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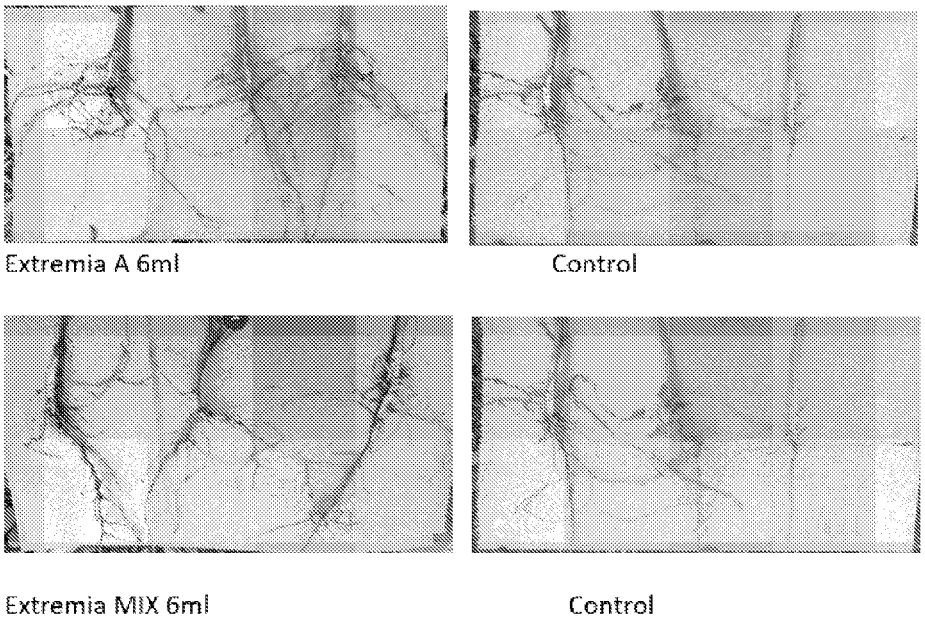

FIG. 6

(57) Abstract: Provided herein are seed treatment formulations that provide improved growth and yield in the plants grown from seeds treated with such formulations, as well as methods of use.

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[Continued on next page]

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SEED TREATMENT FORMULATIONS AND METHODS OF USE

CROSS REFERENCE

[0001] This application claims the benefit of U.S. Provisional Application No. 63/368,135, filed July 11, 2022, and U.S. Provisional Application No. 63/476,280, filed December 20, 2022, each of which is incorporated herein by reference in its entirety.

BACKGROUND

[0002] By 2050, the world population is expected to reach 9.8 billion while more than 500 million hectares of extended wild lands will change to cropland (IRP, 2017). Under current conditions, agricultural production has to face severe challenges due to climate change with extreme weather events and emerging pathogens, while farmers globally have cope with decreasing yields and low operating margins mainly due to the latter (GAP 2017; Sessitsch et al., 2018). When considering both, the expected worldwide population increase and the environmental damage, it is clear that in the next decade it will be a significant challenge to greatly increase agriculture and food production in a sustainable and environmentally friendly manner.

SUMMARY

[0003] Provided herein, in certain aspects, are compositions comprising a microorganism and at least one seed formulation component. In some embodiments, the microorganism is selected from *Klebsiella*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium*, or a combination thereof. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the seed formulation is a nutrient. In some embodiments, the composition further comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml. In some embodiments, the microorganism is selected from *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1, or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae*, is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal

activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization

signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises water.

[0004] In another aspect, there are provided, compositions comprising a microorganism isolated from a plant growing in the high desert and at least one seed formulation component. In some embodiments, the microorganism is isolated from a plant growing in Puna de Atacama. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the microorganism is isolated from a soil or sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes, Bacillus licheniformis*, *Bacillus cereus*, or *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments,

the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises water.

[0005] In another aspect, there are provided treated seeds comprising a plant seed and any one of the compositions provided herein. In some embodiments, the compositions comprise a microorganism and at least one seed formulation component. In some embodiments, the microorganism is selected from *Klebsiella*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof.

In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition further comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1 x 10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml. In some embodiments, the microorganism is selected from *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae*, is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen

reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises a microorganism isolated from a plant growing in the high desert and at least one seed formulation component. In some embodiments, the microorganism is isolated from a plant growing in Puna de Atacama. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the microorganism is isolated from a soil or sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes Bacillus cereus*, *Bacillus licheniformis*, or *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition comprises one or more of peptone, tryptone,

or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1 x 10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some

embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises water.

[0006] In another aspect, there are provided plants grown from treated seeds comprising a plant seed and any one of the compositions provided herein. In some embodiments, the composition comprises a microorganism and at least one seed formulation component. In some embodiments, the microorganism is selected from *Klebsiella*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition further comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml. In some embodiments, the microorganism is selected from *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae*, is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway

signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a

50:50 ratio (CFU/CFU). In some embodiments, the composition comprises a microorganism isolated from a plant growing in the high desert and at least one seed formulation component. In some embodiments, the microorganism is isolated from a plant growing in Puna de Atacama. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the microorganism is isolated from a soil or sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, or *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least

about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises water.

[0007] In another aspect, provided herein are methods of controlling fungal growth, the method comprising contacting a plant seed to any composition provided herein; and germinating the plant seed under a condition capable of exposing the plant seed to a fungus, whereby the seed treatment reduces growth of the fungus on or around the plant seed. In some embodiments, the composition comprises a microorganism and at least one seed formulation component. In some embodiments, the microorganism is selected from *Klebsiella*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition further comprises one or more of peptone, tryptone, or meat extract. In some

embodiments, the microorganism is present at a concentration of greater than about 1 x 10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml. In some embodiments, the microorganism is selected from *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae*, is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth

in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises a microorganism isolated from a plant growing in the high desert and at least one seed formulation component. In some embodiments, the microorganism is isolated from a plant growing in Puna de Atacama. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the microorganism is isolated from a soil or sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, or *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the

composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having

at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises water.

[0008] In another aspect, there are provided methods of protecting plant health, the method comprising contacting a plant seed to any composition provided herein; whereby germination rate, quality of germinated seed, or a combination thereof is improved as compared to an untreated plant seed. In some embodiments, the composition comprises a microorganism and at least one seed formulation component. In some embodiments, the microorganism is selected from *Klebsiella*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition further comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml. In some embodiments, the microorganism is selected from *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae*, is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella*

aerogenes comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises a microorganism isolated from a plant growing in the high desert and at least one seed formulation component. In some embodiments, the microorganism is isolated from a plant growing in Puna de Atacama. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the

microorganism is isolated from a soil or sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, or *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus*

licheniformis comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises water.

[0009] In a further aspect, provided herein are methods of increasing crop yield, the method comprising contacting a set of plant seeds to any composition provided herein; planting the set; growing plants from the planted set to harvest; and harvesting the plants or a portion thereof, wherein the crop yield is increased as compared to crop yield from an untreated set of plant seeds. In some embodiments, the composition comprises a microorganism and at least one seed formulation component. In some embodiments, the microorganism is selected from *Klebsiella*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition further comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml. In some embodiments, the microorganism is selected from *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*,

Exiguobacterium undeae, or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae*, is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU).

In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises a microorganism isolated from a plant growing in the high desert and at least one seed formulation component. In some embodiments, the microorganism is isolated from a plant growing in Puna de Atacama. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the microorganism is isolated from a soil or sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, or *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene

having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus*

comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises water.

[0010] In another aspect, provided herein are methods of promoting growth of a plant, the method comprising contacting seed of the plant to any composition provided herein; germinating the seed of the plant; and growing the resulting plant for a time period sufficient to develop leaves and roots, whereby biomass of the plant, root development of the plant, or a combination thereof is improved compared to a plant grown from an untreated seed. In some embodiments, root development comprises length of the roots, number of lateral roots, or a combination thereof. In some embodiments, the composition comprises a microorganism and at least one seed formulation component. In some embodiments, the microorganism is selected from *Klebsiella*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition further comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1 x 10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml. In some embodiments, the microorganism is selected from *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae*, is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%,

99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 26. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises a microorganism isolated from a plant growing in the high desert and at least one seed formulation component. In some embodiments, the microorganism is isolated from a plant growing in Puna de Atacama. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the microorganism is isolated from a soil or

sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene. In some embodiments, the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a nitrogen pathway signature

comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises water.

[0011] In another aspect, provided herein are methods of preparing a seed treatment, the method comprising growing a microorganism selected from a genus of Klebsiella, *Bacillus*, *Exiguobacterium*, or a combination thereof to at least 1 x 10^8 CFU/g in a liquid media; and preparing a composition comprising a liquid media, the microorganism, at least one formulation component selected from polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the microorganism is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the method further comprises applying the seed treatment to a plant seed. In some embodiments, the liquid media comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a

concentration of greater than 1 x 10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml. In some embodiments, the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml for at least 6 months at 25 °C. In some embodiments, the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml for at least 6 months at a temperature from about 20 °C to about 35 °C. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml for at least 6 months at 25 °C. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml for at least 6 months at a temperature from about 20 °C to about 35 °C.

[0012] In another aspect, provided herein are compositions comprising a microorganism and at least one soil or plant amendment component, wherein the microorganism is selected from *Klebsiella*, *Bacillus cereus*, *Exiguobacterium undeae,* or a combination thereof. In some embodiments, the soil or plant amendment comprises an adjuvant, a stabilizer, or an additive. In some embodiments, the soil or plant amendment comprises polyvinylpyrrolidone (PVP), gum Arabic, or Xanthan gum. In some embodiments, the composition further comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1 x 10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml. In some embodiments, the microorganism is selected from *Klebsiella aerogenes, Bacillus cereus*, *Exiguobacterium undeae,* or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae,* is a strain CK3 or a derivative thereof. In some embodiments, the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum.* In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the composition comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce

carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises water.

[0013] In another aspect, provided herein are compositions comprising a microorganism isolated from a plant growing in the high desert and at least one soil or plant amendment component. In some embodiments, the microorganism is isolated from a plant growing in Puna de Atacama. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the microorganism is isolated from a soil or sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes*, *Bacillus cereus*, or *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the soil or plant amendment comprises an adjuvant, a stabilizer, or an additive. In some embodiments, the soil or plant amendment component comprises polyvinylpyrrolidone (PVP), gum Arabic, or Xanthan gum. In some embodiments, the composition comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1 x 10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 6 months. In some embodiments, the composition is a liquid. In some embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae Septoria sp.*, or *Sclerotinia sclerotiorum*. In some embodiments, the composition confers plant growth regulatory activity. In some embodiments, the composition comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some

embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa). In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises water.

[0014] In another aspect, provided herein are plants grown with the composition comprising soil or plant amendments according to various embodiments herein.

[0015] In another aspect, provided herein are method of controlling fungal growth, the method comprising contacting a plant to the composition comprising soil or plant amendments according to various embodiments herein; and growing the plant under a condition capable of exposing the plant to a fungus, whereby the composition reduces growth of the fungus on or around the plant.

[0016] In another aspect, provided herein are methods of protecting plant health, the method comprising contacting a plant to the composition comprising soil or plant amendments according to various embodiments herein; whereby plant growth is improved as compared to an untreated plant.

[0017] In another aspect, provided herein are methods of increasing crop yield, the method comprising contacting a set of plants to the composition comprising soil or plant amendments according to various embodiments herein; growing plants from the set of plants to harvest; and harvesting the plants or a portion thereof, wherein the crop yield is increased as compared to crop yield from an untreated set of plants.

[0018] In another aspect, provided herein are methods of promoting growth of a plant, the method comprising contacting the plant to the composition comprising soil or plant amendments according to various embodiments herein; growing the plant for a time period sufficient to develop leaves and roots, whereby biomass of the plant, root development of the plant, or a combination thereof is improved compared to an untreated plant. In some embodiments, root development comprises length of the roots, number of lateral roots, or a combination thereof.

[0019] In another aspect, provided herein are methods of increasing fertility of a soil, the method comprising contacting a plurality of plants to the composition comprising soil or plant amendments

according to various embodiments herein; and growing a plurality of plants in the soil, thereby increasing the fertility of the soil.

[0020] In another aspect, provided herein are methods of preparing a soil or plant amendment, the method comprising growing a microorganism selected from a genus of *Klebsiella*, *Bacillus*, *Exiguobacterium*, or a combination thereof to at least 1 x 10^8 CFU/g in a liquid media; and preparing a composition comprising a liquid media, the microorganism, at least one formulation component selected from polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the microorganism is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the method further comprises applying the seed treatment to a plant seed. In some embodiments, the liquid media comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml. In some embodiments, the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml for at least 6 months at 25 °C. In some embodiments, the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml for at least 6 months at a temperature from about 20 °C to about 35 °C. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml for at least 6 months at 25 °C. In some embodiments, the microorganism is present at a concentration of greater than from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml for at least 6 months at a temperature from about 20 °C to about 35 °C.

INCORPORATION BY REFERENCE

[0021] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] An understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

[0023] **FIG. 1** shows viability of CK1 in M1 medium after one month.

[0024] **FIG. 2** shows a comparison of reducing sugars before and after heat by sterilization in M1 and M2 culture media.

[0025] **FIG. 3** shows viability of CD1-M2 over time.

[0026] **FIG. 4** shows KP, AN, and LB culture media for CD1 and CK2 growth.

[0027] **FIG. 5** shows viability of CK1 and CK2 in AN, KB, and LB culture media for two months.

[0028] **FIG. 6** shows crop pictures TUCUMAN (V5) site; A= CK1 + CK2 6 m, B= Control vs CK1 6ML, C= Control vs CK1+CK2 5ml.

[0029] **FIG. 7** shows crop pictures SAN JERONIMO NORTE (V5) site; A= CK1 + CK2 6 m, B= Control vs CK1 6ML, C= Control vs CK1+CK2 5ml.

[0030] **FIG. 8** shows phosphate solubilization genes in CK1.

[0031] **FIG. 9** shows phosphate solubilization genes in CK2.

[0032] **FIG. 10** shows CK1 pathogenicity.

[0033] **FIG. 11** shows biofungicide activity against *Sclerotinia sclerotium*.

[0034] **FIG. 12** shows biofungicide activity against *Fusarium*.

[0035] **FIG. 13** shows treated soybean seeds were planted to analyze the effects of the products against *F. tucumaniae*.

[0036] **FIG. 14** shows results of a greenhouse trial to evaluate the effectiveness of seed treatments against *F. tucumaniae* in soybean (DM5958) at 20 days after planting.

[0037] **FIG. 15** shows treated soybean seeds (M6410 IPRO) were planted to analyze the effects of the products against *M. phaseolina*.

[0038] **FIG. 16** shows results of seed treatment assay against *M. phaseolina* in soybean (M6410) 10 days after planting.

[0039] **FIG. 17** shows an average nucleotide identity heatmap with ANI values. The closest strain to *B. cereus* CK2 is *B. cereus* A1 with an ANI value of 0.99.

[0040] **FIG. 18** shows a phylogenetic tree reconstruction based on ANI values distance matrix using the neighbor joining method with PHYLIP. Strain CK2 is placed in the *B. cereus* species.

[0041] **FIG. 19** shows imaging of roots with Confocal Laser Scanning Microscope (left panel) control and (right panel) CK1-GFP.

[0042] **FIG. 20** shows imaging of leaves with Confocal Laser Scanning Microscope (left panel) control and (right panel) CK1-GFP.

[0043] **FIG. 21** shows imaging of stems with Confocal Laser Scanning Microscope (left panel) control and (right panel) CK1-GFP.

[0044] **FIG. 22** shows ion exchange chromatography in DE52 of the EPS sample. In a dotted line, the concentration of NaCl in the elution is plotted.

[0045] **FIG. 23** shows a spectrum ^{1}H NMR of purified EPS. Above, the spectrum between 5.6 and 3 ppm is illustrated. Below, the resonances of the identified anomeric protons (A-H) in the zone between 5.6 and 4.8 ppm are indicated.

[0046] FIG. 24 shows ^{1}H-^{13}C-HSQC spectra superimposed on hydrolyzed EPS (blue) and D-Mannose (alpha and β) (light blue), D-Glucose (alpha and β) (green), D-Galactose (alpha and β) (red) and D-Glucosamine (alpha and β) (brown). Peaks in the spectrum of hydrolyzed EPS that do not overlap with standards belong to remaining non-hydrolyzed EPS molecules.

[0047] FIG. 25 shows HPAEC-PAD analysis of hydrolyzed EPS. The circumvention times of the different monosaccharides identified are indicated by arrows.

[0048] FIG. 26 shows HPAEC-PAD analysis of hydrolyzed EPS.

[0049] FIG. 27 shows a spectrum ^{1}H-^{13}C-HSQC of MRI of purified EPS. The region of the spectrum corresponding to anomeric protons and carbons is plotted.

[0050] FIG. 28 shows ^{1}H-^{1}H-TOCSY spectrum of purified EPS NMR. The spectrum region is plotted between 5.6 and 4.6 ppm. The correlations between the anomeric ^{1}H and $^{1}H2$ of each residue are indicated.

[0051] FIG. 29 shows ^{1}H-^{1}H-NOESY MRI spectrum of purified EPS. The spectrum region is plotted between 5.6 and 4.6 ppm. Correlations between anomeric ^{1}H and ^{1}HX between residues are indicated.

[0052] FIG. 30 shows five panels of mass spectra of monosaccharides derived from purified EPS. Panels 1, 2, 3, 4 and 5 correspond to species 1, 2, 3, 4 and 5 identified in Table 48, respectively.

DETAILED DESCRIPTION

[0053] Providing improved crop yields in an ever increasing hostile climate will be essential to a growing worldwide population. Provided herein are certain compositions comprising bacterial strains, including seed treatment compositions, that increase the fitness of the plants from treated seeds or soils. In some cases, these bacterial compositions allow crop growth in poor soils that have been degraded by drought, high salinity, and other effects of climate change.

Compositions

[0054] Accordingly, provided herein are compositions comprising mixtures of bacterial strains and methods of use in crop cultivation. In one aspect, there are provided compositions comprising a microorganism and at least one seed formulation component. In some embodiments, the microorganism is selected from *Klebsiella*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae,* or a combination thereof. In some embodiments, the microorganism is selected from *Klebsiella aerogenes, Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae,* or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae,* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the composition is a soil amendment. In some embodiments, the composition is a plant amendment. In some embodiments, the composition comprises water.

[0055] In another aspect, there are provided compositions comprising a microorganism isolated from a plant growing in a harsh environment, such as the high desert, and at least one seed formulation component. As used herein, "harsh environment" refers to a climate with suboptimal rainfall, extremes of heat and cold, and/or high elevation compared to a temperate climate. As used herein, the "high desert" refers to a desert region that is located at a high elevation, such as over 3000 feet (900 meters). In some embodiments, the microorganism is isolated from a plant growing in Puna de Atacama. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the microorganism is isolated from a soil or sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes*, *Bacillus cereus*, *Bacillus licheniformis*, or *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the composition is a soil amendment. In some embodiments, the composition is a plant amendment. In some embodiments, the composition comprises water.

[0056] In embodiments, the seed formulation component comprises any suitable substance for stabilizing the seeds and/or the bacterial strains. In some embodiments, the seed formulation component is a polymer or a detergent. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. For example, in some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition comprises a nutrient source. For example, in some embodiments, the composition comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^4, about 1×10^5, about 1×10^6, about 1×10^7, about 1×10^8 about 1×10^9, or about 1×10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 2 months, about 3 months, about 4 months, about 5 months, about 6 months, about 7 months, about 8 months, about 9 months, about 10 months, about 11 months, or about 12 months. In some embodiments, the composition is a liquid. In some embodiments, the composition is a gel or suspension. In some embodiments, the composition is a soil amendment. In some embodiments, the composition is a plant amendment. In some embodiments, the composition comprises water.

[0057] In embodiments, the composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*.

[0058] In embodiments, the composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene.

[0059] In embodiments, the seed treatment comprises *Klebsiella aerogenes*. In some embodiments, the *Klebsiella aerogenes* comprises a nitrogen pathway signature. In some embodiments, the nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25.

[0060] In embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29.

[0061] In embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35.

[0062] In embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa).

[0063] In embodiments, the composition comprises *Bacillus licheniformis*. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature. In some embodiments, the nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26.

[0064] In embodiments the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29.

[0065] In embodiments, the composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46.

[0066] In embodiments, compositions herein comprise a combination of *Klebsiella aerogenes* and *Bacillus licheniformis*. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 10:90, 20:80, 30:70, 40:60, 50:50, 60:40, 70:30, 80:20, or 90:10 ratio (CFU/CFU). In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises water.

[0067] In embodiments, the composition comprises *Bacillus cereus*. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature. In some embodiments, the nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26.

[0068] In embodiments the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29.

[0069] In embodiments, the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46.

[0070] In embodiments, compositions herein comprise a combination of *Klebsiella aerogenes* and *Bacillus cereus*. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 10:90, 20:80, 30:70, 40:60, 50:50, 60:40, 70:30, 80:20, or 90:10 ratio (CFU/CFU). In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition is a soil amendment. In some embodiments, the composition is a plant amendment. In some embodiments, the composition comprises water.

Treated Seeds and Plants Grown from Treated Seeds

[0071] In another aspect, provided herein are treated seeds comprising a plant seed and a seed treatment composition disclosed herein. In some embodiments, the seed treatment composition comprises a microorganism selected from *Klebsiella*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae,* or a combination thereof. In some embodiments, the microorganism is selected from *Klebsiella aerogenes, Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae,* or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae,* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323.

[0072] In another aspect, there are provided treated seeds comprising a plant seed and a seed treatment composition comprising a microorganism isolated from a plant growing in a harsh environment, such as the high desert. In some embodiments, the microorganism is isolated from a plant growing in Puna de

Atacama and at least one seed formulation component. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the microorganism is isolated from a soil or sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323.

[0073] In a further aspect, there are provided plants grown from treated seeds provided herein.

[0074] In embodiments, the seed treatment composition comprises any suitable substance for stabilizing the seeds and/or the bacterial strains. In some embodiments, the seed formulation component is a polymer or a detergent. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. For example, in some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition comprises a nutrient source. For example, in some embodiments, the composition comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1 x 10^4, about 1 x 10^5, about 1 x 10^6, about 1 x 10^7, about 1 x 10^8 about 1 x 10^9, or about 1 x 10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 2 months, about 3 months, about 4 months, about 5 months, about 6 months, about 7 months, about 8 months, about 9 months, about 10 months, about 11 months, or about 12 months. In some embodiments, the composition is a liquid. In some embodiments, the composition is a gel or suspension.

[0075] In embodiments, the seed treatment composition confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*.

[0076] In embodiments, the seed treatment composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene.

[0077] In embodiments, the seed treatment comprises *Klebsiella aerogenes*. In some embodiments, the *Klebsiella aerogenes* comprises a nitrogen pathway signature. In some embodiments, the nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella*

aerogenes comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25.

[0078] In embodiments, the seed treatment composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29.

[0079] In embodiments, the seed treatment composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35.

[0080] In embodiments, the seed treatment composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa).

[0081] In embodiments, the composition comprises *Bacillus licheniformis*. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature. In some embodiments, the nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26.

[0082] In embodiments the seed treatment composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29.

[0083] In embodiments, the seed treatment composition comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46.

[0084] In embodiments, the seed treatment composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis*. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 10:90, 20:80, 30:70, 40:60, 50:50, 60:40, 70:30, 80:20, or 90:10 ratio (CFU/CFU). In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU).

[0085] In embodiments, the composition comprises *Bacillus cereus*. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature. In some embodiments, the nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26.

[0086] In embodiments the seed treatment composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments,

the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29.

[0087] In embodiments, the seed treatment composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46.

[0088] In embodiments, the seed treatment composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus*. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 10:90, 20:80, 30:70, 40:60, 50:50, 60:40, 70:30, 80:20, or 90:10 ratio (CFU/CFU). In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU).

Soil or Plant Amendments

[0089] In another aspect, provided herein are soil or plant amendments comprising a composition disclosed herein. In some embodiments, the composition comprises a microorganism selected from *Klebsiella*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae,* or a combination thereof. In some embodiments, the microorganism is selected from *Klebsiella aerogenes, Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae,* or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae,* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the composition comprises water.

[0090] In another aspect, there are provided soil or plant amendments comprising a microorganism isolated from a plant growing in a harsh environment, such as the high desert. In some embodiments, the microorganism is isolated from a plant growing in Puna de Atacama and at least one seed formulation component. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the microorganism is isolated from a soil or sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323. In some embodiments, the composition comprises water.

[0091] In a further aspect, there are provided plants grown using soil or plant amendments provided herein.

[0092] In embodiments, the soil or plant amendment comprises any suitable substance for stabilizing the bacterial strains. In some embodiments, the soil or plant amendment comprises a nutrient source. For example, in some embodiments, the soil or plant amendment comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^4, about 1×10^5, about 1×10^6, about 1×10^7, about 1×10^8 about 1×10^9, or about 1×10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 2 months, about 3 months, about 4 months, about 5 months, about 6 months, about 7 months, about 8 months, about 9 months, about 10 months, about 11 months, or about 12 months. In some embodiments, the composition is a liquid. In some embodiments, the composition is a gel or suspension. In some embodiments, the composition comprises water.

[0093] In embodiments, the soil or plant amendment confers anti-fungal activity. In some embodiments, the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*.

[0094] In embodiments, the seed treatment composition confers plant growth regulatory activity. In some embodiments, the microorganism comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a signature gene.

[0095] In embodiments, the soil or plant amendment comprises *Klebsiella aerogenes*. In some embodiments, the *Klebsiella aerogenes* comprises a nitrogen pathway signature. In some embodiments, the nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 25.

[0096] In embodiments, the soil or plant amendment comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29.

[0097] In embodiments, the soil or plant amendment comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35. In some embodiments, the *Klebsiella aerogenes* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 35.

[0098] In embodiments, the soil or plant amendment comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa).

[0099] In embodiments, the composition comprises *Bacillus licheniformis*. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature. In some embodiments, the nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus licheniformis* comprises a nitrogen pathway signature gene set forth in Table 26.

[00100] In embodiments the soil or plant amendment comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a phosphate solubilization signature gene set forth in Table 29.

[00101] In embodiments, the soil or plant amendment comprises *Bacillus licheniformis* and the *Bacillus licheniformis* comprises a plant growth regulatory signature gene set forth in Table 46.

[00102] In embodiments, the soil or plant amendment comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis*. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 10:90, 20:80, 30:70, 40:60, 50:50, 60:40, 70:30, 80:20, or 90:10 ratio (CFU/CFU). In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus licheniformis* in a 50:50 ratio (CFU/CFU).

[00103] In embodiments, the soil or plant amendment comprises *Bacillus cereus*. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature. In some embodiments, the nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification. In some embodiments, the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a nitrogen pathway signature gene set forth in Table 26.

[00104] In embodiments the soil or plant amendment comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a phosphate solubilization signature gene set forth in Table 29.

[00105] In embodiments, the soil or plant amendment comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46. In some embodiments, the *Bacillus cereus* comprises a gene having at least about 70%, 80%, 90%, 95%, 99%, or 100% identity to a plant growth regulatory signature gene set forth in Table 46.

[00106] In embodiments, the soil or plant amendment comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus*. In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 10:90, 20:80, 30:70, 40:60, 50:50, 60:40, 70:30, 80:20, or 90:10 ratio (CFU/CFU). In some embodiments, the composition comprises a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU). In some embodiments, the composition comprises water.

Methods of Controlling Fungal Growth and Protecting Plant Health

[00107] In another aspect, provided herein are methods of controlling fungal growth. In some embodiments, the method comprises contacting a plant seed to any composition provided herein. In some embodiments, the method comprises germinating the plant seed under a condition capable of exposing the plant seed to a fungus. In some embodiments, the seed treatment reduces growth of the fungus on or around the plant seed. In some embodiments, the fungus comprises one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*.

[00108] In a further aspect, provided herein are methods of protecting plant health. In some embodiments, the method comprises contacting a plant seed to any composition provided herein. In some embodiments, germination rate, quality of germinated seed, or a combination thereof is improved as compared to an untreated plant seed. In some embodiments, the composition is a soil amendment. In some embodiments, the composition is a plant amendment.

Methods of Increasing Crop Yield and Plant Growth

[00109] In another aspect, provided herein are methods of increasing crop yield. In some embodiments, the method comprising contacting a set of plant seeds to any composition provided herein. In some embodiments, the method comprises planting the set. In some embodiments, the method comprises growing plants from the planted set to harvest. In some embodiments, the method comprises harvesting the plants or a portion thereof. In some embodiments, the crop yield is increased as compared to crop yield from an untreated set of plant seeds. In some embodiments, the crop yield is increased by about 5%, about 10%, about 15%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, about 100%, about 120%, about 140%, about 160%, about 180%, about 200% or more compared to crop yield from an untreated set of plant seeds.

[00110] In another aspect, provided herein are methods of promoting growth of a plant. In some embodiments, the method comprises contacting seed of the plant to any composition provided herein. In some embodiments, the method comprises germinating the seed of the plant. In some embodiments, the method comprises growing the resulting plant for a time period sufficient to develop leaves and roots. In some embodiments, biomass of the plant, root development of the plant, or a combination thereof is improved compared to a plant grown from an untreated seed. In some embodiments, root development comprises length of the roots, number of lateral roots, or a combination thereof. In some embodiments, the biomass of the plant, root development of the plant, or a combination thereof is increased by about 5%, about 10%, about 15%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, about 100%, about 120%, about 140%, about 160%, about 180%, about 200% or more compared to the biomass of the plant, root development of the plant, or a combination thereof from an untreated set of plant seeds. In some embodiments, the composition is a soil amendment. In some embodiments, the composition is a plant amendment.

Methods of Preparing Seed Treatments

[00111] In an aspect, provided herein are methods of preparing a seed treatment. In some embodiments, the method comprising growing a microorganism selected from a genus of Klebsiella, *Bacillus*, *Exiguobacterium*, or a combination thereof to at least 1 x 10^8 CFU/g in a liquid media. In some embodiments, the method comprises preparing a composition comprising a liquid media, the microorganism, at least one formulation component. In some embodiments, the formulation component is a polymer or a detergent. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the microorganism is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323.

[00112] In an aspect, provided herein are methods of preparing a seed treatment. In some embodiments, the method comprises growing a microorganism isolated from a plant growing in a harsh environment, such as the high desert. In some embodiments, the microorganism is isolated from a plant growing in Puna de Atacama. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the microorganism is isolated from a soil or sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, or *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323.

[00113] In aspects, the method further comprises comprising applying the seed treatment to a plant seed.

[00114] In embodiments, the seed formulation component comprises any suitable substance for stabilizing the seeds and/or the bacterial strains. In some embodiments, the seed formulation component is a polymer or a detergent. In some embodiments, the seed formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. For example, in some embodiments, the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the composition comprises a nutrient source. For example, in some embodiments, the composition comprises one or more of peptone, tryptone, or meat extract. In

some embodiments, the microorganism is present at a concentration of greater than about 1 x 10^4, about 1 x 10^5, about 1 x 10^6, about 1 x 10^7, about 1 x 10^8 about 1 x 10^9, or about 1 x 10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 2 months, about 3 months, about 4 months, about 5 months, about 6 months, about 7 months, about 8 months, about 9 months, about 10 months, about 11 months, or about 12 months. In some embodiments, the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml for at least 6 months at 25 °C. In some embodiments, the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml for at least 6 months at a temperature from about 20 °C to about 35 °C. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml for at least 6 months at 25 °C. In some embodiments, the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml for at least 6 months at a temperature from about 20 °C to about 35 °C. In some embodiments, the composition is a liquid. In some embodiments, the composition is a gel or suspension.

Methods of Preparing Soil or Plant Amendments

[00115] In an aspect, provided herein are methods of preparing a soil or plant amendment. In some embodiments, the method comprising growing a microorganism selected from a genus of Klebsiella, *Bacillus*, *Exiguobacterium*, or a combination thereof to at least 1 x 10^8 CFU/g in a liquid media. In some embodiments, the method comprises preparing a composition comprising a liquid media, the microorganism, at least one formulation component. In some embodiments, the formulation component is a polymer or a detergent. In some embodiments, the formulation component is an adjuvant, a stabilizer, an additive, or a combination thereof. In some embodiments, the formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum. In some embodiments, the microorganism is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323.

[00116] In an aspect, provided herein are methods of preparing a soil or plant amendment. In some embodiments, the method comprises growing a microorganism isolated from a plant growing in a harsh environment, such as the high desert. In some embodiments, the microorganism is isolated from a plant growing in Puna de Atacama. In some embodiments, the microorganism is isolated from a rhizosphere of the plant. In some embodiments, the microorganism is isolated from a soil or sediments of the plant. In some embodiments, the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*. In some embodiments, the bacterium is *Klebsiella aerogenes*, *Bacillus licheniformis*, *Bacillus cereus*, or *Exiguobacterium undeae*. In some embodiments, the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof. In some embodiments, the strain CK1 has a DSMZ accession number DSM 34332. In some

embodiments, the *Bacillus licheniformis* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* is a strain CK2 or a derivative thereof. In some embodiments, the *Bacillus cereus* strain CK2 has a DSMZ accession number DSM 34322. In some embodiments, the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof. In some embodiments, wherein the strain CK3 has a DSMZ accession number DSM 34323.

[00117] In aspects, the method further comprises comprising applying the soil or plant amendment to a plant or a plant seed.

[00118] In embodiments, the soil or plant amendment comprises any suitable substance for stabilizing the bacterial strains. In some embodiments, the seed formulation component is a polymer or a detergent. In some embodiments, the soil or plant amendment comprises an adjuvant, a stabilizer, or an additive. For example, in some embodiments, the soil or plant amendment comprises polyvinylpyrrolidone (PVP), gum Arabic, or Xanthan gum. In some embodiments, the soil or plant amendment comprises a nutrient source. For example, in some embodiments, the soil or plant amendment comprises one or more of peptone, tryptone, or meat extract. In some embodiments, the microorganism is present at a concentration of greater than about 1×10^4, about 1×10^5, about 1×10^6, about 1×10^7, about 1×10^8 about 1×10^9, or about 1×10^{10} CFU/ml. In some embodiments, the composition has a shelf life of at least about 2 months, about 3 months, about 4 months, about 5 months, about 6 months, about 7 months, about 8 months, about 9 months, about 10 months, about 11 months, or about 12 months. In some embodiments, the microorganism is present at a concentration of greater than 1×10^8 CFU/ml for at least 6 months at 25 °C. In some embodiments, the microorganism is present at a concentration of greater than 1×10^8 CFU/ml for at least 6 months at a temperature from about 20 °C to about 35 °C. In some embodiments, the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml for at least 6 months at 25 °C. In some embodiments, the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml for at least 6 months at a temperature from about 20 °C to about 35 °C. In some embodiments, the composition is a liquid. In some embodiments, the composition is a gel or suspension.

EXAMPLES

[00119] The following examples are given for the purpose of illustrating various embodiments of the invention and are not meant to limit the present invention in any fashion. The present examples, along with the methods described herein are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the invention. Changes therein and other uses which are encompassed within the spirit of the invention as defined by the scope of the claims will occur to those skilled in the art.

Example 1: Media Evaluation and Seed Treatment Formulation

[00120] Bacterial strains CK1 (*Klebsiella aerogenes*), CK2 (*Bacillus cereus*) were isolated from the rhizosphere of plants growing next to Volcán Galán, provincia de Catamarca, Argentina.

[00121] CK1 and CK2 were evaluated for their ability to form viable colonies after growth in a variety of culture media.

[00122] For all assays the bacterial cultures were grown at 30°C and 230 rpm. After 10 hours of culture, CFU/mL and pH of each culture was measured. The components of each culture media were listed in Table 1, all media sterilizations were carried out with autoclave, at 121°C for 15 minutes.

[00123] In all cases, first the selection of a culture medium was based on achieving a high CFU/ml count during cultivation, then its shelf life was controlled by addition of the adjuvant (formulated). Xanthan gum (Phernhofen) was used as an adjuvant, and it was added to culture broth when shelf life was evaluated in 0.5% final concentration.

[00124] For check viability the samples were kept at room temperature, protected from light.

Table 1: Components and concentrations used for different culture media tested

Culture Media	**Previous denomination**	**$(NH_4)_2HSO_4$ g/L**	**Yeast Ext. g/L**	**Soy peptone g/L**	**Glucose g/L**	**K_2HPO_4**	**KH_2PO_4**
M1	ECO	5	3	-	3	-	-
M2	M7	3	3	-	3	-	-
M3	Medio 1			5	15	4	6
M4	Medio 2	2	1.5	-	-	0.125	-
M5	Medio 4	-	5	10	2	-	-
M6	Medio 5	-	0.5	10	-	-	-
M7	2 ‘ (prima)	2	3	-	-	0.125	-
M8	2A	2	-	3	-	0.125	-
AN		-	-	-	-	-	-
LB		-	5	-	-	-	-
KB		-	-	-	-	-	-
Culture Media	**$(NH_4)_2SO_4$**	**$MgSO_4.7H_20$**	**KCl**	**$MnSO_4.7H_20$**	**NaCl**	**$FeSO_4.7H_2O$**	**Trisodium citrate g/L**
M1	-	-	-	-	-	-	-
M2	-	-	-	-	-	-	-
M3	2	0.2	-	-	-	-	1
M4	-	0.2		-	-	-	7.5
M5	-	-	-	-	-	-	-
M6	0.5	0.1	0.2	0.004	0.2	0.002	-
M7	-	0.2	-		-	-	-
M8	-	0.2	-	-	-	-	-
AN	-	-	-	-	-	-	-
LB	-	-	-	-	-	-	-
KB	-	-	-	-	-	-	-
Culture Media	**Sucrose g/L**	**meat extract**	**Tryptone**	**Pluri-peptone**	**Meat peptone**	**Sodium Chloride**	**K_2PO_4**	**$MgSO_4$**
M1	-	-	-	-	-	-	-	-
M2	-	-	-	-	-	-	-	-
M3	-	-	-	-	-	-	-	-
M4	-	-	-	-	-	-	-	-
M5	-	-	-	-	-	-	-	-
M6	-	-	-	-	-	-	-	--
M7	7.5	-	-	-	-	-	-	-

M8	7.5	-	-	-	-	-	-	-
AN	-	3	-	5	-	8	-	-
LB	-	-	10	-	-	10	-	-
KB	-	-	10	-	10	-	1.5	1.5

[00125] CK1 and CK2 were routinely cultivated in M1 medium. Even when the CFU/ml value for both strains was adequate (Table 2), this culture medium was discarded because the development of the formulation required a culture medium that sustains the viability of the cells over time. As shown in FIG. 1, when CK1 strain viability was tested in M1, a significant loss of viability after 15 days of storage was observed.

Table 2: Parameters evaluated for CK1 and CK2 growth in M1 medium

	M1		
Strain	**pH (after culture)**	**OD600 nm**	**CFU/ml**
Klebsiella aerogenes CK1	4.80	1.24	2.65E+09
Bacillus cereus CK2	5.10	1.25	1.53E+08

[00126] On the other hand, M1 medium was seen that after sterilization the Maillard reaction was produced in the culture medium used. The Maillard reaction is a non-desirable chemical reaction that occurs in the presence of heat between carbonyl compounds, especially reducing sugars like glucose, with compounds which possess a free amino group, such as amino acids, amines, and protein. This generates a brownish color and a decrease of reducing sugars, which should be available for consumption by the bacteria for their growth.

[00127] The reducing sugars were determined by DNS technique and the values obtained before and after heat are shown in FIG. 2. The reducing sugar in M1 culture medium decreased an 18%, from 3.04 g/L to 2.51 g/L after being exposed to heat. In contrast, M2 medium, containing sucrose (non-reducing sugar) instead of glucose as a carbon source, emerges as a viable alternative to M1 medium, because of showed a sugar loss only of 2.6% after the sterilization process.

[00128] M2 medium leading to CFU/mL values similar to M1 medium for both CK1 and CK2 strains (Table 3). Later, it was also discarded, since acidification was observed, which resulted in a loss of viability in a short time as shown in FIG. 3.

Table 3: Parameters evaluated for CK1 and CK2 growth in M2 medium

	M2		
Strain	**pH (after culture)**	**OD600**	**CFU/ml**
Klebsiella aerogenes CK1	6.10	1.04	2.5E+09
Bacillus cereus CK2	5.90	0.97	2.3E+08

[00129] Due to the results obtained, it was presumed that the sugars (glucose in M1 and sucrose in M2) caused the acidification of the media (see Table 2 and Table 3), which led to the loss of viability, so it was decided to evaluate new culture media without a defined carbon source. Thus, three new culture media (without sugars as C-source) were evaluated for CK1 and CK2 growth.

[00130] "AN", "KB" and "LB" medium were the media selected for the assays (the composition was shown in Table 1). The results (FIG. 4) demonstrated that the three culture media evaluated were

adequate for the growth of CK1, the bacterial load of 10^9 CFU/mL was reached in AN and KB while in LB the bacterial count was higher (10^{10} CFU/mL). For CK2, LB and AN media were better than KB.

[00131] The shelf life for CK1 and CK2 in LB, KB and AN (plus xanthan gum 0.5 %) was also evaluated. As shown in FIG. 5, the AN medium was the most suitable and showed better stability in the evaluated time (60 days). In LB medium, even when the higher CK1 CFU/mL value was obtained, the drop in bacterial concentration was large after one month of storage whereas in KB medium the decrease in viability was registered after 30 days.

[00132] For CK2, even when CFU/mL drops drastically over time, the AN culture medium seemed to be the most suitable for maintaining higher viable cell numbers at 60 days.

[00133] During the 2021 year, the field assays were carried out by both strains growth in AN medium. The product formulated as "CK1 + xanthan" or "CK1 +CK2 + xanthan" was designated as "Extremia A" and "Extremia MIX" respectively.

[00134] CK1 and CK2 growth for field testing were carried out in stirred tank reactors (STR), in a volume of 750 L for each strain. A sterile antifoam AF10 silicone was added to the culture media (1/1000) to avoid the generation of high levels of foam, which is a common problem in STR productions due to the high levels of aeration and agitation used.

[00135] To obtain the final formulation, the culture broth was mixed with 2% (w/v) xanthan gum (proportion 75% v/v of culture broth + 25 % v/v of xanthan gum). For Extremia MIX the culture broths for each strain were mixed (50% v/v). Finally, the formulations obtained were packaged in sterile bags of 5 L. The product was stored at room temperature and viability was assessed by measurement of CFU/mL and pH values.

[00136] Extremia A reached 1 x 10^9 CFU/mL while in extremia MIX the bacteria load was 5 x 10^8 CFU/mL for CK1 and 1 x 10^8 CFU/mL for CK2.

Table 4: Viability of Extremia A and Extremia MIX at monthly interval

Product	Time	Strain	CFU/ml	pH
Extremia Mix	T0	*Klebsiella aerogenes* CK1	3.6E+08	7.45
		Bacillus cereus CK2	1.2E+08	
	T30 days	*Klebsiella aerogenes* CK1	4E+08	-
		Bacillus cereus CK2	1.5E+07	
	T60 days	*Klebsiella aerogenes* CK1	1.84E+08	7.75
		Bacillus cereus CK2	1.09E+07	
	T90 days	*Klebsiella aerogenes* CK1	2.6E+07	8.36
		Bacillus cereus CK2	6E+06	
Extremia A	T0	*Klebsiella aerogenes* CK1	1.55E+09	7.42
	T30 days	*Klebsiella aerogenes* CK1	2.7E+08	-
	T60 days	*Klebsiella aerogenes* CK1	1.64E+08	8.03
	T90 days	*Klebsiella aerogenes* CK1	3.7E+07	8.36

[00137] For field testing the method used for applying the inoculant was the "seed dressing" and the product was mixing with pesticides frequently used. The dose of the Extremia used in the tests was 5ml per kg of seed.

[00138] In a next step, taking into account the drop in CFU/mL after 90 days for both Extremia A and Extremia mix, it was decided to search an alternative culture medium in which a higher CFU/mL count could be achieved, especially for CK2. Thus, new culture media were tested (see Tables 5 and 6). Also, as shown below in Example 2, new formulation alternatives (with adjuvants, cell protector and surfactant) were tested with the aim of getting a better viability in Extremia products.

[00139] M3, M4, M5 and M6 culture media (Table 5) were evaluated for CK1 and CK2, nevertheless its use corroborated that the glucose was responsible for dropping the pH value in the medium. As shown in Table 6, in the M4 medium, the pH values remained close to neutrality, and even when CK1 reached a higher CFU/ml, CK2 did not grow enough under those conditions.

[00140] To obtain a higher CFU/ml count for CK2, two alternative media, M7 and M8 were tested. In M7 medium the amount of yeast extract was doubled than M4 (1.5 g/L to 3.0 g/L). M8 contained soy peptone instead of yeast extract, which has been described as an alternative and appropriate substrate for *Bacillus* genus.

Table 5: Evaluation of M3, M4, M5, and M6 culture media for *Klebsiella aerogenes* CK1 and *Bacillus cereus* CK2

Medium	Strain	DO_{600nm}	pH_{final}	CFU/mL
M3	CK1	0.807	6.09	7.50E+09
M3	CK2	0.787	5.01	4.50E+08
M4	CK1	0.892	7.21	1.84E+09
M4	CK2	0.297	7.21	8.2E+07
M5	CK1	0.96	4.78	4.90E+09
M5	CK2	0.885	4.72	9.00E+08
M6	CK1	0.427	3.55	7.10E+09
M6	CK2	0.857	3.89	4.30E+07

Table 6: Evaluation of M6 and M8 for *Klebsiella aerogenes* CK1 and *Bacillus cereus* CK2

Medium	Strain	DO_{600nm}	pH	CFU/mL
M7	CK1	0.743	7.25	2.57E+09
M7	CK2	0.598	7.07	1.06E+08
M8	CK1	0.754	7.18	2.9E+09
M8	CK2	0.683	7.52	6.5E+08

[00141] No significant difference in CK1 growth between M7 and M8 were obtained, however the CFU/ml value for both CK1 and CK2 in M8 medium were slightly higher than M7 medium (Table 4).

[00142] M8 culture medium was selected for the growth of both strains (CK1 and CK2) due this allowed the design of a product Extremia mix in which the two bacterial genera are together CK1+CK2.

Example 2: Cell Protectants

[00143] It has been reported that cell protectants are able to improve bacterial homeostasis. Therefore, different cell protectants and additives were evaluated to optimize the shelf life of the products.

[00144] The culture media evaluated were AN and M8 described in Table 1. Polymers as polyvinylpyrrolidone (PVP) 2.5% (p/v), Arabic and Xanthan gums were used as cell protectants. Tween

20 2.5% (v/v) was evaluated as surfactant. All additives were added to the culture media during their preparation. The culture media were sterilized by autoclave (15 min).

[00145] Xanthan gum and Arabic gum were dissolved in physiological solution (NaCl 8g/l).

[00146] Inoculation: Before inoculating, sterile AF10 silicone antifoam was added to the culture media (1/1000).

[00147] Incubation: Culture media were incubated at 30ºC, 200 rpm. 8 hours and after growth CFU/ml of the culture broths of each strain (CK1, CK2) are made.

[00148] The different formulations were prepared as described below:

[00149] A) Xanthan gum (2% w/v). Proportion: Xanthan 25% -75% culture broth. Xanthan concentration in the formulation: 0.5%.

[00150] B) Carboxymethylcellulose (CMC, 1% w/v). Proportion: CMC 25% - 75% culture broth. CMC concentration in the formulation: 0.25%.

[00151] C) Nothing was added.

[00152] The product was packaged in plastic bottles and stored at room temperature protected from light.

Table 7: Carrier formulation materials for microbial inoculant

Culture media	Strain	Additive
M8 + G. Arabic 0.6% (p/v) + Tween 0.025% (v/v)	*Klebsiella aerogenes* CK1	none
M8 + G. Arabic 0.6% (p/v) + Tween 0.025% (v/v)	*Klebsiella aerogenes* CK1	Xanthan 2 % (p/v) en FS
M8 + G. Arabic 0.6% (p/v) + Tween 0.025% (v/v)	*Klebsiella aerogenes* CK1	CMC 1 % (p/v) en FS
M8 + G. Arabic 0.6% (p/v) + Tween 0.025% (v/v)	MIX (*Klebsiella aerogenes* CK1. *Bacillus cereus* CK2)	none
M8 + G. Arabic 0.6% (p/v) + Tween 0.025% (v/v)	MIX (*Klebsiella aerogenes* CK1. *Bacillus cereus* CK2)	Xanthan 2 % (p/v) en FS
M8 + G. Arabic 0.6% (p/v) + Tween 0.025% (v/v)	MIX (*Klebsiella aerogenes* CK1. *Bacillus cereus* CK2)	CMC 1 % (p/v) en FS
M8 + PVP 2.5% (p/v) + Tween 0.025% (v/v)	*Klebsiella aerogenes* CK1	none
M8 + PVP 2.5% (p/v) + Tween 0.025% (v/v)	*Klebsiella aerogenes* CK1	Xanthan 2 % (p/v) en FS
M8 + PVP 2.5% (p/v) + Tween 0.025% (v/v)	*Klebsiella aerogenes* CK1	CMC 1 % (p/v) en FS
M8 + PVP 2.5% (p/v) + Tween 0.025% (v/v)	MIX (*Klebsiella aerogenes* CK1. *Bacillus cereus* CK2)	none
M8 + PVP 2.5% (p/v) + Tween 0.025% (v/v)	MIX (*Klebsiella aerogenes* CK1. *Bacillus cereus* CK2)	Xanthan 2 % (p/v) en FS

M8 + PVP 2.5% (p/v) + Tween 0.025% (v/v)	MIX (*Klebsiella aerogenes* CK1. *Bacillus cereus* CK2)	CMC 1 % (p/v) en FS
AN+ NaCl 0.8% + G. Arabic 0.6% (p/v) + Tween 0.025% (v/v)	*Klebsiella aerogenes* CK1	none
AN+ NaCl 0.8% + G. Arabic 0.6% (p/v) + Tween 0.025% (v/v)	*Klebsiella aerogenes* CK1	Xanthan 2 % (p/v) en FS
AN+ NaCl 0.8% + G. Arabic 0.6% (p/v) + Tween 0.025% (v/v)	*Klebsiella aerogenes* CK1	CMC 1 % (p/v) en FS
AN+ NaCl 0.8% + G. Arabic 0.6% (p/v) + Tween 0.025% (v/v)	MIX (*Klebsiella aerogenes* CK1. *Bacillus cereus* CK2)	none
AN+ NaCl 0.8% + G. Arabic 0.6% (p/v) + Tween 0.025% (v/v)	MIX (*Klebsiella aerogenes* CK1. *Bacillus cereus* CK2)	Xanthan 2 % (p/v) en FS
AN+ NaCl 0.8% + G. Arabic 0.6% (p/v) + Tween 0.025% (v/v)	MIX (*Klebsiella aerogenes* CK1. *Bacillus cereus* CK2)	CMC 1 % (p/v) en FS
AN+ NaCl 0.8% + PVP 2.5% (p/v) + Tween 0.025% (v/v)	*Klebsiella aerogenes* CK1	none
AN+ NaCl 0.8% + PVP 2.5% (p/v) + Tween 0.025% (v/v)	*Klebsiella aerogenes* CK1	Xanthan 2 % (p/v) en FS
AN+ NaCl 0.8% + PVP 2.5% (p/v) + Tween 0.025% (v/v)	*Klebsiella aerogenes* CK1	CMC 1 % (p/v) en FS
AN+ NaCl 0.8% + PVP 2.5% (p/v) + Tween 0.025% (v/v)	MIX (*Klebsiella aerogenes* CK1. *Bacillus cereus* CK2)	none
AN+ NaCl 0.8% + PVP 2.5% (p/v) + Tween 0.025% (v/v)	MIX (*Klebsiella aerogenes* CK1. *Bacillus cereus* CK2)	Xanthan 2 % (p/v) en FS
AN+ NaCl 0.8% + PVP 2.5% (p/v) + Tween 0.025% (v/v)	MIX (*Klebsiella aerogenes* CK1. *Bacillus cereus* CK2)	CMC 1 % (p/v) en FS

[00153] The additives were evaluated in different proportions according to the bibliography, as shown in Table 8. The selection of the best concentration was made based on the CFU/mL count obtained compared to the control (medium without additives).

[00154] In all cases the lowest concentration in which growth was greater or the same than the control was selected.

Table 8: Additives and concentration used

Properties	**Additives**
Cell protectants	Glycerol 5 mM
Cell protectants	Glycerol 10 mM
Cell protectants	Glycerol 15 mM
Cell protectants	Glycerol 20 mM

Surfactant	Tween 20 0.025%
Surfactant	Tween 20 0.5%
Protectant	Arabic gum 0.6%
Protectant	Arabic gum 0.8%
Preservative	Potassium sorbate 0.2%
Protectant	PVP 2.5%
Protectant	PVP 2%
Protectant	Sodium Alginate 0.1%
Adjuvant	CMC 0.1%
Adjuvant	Xanthan 2%

[00155] The best counts (CFU/mL) were obtained with the combination of tween, Arabic gum and PVP. It is important to note that the pH values remained close to neutrality. These results were not obtained with glycerol, which produced acidification in the culture medium. Potassium sorbate affected the growth of CK2, this strain grew less in its presence, so it was discarded and, on the other hand this protectant combined with PVP alkalinized the medium with CK1.

Table 9: Effect of different additives on the population of *Klebsiella aerogenes* CK1 and *Bacillus cereus* CK2

	Product	Protectant	Surfactant	CFU/ml	pH
1	*Klebsiella aerogenes* CK1	PVP 2.5%	Sorbitol K 0.2%	$1.8x\ 10^9$	7.73
1	*Bacillus cereus* CK2			$1.9x\ 10^7$	6.61
3	*Klebsiella aerogenes* CK1	Alginate 0.1%	Sorbitol K 0.2%	$1x2x\ 10^9$	6.97
3	*Bacillus cereus* CK2			$2x\ 10^7$	6.55
5	*Klebsiella aerogenes* CK1	Glycerol 5%	Sorbitol K 0.2%	$4.15x\ 10^8$	5.60
5	*Bacillus cereus* CK2			$6.7x\ 10^7$	6.05
7	*Klebsiella aerogenes* CK1	PVP 2.5%	Tween20 0.025%	$1.1x\ 10^9$	6.82
7	*Bacillus cereus* CK2			$1.54x\ 10^8$	6.56
8	*Klebsiella aerogenes* CK1	Arabic gum 0.6%	Tween20 0.025%	$1.9x\ 10^9$	6.67
8	*Bacillus cereus* CK2			$1.4x\ 10^8$	6.49
CTRL	*Klebsiella aerogenes* CK1	------	------	$1.6x\ 10^9$	7.06
CTRL	*Bacillus cereus* CK2	------	-------	$1.6x\ 10^8$	6.52

[00156] The process was simplified by adding all the components to the culture medium before inoculating. At the end of the process the xanthan gum or CMC were added.

[00157] To select the best formulation, CFU/mL were evaluated every month, as shown in Table 10. The addition of Arabic gum/PVP, tween 20 and xanthan/CMC improved the stability of the product, especially for CK1 in the Mix product. Spores' formation was identified for CK2 during time.

Table 10: Effect of additives on the pH and CFU/mL of *Klebsiella aerogenes* CK1 and *Bacillus cereus* CK2 during time.

CK1 A /M8							
Days	M8+XANT	M8+GA+T	M8+GA+T+XANT	M8+GA+T+ CMC	M8+PVP+T	M8+PVP+T+XANT	M8+PVP+T+CMC

0	1.22E+09	1.73E+09	1.10E+09	1.47E+09	1.78E+09	1.65E+09	1.80E+09
30	3.00E+07	3.00E+07	1.10E+08	1.85E+08	1.85E+07	1.20E+08	1.21E+08
60	4.75E+07	1.60E+08	2.20E+08	1.75E+08	3.80E+07	1.08E+08	3.70E+07
pH							
0		6.99	7.05	6.9		6.95	7.25
30	7.27	7.47	7.22	7.4	7.76	8.23	8.45
60	8.35	7.69	7.45	7.48	7.98	8.17	8.12
CK1+CK2/M8							
Days/ CK1	**M8+XANT**	**M8+GA+ T**	**M8+GA+T+ XANT**	**M8+GA+ T+ CMC**	**M8+PVP+ T**	**M8+PVP+ T+XANT**	**M8+PVP+ T+CMC**
0	1.73E9	9.40E+08	4.97E+08	4.10E+08	2.13E+09	1.33E+09	1.27E+09
30	3.00E+07	4.30E+07	5.10E+08	2.90E+08	4.50E+08	7.50E+08	2.90E+08
60	1.85E+07	3.00E+07	1.2E8	2.60E+08	3.40E+07	1.90E+08	1.60E+08
Days/CK2							
0	6.50E+07	7.70E+07	4.00E+07	3.20E+07	2.35E+07	4.35E+07	2.50E+07
30	-	1.80E+06	4.25E+06	1.80E+06	-	2.50E+06	2.00E+07
60	-	2.00E+06	-	1.00E+06	1.10E+06	1.00E+05	3.10E+06
CK1/AN							
Days	**AN+XANT**	**AN+GA+ T**	**AN+GA+T+ XANT**	**AN+GA+ T+ CMC**	**AN+PVP+ T**	**AN+PVP+ T+XANT**	**AN+PVP+ T+CMC**
0	1.40E+09	2.43E+09	2.30E+09	2.00E+09	2.50E+09	2.50E+09	2.00E+09
30	1.44E+08	3.30E+08	4.00E+07	2.3E+08	2.20E+08	4.00E+07	3.00E+08
pH							
0		6.72	6.94	6.88	6.75	6.68	6.85
30		6.87	6.93	7.01	7.07	6.88	6.99
CK1+CK2/AN							
Days/ CK1	**AN+XANT**	**AN+GA+ T**	**AN+GA+T+ XANT**	**AN+GA+ T+ CMC**	**AN+PVP+ T**	**AN+PVP+ T+XANT**	**AN+PVP+ T+CMC**
0	1.38E+08	7.50E+08	1.16E+09	1.00E+09	1.14E+09	1.46E+09	1.06E+09
30		2.00E+08	1.5E8	4.00E+08	4.44E+07	4.40E+07	7.00E+07
Days/CK2							
0	2.57E+07	4.60E+06	3.00E+07	1.00E+07	2.00E+06	7.50E+07	3.00E+06
30		3.1E7	> 1E4	1.00E+07	< 1E4	2.00E+04	< 1E4

[00158] The results showed that in M8 medium " M8+GA+T+XANT" was the best combination evaluated. Although in the first month it experienced a drop in the CFU/mL, then the pH values were maintained in this formulation. This was not observed with the use of "M8+PVP+T+XANT" and "M8+PVP+T+XANT" in which the medium was alkalinized, values greater than 8 were reported.

[00159] Regarding CK1 and CK1+CK2 in AN medium, the best results were reported with CM.

[00160] The combinations "AN+GA+T+XANT" and "AN+PVP+T+XANT" were not effective. Furthermore, the results reported shown that the use of PVP in CK1+CK2 was not useful. At 30 days the CFU/mL counts were less than 1E4.

Example 3: CK2 Sporulation

[00161] Bacterial spores have been defined as small oval structures exhibiting a strong resistance to high temperatures, desiccation, radiation, and chemical agents. Products based on spores could improve the survival of the bacteria over time, thus enhancing products shelf life, and the resistance of the product to stress conditions. Therefore, CK2 sporulation capacity was evaluated.

[00162] CK2 was grown in different media and then evaluated for the induction of sporulation (see protocol above). CK2 cultures were grown, and CFU/mL count and pH were measured as described in Example 1. The CK2 morphology was controlled using an optical microscope Samples were measured at 24 hrs, 48 hrs, and 72 hrs.

[00163] The culture media tested, and results are shown in Table 11 and 12 respectively.

[00164] *Sporulation protocol: TOTAL CELLS AND SPORES COUNT*

[00165] The number of total cells (vegetative cells + germinative cells or spores) and the number of spores produced in each tested condition were evaluated at different times. CFU/mL count was performed before and after heating the sample following the next protocol:

[00166] 1 mL of the growth medium containing CK2 was sampled.

[00167] 100 µL were used to perform CFU/mL.

[00168] The remaining sample was heated at 70°C or 80°C for 20 min.

[00169] The spore count (CFU/mL) of the heated sample was measured. Overall, one less dilution should be plated than in the count without heating, unless the entire sporulated culture is observed under a microscope, in which case the same dilutions should be plated.

Table 11: Culture Media for Spore Production in *Bacillus cereus* CK2

(g/L)	Glucose	Soy flour	Cornstarch	$MgSO_4 \cdot 7H_2O$	$MnSO_4$	CaCl
S1	1.2	-	-	0.5	-	-
S2	1.2	-	-	0.5	-	-
S3	1.2	35	30	0.3	0.3	3
S4	1.2	-	-	0.5	0.3	-
S5	2.41	10.13	16.89	0.45	-	-
S6	2	9.5	9	-	0.3	1.55
S7	-	-	-	-	-	5
S8	-	-	-	-	-	-
S9	-	-	11.1	-	-	5
S10	-	-	12.5	-	-	-
S11	-	-	-	0.15	0.04	0.04
S12	-	-	-	-	-	-
S13	-					
S15	1.2	-	-	0.5	0.04	-
S16	-	-	-	0.2	-	-
S17	-	-	-	0.5	0.04	-
S18	1.2	-	-	-	0.04	-
S19	1.2	-	-	0.5	0.04	-
S20	1.2	-	-	0.5	-	-
S21	1.2	-	-	0.5	0.04	-
S22	1.2	-	-	0.5	0.04	-
S23	-	-	-	0.5	-	-
AN	-	-	-	-	-	-
(g/L)	Meat ext.	KH_2PO_4	Triptein	$(NH_4)_2HSO_4$	Na Cl	Soluble potato starch
S1	5	-	3	-	-	-
S2	3	-	-	-	-	-
S3	-	-	-	-	-	-
S4	5	6	3	-	-	-

S5	-	-	1.13	7.96	4.5	-
S6	7.2	-	-	-	-	-
S7	-	-	-	-	-	11.1
S8	-	-	-	1	-	12.5
S9	-	-	-	-	-	-
S10	-	-	-	1	-	-
S11	-	1	5	-	-	-
S12	2,5	-	-	-	-	-
S13	3,75					
S15	-	-	-	-	-	-
S16	-	-	-	2	-	-
S17	1.5	-	-	-	-	-
S18	1.5	-	-	-	-	-
S19	1.5	-	-	-	-	-
S20	1.5	-	-	-	-	-
S21	1.5	-	-	-	-	-
S22	-	-	-	-	-	-
S23	1.5	-	-	-	-	-
AN	1.5	-	-	-	-	-
(g/L)	**$FeCl_3 \cdot 6H_2O$**	**Yeast Ext.**	**K_2HPO_4**	**Pluripeptone**	**Sodium citrate**	
S1	-	-	6	-	-	
S2	-	-	6	5	-	
S3	-	-	-	-	-	
S4	-	-	-	-	-	
S5	-	-	-	-	-	
S6	-	-	-	-	-	
S7	-	3	-	-	-	
S8	-	10	-	-	-	
S9	-	3	-	-	-	
S10	-	10	-	-	-	
S11	0.3	3	-	-	-	
S12	-	-	-	1,5	-	
S13			-	2,25	-	
S15	0.3	1.5	1	2.5	-	
S16	-	-	0.125	-	7.5	
S17	0.3	-	1	2.5	-	
S18	0.3	-	1	2.5	-	
S19	0.3	-	-	2.5	-	
S20	0.3	-	1	2.5	-	
S21	-	-	1	2.5	-	
S22	0.3	-	1	-	-	
S23	0.3	-	1	2.5	-	
AN	-	-	-	2.5	-	

Table 12: Evaluation of Spore Production in *Bacillus cereus* CK2 (First Stage)

Culture media	Strain	Incubation time	pH	CFU/mL	Spores/mL
S1	CK2	24 h	7,15	8.00E+08	2,7E+05
		48 h	-	1,5E+08	2.00E+04
S2	CK2	24 h	7,08	1,36E+09	-
		48 h	-	2,8E+08	-
S3	CK2	24 h	4,83	1,3E+08	-

		48 h	6,06	9.00E+08	-
		72 h	-	-	-
S4	CK2	24 h	6,43	1,25E+08	-
		48 h	6,72	3,96E+08	4.00E+05
		72 h	7,30	6,6E+07	2.00E+07
S5	CK2	24 h	4,84	1.00E+08	-
		48 h	4,83	8.00E+06	-
		72 h	-	-	-
S6	CK2	24 h	4,84	3,58E+08	2.00E+06
		48 h	4,79	6.00E+06	-
		72 h	-	-	-
S7	CK2	24 h	4,57	1,1E+07	-
		48 h	4,51	-	5.00E+06
		72 h	4,69	-	1.00E+06
S8	CK2	24 h	5,92	4,35E+08	-
		48 h	5,92	3.00E+07	2.00E+07
		72 h	-	-	-
S9	CK2	24 h	5,81	1.00E+08	-
		48 h	5,83	1.00E+08	-
		72 h	-	-	-
S10	CK2	24 h	5,28	2,18E+08	-
		48 h	5,18	6.00E+06	3.00E+07
		72 h	5,06	3,2E+07	6,5E+06
S11	CK2	24 h	-	2,25E+08	1,7E+06
		48 h	6,91	2.00E+08	6.00E+06
		72 h	7,63	1.00E+08	3.00E+06
S12	CK2	24 h	6,67	2,18E+08	3.00E+06
		48 h	-	1.00E+08	1.00E+05
		72 h	7,01	1,49E+08	1,4E+05
S13	CK2	24 h	6,46	7.00E+07	3.00E+06
		48 h	-	1,26E+08	-
		72 h	7,07	1,1E+08	6,2E+05

[00170] The first culture media evaluated for CK2 sporulation were S1 and S2. The results obtained in S1 and S2, indicated an optimal CFU/mL count and the presence of some refringent spores inside the CK2 vegetative cells under a microscope. However, CK2 was not able to sporulate.

[00171] Since nutrient deprivation (C, N and/or P) has been described a key factor to trigger bacterial sporulation, these results could be linked to an excess of nutrients in the culture media, which prevented them from becoming limiting in the times evaluated and therefore the sporulation could not take place.

[00172] Regarding the pH value, it remained neutral. It has been shown that in some *Bacillus* species, the sporulation process depends on the pH value. Nevertheless, in other cases, it was possible to work at a free pH without affecting the sporulation capacity of the bacteria. Despite these differences, overall, it has been reported that the sporulation process increases the pH of the medium above 7.5.

[00173] Further studies are needed to elucidate the influence of the pH on the sporulation process of the CK2 strain.

[00174] Regarding the culture media S3, S4, S5, S6, S7, S8, S9, S10, S11, S12 and S13, an optimal CFU/mL count was reached. However, in most of them, the spores number obtained was low.

[00175] Particularly, S3, S5, S6 and S9, exhibited no spores after 48 hours of incubation, thus they were discarded.

[00176] Despite S8 medium, showed 2.00E+07 spores/mL, it was discarded since it was composed of soluble potato peptone as a sole carbon source. Potato peptone is manufactured by a controlled enzymatic hydrolysis of potato proteins, and its composition usually changes between production batches, changing the spore's concentration in the culture medium. In addition, its commercial availability was low. Therefore, corn starch was added (S9 culture medium) as a replacement of potato peptone. However, no spore formation was observed in S9, under the studied conditions.

[00177] After 48 hours, S4, S6, S10 and S11 reached 4.00E+06, 5.00E+06, 3.00E+07 and 6.00E+07 spores/mL, respectively. At 72 hours, S4 medium exhibited an increment of the spore's quantity. No changes were obtained for S7 and S11 culture media. In contrast, spores/mL decreased in the S10 medium.

[00178] Even though spore's production in S12 and S13 was evaluated up to 72 hours, the highest number of spores/mL was registered at 24 hours.

[00179] Regarding the pH, it has been observed that the higher the spores/mL, the higher the pH value, when CK2 was grown in S4 medium. Conversely, no pH changes were registered in S10 medium. Furthermore, the pH values were lower (around 5) than the ones obtained in S4.

[00180] Finally, S11, S12 and S13 showed an increase in pH over time. As it was mentioned before, it has been reported that the bacterial sporulation process usually provokes a culture medium alkalinization raising the pH value.

[00181] In spite of having found some culture media capable of exhibiting spores' formation, the concentration of them was still low. Therefore, new culture media was evaluated.

[00182] CK2 was grown in S15, S16 and AN media. The protocol followed to grow CK2 was slightly different from the one previously described. In all cases, it was decided to use CaCl2 1.55 g/L (2 Mm) as inducer of the sporulation process. Thus, CK2 was incubated at 30°C and 230 rpm, to obtain a CK2 culture in stationary phase. At 20 hours, the inducer (CaCl2 1.55 g/L) was added, and sporulation was evaluated at different times: 0, 2, 4, 6, 24 hours and 4 days after the addition of the inducer.

Table 13 Evaluation of spore production in *Bacillus cereus* CK2 (second stage)

Time (h) Inducer aggregate	spores/mL S15	spores/mL S16	spores/mL AN
0	1.1E+05	1.83E+07	1.5E+05
2	4.5E+05	1.1E+07	2.5E+06
4	1.6E+08	1.1E+07	3.6E+07
6	2.2E+08	1.2E+07	1.9E+07
24	2.4E+08	8.0E+06	3.31E+08
96	4.0E+08	1.6E+07	1.71E+08

[00183] According to the results (Table 13), although CK2 sporulation was quickly reached in S16 culture medium, the growth of the strain was low (1.0E+7). The pH value registered was 7.4 at 24 hours after adding the inducer and 8.5 after 4 days. Free spores were found in the culture medium at 4 days of

growth. In addition, no induction of the sporulation process was observed after adding CaCl2. Since CK2 growth was inferior than expected, and the spores concentration was lower than the values reached in S15 and AN, the use of S16 was discarded.

[00184] Regarding S15 and AN culture media, the results showed that the sporulation process was triggered a few hours earlier in S15 compared to AN medium. In both culture media, the addition of CaCl2 was able to induce the sporulation in CK2.

[00185] According to the results, AN optimization was abandoned. In contrast, it was decided to continue working on the optimization of the medium S15.

[00186] In a third stage, the effect of adding a higher volume of the initial inoculum in the process was tested. Two different conditions were compared following the next protocol:

CONDITION 1

[00187] Approximately 100 mL of S15 medium were placed in a 250 mL Erlenmeyer flask. Erlenmeyer flask was inoculated with 1 mL (0.1%) of CK2, previously grown in S15 culture grown (approx. 20 hours). Erlenmeyer flask was then incubated during 18h, at 30°C and 230 rpm, to obtain a CK2 culture in stationary phase. After 18 hours of culture, the inducer was added (CaCl2 1.55 g/L, approx. 2mM). The following incubation was performed at 30°C, 230 rpm and the sporulation of the culture was evaluated at different times: 0, 2, 4, 6, 8, 24 and 48 hours after the addition of the inducer.

CONDITION 2:

[00188] The steps were the same described for condition 1, but the Erlenmeyer flask was inoculated with 10 mL (10%) of CK2 instead of 1 ml.

[00189] The results are shown in Table 14. Under the tested conditions, the volume of the initial CK2 inoculum affected the sporulation process. The increase of the volume of the initial CK2 inoculum (from 0.1% to 10%) accelerated the sporulation process. Total sporulation was achieved two hours after the addition of CaCl2. In contrast, when 0.1% of the inoculum was used, complete sporulation was reached after 24 hours of adding CaCl2.

[00190] Therefore, hereinafter the initial CK2 inoculum was used at 10%, regardless the final culture volume.

Table 14 Evaluation of spore production in *Bacillus cereus* CK2 (third stage)

	S15 10% initial inoculum		S15 0.1% initial inoculum	
Time (h) Inducer aggregate	**Spores/mL**	**Sporulation percentage (%)***	**Spores/mL**	**Sporulation percentage (%)**
0	1.3E+07	7.3%	2.8E+05	≤1%
2	5.9E+08	100%	1.0E+05	≤1%
4	4.93E+08	100%	3.0E+06	1.3%
6	5.72E+08	100%	2.0E+07	10%
8	6.6E+08	100%	7.5E+07	34%
24	3.5E+08	70%	3.7E+08	100%
48	3.4E+08	85%	2.0E+08	100%

***Sporulation percentage (%):** Sporulation efficiency (%) = (Final number of spores/Final number of total cells)*100

[00191] Finally, in a fourth stage, the optimization of the S15 culture medium was performed. The influence of the different components was evaluated. In addition, the inducer (CaCl2) was added to the culture medium at the beginning of the growth. The incubation was stablished at 30°C, 230 rpm during 18h. The parameters evaluated are described in Table 15.

Table 15 Evaluation of spore production in *Bacillus cereus* CK2 (fourth stage)

Culture media	Initial pH	Final pH	CFU/mL	Spores/mL
S15	7.5	7.4	1.81E+08	2.8E+8
S17	7.5	7.5	1.6E+08	3.6E+08
S18	7.5	7.25	1.81E+08	1E+06
S19	7.5	7.60	1.93E+08	2.5E+08
S20	7.5	7.36	2E+08	6.4E+08
S21	7.5	7.24	2E+08	4E+06
S22	7.5	5.98	2E+07	2.3E+07
S23	7.5	7.69	2.53+08	7E+08

[00192] According to the results, the cations Mg2+ and Fe3+, showed to be important in the composition of the S15 medium since removing any of the cations the sporulation process was delayed. The spore count in the S17, S19 and S20 media (without glucose, dibasic phosphate, and manganese, respectively) was comparable to the S15 medium. In contrast, S18 and S21 showed a lower number of spores compared to S15. On the other hand, S22 (without pluripeptone and meat extract), exhibited a spore count one order lower than the control (S15). However, CK2 growth was also lower in this condition.

[00193] Regarding the pH value, in all culture media (including the control) it remained between 7.24 and 7.60, except for S22, in which a decrease in pH (5.98) was observed. It could be explained by the presence of glucose in the culture medium since its metabolism induced the acidification of the culture medium.

[00194] Overall, the presence of Fe3+ and Mg2+ ions was important to reach the sporulation of CK2 within 18 hours of growth. The same was found for pluripeptone and meat extract. In contrast, glucose, Mn2+ and/or dipotassium phosphate could be removed from the S15 medium, without negatively affecting the growth and sporulation process. Therefore, S17 medium was selected to perform the last optimization removing the Mn2+ ions.

[00195] As it shown in Table 15, S23 culture medium exhibited the highest number of spores as well as the greater growth. Thus, S23 was chosen as the sporulation culture medium for CK2 and to evaluate the viability over time of the strain.

Example 4: Field testing- Extremia A and Extremia MIX treated seeds improve crop yields

[00196] Field trials were performed with either the Extremia A or Extremia MIX.

[00197] Products were manufactured by growing the bacteria in AN culture medium, containing 10 gxL^{-1} peptone, 10 gxL^{-1} meat extract and 5 gxL^{-1} sodium chloride. Growth conditions were settled as follows:

[00198] Temperature: 30°C.

[00199] Growth time: between 6 and 8 hours.

[00200] Bacterial final concentration: Extremia A, containing CK1 strain, reached 1x109 CFU/mL. Extremia MIX presented $3x10^8$ CFU/mL of CK1 and $1x10^8$ CFU/mL of CK2. For Extremia MIX the culture broths for each strain were mixed (50% v/v).

[00201] The cultures were then mixed with the stabilizer in a ratio of 7.5:2.5 (vol./vol.) respectively.

[00202] The stabilizer selected for the mixture was xanthan gum FF fine food (Phernhofen). At the beginning the xanthan gum was prepared at 2% (weight / vol.) using distilled water to dissolve it. Later, the dissolvent was replaced by physiological solution (NaCl 8 g x L^{-1}) since it helps to stabilize the osmotic pressure in the medium.

[00203] The initial preparation of the xanthan gum included a magnetic stirring and dissolution of remaining lumps with a spoon. Currently, a propeller stirrer (Dlab brand, model OS40-S) is used at 1000-1400 rpm (approx.) until complete dissolution.

[00204] An antifoam (AF10 silicone from Permaquim) is mixed with the xanthan gum before sterilizing. The antifoam is diluted 1/1000.

[00205] The sterilization of the xanthan gum with the silicone is performed in an autoclave. The sterilization time depends on the volume of xanthan gum placed in the container. Generally, 500 mL is placed and sterilized for at least 20 minutes to ensure sterility.

[00206] Finally, the mixture was packed in either sterile 100 mL plastic bottles or 2L/5L plastic bladders and preserved at room temperature (~25°C).

[00207] Soybean seeds were inoculated with either the Extremia A Product or Extremia MIX, a commercial *Bradyrhizobium* inoculant (CKC liquid soybean, 0.96 mL per kg of seed) or a combination of Extremia A and *Bradyrhizobium* (2.5 mL and 0.48mL respectively).

[00208] Control treatment seeds were not inoculated. Seeds were inoculated with either Extremia A Product or Extremia MIX at 5 mL of inoculant per kg of seed or 6 mL of inoculant per kg of seed.

[00209] Seed dressing was the method used by seed treatment. The liquid formulation was mixed with pesticides frequently used. The seeds were treated with the liquid inoculant according to the producer; it can be mechanical or manual (using different containers to make the mixture).

[00210] The treated seeds were grown under different locations and conditions, and the subsequent development of the crops was evaluated.

[00211] Seeds were planted, grown, and harvested under various environmental and soil conditions representative of potential agricultural conditions. The locations and conditions are listed in Table 16.

[00212] Seed planted was carried out with an experimental direct seeders machine at 52 cm between rows.

[00213] Four central rows were harvested, and Yield (kg/ha) was determined in each Experimental unit (Number of pods per plant, N° grains/pod and grain weight). A sample (1 kg) of the harvested seeds from each experimental unit was subjected to quality analysis.

Table 16 Seed growth conditions

Location	Previous crop	Soil types	Fertilization	rainfall cycle	M.O %	Phosphorus ppm	pH

Tucuman	Corn	Typical hapludoll	yes	Normal	3.36	17.3	7.66
San Jeronimo Norte	Barley		Yes	Normal	2.3	19	5.83
F. Ameghino Bs As	Corn	Hapludoll	Yes	Stress		9.5	
Pergamino Bs As	Corn	Typic argiudolls	Yes	Low	3	14.6	5.6
Tres Arroyos Bs As	Barley	Petrocalcic Argiudolls	yes	Stress	3.4	9	6.1
Colonia Caroya CBA	Corn		No	Stress	N/A	N/A	N/A
Diamante ER	Wheat	Aquic argiudolls	No	Low	2.6	58.1	6.2

[00214] Results are shown in Table 17. The data showed that all treatments with Extremia A and Extremia MIX Products had average increased yield between 9.8% and 16.7% over untreated seed, compared to 3.9% increased yield of the commercial *Bradyrhizobium* product evaluated.

[00215] To calculate yield, the four central rows (8 meters long) of each experimental unit were harvested. Measurements of yield (translated to kg./ha), pods per plant, seeds per pod, and seed size were calculated. Adjustments for moisture content were also made to each treatment.

[00216] The win rate was defined as the percentage of trials in which one treatment presented higher yields than the control untreated seeds. Four different Extremia A and Extremia MIX Product treatments had a 100% response rate. Extremia A 6 mL had an 85.7% response rate. In the same experiments, the commercial *Bradyrhizobium* product's response rate was 71.4%.

Table 17 Yield evaluation comparison to control treatment

Yield vs. Control	Extremia A + *Brady*	Extremia A 6mL	Extremia MIX 6mL	Extremia A 5mL	Extremia MIX 5mL	Brady
Pergamino Bs As	22%	15%	13%	6%	6%	3%
F. Ameghino Bs As	30%	9%	17%	4%	17%	6%
San Jerónimo Norte	21%	45%	15%	40%	8%	15%
Tucumán	3%	3%	9%	8%	1%	-3%
Tres Arroyos Bs As	2%	0%	1%	9%	16%	-4%
Jesus María	10%	9%	7%	10%	14%	6%
Entre Ríos	29%	-3%	6%	14%	10%	3%
Average trials (7 treatments)	16.7%	11.2%	9.8%	13.0%	10.4%	3.9%
Win rate	100.0%	85.7%	100.0%	100.0%	100.0%	71.4%

[00217] Crop yield data was further analyzed to compare yields of Extremia A and Extremia MIX Products treated seeds versus the commercial *Bradyrhizobium* product treated seeds. Results are shown in Table 18.

[00218] The data showed that Extremia A and Extremia MIX Product treatments generally increased yield for all treatments compared to untreated seeds. Yield levels were much higher for Extremia A and Extremia MIX Product treated seeds than seeds treated with traditional *Bradyrhizobium* based products. Seeds treated with Extremia A and Extremia MIX Products exhibited 6-12% higher yields than seeds treated with the commercial *Bradyrhizobium* product. Seeds treated with Extremia A and Extremia MIX Products exhibited higher yields than seeds treated with the commercial *Bradyrhizobium* products in 6 of 7 trials, or up to the 7 trials in the case of Extremia A+ Bradyrhizobium.

[00219] The combined analysis of the field trials demonstrated that the Extremia A and Extremia MIX formulation treatments presented significant performance improvements of ~ 10-17% versus a control treatment without inoculation, and improvements of ~ 6-12% when compared to the commercial *Bradyrhizobium* based product. The Extremia A and Extremia MIX Product treatments exhibited higher consistency of response rates, between 87-100%, compared to response rates of 71% for the Bradyrhizobium-based product. Fisher's statistical analysis showed that all Extremia A and Extremia MIX Product treatments showed significant differences in performance against the uninoculated control and against the commercial *Bradyrhizobium* product.

Table 18 Yield evaluation comparison to *Bradyrhizobium* treatment

Yield vs. *Bradyrhizobium*	Extremia A + Brady	Extremia A 6mL	Extremia MIX 6mL	Extremia A 5mL	Extremia MIX 5mL
Pergamino Bs As	18%	12%	10%	3%	2%
F. Ameghino Bs As	22%	3%	10%	-3%	10%
San Jerónimo Norte	6%	26%	0%	22%	-6%
Tucumán	5%	6%	12%	11%	4%
Tres Arroyos Bs As	7%	5%	6%	14%	22%
Jesus María	4%	2%	1%	4%	8%
Entre Ríos	25%	-7%	2%	10%	7%
Average vs. *Brady*	**12%**	**7%**	**6%**	**9%**	**7%**

[00220] Results are shown in Table 19.

[00221] Yield data comparison with the *Bradyrhizobium* treatment showed that, on average, the combination of Extremia A exhibited the highest yield improvement. However, this treatment exhibited the top yield in only 3 out of the 7 trials, showing that treatment performance could be affected by the environmental conditions and other factors such as rainfall, existing microbiome, and soil characteristics.

Table 19

Location / Treatment	**Extremia A + Brady**	**Extremia A 6ml**	**Extremia MIX 6ml**	**Extremia A 5ml**	**Extremia MIX 5ml**	***Brady***	**Control**	**Location average yield**
Pergamino	4272	4052	3977	3723	3704	3629	3508	**3838**
F. Ameghino	5292	4453	4771	4223	4783	4343	4079	**4563**
San	2900	3472	2744	3347	2577	2748	2388	**2882**

Jeronimo Norte								
Tucumán	3216	3220	3422	3388	3166	3052	3134	**3228**
Tres Arroyos	2991	2943	2971	3201	3414	2805	2933	**3037**
Jesús María	3399	3356	3309	3406	3522	3275	3083	**3336**
Entre Ríos	2390	1794	1964	2112	2047	1919	1856	**2012**
Bengolea	3199			3643	3562		3098	**3376**
Cnel. Moldes	3950			3526	3756		3369	**3650**

[00222] *Yield matrix*

[00223] At each trial location, four central rows of every experimental unit were harvested, and Yield (kg/ha) was determined in each Experimental unit through measuring its components (Number of pods per plant, N° grains/pod and grain weight).

[00224] For the 7 trials, results were compared among treatments to analyze superiority of one treatment over others. Table 9 shows the results from the comparative analysis.

[00225] Key conclusions were that all the treatments that included Extremia A or Extremia MIX Products, were superior to Bradyrhizobium in at least ~86% of the trials. In addition, not enough evidence showed superiority of using 6ml vs. 5ml for both Extremia A and Extremia MIX Products, but there was a slight advantage to the lower dosages (better results in 57% of trials). Finally, by calculating the total number of comparisons that were superior for each treatment, it was found that Extremia A 5ml and Extremia A +Brady exhibited the best results, showing an advantage in 63% of the comparisons.

Table 20

Row vs. Column comparison*	**Extremia A + Brady**	**Extremia A 6ml**	**Extremia MIX 6ml**	**Extremia A 5ml**	**Extremia MIX 5ml**	**Brady**	**% ""battles" won**
Extremia A + Brady		71%	43%	43%	57%	100%	**63%**
Extremia A 6ml	29%		43%	43%	43%	86%	**49%**
Extremia MIX 6ml	14%	57%		43%	43%	86%	**49%**
Extremia A 5ml	57%	57%	57%		57%	86%	**63%**
Extremia MIX 5ml	29%	57%	57%	43%		86%	**54%**
Brady	0%	14%	14%	14%	14%		**11%**
***Row is superior to Column in X% of the time**							

Example 5: Root Evaluation of seeds treated with Extremia A and Extremia MIX

[00226] Soybean seeds were inoculated with either Extremia A or Extremia MIX at 5 mL of inoculant per kg of seed or 6 mL of inoculant per kg of seed. Seeds were planted, grown, and harvested in Moldes and Bengolea , in the Province of Córdoba or in Tucuman and San Jeronimo Norte regions as described in Example 4.

[00227] Roots of the soybean plants were measured for their length and the number of secondary (lateral) roots. The measurements were carried out 28 days (Moldes) and 29 days (Bengolea) after planting. Results are shown in Table 21 and Table 22. The results indicated that both Extremia A and Extremia Mix have plant growth promoter activity based on the analysis of the development of soybean crop root length and secondary root structure. The crops harvested from Moldes that were treated with Extremia A and Extremia MIX exhibited both an increase in the length of the main root, and an increase in the number of lateral roots. The crops harvested from Bengolea that were treated with Extremia A and Extremia MIX showed an increase in the number of lateral roots.

[00228] FIG. 6 and FIG. 7 show representative images of crops from the Tucuman and San Jeronimo Norte regions, respectively. As shown, soybean plants treated with Extremia A and Extremia MIX exhibited an increase in root growth development, as well as an increase in biomass.

[00229] The cufflinks program was used to calculate the fragments per kilobase per million (FPKM) to calculate the abundance of each gene. This quantification is optimal for making comparisons with other genes in the same genome. Considering the length of the gene we can estimate whether gene X is more abundant than gene Y in each genome. However, the comparison between different genomes is not valid. Results of this analysis is found in FIG. 8 and FIG. 9.

Table 21: Soybean main root length

	Length of main roots (cm)		
Treatments	Bengolea	Moldes	Average
Control	18.4	13.9^{B}	16.2
Extremia A	18.3	19.8^{A}	19.1
Extremia Mix	17.9	17.7^{AB}	17.8
ANOVA	NS	0.0484	NS

Table 22: Soybean lateral root length

	Number of lateral roots		
Treatments	Bengolea	Moldes	Average
Control	44.0^{B}	35.8	39.9^{B}
Extremia A	67.2^{A}	43.3	52.2^{A}
Extremia Mix	66.2^{A}	37.9	52.1^{A}
ANOVA	-0.0001	NS	0.0001

^{A} or ^{B} indicates statistically significant.

Example 6: Genomic characterization of CK1 and CK2

[00230] The CK1 and CK2 strains were characterized by whole genome sequencing as described in Carriço et al. (Clinical Microbiology and Infection (2018) 24(4):P342-349). The genome assembly analysis for the strains in shown in Table 23. Based on the average nucleotide identity to publicly available species, it was determined that CK1 is most related to *Klebsiella* and CK2 to *Bacillus*. Neither strain shared 100% identity to any publicly available genome sequence. An analysis of the genomic sequence for CK1 and CK2 for coding regions, rRNA, repeat regions and tRNA regions is shown in Table 24.

Table 23: Genome assembly analysis of CK1 and CK2

	CK1 (*Klebsiella aerogenes*)	CK2 (*Bacillus cereus*)

# contigs (>= 0 bp)	329	110
# contigs (>=500 bp)	40	18
# contigs (>= 1000 bp)	26	18
Largest contig	1511170	1010096
Total length	5005304	4285098
Total length (>= 0)	5068702	4303100
Total length (>= 1000)	4995476	4285098
N50	537496	610525
N75	32808	516531
L50	3	3
L75	6	5
GC (%)	55.16	45.91

Table 24: Genome annotation analysis of CK1 and CK2		
	CK1 (*Klebsiella aerogenes*)	**CK2 (*Bacillus cereus*)**
CDS	4645	4415
rRNA	6	8
Repeat region	0	1
tRNA	77	95

Example 7: Nitrogen fixation genome analysis of CK1 and CK2

[00231] Using the genomic sequence obtained for CK1 and CK2 in Example 6, the genomes of these strains were analyzed for the presence of N2 metabolic pathways. Paired-end sequences were filtered for quality using the Trimmomatic program and observed through FastQC. The sequences of each strain were filtered. The assembly of the reads was carried out by means of the Spades program. The annotation of the sequence obtained through Spades was made through the Prokka program. Using the annotated genome data, the presence of enzymes corresponding to the nitrogen cycle was searched (N2 fixation, assimilative and dissimilative reduction, denitrification, and nitrification). For this analysis, the FASTA sequences of all the genes of interest related to the metabolic pathway were downloaded from the Uniprot database and only curated sequences were used. With each sequence downloaded, a Psi-blast was performed to obtain a list of 500 homologous sequences that maintained the conserved regions of each sequence and was iterated a minimum of 4 times to obtain sequences as distant as possible.

[00232] First, the cdhit program was used to remove redundant sequences. Then, the Clustal program was used to perform a multiple alignment of the 500 sequences corresponding to each enzyme of interest. Finally, multiple alignment was used to obtain a hidden Markov model (HMM) of each enzyme and then this model was used to thin it against the faa file of each annotated genome. In this way, all the sequences present in the genomes that are similar to the enzymatic sequences of interest were searched manually.

[00233] Results of genome analysis are shown in Tables 25 and 26, indicating the presence and absence of enzymes for steps involved in nitrogen fixation. The presence and absence of the pathways is summarized in Table 27. Table 28 lists the gene names, enzymes, and protein sequences searched. The results indicated the presence of an incomplete subset of nitrogen fixation pathway enzymes in CK1 and CK2.

Table 25: *Klebsiella aerogenes* CK1 Nitrogen fixation gene signature

Pathway	Gene	EC	HMM found (E-value < 10^{-3})	Protein name	Present
Nitrogen fixation	niKDH	1.18.6.1	-	-	No
	anfGD		-	-	
	vnfDKG	1.18.6.	-	-	
Assimilatory nitrate reduction	nasA; narB	1.7.7.2 1.7.1.4	CIKKEGMN_01222	Nitrate Reductase	Yes
	nasB (igual que nirB)		CIKKEGMN_02470	Nitrite Reductase	
	nirA	1.7.7.1	-	-	
Dissimilatory nitrate reduction (DNR)	NarG	1.7.5.1	CIKKEGMN_01227 CIKKEGMN_00439	Respiratory nitratereductase alpha	Yes
	narH		CIKKEGMN_00440 CIKKEGMN_01228	Respiratory nitrate reductase beta chain	
	narI		CIKKEGMN_01230 CIKKEGMN_00442	Respiratory nitrate reductase gamma	
	napA	1.9.6.1	-	-	
	nirB (igual que nasB)	1.7.1.1.5	CIKKEGMN_02470	Nitrite Reductase large subunit	
	nirD		CIKKEGMN_01227	Respiratory nitrate reductase	
Denitrification	narGHI (igual que en DNR)	1.7.5.1 1.9.6.1	CIKKEGMN_01227	-	No
	napA (igual que enDNR)		-	-	
	nirK	1.7.2.1	-	-	
	nirS		-	-	
	norB	1.7.2.5	-	-	
	nosZ	1.7.2.4	-	-	
Nitrification	amoA	1.14.99.39	-	-	No
	amoB		-	-	
	Hao1	1.7.2.6	-	-	

Table 26: *Bacillus cereus* CK2 Nitrogen gene signature

Pathway	Gene	EC	ck2 ID	Protein name	Present
Nitrogen Fixation	*nifKDH*	1.18.6.1	—	—	**No**
	anfGD		—	—	
	vnfDKG	1.18.6.	—	—	
	NRT, narK, nrtP, nasA		AHCFPGON_00953	MFS transporter, NNP family, nitrate/nitrite transporter	

Assimilatory nitrate reduction	*narGHI (igual que en DNR)*	1.7.99.-	AHCFPGON_00963 AHCFPGON_00962 AHCFPGON_00960	Nitrate reductase	**Yes**
	nasE	1.7.7.4	AHCFPGON_05730	Nitrite Reductase small subunit	
	nasD		AHCFPGON_05731	Nitrite Reductase large subunit	
Dissimilatory nitrate reduction (DNR)	*narG*	1.7.5.1	AHCFPGON_00963	Respiratory nitrate reductasealpha chain	**Yes**
	narH		AHCFPGON_00962	Respiratory nitrate reductasebeta chain	
	narI		AHCFPGON_00960	Respiratory nitrate reductasegamma chain	
	napA	1.9.6.1	—	—	
	nirB	1.7.1.15	AHCFPGON_00946	Nitrite Reductase large subunit	
	nirD		AHCFPGON_00947	Nitrite Reductase small subunit	
Denitrification	*narGHI (igual que en DNR)*	1.7.5.1 1.9.6.1	AHCFPGON_00963 AHCFPGON_00962 AHCFPGON_00960	Respiratory nitrate reductase	**No**
	napA (igual que en DNR)		—	—	
	nirK	1.7.2.1	—	—	
	nirS		—	—	
	norB	1.7.2.5	—	—	
	nosZ	1.7.2.4	—	—	
Nitrification	*amoA*	1.14.99.39	—	—	**No**
	amoB		—	—	
	hao1	1.7.2.6	—	—	
	nxrAB		AHCFPGON 00963	Nitrate reductase/ nitrite oxidoreductase	

Table 27: Summary of Nitrogen Fixation Gene Signature in *Klebsiella aerogenes* CK1 and *Bacillus cereus* CK2

Pathway	CK1	CK2
N2 fixation	ABSENT	ABSENT
Assimilatory nitratereduction	PRESENT	PRESENT
Dissimilatory nitratereduction (DNR)	PRESENT	PRESENT
Denitrification	ABSENT	ABSENT
Nitrification	ABSENT	ABSENT

Table 28: Nitrogen Cycle Enzyme Genes

Enzyme name	Gene name	*Bacillus cereus* CK2 ID	FASTA protein sequence
MFS transporter, NNP family, nitrate/nitrite transporter	narK, nasA, NRT, nrtP	AHCFPGON_00953	>AHCFPGON_00953 putative nitrate transporter NarT MKSPNFQLSLQTSNLIIGFMVWVILSS LMPYIKVDIPLTAGQISMVTAVPVIL GSVLRIPIGYWTNRFGARKLFFISFILL LLPVFYISVANSMMDLIIGGLFVGIGG AVFSVGVTSLPKYFPKESHGFVNGIY GVGNAGTAITSFLAPVIATSVGWRTT VQCYLVLLAAFALMNFLLGDRKEKK VNTPLMEQIKGVYKNEKLWFLCIFYF LTFGSFVAFTVYLPNFLVSHFGLEKV DAGMRTAGFIVLATIMRPIGGWLGD KFNPFKILIFVFIGLTLSGIILSFMPSM NVYTFGCLLVAFCAGIGNGTIFKLVP MYFSEQAGIVNGLVSALGGLGGFFPP LILTLLFQLTGHYAIGFMALSEVALA CLIITVWMYSQEKLLVMLKNH
Nitrite Reductase [1.7.7.4]	nasD	AHCFPGON_00946	>AHCFPGON_00946 Nitrite reductase [NAD(P)H] MKKRLVMIGNGMAGIRCMEEILKHD SDSYEITIFGDEPHPNYNRIMLSHVLQ GKTNIQDIIMNEYSWYEENEITLYTN ERVQSINREEKIIITEKKRTLTYDKLII ATGSSAFILPVEGSALSGVTGFRTIED TQFMIDTAKEKKKAVVIGGGLLGLE AARGLIDLGMDVHVVHLMPSLMEQ QLDTKAAALLREDLEAQGMKFLME KKTVKILGTDHVEGIQFEDGEVVDC DLIVMAVGIRPNTQIAKDAGLIVNRG IVVNDYMLTNDESIYAVGECAEHDGI AYGLVAPLYEQGAILAKHITNLQTD GYSGSIVGTQLKVAGCDLFSAGQIYE DDQTKAISIFNECKRSYKKILIRDNKV VGIVLYGDTADGTRLFSILKKEEDIQ EYTPASILHKAGEECELDVATMSAD DTICGCNGVTKGTIVHAILEQELKTF EEVKACTKAAGSCGKCRPLVEQVLS HTLGDAFDASAQSTGMCGCTPLSRD EVVAAIHEKGLKSPKEVRNVLGFVH EDGCSKCRPALNYYLRMAIPEEYED DKSSRFVNERMNGNIQHDGTFSVIPR MYGGVTTADDLMKIAEVAKKYDVP LVKITGASRIGLYGVKKQDLPNVWA ELNMASGYAYSKSLRNVKSCVGSRF CRFGTKDSLGLGMLLEQSLEMVDTP HKMKMGVTGCPRNCAEVLTKDFGV VCVENGYQLYIGGNGGTEVREADFV IIVPTEDDVLRIATAYMQYYRETGIY

			GERTAYWTERLGFDHIKEILQDANM VTKLNERFQKARGTYKEAWGQALE TKSLKAMYEVETVK
	nasE, nirD	AHCFPGON_00947	>AHCFPGON_00947 Assimilatory nitrite reductase [NAD(P)H] small subunit MIQTKEKIKVMRAEDLPIQIGKEVQM KGMSFALFRLSNGDIRAVENRCPHK KGPLAEGIVSGEFVFCPLHDWKISLL TGEVQKPDDGCIQTYEVEVIDGDIYI YM
Nitrite Reductase [1.7.7.4]	nasD	AHCFPGON_05731	>AHCFPGON_05731 Nitrite reductase [NAD(P)H] MCGCTPLSRDEVIAAIHEKGLKSPKE VRNVLGFAHEDGCSKCRPALNYYLR MTIPEEYEDDKSSRFVNERMNGNIQH DGTFSVIPRMYGGVTTADDLMKIAE FAKKYDVPLVKITGASRIGLYGVKK QDLPNVWAELNMTSGYAYSKSLRN VKSCVGSRFCRFGTKDSLGLGMLLE QSLEMVDTPHKIKMGVTGCPRNCAE VLTKDFGIVCVENGYQLYIGGNGGT EVREADFVMIVPTEDDVLRIATAYM QYYRETGIYGERTAYWTERLGFDHI KEILQDANMVTKLNERFQTARGTYK EAWGQALETKSLKAMYGVETVK
	nasE, nirD	AHCFPGON_05730	>AHCFPGON_05730 Assimilatory nitrite reductase [NAD(P)H] small subunit MLQSKEKFKIMRAEDLPFQIGKEVQ MKGISIILFRLLNGDIRAVENHCPHKN GPLAEGIVSGEFVFFPLHDWKISLVT GEVQKPDDGCIQTYEVEVIDGDIYIY M

nitrate reductase / nitrite oxidoreductase [EC:1.7.5.1 1.7.99.-]	narG, narZ, nxrA	AHCFPGON_00963	>AHCFPGON_00963 Respiratory nitrate reductase 1 alpha chain MKKKTSALMRRLKYFSPIDRYNDNH TQETYEDREWENVYRKRWQHDKVI RSTHGVNCTGSCSWNIYVKDGIVTW EGQELNYPTTGPDMPDFEPRGCPRG ASFSWYIYSPLRVKYPYVRGVLWNM WQEELQNNESPLEAWKSIVENREKA RTYKQARGKGGFIRVNWDEVLQLVS ASLLYTVMKYGPDRNVGFSPIPAMS MLSHAAGSRFMQLMGGPMLSFYDW YADLPPASPQIWGDQTDVPESSDWY NSGYIMTWGSNVPMTRTPDAHFLAE VRYKGTKVVSVSPDFAESTKFADDW ISVKQGTDGALAMAMGHVILQEFYV DNQVEYFTKYVKQYTDFPFFVTLKQ KGDQFVADRFLNASDIGRETKLGEW KPVLWNENTNDFATPHGTMGSRWD NEKKWNLRLEDEETGEKIDPRLSLLG MEDSVQTVQIPYFSDDGNKILERTIP VKKVMTEEGELFVTTVYDLTLANYG VNRGVGGQEPKDFNDDIPFTPAWQE KMTGVKRELIIQIAREFAQNAVDTNG RSMIIVGAGINHWFNSDTIYRAVLNL VLLVGAQGVNGGGWAHYVGQEKL RPAEGWQTIAMAKDWQGPPKLQNG TSFFYFVTDQWRYEDTPVGHLASPV EGNSRYQHHGDYNVLAARLGWLPS YPTFEKNGIELYKEAVAAGATTQEEI GKYVAQKLKEKELKFAIEDPDNKNN FPRNLFVWRANLISSSGKGHEYFLKH LLGTTNGLMNDDSDSLRPEEIKWHE EAPEGKLDLLINLDFRMAGTALYSDI VLPASTWYEKHDLSSTDMHPFVHPF NPAIGSPWEARSDWDIFTSLSKAVSD LAKKIDLEPMKEVVATPLLHDTPQEL AQPLGKIKDWSKGECEPIPGKTMPQI HVVERDYKTIYDKMTALGPNAGKQP IGTKGISWSAEKEYEQLKSKLGVVRT DSIAKGCPDIKEAINAAEAVLTLSSTT NGHMAVKAWEALEKQTDLKLRDLA EEREEECFTFEQITAQPKTVITSPAFT GSEKGGRRYSPFTTNVERLIPWRTIT GRQSFYLDHDMMKEFGETMATFKPI LQHKPFRKSRPEVEGKEITLNYLTPH NKWSIHSMYFDSLPMLTLFRGGPTV WMNKEDAAEAGVADNDWIECFNRN GVVVARAVVTHRIPRGMAFMHHAQ DRHINVPGTKLTSNRGGTHNSPTRIH

			VKPTHMIGGYGQLSYGFNYYGPTGN QRDLNVVIRKLKEVDWLED
	narY, narH, nxrB	AHCFPGON_00962	>AHCFPGON_00962 Respiratory nitrate reductase 2 beta chain MKIKAQVGMVMNLDKCIGCHTCSV TCKNTWTNRPGAEYMYFNNVETKP GIGYPKQWEDQEKYKGGWELKNGEI QLKSGSKMKRLMNIFHNPDQPTIDD YFEPWNYDYETLTNSPQRKHQPVAR PKSAITGEFIDKIEWGPNWEDDLAGG HITGLQDPNVKKMEEEIKTDFENVF MMYLPRICEHCMNPSCVSSCPSGAM YKREEDGIVLVDQNACRAWRFCVSS CPYKKVYFNWQTNKAEKCTMCFPRI EAGMPTICSETCVGRIRYIGVMLYDA DKVKEAASVEDEKDLYESQLTVFLD PNDPEIAAEAKKQGIPEEWIKAAQQS PIYKMIIDWKIALPLHPEYRTMPMVW YIPPLSPIMNMVEGKGSNWQAEEVFP AIDNMRIPIQYLANLLTAGDESHIRLT LKKMAVMRTYMRALQINKEPNEAV LKELGLAKQDVEDMYRLLAIAKYKD RFVIPTSHREQVADLYSEQGSCGLSF TGGPGSCMTIS
	narJ, narW	AHCFPGON_00961	>AHCFPGON_00961 Nitrate reductase-like protein NarX MRQSLQTAFSCSSFLLSYPELGWREA VTELQEEVETIKQEDVKASLTAFIKQ

			VLNKTNDQLIDSYVYTFDFGKKTNM YLTYMNTGEQRERGIELLELKQHYK KSGFEVTDKELPDYLPLLLEFFANAN EIDSEPIMSKYTENIQALHVQLKEAD SMYEPILAAVLLAIETWGVQTN
	narI, narV	AHCFPGON_00960	>AHCFPGON_00960 Nitrate reductase-like protein NarX MMDQFLWVLFPYIIFAIFIGGHIFRYN YDQFGWTSKSSELLEKKMLRVGSLL FHFGIMFVIGGHVMGILIPEAVYRSIG ISEHMYHVVAISFGLPAGVASIIGLIIL TYRRVTVKRIIATSTKGDYIALILLLI VMLAGLSSTFLNIDSKGFDYRTTIGP WFRSLFIFQPKVEYMMEVPIWFKIHI LAGMGLFAVWPFTRLVHVFSAPIKY VSRSYVIYRRRIPNELKK
nitric-oxide synthase, bacterial [EC:1.14.14.47]	nos	AHCFPGON_04505	>AHCFPGON_04505 Nitric oxide synthase oxygenase MSKTKQLIEEASNFITICYKELHKEQL IEERIKEIQIEIEKTGTYEHTFEELVHG SRMAWRNSNRCIGRLFWSKMHILDA REVNDEEGVYNALIHHIKYATNDGK VKPTITIFKQYQGEENNIRIYNHQLIR YAGYKTETGVIGDSHSATFTDFCQEL GWQGEGTNYDVLPLVFSIDGKAPIY KEIPREEVKEVPIEHPEYPISSLGVKW YGVPMISDMRLEIGGISYTAAPFNGW YMGTEIGARNLADHDRYNLLPAVAE MMDLDTSRNGTLWKDKALIELNIAV LHSFKKQGVSIVDHHTAAQQFQQFE KQEAACGRVVTGNWVWLIPPLSPAT THIYHKPYPNEILKPNFFHK

Table 46: *Bacillus cereus* genes involved in plant growth promoting features		
Enzyme name	**Gene name**	**FASTA protein sequence**
nitric-oxide synthase, bacterial [EC:1.14.14.47]	nos	>AHCFPGON_04505 Nitric oxide synthase oxygenase MSKTKQLIEEASNFITICYKELHKEQLIEERIKEIQIEIEKTGTYEHTFEE LVHGSRMAWRNSNRCIGRLFWSKMHILDAREVNDEEGVYNALIHHI KYATNDGKVKPTITIFKQYQGEENNIRIYNHQLIRYAGYKTETGVIGD SHSATFTDFCQELGWQGEGTNYDVLPLVFSIDGKAPIYKEIPREEVKE VPIEHPEYPISSLGVKWYGVPMISDMRLEIGGISYTAAPFNGWYMGT EIGARNLADHDRYNLLPAVAEMMDLDTSRNGTLWKDKALIELNIAV LHSFKKQGVSIVDHHTAAQQFQQFEKQEAACGRVVTGNWVWLIPPL SPATTHIYHKPYPNEILKPNFFHK
salicylate biosynthesis	pchA	>AHCFPGON_00781 Isochorismate synthase DhbC MNEHIAVKELSEKLLEDYKTESSFFFASPTRTILAEGEFTTVKHREIES

isochorismate synthase [EC:5.4.4.2]		FPELVQAKLSNAKQAGNPNPIVVGALPFDRRKEVQLIVPEYSRISERL QLDTTNQLETNENVTFEMTPVPDPEVYMNGVKQGIEKIQDGDLKKI VLSRSLDVKSSEKIDKQKLLRELAEHNKHGYTFAVNLPKDEKENSKT LIGASPELLVSRNGMQVISNPLAGSRPRSEDPVEDKRRAEELLSSPKD LHEHAVVVEAVAAALRPYCHTLHVPEKPSVIHSEAMWHLSTEVKGE LKDPNTSSLQLAIALHPTPAVCGTPMEKAREAIQHIEPFDREFFTGML GWSDLNGDGEWIVTIRCAEVQENTLRLYAGAGVVAESKPEDELAET SAKFQTMLKALGLRDSSLNEK
salicylate biosynthesis isochorismate synthase [EC:5.4.4.2]	pchA	>AHCFPGON_02841 Salicylate biosynthesis isochorismate synthase MIQTKQKGLQEVLSAAIKHATDEKILVSFVKQIDWMDPLLFYAAGK RIALENRCYFADPAQHVIFAGIGSVFTIANSSHKRFQAARDEWDKVK EKAFVQREKYEFGTGPLLFGGFSFDQEKEKTDLWKEFDDTTFSLPAF LLTVKNEKAWLTMNTFVSATDCAETLYNEIVSLEEKIFGESKCALEG SKLTVTSKVEVDPKGWMKAIEKVQDEMKQGNVQKVVLARELKVE MDHHIDSALVLEALRIGQPDCYVFSFDYKGACFLGATPERLIRKEDE KFTSMCLAGSTGHGQSIEESKRNSNALLHDEKNLAEHGYVVNMIRS VLNEHCEYVNIPESPGLLTTKNLIHLYTPVEAKGTASLLTMVEELHPT PALGGTPRLEAMKLIRDVELLDRGLYGAPIGWIDDEGNGEFAVALRC GLLNGEKASLFAGCGIVIDSVPQLEYEETSLKFRPMLGALEELMK
isochorismate pyruvate lyase [EC:4.2.99.21]	pchB	>AHCFPGON_00157 Protein AroA(G) MANHELDQLRKQVDEINLQLLHLLNKRGEIVQKIGEQKQVQGTKRF DPVREREVLDMIAEHNEGPFETSTVQHIFKTIFKASLELQEDDNRKAL LVSRKKKQENTIVDVKGELIGNGTQTFIMGPCAVESLEQVRQVGQA MKDQGLKLMRGGAFKPRTSPYDFQGLGVEGLQILRQVADEFDLAIIS EILNPNDVEMALDYVDVIQVGARNMQNFDLLRAVGKVNKPVLLKR GLAATIDEFINAAEYIIAQGNDQIILCERGIRTYERATRNTLDISAVPIL KKETHLPVIVDVTHSTGRRDLLLPTAKAALAIGADAVMAEVHPDPA VALSDSAQQMDIPEFHRFMDELKGFKNKLS
isochorismate pyruvate lyase [EC:4.2.99.21]	pchB	>AHCFPGON_03019 Protein AroA(G) MASQQLGRLRSEIDQLNLQILELLNERGRLVQEVGNLKEVQGVKRF DPVRERNMLDLIAENNNGPFETSTLQHIFKQIFQAGLELQEDDHRKA LLVSRKKKTEDTIVEINGEKIGDGNQHFIMGPCAVESYEQVRQVAEA MKEQGLKLMRGGAFKPRTSPYDFQGLGLEGLQILRQVADEYDLAVI SEILNPNDIEMSLDYVDVIQIGARNMQNFDLLRAAGAVNKPVLLKRG LSATIEEFINAAEYIMAKGNGNIILCERGIRTYERATRNTLDISAVPILK KETHLPVVVDVTHSTGRRDLLLPTAKAAMAIGADAIMAEVHPDPAV ALSDVAQQMNIPQFNDFMNELKSFGSKL
pyochelin biosynthetic protein PchC	pchC	>AHCFPGON_00778 Dimodular nonribosomal peptide synthase MPNSQKIRHSLSSAQSGMWFAQQLDPLNPIYNTGEYVEINGNIHQEIF ELAVRKVVIEAEALHVRFEEDEIGPWQVIEESQFHMHFIDVRKEENPE EAAKVWMKNDLSMPVDLKKDTLFTEALIQVENNRFFWYQRIHHIV MDGYGFSLLSQKVANEYTSLIEETNKNEKPFGSLTKVVQEDIEYRDS KKFQEDRTFWLEKFADEPEVVSLAERAPRTSNGFSRETAYLSSSSTK TLLEDINISLTSWPEFIVAVTSIYMHKLTGANDIVLGLPMMGRLGSVS IHTPSMVMNLVPLRITVTPNITLAELLQQVSKEIRDVRRHYKYRHEEL RRDLKLLGENQRLFGPLVNVMPFDYGLNFAGNRGITHNLSAGPVDD LSINVYKRFDQNKLMIHFDANPEVYNGAELALHKERFMSLFELVVN NYEKNESIGKINITLPEENHKVLLEWNETKEDDELLSLPISFEKQVQK NPNKLAITCDGVNLTYKELNARANELAHYLVEEGIRPNQFVALVFPR SIEMVVSMLAVLKAGAAYLPIDPEYPAERINYIVNDAKPVCIITHSSV SSKLVIENDMKKIVLDEEETKLALHTYSRMNIACKNDVSLLNPAYTI YTSGSTGNPKGVIVPMRGLSNFLMAMQQKFSLNENDHLLAVTTFAF DISALEIYLPLISGASLTIAQKEDIQEPSALTTLLQEERVTIMQATPTLW QALVTDYPEKLQGLNILVGGEALPEHLANKLKELGCSITNLYGPTET TIWSTFMNIDEGEKGIPPIGKPICNTEVYVLDAGLQPVPPGVIGELYIA GEGLASGYLGKPELTAERFIANPYGESGKRMYRTGDLVKWRSDGAL

		EYISRADHQIKIRGFRIELAEIETVLQRHENIQQAVVIVREDRPNDKRII AYIVAEEKEPINLSEIRSYVSESLANYMIPSAFVVLEELPLTPNGKVDR KKLPAPDFNRMDNERVARNPKEEILCDLFAEVLGVSRISIDDNFFEM GGHSLLASRLMARIRETLSVELGIGKLFESPTVAELAKQLNHAKSAR PAIQKASRPNEVPLSFAQRRLWFLNCLEGPSPTYNIPLVIRMNGILNR EALQGAFYDVVEKHETLRTIFPNVLGSSYQRILDMENLNLEMVITNT CKDELESVFSEAVRYSFNLDFEPAVRLQLFTVSENEHVLLILLHHIVG DGWSLQPLTRDFTAAYKARCQGDRVQLETLSVQYADYALWQQQLL GDETTPESLISTQLDFWKEELKGLPDQMELPTDFQRPIETSYRGETIHF HIDEGMHSRLVELARKNGVSLFMVLQAGLSALFTRLGAGTDIPIGSPI AGRNDDVLSDIVGLFVNTLVLRTNTSGDPSFKELLNRVKQVNLAAY ENQDVPFERLVEVLNPVRTRNSHPLFQVMLAFQNTPEAIFDAPDIEAS LEIQSVGSAKFDLTFEISESNGVDGTPNGLHGLLEFSTDLYKRETVQK LIERFILLLDDAATNPDQSIGRLEILTVAEKNTVLEKWNGGFQIAPEM TLPQLFEKQVHINPNSIAVVFEDKKLTYEELNRKANKIARFLIAKGIG PDQLVALAMPRSLNMVVSLLAVLKAGAGYLPLDPDYPADRISFMLH DAKPTCVLTNSEVEIECNEALKVLVDDVKVIAEVEKYSEENIDEVERI KPLSPSHIAYVIYTSGSTGRPKGVMIPHQNVVRLLGATDHWFQFDGN DVWTMFHSYAFDFSVWEIWGPLLYGGRLVVVPHTVSRSPKEFLQLL VKEKVTVLNQTPSAFYQLMQADRENEEIGQKLSLRYVVFGGEALEL SRLEDWYSRHPHNAPKLINMYGITETTVHVSYIELDETIVSLRANSLI GCSIPDLKVYVLDNYLQPVPPGVVGEMYVAGAGLARGYLGRAGLT AERFIADPFGKPGTRMYRTGDLARWRKDGTLDYIGRADHQIKIRGFR IELGEIEAVIMKHPKVEQVVVIVREDQPGDKRLVSYIVASNNEAIDTN EMRQFASGSLPDYMVPYDFVVVNELPLTPNGKLDRKALPAPEFIASS SSRGPRTPQEEMLCDLFTEVLSVPQIGIDDGFFDLGGHSLLAVQLMSR MKEALGVELNIGTLFAAPTVAGLAERLEMGNGQSALDVLLSLRASG DQLPLFCVHPAGGLSWCYAGLMKSLGTDYPIYGVQARGIAKNEELP KSLEEMAADYLKQVREVQPHGPYRLLGWSLGGNVVHAMAAQLQN EGEEVELLVMLDSYPGHFLPNTEAPTEEEALIALLALGGYDPDNMDG KPLTMESAVEILRKDGSALASLEEETILNLKETYVNSVGLLGKYVPK VYNGDILFFRSTVIPDWFDPISPNTWLNYLDGQIVQHDIDCRHKDLC QPGPLTEIGQVLAKYLQNKKGVSRV
pyochelin biosynthesis protein PchD	pchD	>AHCFPGON_00780 2,3-dihydroxybenzoate-AMP ligase MLVGYTEWPKEFADRYREAGCWLGETFGGVLRERAEKYGDRIAVV SGKKHITYSELNKKVDRLAAGLLNLGIKKEDRVVIQLPNIIEFFEICFA LFRIGALPVFALPSHRSSEISYFCEFGEASAYVISDKALGFDYRKLARE VKEKVPTLQHVIVVGEEEEFVNINDLYMDPVSLPEVQPSDVAFLQLS GGTTGLSKLIPRTHDDYIYSLRVSAEICNLNAESVYMAVLPVAHNYP MSSPGTFGTFYAGGKVVLATGGSPDEAFALIEKEKVTITALVPPLAMI WLDAASSRNADLSSLEVIQVGGAKFSAEVAKRIRPTFGCTLQQVFG MAEGLVNYTRLDDPEEFIIYTQGRPMSALDEVRVVDENDNDVQPGE VGSLLTRGPYTIRGYYKAEEHNARSFTKDGFYRTGDLVKVNEQGYII VEGRDKDQINRGGEKVAAEEVENHLLAHDSVHDVAIVSMPDDYLG ERTCAFVIARGQVPAVSELKMFLRERGIAAYKIPDRIEFIEAFPQTGV GKVSKKELRKVIAEKLITVKQ
dihydroaerugi noic acid synthetase	pchE	>AHCFPGON_00779 Isochorismatase MAIPSISVYKMPIESELPKNKVNWTPDPKRAVLLIHDMQEYFLDAYS DKESPKVELISNIKMIREKCKELGIPVVYTAQPGGQTLEQRGLLQDF WGDGIPAGPDKKKIVDELTPDEDDIFLTKWRYSAFKKTNLLEILNEQ GKDQLIICGIYAHIGCLLTACEAFMDGIEPFFVADAVADFSLEHHKQA LEYASNRCAVTTSTNLLLNDLQSVKDDESEGITIQEVHELVAQLLREP VESIDIDEDLLNRGLDSVRIMSLVEKWRREGKEITFAHLAERPTVAG WYSLLSSQTAQVL
tryptophan synthase	trpA	>AHCFPGON_02664 Tryptophan synthase alpha chain MGVEKIKAAFENGKKAFIPYVMGGDGGFEKLKERIRFLDEAGASIVE

[EC:4.2.1.20]		IGIPFSDPVADGPTIQRAGKRALDSGVTVKGIFQALIEVRKEVQIPFVL MTYLNPVLAFGKERFIENCIEAGVDGIIVPDLPYEEQDIIAPLLREANV ALIPLVTITSPIERIEKITSESKGFVYAVTVAGVTGVRQNFKEEIHSYLE KVKSHVNLPVVAGFGISTKEHVEEMVTICDGVVVGSKIIELLENEKQ EEICELIYATKQKEEA
	trpB	>AHCFPGON_02665 Tryptophan synthase beta chain MNYAYPDEKGHYGIYGGRYVPETLMQSVLELEEAYKEAMQDEAFQ KELNHYLKTYVGRETPLYFAENLTKYCGGAKIYLKREDLNHTGAHK INNTIGQALLAVRMGKKKVVAETGAGQHGVATATVCALLGLECVIF MGEEDVRRQKLNVFRMELLGAKVESVAAGSGTLKDAVNEALRYW VSHVHDTHYIMGSVLGPHPFPQIVRDFQSVIGNETKKQYEELEGKLP EAVVACIGGGSNAMGMFYPFVHDEEVALYGVEAAGKGVHTEKHA ATLTKGSVGVLHGSMMYLLQNEEGQIQEAHSISAGLDYPGVGPEHS LLKDIGRVSYQSITDEEALEAFQLLTKKEGIIPALESSHAVAYALKLA PKMKEDEGLVICLSGRGDKDVESIKRYMEEV
indole-3-glycerol phosphate synthase [EC:4.1.1.48]	trpC	>AHCFPGON_02667 Indole-3-glycerol phosphate synthase MGTILDKIVEQKKKEVAELYEIYTPVKAKRKAHSLVEALQQFTVIAE VKRASPSKGDINLHVDVRKQVGTYEKCGAGAVSVLTDGQFFKGSFH DLQTAREESNIPLLCKDFIIDKIQIDRAYEAGADIILLIVAALTKEKLKE LYSYVLEKGLEAIVEVHDEQELETAIVLNPHVIGINNRNLKTFEVDLS QTEKLGKRLNEEKLLWISESGIHSKEDIIRVKRAGAKGVLVGEALMT SSSISSFFEDCKVNI
anthranilate phosphoribosyltransferase [EC:2.4.2.18]	trpD	>AHCFPGON_02668 Anthranilate phosphoribosyltransferase 2 MNNYLRKLVEGQHLTEEEMYKAGLLLLSENILESEIAAFLVLLKAKG ETAEEIYGLVRALREKALPFSNHIQGAMDNCGTGGDGAQTFNISTTS AFVLAGAGVKVAKHGNRAVSSKTGSADLLEELGVNISSTPNEIDYLL EHVGIAFLFAPAMHPALRRIMKIRKELNVPTIFNLIGPLTNPVNLETQF VGIYKRDMLLPVAQVLQKLGRKQALVVNGSGFLDEASLQGENHVV LLKDNEIVEMSIDPEKYGFSRVKNEEIRGGNSKENAKITLEVLSGEKS VYRDTVLLNAGLALFANGKTETIEEGIKLAAHSIDSGKALTKLNLLIA ASNEKLERVN
indole-3-glycerol phosphate synthase [EC:4.1.1.48]	trpC	>>AHCFPGON_02667 Indole-3-glycerol phosphate synthase MGTILDKIVEQKKKEVAELYEIYTPVKAKRKAHSLVEALQQFTVIAE VKRASPSKGDINLHVDVRKQVGTYEKCGAGAVSVLTDGQFFKGSFH DLQTAREESNIPLLCKDFIIDKIQIDRAYEAGADIILLIVAALTKEKLKE LYSYVLEKGLEAIVEVHDEQELETAIVLNPHVIGINNRNLKTFEVDLS QTEKLGKRLNEEKLLWISESGIHSKEDIIRVKRAGAKGVLVGEALMT SSSISSFFEDCKVNI
anthranilate phosphoribosyltransferase [EC:2.4.2.18]	trpD	>AHCFPGON_02668 Anthranilate phosphoribosyltransferase 2 MNNYLRKLVEGQHLTEEEMYKAGLLLLSENILESEIAAFLVLLKAKG ETAEEIYGLVRALREKALPFSNHIQGAMDNCGTGGDGAQTFNISTTS AFVLAGAGVKVAKHGNRAVSSKTGSADLLEELGVNISSTPNEIDYLL EHVGIAFLFAPAMHPALRRIMKIRKELNVPTIFNLIGPLTNPVNLETQF VGIYKRDMLLPVAQVLQKLGRKQALVVNGSGFLDEASLQGENHVV LLKDNEIVEMSIDPEKYGFSRVKNEEIRGGNSKENAKITLEVLSGEKS VYRDTVLLNAGLALFANGKTETIEEGIKLAAHSIDSGKALTKLNLLIA ASNEKLERVN

anthranilate synthase component I [EC:4.1.3.27]	trpE	>AHCFPGON_02670 Anthranilate synthase component 1 MMTKEEFIKQKRERKTFLVITEEEGDSITPISLYRRMKGKKKFLLESS QLHQDKGRYSYLGCNPYGEVKSVGTEVERTIFGRAEKLQGNVLQVL EEVIAPSQVDSPFPFCGGAVGYIGYDVIRQYENIGADLHDPLNIPEVH LLLYREFIVYDHLRQKLSFVYVCREDDSTDYEEVYERLRVYKEEVLQ GEEAEVNAIQSPLSFTSSITEKEFCEMVEIAKEYIRAGDIFQVVLSQRL QSECIGDPFALYRKLRIANPSPYMFYIDFQDYVVLGSSPESLLSVRED KVMTNPIAGTRPRGKTKREDEEIAKELLGNEKERAEHMMLVDLGRN DIGRVSEIGSVTIDKYMKVEKYSHVMHIVSEVYGTLRKQMGGFDAL AYCLPAGTVSGAPKIRAMEIINELENEKRNVYAGAVGYVSFSGNLD MALAIRTMVVKDEKAYVQAGAGVVYDSDPVAEYEETLNKARALLE VMK
phosphoribosylanthranilate isomerase [EC:5.3.1.24]	trpF	>AHCFPGON_02666 N-(5'-phosphoribosyl)anthranilate isomerase MKVKICGITDMETAKSACEYGADALGFVFAESKRKITPKRAKEIIQEL PANVLKIGVFVNESVEVIQKIADECGLTHVQLHGDEDNYQIRRLNIPS IKSLGVTSESDMKNAQGYETDYILFDSPKEKFHGGNGKTFSWELLGH MPKELRKKTILAGGLNALNIEEAIRTVRPYMVDVSSGVETEGKKDVE KIKQFIIKAKECSK
indoleacetamide hydrolase [EC:3.5.1.-]	gatA, iaaH	>AHCFPGON_03992 Glutamyl-tRNA(Gln) amidotransferase subunit A MKKWVKVTLSITGGIVLLACAGGYYVYKNYFPKESERIVYDKERVL QPIHNQLKGINIENVKIKEKEVVNATVDELQKMIDDGKLSYEELTSIY LFRIQEHDQNGITLNSVTEINPNAMEEARKLDQERGRNKNSNLYGIP VVVKDNVQTEKVMPTSAGTYVLKDWIADQDATIVKQLKEEGAFVL GKANMSEWANYLSFTMPSGYSGKKGQNLNPYGPITFDTSGSSSGSA TVVAADFAPLAIGTETTGSIVAPAAQQSVVGLRPSLGMVSRTGIIPLV ETLDTAGPMARTVKDAATLFNAMIGYDEKDVMTEKMKDKERIDYT KDLSIDGLKGKKIGLLFSVDQQDENRKAVAEKIRKDLQDAGAILTDN IQLSAEGVDNLQTLEYEFKHNVNDYLSQQKNVPVKSLEEIIAFNKKD SKRRIKYGQTLIEGSEKSVITKEEFENVVQTSQENARKELDRYLVEKG LDALVMINNDEVLLSAVAGYPELAVPAGYDKNGEPIGVVFVGKQFG EKELFNIGYAYEQQSKNRKLPSL
indoleacetamide hydrolase [EC:3.5.1.-]	gatA, iaaH	>AHCFPGON_04124 Glutamyl-tRNA(Gln) amidotransferase subunit A MSLFDHSVSELHKKLNSKEISVTDLVEESYKRIADVEDNVKAFLTLD EENARAKAKELDAKIGAEDNGLLFGMPIGVKDNIVTNGLRTTCASKI LANFDPIYDATVVQKLKAADTITIGKLNMDEFAMGSSNENSGFYAT KNPWNLDYVPGGSSGGSAAAVAAGEVLFSLGSDTGGSIRQPAAYCG VVGLKPTYGRVSRYGLVAFASSLDQIGPITRTVEDNAYLLQAISGIDR MDATSANVEVGNYLAGLTGDVKGLRIAVPKEYLGEGVGEEARESV LAALKVLEGMGATWEEVSLPHSKYALATYYLLSSSEASANLSRFDG VRYGVRSDNVNNLLDLYKNTRSEGFGDEVKRRIMLGTFALSSGYYD AYYKKAQQVRTLIKNDFENVFANYDVIIGPTTPTPAFKVGEKVDDP MTMYANDILTIPVNLAGVPAISVPCGFGANNMPLGLQIIGKHFDEATI YRVAHAFEQATDYHTKKASL
indolepyruvate decarboxylase [EC:4.1.1.74]	ipdC	>AHCFPGON_00678 Indole-3-pyruvate decarboxylase MKKQYTVSTYLLDRLHELGIEHIFGVPGDYNLAFLDDVVAHKNLKW IGNCNELNAAYAADGYARIKGIAALITTFGVGELSAINGIAGSYAENV PVIKITGTPPTKVMENGAIVHHTLGDGKFDHFSNMYREITIAQTNVTP EHAAEEIDRVLRACWNEKRPGHINLPIDVYNKPINKPTEPIINKPILSN KEALNKMLLHAISKINSAKKPVILADFEVDRFHAKESLHQFVEKTGF PIATFSMGKGIFPEKHPQFIGVYTGDVSSPYLRKRIDESDCIISIGVKLT DTITGGFTQGFTKEQVIEIHPYTVKIIDKKYGPVVMQDVLQHLSDSIE HRNKDTLDVKPFILESSPFTEEFNPKAQMVTQKRFWQQMYHFLQEN DVLIVEQGTPFFGSAAIPLPNNTAYVGQPLWGSIGYTLPALLGTQLAN LSRRNILIIGDGSFQVTAQELSTILRQNLKPIIFLINNNGYTVERAIHGQ NQLYNDIQMWDYNKLSMVFGSEEKSLTFKVENEAELAEVLTNITFN KNQLIFIEVIMSQSDQPELLAKLGKRFGQQNS

arginine decarboxylase [EC:4.1.1.19]	speA	>AHCFPGON_01260 Arginine decarboxylase MSQYETPLFTALVEHSKRNPIQFHIPGHKKGQGMDPTFREFIGHNAL AIDLINIAPLDDLHHPKGMIKEAQDLAAAAFGADHTFFSIQGTSGAIM TMVMSVCGPGDKILVPRNVHKSVMSAIIFSGAKPIFMHPEIDPKLGIS HGITIQSVKKALEEHSDAKGLLVINPTYFGFAADLEQIVQLAHSYDIP VLVDEAHGVHIHFHDELPMSAMQAGADMAATSVHKLGGSLTQSSIL NVKEGLVNVKHVQSIISMLTTTSTSYILLASLDVARKRLATEGTALIE QTIQLAEHVRDAINSIEHLYCPGKEMLGTDATFNYDPTKIIVSVKDLG ITGHQAEVWLREQYNIEVELSDLYNILCLITLGDTESDTNTLIAALHD LAATFRNRADKGVQIQVEIPEIPVLALSPRDAFYSETEVIPFENAAGRI IADFVMVYPPGIPIFTPGEIITQENLEYIRKNLEAGLPVQGPEDMTLQT LRVIKEYKPIS
arginine decarboxylase [EC:4.1.1.19]	speA	>AHCFPGON_05447 Arginine decarboxylase MNQNRMPLYEALIEFKERGPLSFHVPGHKNGLNFPQEAIREFKDILSI DVTELAGLDDLHSPFECIDEAQQLLAEVYNTKRSYFLINGSTVGNLA MILSCCGEHDIVLVQRNCHKSIINALKLAGANPIFLDPWIDEAYNVPV GVRNEIIKKAIEKYPNAKALILTHPNYYGMGMDLEASIAFAHAHKIP VLVDEAHGAHLCLGEPFPKSALTYGADIVVHSAHKTLPAMTMGSYL HINSHLVDEEKVTTYLSMLQSSSPSYPIMASLDIARFTMARIKEEGHS EIVEFLRKFKEQLRSISQIAILEYPLQDELKVTVQTRCQLSGYELQSVF EKVGIYTEMADPYNVLFILPLQVNGGYMKVIEMIRVALQHYEVKDK RESIRYTYKGEFSLLPYTYKQLDGYETKIVSIEDAVGMIAAEMVIPYP PGIPLIMYGERITSEHKEQIMYLERAGARFQCNTKYMKVYDIESRF
agmatinase [EC:3.5.3.11]	speB	>AHCFPGON_04579 Agmatinase MRFDEAYSGKVFIKSHPSFEESKVVIYGMPMDWTVSYRPGSRFGPAR IREVSIGLEEYSPYLDRELEEVKYFDAGDIPLPFGNAQRSLDMIEEYVS KLLDADKFPLGLGGEHLVSWPIFKAMAKKYPDLAIIHMDAHTDLRE SYEGEPLSHSTPIRKVCDLIGPENVYSFGIRSGMKEEFEWAKEVGMN LYKFDVLEPLKEVLPKLAGRPVYVTIDIDVLDPAHAPGTGTLEAGGIT SKELLDSIVAIANSNINVVGADLVEVAPVYDHSDQTPVAASKFVREM LLGWVK
S-adenosylmethionine decarboxylase [EC:4.1.1.50]	speH, speD, AMD1	>AHCFPGON_03112 S-adenosylmethionine decarboxylase proenzyme MDTMDTMGRHVIAELWDCDFDKLNDMPYIEQLFVDAALKAGAEV REVAFHKFAPQGVSGVVIISESHLTIHSFPEHGYASIDVYTCGDRIDPN VAAEYIAEGLNAKTRESIELPRGTGSFEIKQRETKAL
spermidine synthase [EC:2.5.1.16]	speE, SRM	>AHCFPGON_04578 Polyamine aminopropyltransferase MELWFTEKQTKHFGITARINRTLHTEQTEFQKLDMVETEEFGNMLIL DGMVMTTEKDEFVYHEMVAHVPLFTHPNPENVLVVGGGDGGVIRE VLKHPSVKKATLVEIDGKVIEYSKQYLPSIAGALDNERVEVKVGDGF LHIAESENEYDVIMVDSTEPVGPAVNLFTKGFYAGISKALKEDGIFVA QTDNPWFTPELITTVFKDVKEIFPITRLYTANIPTYPSGLWTFTIGSKK HDPLQVSEERFHEIETKYYTKELHNAAFALPKFVGDLIK
acetolactate decarboxylase [EC:4.1.1.5]	alsD, budA, aldC	>AHCFPGON_03760 Alpha-acetolactate decarboxylase MTVAQLIDIDAKKTKTSNEVYQTSTMLALLDGIYDGVISFEDLKKHG DFGIGTFDQLDGEMIAFDNGFYHLRSDGSAEKVEPEETTPFATVTFFE KEMSYTVERSMNREEVEALLHELMPSKNLFYAIRMDGTFREVRTRT VPRQEKPYTPLVEVTKSQPIFSFENTEGTLAGFWTPDYAQGIGVAGF HLHYIDDERSGGGHVFDYVVENCTIQICQKAHMHLALPETADFMAA ELSRENLEDNIATAEGAE
acetolactate synthase, catabolic	alsS	>AHCFPGON_03761 Acetolactate synthase MSTGVKANDVKTKTKGADLVVDCLIKQGVTHVFGIPGAKIDSVFDV LQERGPELIVCRHEQNAAFMAAAIGRLTGKPGVCLVTSGPGTSNLAT GLVTANAESDPVVALAGAVPRTDRLKRTHQSMDNAALFEPITKYSV EVEHPDNVPEALSNAFRSATSTNPGATLVSLPQDVMTAETTVESIGA LSKPQLGIAPTHDITYVVEKIKSAKLPVILLGMRASTNEVTKAVRKLI

		ADTELPVVETYQAAGAISRELEDHFFGRVGLFRNQPGDILLEEADLVI SIGYDPIEYDPKFWNKLGDRTIIHLDDHQADIDHDYQPERELIGDIAL TVNSIAEKLPKLVLSTKSEAVLERLRAKLSEQAEVPNRASEGVTHPL QVIRTLRSLISDDTTVTCDIGSHSIWMARCFRSYEPRRLLFSNGMQTL GVALPWAIAATLVEPGKKVVSVSGDGGFLFSAMELETAVRLNSPIVH LVWRDGTYDMVAFQQMMKYGRTSATEFGDVDLVKYAESFGALGL RVNTPDELEGVLKEALAADGPVIIDIPIDYRDNIKLSEKLLPNQLN
acetolactate synthase [EC:2.2.1.6]	ilvH, ilvN	>AHCFPGON_02519 Acetolactate synthase small subunit MKRIVTATVRNQSGVLNRITGVMTRRHFNIESISVGHTESSDISRMTI VVHVESEQQVEQLIKQLHKQIDVLKVSDITEEAMIARELALIKVATSV ARAELYSLIEPFRAAVIDVGKDSIVVQVTGTQDKVEALIELLRPYGLK EIARTGVTAFTRSMKKQDKQVMLIQ >AHCFPGON_02520 Acetolactate synthase large subunit MSSKTEEKLATGAQLLLEALEKEGVEVIFGYPGGAVLPLYDALYDC EIPHILTRHEQGAIHAAEGYARITGHPGVVIATSGPGATNVITGLADA MIDSLPLVVFTGQVATTLIGSDAFQEADIMGLTMPVTKHNYQVRKA SDLPRIIKEAFHIAKTGRPGPVVIDLPKDMVVEKGEQCSNVQMDLPG YNPNYEPNLLQINKLLKVIETAKKPLILAGAGILHAKASKELTNFARK YEIPVVHTLLGLGGFPPDDELFLGMGGMHGSYTANMALYECDLLINI GARFDDRLTGNLAYFAKGATVAHIDIDPAEIGKNVPTEIPIVASAKRA LEVLLEPEGGKENHHEWITLLKGRKEQYPFSYKRNSESIKPQYAIDM LYEITKGEAIVTTDVGQHQMWAAQYYPLKNPDKWVTSGGLGTMGF GFPAAIGAQIAKPEELVIAIVGDAGFQMTLQELSVLKEHALPVKVFIL NNEALGMVRQWQDEFYNQRYSHSLLPCQPDFVALANAYGIKGIRID DPLLAKKQIQHAIELQEPVVIDCRVLQSEKVMPMVAPGKGVHQMEG VEKG
acetolactate synthase [EC:2.2.1.6]	ilvH, ilvN	>AHCFPGON_04053 Acetolactate synthase small subunit MSHTFSLVIHNEPSVLLRISGIFARRGYYISSLHLNERDTSGVSEMKLT AVCTENEATLLVSQLKKLIDVLQVNKL
	ilvB, ilvG, ilvI	>AHCFPGON_04054 Acetolactate synthase large subunit MKQQYTAYEKLQCEEMTGAGHVIQGLKKLGVTTVFGYPGGAILPV YDALYESGLKHVLTRHEQAAIHAAEGYARASGKVGVAFATSGPGAT NLVTGLADAYMDSIPLVVITGQVATPLIGKDGFQEADVVGITVPVTK HNYQVRDVNHVSRIVQEAFYIAKSGRPGPVLIDIPKDVQNAKVTSFF NEEVDIPGYKPELVPDSMKLREVAKAISKSKRPLLYIGGGVIHSGGSD ELFEFARENRIPVVSTLMGLGAYPPGDPLFLGMLGMHGTYAANMAV TECDLLLALGVRFDDRVTGKLELFSPHSKKVHIDIDPSEFHKNVTVE HPIVGDVKKALHMLLHMSIYTQTDEWLQKVKAWKEEYPLSYKQKE SELKPQHVINLVSELTNGEAIVTTEVGQHQMWAAHFYKARKPRTFL TSGGLGTMGFGFPAAIGAQLAKEEELVVCIAGDASFQMNIQELQTIA ENNIPVKVFIINNRFLGMVRQWQEMFYENRLSESKIGSPDFVKVAEA YGVKGLRATNSTEAKQVVLEAFAHEGPVVVDFCVEEGENVFPMVLP NKGNNEMIMKRWEE
hydrogen cyanide synthase [EC:1.4.99.5]	hcnA	>AHCFPGON_00274 hypothetical protein MSRITHHPILGTLQSSKRITFQFNGHQYKAYEHETIAAALLANGIRTV RVHEDSGTPQGIYCNIGHCSECRMTVNNQTNVRACLTVVEENMVVE SGKQHPNIVREMVKKR
	hcnB	>AHCFPGON_00273 Hydrogen cyanide synthase subunit HcnB MSDVIIIGAGPAGLSASISCARFGLKVLVIDEFMKPGGRLLGQLHQEP TGEWWNGIKESKRLHEEAESLSVHIRCGVSVYNLDRDENNWFVHTN IGTLEAPFVLLATGAAEYSIPLPGWTLPGVMSIGAAQVMTNVHRVQV GKKGIIIGANILSFAILSELQLAGITVDHIVLPEKSELSQKAGEPEEVLN SLLNAAHLAPSAILRIGSHFMKYDWIRKAGLTFYPNSGMKINGTPLH LRKAALEIIGTDQVEGVRVANIDSKGNVINGSEKIYEADFVCIAGGLY PLAELAAVAGCPFHYISELGGHVPLHSETMETPLPGLFVAGNITGIES GKIAMAQGTVAGLSIAKYASKKRDIVDQQLYHAIQNVHSVRQKAAI

		QFNPMVDIGRRKMNDLWHKFQTNDKDFYKQQEII
	hcnC	>AHCFPGON_00277 Hydrogen cyanide synthase subunit HcnC MRHCDVLIIGGGIIGCSIAYYTSKYGRDVTIIEKGEFVSGTSSRCDGNI LAIDKDPGFDSQMSLVSQKLVTDLSEELEHSFEYRAPGSILVCESDEE MEAAQQWVNRQQEAGLPFRMLDRQDIREESPFFADDLLGGLECATD STVNPYLLAFSLLSEAQKFGAKAFKQTEVKSMEIETDGSFVVETTNG TFTAQQVVNAAGVWAPKIGQMLNINIPIEPRKGHIIVASRQQHVGCR KVMEFGYLISKFGGKRKVDALTEKYGVALVFEPTESQNFLIGSSREF VGFHTRINNEVIKCIANRAIRFYPKMADMMVIRSYAGLRPWTEDHLP IISRVEHIPNYFIAAGHEGDGISLAAVTGKVIEELLNEKETIIPIEPLRLS RFTERVLNK
flagellar basal-body rod protein FlgC	flgC	>AHCFPGON_04666 Flagellar basal-body rod protein FlgC MFQAINASGSGLTTARKWMEVTSNNIVNANTTAAPGADLYERRSVV LESNNSFASMLDGAPTNGVKIKSIEADKTENLVYDPTHPHANEEGYV RYPNIDVTAEMTNVMVAQKMYEANTSVLNANKKMLDKDLEIGRG
flagellar basal-body rod modification protein FlgD	flgD	>AHCFPGON_04674 hypothetical protein MPTVGLNTTSTNHIPLQAGAQTKNASVNGVQSPVQQTNGVSASNQK TPGIMDKDDFLKLFLASFQHQDPFNAMDMNQMMNQTAQLSLMEQV QNMTKAVDKLQSTMYTTALDGGMKFLGKYVRGINNKGEQVTGQV ETVRLAENNDVQLIVDNQVVSLRFVERVSDKPIAETNPEDEKKDDIE KNEEVKQN
flagellar hook protein FlgE	flgE	>AHCFPGON_04675 Flagellar hook protein FlgE MIKALYTSITGMNAAQNALSVTSNNIANAQTVGYKKQKAIFDDLLY NNTVGSRGDGAYAGTNPKSIGNGVKFSGTSTDFSDGSITLTSDKMET AIEGNGLFLVGDRNSGNVEYTRKGSFGVSKDNYVTNTSGQYVLGYG VKTGTQEIDFSSRPSPIHIPMGSAVGGIQTDKATIGGNLPRNQNALSH EFTVFDEEGNSLTLRVNIKQKTTKETVDGKEVEKPVPGEYTYTVSVR NDSKNEKEFKPVEGMTGEKNLKFDTLGNLKETDEAVQKNPVTGEIT KGGTVKIPFGKGLTLDLSGLTNYPTGKTISTTEVTGRPAAIANDYSIS DGGFVMMRYSDGSMKVVGQLAVATFPNSGGLMKTGNGNYIATPSA GIPGIGVAGENGAGNVRGSAKESSNVDLSVEFVDLMLYQRGFQGNA KVIKVSDEVLNEVVNLIR
flagellar hook-associated protein 1 FlgK	flgK	>AHCPGON_04660 hypothetical protein MRLSDYNTPLSGMLAAQMGLQTTKQNLSNIHTPGYVRQMVNYGSA GGSKGYAPEQRIGYGVQTLGVDRITDEVKTKQYNDQMSQFSYYAY MNSTLSRVESMVGTTGKNSLSSLMDGFFNAFREVAKNPEQSNYYDT LIAETGKFTSQVSRLAKNLDTVEAQTTEDIEAHVNEFNRLAASLAEA NKKIGQAGTQVPNQLLDERDRIMTEMSKYADIEVSYEATNPNIASVR MNGVLTVNGQDTYPLQLQKDKKPMSVQISGTDIPLSGGTILSAIDTK AKITNYKDNLNEFVNSLKKQVNNTMKKELFVGEDAKKLELNPDFIK DISKMKISAETANNLAAITDKGYKDGLTYKQALDQFLVGVASDKSS VNAYQNIHKDLLEGIQQEKMSIEGVNMEEEMVNLMAFQKYFVANS KAITTMNEVFDSLFSIIR
flagellar hook-associated protein 3 FlgL	flgL	>AHCFPGON_04661 Flagellar hook-associated protein 3 MRVSTFQNANWAKNQLMDLNVQQQYHRNQVTSGKKNLLMSEDPL AASKSFAIQHSLANMEQMQKDIADSKNVLTQTENTLQGVLKSLTRA DQLTVQALNGTNSEKELQAIGVEIDQILKQVVYLANTKEQGRYIFGG DSAKNPPFTEDGTYQGGKNDVNWKLNDGYEFKAFRNGGALLSPVIK TLKQMSEAMKNGDQKALKPLLEGNKQNLDGIINRTTEVGSTMNTM ETFKTILNEQNVALQENRKEIEDVDLAVAISDLAYINATYEATLKAVS TMSKTSILDYM
flagellar biosynthesis protein FlhA	flhA	>AHCFPGON_04694 Flagellar biosynthesis protein FlhA MFKIESARTYFSIFLAASFVVALLIPLPPFILDIIIVFLLSMSVLIYMRAT SINEWDELKSFPTMLLLIGIFRVSINVSTTRAILTDGNAGHVIEEFGQF VIGGNLLIGIVIFTVLIIFQFIVANGASRTAEVAARFTLDSLPGKQMSID ADLNQRIISEKDAQAKRKKLNMETEFYGAMDGAGKFIKGDVIFGIVI

		LFVNIIFGLIVGMMQQGMSFADAALHYTQLTVGDGIVNQIGSLMLAI STGIIVTRVFDGSPDTVTEGIFKELLAHEVVVYALGGLFIAMGIFTPLP FLPFALVGGTIIFLGIRNKNRIKKEKEDELQKEIEMIQGEDEQLQQVED SFGVFTDKYPIIVELGLDLAALVKQKINGETARDKVVLMRKSIITDLG INVPGINFKDNTSFRPRGRYIIRIKGAKAAEGVLKSGYLLALKTPNVM ADLDAEPAKDPIFGEDGYWILEHMVQDAQMKGYQVLEPLSILITHLD VVVRRNLHELIQRQHVKDLINSLENDNGVLLEEIKKKEIDLSLVQNVI KQLLKEGISIRDLPTIIEGIIDGKEIYQNHVDGVTSFVRECISKVICENA KNPDGKIYAALFSDSIELDADVVNNSYQGYLLNWDLDLETRVVEQV QRVFKQARLMGREPVLLTRRKDFRFAIVRLLERYQVEAQVLCISELA PEIVVDQIAYIE
flagellar biosynthetic protein FlhB	flhB	>AHCFPGON_04693 Flagellar biosynthetic protein FlhB MAKDNKTEKATPQKRKKSREEGNIARSKDLNNLFSILVLAVVVYFF GDWLGFEIANSVSVLFNQIGKNTDSTEYFYLMGILLLKVSAPILILVY AFHLFNYMIQVGFLFSSKVIKPKASRINPKNYFTRLFSRKSLVDILKSL FYMGLIGYVAYVLFKKNLEKIVSMIGFNWTASLTEIIRQIKFIFLAILII LIVLSIIDFIYQKWEYEQDIKMKKEEVKQEHKDNEGDPQVKGKRKNF MHAILQGTIAKKMDGATFIVNNPTHISVVLRYNKHVDAAPIVVAKG EDELALYIRTLAREQEIPMVENRPLARSLYYQVEEDETIPEDLYVAVI EVMRYLIQTNELEV
flagellin	hag, fliC	>AHCFPGON_04680 Flagellin MRIGTNVLNMNARQSLYENEKRMNVAMEHLATGKKLNHASDNPA NIAIVTRMHARASGMRVAIRNNKDAISMLRTAEAALQTVTNILQHM RDLAVQSSNGTNSNKNRNSLHKEFQSLTEEIGYIVETTEFNDLSVFDG QNRPITLDDNGHTINMMKHIPPSPTQHDIKISTEQEARAAILKIEEALQ SVSLHRADLGAMINRLQFNIENLNNQSMALTDAASRIEDAEMAQEM SDFLKFKLLTEVAICMVSQANQIPQMVSKLLQS
flagellin	hag, fliC	>AHCFPGON_04681 Flagellin MRINTNINSMRTQEYMRQNQDKMNTSMNRLSSGKSINSAADDAAG LAIATRMRAKEGGLNVGARNTQDAMSALRTTDSALNSISNILLRMR DLATQSANGTNDGKDKDSLNLEFKELQEEINHIAGKTNFNGKNLLA AAGTDKNISIQLSDVASDNLTITAVDATTGATGLGLTKTIGAPAAPVI PAPPAPAADNDAAGAIVQLDAAIQKVADMRATFGSQLNRLDHNLN NVNSQATNMAASASQIEDADMAKEMSEMTKFKILNEAGISMLSQAN QTPQMVSKLLQ
flagellin	hag, fliC	>AHCFPGON_04682 Flagellin MRINTNINSMRTQEYMRQNQDKMNTSMNRLSSGKSINSAADDAAG LAIATRMRAKEGGLNVGARNTQDAMSALRTTDSALNSISNILLRMR DLATQSANGTNDGKDQDSLNLEFKELQGEIDHIAGKTNFNGKSLLA AKGTDIDIQLSDISGDKLTIASVDATTGADGLNLTKTIASTGKGGDAA ESIKELDKAIQSVADMRATFGSQLNRLDHNLNNVNSQATNMAASAS QIEDADMAKEMSNMTKFKILNEAGISMLSQANQTPQMVSKLLQ
flagellin	hag, fliC	>AHCFPGON_04683 Flagellin MRINTNINSMRTQEYMRQNQDKMNTSMNRLSSGKSINSAADDAAG LAIATRMRAKEGGLNVGARNTQDAMSALRTTDSALNSISNILLRMR DIATQSANGTNETKDQASLDLEFQELHKEIDHIAEKTNFNGKNLLAA TGADIDIQLSDVSGDKLTIASINAKADTLLTATGTNVKTTADASTAIT NLDKAIQTVADNRATFGSQLNRLDHNLNNVNSQSTNMAAAASQIED ADMAKEMSNMTKFKILNEAGISMLSQANQTPQMVSKLLQ
flagellin	hag, fliC	>AHCFPGON_04684 Flagellin MRINTNINSMRTQEYMRQNQDKMNTAMNRLSSGKSINSAADDAAG LAIATRMRAKEGGLNVGARNTQDAMSALRTTDSALNSISNILLRMR DIATQSANGTNDTKDQDSLDLEFQELKGEITHIAEKTNFNGKTLLAG VAAANNIDVQLSDVSGDKLTITAIDATAATLKITGDVKSTKNASDSIT ALDAAIQTVADNRATFGSQLNRLDHNLNNVNSQSTNMAAAASQIED ADMAKEMSNMTKFKILNEAGISMLSQANQTPQMVSKLLQ

flagellar hook-associated protein 2	fliD	>AHCFPGON_04662 B-type flagellar hook-associated protein 2 MAGTISNYGDRQQIWNLGNNIIDTKKLVDLELQALEMKKSPYTTQK QTLTNENKVYASMKKEFANFVQVFKDLNTFKGDEKKTTLSKDGFM TAQADAAAIPGTYTITVERVAERHQITTAPLTPPKTPEGTEQKFSLDL KLGVDDVFQINGKEVKISKDMTYKDLVNKINNGNYGASVYTLGDQ LFFTSTTAGEAGELKLTDGANGFLQNIGLVTSAKNPDGTNVVAHQV TGAINAEYTINGIKGTSKTNKIDTIPGLTINLEKVTTEPIKLTIEDSDIKN SIDLIKKMKDEYNNAVKSLDLFSGENGVMQGNNVSFAISNAMTSIFK FSQDDKYLFSFGIQIDKTGNMTLDEEKLKIAFKENPESTKQFFFGFNGI GHDIDKKLEGIFGDEGIIGKRSKSIEKQVTDLERKIQDIDTINKKKQESI IDKYAKLESQLALLDSQLQTIKAMTKTKSDD
flagellar hook-associated protein 2	fliD	>AHCFPGON_05877 Flagellar hook-associated protein 2 MAQISQRAGKATDTSLDNYTLGKRMKDIDSRITNFERRLELTEARY WRQFSEMERAISMMNQQSSMLMSNFGSGMAQG
flagellar hook-basal body complex protein FliE	fliE	>AHCFPGON_04667 Flagellar hook-basal body complex protein FliE MKIQPMLHTQPFGAIQSIGAPKTSQTSVVEGKKFIDLLEDMNQTQNN AQTAVYDLLTKGVGETHDVLIQQKKAESQMKTAALVRDNLIENYKS LINMQI
flagellar M-ring protein FliF	fliF	>AHCFPGON_04668 hypothetical protein MEKMKNVIQSLKTWHKLVIGAALLAIVTGALLYFTLPDKYVVVYQN LNDADKQEITAELSKLGVDYQLAADGSIRVQKNDAPWVRKEMNGM GLPFNSKSGEEILLESSLGSSEQDKKMKQIVGTKKQLEQDIVRNFATV ETANVQITLPEKETIFDEEKAKGTAAITVGVKRGQLLTADQVAGIQQ MISAAVPGVKAEEVSVIDSKKGVISKGADEAHSSSSSSYEKEVEMQH QLEGKLKQDIDATLMTMFKPNEYKVNTKVSVNYDEVTRQSEKYGD KGVLRSKQEQEESSTAQEGADTKQGAGITANGEVPNYGTNNNQNG KVVYDNKNGNKIENYEIDKTVETIKKHPELTKTNVVVWVDNDTLVK RKIDMTTFKEAIGTAAGLQADPNGNFINGQVNVVTVQFDQPKAEKE KEPEKSGMNWWLFGGITAGLLAIGGLVWFLLARRKRKKEEEEYEEY LAEEEIAASNESILEIPEEKIVPEPKPEPEEPKEPTLDEQVQDATKEHVE GTAKVIKKWLNGQ
flagellar motor switch protein FliG	fliG	>AHCFPGON_04669 Flagellar motor switch protein FliG MLDEISSKEKAAILIRTLEEGVAAKVIEYMTAEEKEVLLREIAKFRVY KPETLENVLGEFLYELNVKELNLVTPDKEYIRRIFKNMPEDELEKLLE DLWYNKDNPFEFLNSLTDLEPLLTVLNDESPQTIAIIASYIKPQLASQL IERLPDHKRVETVMGIAKLEQVDGELINQIGELLKSKLNNMAFSAIN KTDGLKTIVNILNNVSRGVEKTVFQKLDEVDYELSEKIKENMFVFED LLGLEDLALRRVLEEITDNGVLAKALKIAKEEIKEKLFTCMSSNRKE MILEELDGLGPLKMTDAEKAQQTITGTVKKLEKEGRIIVQRGEEDVLI
flagellum-specific ATP synthase [EC:7.4.2.8]	fliI	>AHCFPGON_04671 putative ATP synthase YscN MSRLLMNENEKWNKFIETPLYTKVGKVHSVQEQFFVAKGPKAKIGD VCFVGEHNVLCEVIAIEKENNMLLPFEQTEKVCYGDSVTLVSEDVVV PRGNHLLGKVLSANGEVLNEEAENIPLQKIKLDAPPIHAFEREEITDV FGTGIKSIDSMLTIGIGQKIGIFAGSGVGKSTLLGMIAKNAKADINVIS LVGERGREVKDFIRKELGEEGMRKSVVVVATSDESHLMQLRAAKLA TSIAEYFRDQGNNVLLMMDSVTRFADARRSVDIAVKELPIGGKTLL MESYMKKLLERSGKTQKGSITGIYTVLVDGDDLNGPVPDLARGILD GHIVLKRELATLSHYPAISVLDSVSRIMEEIVSPHHWQLANDVRKILSI YKENELYFKLGTIQQNEENAYIFECKNKVEGINTFLKQGRSDSFQFD DIVEAIQHIV
flagellar motor switch protein FliM	fliM	>AHCFPGON_04687 Flagellar motor switch protein FliM MSGEKLSQEQIDALLKAVNEGEEMPAFAQEAGKQEKFQEYDFNRPE KFGVEHLRSLQAIASTFGKQTSQTLSARMRIPIELEPSTVEQVPFTSEY VEKMPKDYYLYCVIDLGLPELGEIVIEIDLAFVIYIHECWLGGDSKRN FTMRRPLTAFEFLTLDNIFLLLCKNLEQSFESVVAIEPKFVTTETDPNA LKITTASDIISLLNVNMKTDFWNTTVRIGIPFLSVEEIMDKLTSENIVE

		HSSDKRKKYTSEVEVKVNQVYKPVHVAIGEQKMTMSEIEQIEEGDII PLHTKVSDELLGYVDGKHKFNCFIGKDGTRKALLFKSFVE
flagellar biosynthetic protein FliP	fliP	>AHCFPGON_04690 hypothetical protein MRIKKQLSLLAVIFVFSIVFSIIFVNPAYAAPNGFINFENGKEFTSNSSV QLFALVTLLSLSSSIVLLFTHFTYFMIVLGITRQGLGVMNLPPNQVLV GLALFLSLFTMQPVLGQLKSDVWDPMTKEKITVSQAAETTAPIMKE YMSKHTYKHDLKMMLKVRGEELPKDLKDLSLFTLVPSFTLTQIQKG LLTGMFIYLAFVFIDLIISTLLMYLGMMMVPPMILSLPFKILVFVYLG GYTKIVDIMFKTVA
flagellar biosynthetic protein FliQ	fliQ	>AHCFPGON_04691 hypothetical protein MNTSPIIDIFQTFFYKGVMILMPVAGVSMIVVIIIAVIMAMMQIQEQTL TFLPKMASIVLVIIILGPWMFQELTTLILDLFDKIPSLLRSY
flagellar biosynthetic protein FliR	fliR	>AHCFPGON_04692 Flagellar biosynthetic protein FliR MNMELWAATFFAFCRITSFLYFLPFFSGRSIPAMAKVTVGLALSITVA DQVDVSHIKTVWDVAAYAGTQIVIGLSLSKIVEMLWNIPKMAGHIL DFDIGLSQASLFDVNAGSQSTLLSTIFDIFFLIIFISLGGINYFVATILKSF QYTEAISKLLTTSFLDSLLATLLFAITSAVEIALPLMGSLFIINFVLILIA KNAPQLNVFMNAYVIKITCGILFIAMSVPMLGYVFKNMTDVLLEEYT KLFNFFLTK
flagellar protein FliS	fliS	>AHCFPGON_04663 hypothetical protein MQAWQRYMQNDIMTSNPIKNTIFIYERCIVEFRKLEELLNTFKLQEG DDLLEKLERIFEELKLQLNPDISKDLYDSLFGLYDWISIQIQTMKVTR EAKDIDAIVQVLQDLIDGYRGALENEQ
Chemotaxis protein	motA	>AHCFPGON_03184 Chemotaxis protein PomA MDFATIIGLILGFVAVVVGMVVKGADITALLNPAAALIIFIGTFAAVCI AFPMNQLKRVPKLFKVLFGSNKKDLSYEQLLELFVHWTSESRKYGIL SLEQQLDKIQDEFLLRGMKFVIDGVSAEDLEQILESELEAIEERHAKG AAIFSQAGTYAPTLGVLGAVIGLVAALGNLTDIEKLGHAISGAFIATIF GIFSGYVLWHPFANKLKQKSSAEIEKKRLIIDCLLMLQEGTYPFIMKN RILGALSATERKKLEKGAEKNAE
	motB	>AHCFPGON_03185 Motility protein B MRSKKNRRGKKKKHDEHIDETWLIPYSDMLTLLFALFIVLFAMSSID AAKFKQMAVAFRSELAGGTGNKEFLSDQKPNDEKELSASSLEAEQT KKQEEARAKEKKEMDELKALQKKIDQYINEKQLSSSFQTKLTEKGL MVTILENILFDSGKADVKLESLGIAKEMSSLLVSASPREITVSGHTDN VPIANAQFASNWELSTQRAVNFMQVLLQNKELQPEKFSAIGYGEYR SIAPNDTQEGKAKNRRVEVFILPLTEKVK
Chemotaxis protein	motA	>AHCFPGON_04649 Chemotaxis protein PomA MGEKNQVLARPQRRKRKFDISSPVGIIVGFIIVIAAIMLGGGGIKAFKN FLDISSILIVIGGTTATIVVAYRFGEIKKYTKSIFTVLHRREEDLEQLTD LFVDFSKKSKKNGLLSLEVDGEQVDNPFIQKGIRLMLSGYDEDELKE VLLKDIETEVYELRKGAALLDKIGDFAPAWGMIGTLIGLIIMLQNLQ DTSQIGTGMAVAMLTTLYGSVLANMIAIPLAEKVYRGIEDLYTEKKF VIEAISELYRGQIPSKLKLKLDTYVYETKVKKVKGAA
	motB	>AHCFPGON_04650 Motility protein B MSKGPQKGSPRWMTTFTDLTMLLLTFFVLLVATSKQDAVKLSKMLE KFSDTGQVDAKVMENTIPDISHEKNDEKMISKKRMDELYKKLKAYV DNNGISQVNVYREDTGVSVVIVDNLIFDTGDANVKPEAKGIISQLVG FFQSVPNPIVVEGHTDSRPIHNEKFPSNWELSSARAANMIHHLIEVYN VDDKRLAAVGYADTKPIVPNDSPQNWEKNRRVVIYIKE
two-component system, chemotaxis family, sensor kinase CheA	cheA	>AHCFPGON_04652 Chemotaxis protein CheA MQTDLLNIFFEESEEHLQSLNENVLVLEQNPADMDVVGEIFRSAHTF KGMSASMEFTEMADLTHKMENVLDEIRHGNIVVNADIIDVIFECIDN LEKMVADVQQGGMGNIDVASTKQKLEALLNGNVETPTEHIEQNHID TDDAVSHEVHITVEQQAILKAVRAIMCIEALQNVGNIQKTAPSIEEIE ADAFGFEFTVFMDTDCSIEELKQVVLHVSEIEKVEVKQGEPISKEVAS

[EC:2.7.13.3]		KKVVTQEVVQVEEKLQPAVVTQVNSPIEATNQPSSTMPAKSTTKTK NAKVENRSIRVQLEKIERLMNMFEESVIERGRIDELAQTIQNKELIEH LNRLGDISKDIQNVLLNMRMVPIETVFNRFPRMVRMLAKDLGKKID LQITGEDTEVDKIVIDEIGDPLVHLIRNAIDHGVETVEKRRDAGKNET GTIKLEAFHSGNHVVIQITDDGNGINKGKVLEKAIKNGVVTEADANR LTDREVFDLIFQPGFSTAEVVSDLSGRGVGLDVVKHTIHSLGGHLIID SEEGKGSTFRIELPLTLSIIQSMLVQTNDKRYALPLGNIVEAIRIKREDI QSLQGKDVLNYRNQIIEVKHLSTVFGEKTVDEAFASYDGQMVPVLIV RNTHRSYGLIVNTIIGQREIVLKSLGDFFAESSNYFSGATILGDGRVVL ILNPEGL
chemotaxis protein methyltransferase CheR [EC:2.1.1.80]	cheR	>AHCFPGON_03633 Chemotaxis protein methyltransferase MENKYYNFDPSVDTDERTNLEIELLLEAVFKLSGFDFRQYARTSIYR RICNRMQLSNIPTISKLIEKVIHEEGVLEQLLNDFSINVTEMFRNPAFF KALREHVIPELKKQPEIRIWHAGCATGEEVLSMSILLHEEGLSEKSVI YATDMNTNVLEKAKQAILPLNKMQTYTKNYLQAGGTQAFSNYYST DNRFAYFNPSLLQNIIFAQHNLVTDQSFNEFHIILCRNVLIYFTSKLQN QVQHLFYESLSHNGFLCLGNKETLRFSNIMPHYTQFNPSEQIYQKIQ
chemotaxis protein methyltransferase CheR [EC:2.1.1.80]	cheR	>AHCFPGON_04656 Chemotaxis protein methyltransferase MPIVNMIIEQDYDHFIASFKQQFNMDIASYKQDRMRRRIDAFISRKGF ENYTNFLNKLRADQNLFLNFIDYITINVSEFFRNKERWQTLESKALPK LLEQNSGKLKVWSAACAAGEEPYTLSLILSKHLAPFRFEIQATDLDF HILETAKRAQYTERSLKELPTDLKERHFTKENGLYSLHQNIKQNVSF KQHDLLMQSFDTNYDLIICRNVMIYFTEEARIKLYEKFSRSLRKGGV LFVGSTEQILTPERYNLQRFDTFFYEKI
two-component system, chemotaxis family, chemotaxis protein CheY	cheY	>AHCFPGON_04651 Chemotaxis protein CheY MAHKILVVDDAMFMRTMIKNLLKSNAEFEVIGEAENGVEAIQKYKE LQPDIVTLDITMPEMDGLEALKEIIKIDSSAKVVICSAMGQQGMVLD AIKGGAKDFIVKPFQADRVIEALTKVANS
purine-binding chemotaxis protein CheW	cheW	>AHCFPGON_04678 Chemotaxis protein CheV MSQAQSILLESGTNELEIVTYTVGENLFSINVMKVREIINPFPVTTVPE SHHAVEGVVQVRGEILPVINLAMALNLKSTKPLDQTKFIISELNQMK VIFRVDEVHRIQRISWEQIDEPASLSMGLEETTSGIVKLDGKIILLLDY EKIVCEISGTGYDNKSIAGLEQKTDRAEKVIYIAEDSAMLRQILEETLS SAGYTKMNFFSNGAEALAQIEKLAKEQGEKMFEHIHLLITDIEMPKM DGHHLTKVVKDSEVMNRLPVIIFSSLITNELFHKGEAVGANAQVSKP DIQELIGLVDKLVL

Flagellin	hag, fliC	>LOFDPPFF_01689 Flagellin C ATGATTATCAATCACAACATTACAGCACTTAACACACACAACAAA CTTTCGAGCGCATCTTCTGCTCAAAGTAAATCGATGGAGAAATTA GCTTCAGGTCTTCGCATCAATAAAGCAGGCGACGACGCTGCTGGT CTTGCGATTTCTGAAAAAATGCGTGCACAGGTTCGTGGACTTGAC CAAGCTTCACGTAACGCACAAGACGGAATCTCAATGATTCAAAC AGCTGAAGGTGCCTTAAACGAAACACACGATATTCTTCAACGTAT GCGTGAATTAGCAGTTCAGGGTGCAAACGATACGAACGTTACTCA AGACCGCGACGCTATTCAAGAAGAATTAACAGCATTAAAGAGCG AAATCGACCGTATCGGTGAAACAACAGAATTCAACAAACAGACA CTTTTAAATGGTGGACTTGGTGGAACTGTTGATCAAGATGTTGCA ACTACTACAGTTTTAGGTGTTACAGGTGTAGCAGGTGCTTCTACT AACGGTGCTGTCGCTGGATCATATGCAATCACTAGCGGAACTGCT GGCGAATTGACAATGACATTCGGAACTAAAACGCAAACAATCAG CAACGCAAACGGCGCTCAAGACTTGAACTTCTCTGAGTTCGGTAT CTCGATCAAAACAAACGCTGGTTACACTGCAGATGACGCAGTTGG TAACGTTGTTGTAGATCCTGGAGCAGTTACATTCCAAATCGGTGC TAACGAAGACCAAAACTTGAGCTTGAACATCCGTAACATGAAAA CAGACGGCGTATTAAACCTCGCAACTGCAGGACGTGTAGATGTTT CGACTCACGCAACAGCTAAAGCTTCAGTAACAAACATCGAAGGT GCTATCACTGAAGTATCTAAAGAACGTTCGAAACTCGGTGCTTAC CAAAACCGTCTCGATCACACAATCAACAACCTTAAAACTTCTTCT GAAAACCTAACAGCGGCTGAATCACGCGTTCGTGACGTTGATATG GCTAAAGAAATGATGAACCAAACGAAAAACTCAATCCTTGCACA GGCTGCACAAGCAATGTTGGCGCAAGCAAACCAACAACCGCAAG GCGTTCTTCAATTACTTCGTTAA
flagellar hook-associated protein 3 FlgL	flgL	>LOFDPPFF_01708 hypothetical protein ATGTTAACAAAAACGAATATCGGACATTTATCAGCGAGTTATCAA AAGCTGAGCTCGATGCAGGAACAACTGATCAGCGGTAAAAAAAT TCAGCGCCCGTCCGAAGATCCGGTCGTTGCGATGCAAGGCATCCG TTACCGGACAGAAGTCCGGGAAGTGGAACAGTTCAAGAAAAACG TCAATGAAGCGACAGGGTGGATGGATTTGACCGATTCAGCTCTCA ATGAAGTGACATCCGCGATGAGCCGAGTCCGTGAATTGACGACA CAAGCCGCAACGGATACATATGATGCGACCCAGCGAAAAGCCAT CCAAAGTGAAGTTGGTCAATTGATTGAGCATATTGGTACGCTCGC TAATACGAAATACAATGAAAAAGCGATTTTTAATGGGACTAAAA CAGATCAACCCTTCATTTCAATGGAAAATCTGAAGGACTATTTAA CGACATCCGGTAAATCGGTTGATACCGTCTTTACCGATGGAAACC CTGTAACAAAAGAGAATGAAGTGATTCGCTATGAAATATCGTCCG GCATTGAAGTTCAAGTCAATGTTTCGCCAACAAATGTGTTTAGTA CAGAAACTTTCATGACGCTAAAAAAAGTGTATGATGCCTTAGGTG GTACTTCGGACGCAGGTCCCGTCGACAGTTCCAACAATGGAGCTG AACTATCGGGTATGTTGAAAGATCTTGATAGCATGCTTAATCAGA CAGTTGAAACACGAGCCGATCTCGGGGCGCGGGTCAATCGACTT GAGCTGAACGCTTCACGCCTTGAAGATCAAGAAATCATCGCGAA ATCCGTCATGTCGGACAATGAAGATATTGAGGCTGAAAAGGTCAT CATGGAATTGAAGTCATACGAAACGCTACACCGCGCGGCGCTTA GTGCAGGGGCGCGGATCATTCAACCGACTTTGCTCGATTTCTTAC GTTAA
flagellar hook-associated protein 1 FlgK	flgK	>LOFDPPFF_01709 hypothetical protein ATGGGATCAACGTTCATGGGACTTGAGACCGGACGACGTGCACT GACGACCAATCAGTGGGCGCTCCAGTCGACGGGAAACAATATCG CAAATGCAGGGACAGTTGGTTTTTCGCGTCAACGACTGATTATGG CGACGACAGAACAACTTACAATGGCAATCGGAACTGGCAAGATG GGGCAAATTGGAACTGGTGTAAAAGGTGAGATGCTTGAACGTGT

		CCGCGACGTCATGCTCGACAAACAATACCGTGATGAAGCAACGA AGACGTCTTACTATGGCACGAAAGAAGCGGCATTTAGTCGGATG GAAGACGTTATCAATGAGCCATCGGATACAGGACTGTCCAAAGC GTTTGATGGTTTTTGGGAATCATTGCAGACATTGTCGACGAACCC GCAAGACTCTGGTGCCCGCAGTGTTGTTCGTCAAAAAGCAGAGAC GTTGACGCAGACGTTCAACTATATGGCGAAGGCGCTTAATCAAGT ACAAGGGGACTTGAAAAGTGAAATTGAGGTCTCAACCAAAAAAG TGAATGACTTGTTCAAAAAAATTCATAACATCAATGCCGAGATTC ATACCGTCGAGCCGCTTGGTGTTCTGCCAAATGCCTTGTATGATG AGCGCGACCGCTATTTTGATGAACTGTCAGAGTATGTCGATTTTG AAAAAGTGTCTGTCGATGGCGATGCGATTCAACAAGGAACACTT GGAAACACCGTCAAAACGGCTGAAGGCCGAATTGACGTCCGTAT CAAACTCCCTAACGGGGATAAACTGCTGGCAGTGGATTCAGATTT ACCACAAGCAGGAACGCTGACGTTCACAACGGACGATAAAGGTT TGTATACAGGATTTAAAACCGATTCACAAACGATTTCATTCGACG CGGCTGGTGGTTTTTCATCAGGACGTCTGATTGGTTTAATTGAGAT GTACGGACATGTCGAAAATGGTCAAGCAGCAGGCGAATATGTCA AAATGCAAGGACATCTTGATGAGATGGCGGCAACCTTTGCAACTG CTTTTAACGAGGCACATGCTACGAATGTAAAAAAAGATAAGACG GCAGGTACCAATGAATTTTTCGTTTCTTCAAATGGTGGGACCATT ACAGCAAATTCAATTACACTTGGAACGGATATAAAAAAAAGTCT GGATAATATTGCAACTTCGACTGACGGCAATATTGGTGATAGTGC CGGTGCCTTGAAACTTGCCAACATGAAGACCGCAAGCATCCGTTT TGAACGATCGGATACGACGACGACGATCGGTTCGTTTTATCAAAA CGTTATTGGAGATATGGCGGTGGCAACAGATCAAGTCGCACGGCT CGGTCAGAGTTCGGCAGTCTTGATGGAAAGTGCGGAACAACGCC GTATGTCCGTCTCCGCTGTTTCAATTGATGAAGAGATGACAATGA TGATTCAGTATCAACATGCATACAACGCGGCAGCGCGTAATATCA CGACGGTTGATGAAATGCTCGATAAAATCATCAACGGTATGGGA ATCGTAGGACGGTGA
flagella synthesis protein FlgN	flgN	>LOFDPPFF_01710 putative protein YvyG GTGGAACTCATCAACCAGCTCACGACAACGCATATGGATCTGCTG GAACTGGCACACGAAAAGAAACAGGTCCTGATTCAAAACGATAT GCCACGCCTGTCGCAAATCGTCAAGGAAGAACTGGTTTATCTGAA ACGGATGGAGCAGTTGGAACAGCAACGGATTGAACACATGGGAG CGGTGACAATGACGGAATGGCTTCAAGTCCATCCGGAAGATGTC GAGGCCATGCGCCAGTTACTTCAGGCAATCGGTAAGCTCAAAATT ATCAATGAATTGAACGCCGACTTGCTCGAACAATCGTTACAATAC CTCAACTGGCATCTCGAACTATTAGTGCCAGAAGCAGATGATTTT ACATACGGTCAATCGGCGCTTGATCGCGCCCACTTCAATCGAAAC GCCTAA
negative regulator of flagellin synthesis FlgM	flgM	>LOFDPPFF_01711 hypothetical protein ATGCGAATTGATTCTACGAAATGGGTTAACATGCCTAAGACGTAC GAAAGAAATCAAAAAGTAGAAGGAACAGAAGCAACACGTACGA ATCGGCCGGACGAGGTGACGATCTCAAGCGAAGCGCGGATGCGT TTCAGTGAGACAGGCACATCCCGGACCGAGAAGATTGAATCCCTT CGCCAAGCCATTCAGGATGGAACCTATAAACCGGATGCGAAAAA AATCGCAGAACGTTTCTTGAACTTGTAA
alkaline phosphatase [EC:3.1.3.1]	phoA, phoB	>LOFDPPFF_02075 Alkaline phosphatase 3 ATGAAGTTGAAACGAATCATCCCGATTATGGCATTATCGACATTA TCCCTTAGCACGATGATCTCGACAGATAATGCCGAGGCCAAGACG AAATCATCCAAATCTCCGGAAATCCGTAACGTCATCTTTTTGATC GGTGACGGAATGGGTGTTTCTTATACATCTGCTCACCGTTATCTG AAAAACAATCCCGCTACACCTGTCGCTGAGAAAACCGCATTCGAT CAATATCTAGTCGGTCAACAGATGACCTATCCGGAAGATCCGGAA CAAAACGTCACCGACTCTGCTTCTGCCGCAACGGCGATGTCATCC

		GGTGTCAAAACGTATAACGCGGCAATCGCTGTCGACAACGATAA GTCGGAAGTCAAGACCGTCCTTGAAGCGGCAAAACAACGCGGCA AATCGACGGGACTCGTCGCGACGTCCGAAATCACACACGCGACG CCGGCCTCATTCGGGGCGCATGACGAGAACCGCAAGAATATGAA CGCCATCGCCGACGACTATTTCAAAGAACGTGTCAACGGAAAAC ACAAGATTGACGTTCTGCTCGGCGGCGGGAAATCGAACTTCGTCC GTCCGGATGTTGATTTGACGAAATCGTTTAAGAAAGACGGTTACA GCTACGTCACGGATCTTGATCAAATGCAGGCAGATAAGAACAAG CAGGTACTTGGTCTGTTCGCGGACGGCGGACTGCCAAAACGAATC GACCGCGAGAATACCGTCCCGTCTCTCGAGCAGATGACGAACTCG GCCATCAAACGTCTTGATTCGAACAAAAAAGGCTTCTTCTTGATG GTTGAAGGAAGCCAAATCGACTGGGCAGGTCACGATAACGACAT CGTCGGAGCGATGAGCGAGATGGAAGACTTCGAACGTGCCTTCA AAGCAGCGATCGCTTTCGCCAAAAAAGATAAACACACACTCGTC GTCGCAACAGCCGACCATTCGACCGGTGGTTACTCGATCGGAGCA GACGGGATCTACAACTGGTTCGCCGAGCCGATTAAAGCAGCGAA AAAGACGCCGGACTTCATGGCGGCAAAAATCATTGAAGGTGCAG ATGTCCGGAAGACCTTGACGACGTACATCGATCAAAACCGACTTG CCTTGACGGAGGAAGAAATCCAGTCCGTTTCACGTGCCGCGGAGT CGAAGAAAGTGCTCGACGTCGATAATGCGATCGAAGACATCTTC AATAAACGTTCGCACACCGGCTGGACGACAGGTGGACACACCGG GGAAGATGTTCCGGTCTATGCCTTCGGTCCTGCAAAGGAACGATT CGCCGGACAAGTTGATAATACGGATCACGCCAAAATCATCTTCGA TCTGTTGAAATCGAAGAAATAA
pyoverdine synthetase D	pvdD	>LOFDPPFF_02108 D-alanine--D-alanyl carrier protein ligase ATGTCAATCACTTCACTCCGATCACCCTTATTGGAAACCCTAACT AAAATCACAAAACAGACTCCGATGAAAGAAGTATTACTGACGGA AGGCGCTACGTATACCTTAGAAGATATCCGGGTGCGTTCCAATGC GATGGCACACCAACTAGAGAAATCATTTACGACACAAAGATATA TCCCGGTTTATACGACCGACAACGTCCAATCGATCTTCAGCATGT TGGCGTGTTGGAAAGCAGGAAAAGTCTACGTTCCATTGAACCCGC AGACCCCTGTGCCAAAAATCCACCAACTAATGTCCACACTCCACA GTGAGTCGATTTGGACAGATGGACTACCGGAAGAATACGATATC CCGCAGATCATCTTTTCTAAAGAACGAATGGAACATGATGTTGAC GTGGTGGGAACAGAGGTCGCTTATATCCTAATGACATCTGGTAGC ACGGGCGAACCTAAGAAGGTAGAAGTAACGCACGCCAACTTGGA TTGGTTACTGCGTACATTGGAGCAGACCATCCCATTTGCAAAGAA CGATCGTTTTCTCGTCTCGACGCCACCTGCTTTTGATGTCGTCCTT CATGAAATGTTGGCGTTCCTCTATGGAGAGGGACAAGTCGTCTGT TTCCCGGCATATTCGAACATCCAAAAGATTAAGGAATTGCCAAAC TTCGTCAAGCGTTATGACATTACGCATATCGCGTTATCACCATCTG CCTGTACGCAAATCTTGAACCGTGAAAACGAACGCGTGAAGTTG GCTTCTTTACGAAAAGTATTATTAGCGGGAGAGGCGCTAGGAGTA CCGCTCGTCCAAAAACTTCATACACATTTCCCGAACGTCGACGTC TACAATCTATATGGACCGACTGAGACGACAGTCTATGCGACTTGC GTGAAGATTGATGATGTAGTAAATGAAGAGATACCTATCGGAAA AGCACTTGCCGGTACTTCTATTATATTTCGTGATAAAGACGGACA GTTGAACAATTCCGCTGGTGAGATATTGATTGGCGGGAACGGCGT AAGTCGTGGATACCTGGGCAATCCATCATTGACAGAAGAGAAGT TTCTGACCATTGGAGAGGCACGCTATTACGCTACAGGTGACCATG GACGAAAGGACGAGAGCGGCATAATTTTTTACGAGGGAAGACAA GATGATCAAGTGCAGGTGAACGGAATTCGGGTCGAACTCGGAGA AATCAATGCAGCACTCCATGCGGTTCGTCCGACAGGTACCTTCGA AACATTATATCTAGCGAATCGCCTAGTCGTCTTTAGCGATACTCA TTCGTTCACGTCAGAAGATGCGCAAATGTTGAAAGAAGAACTGA AGAAACGAATCCCTTCGTATATGATTCCGAGCATGTATGTGACCG

		TACCAGAATTCAAAATGACGGCCAACCGTAAGCTGGACCGTCGTT ATCTCGAGTCTTTCATCGAGACGACGGATATAGGAGAGCTCGTTA AGGAGGAATCAGTTCAAAATATGGATCAACTTTTGGTGCGTGTTT CGAATCACTACGGTCGTCCAGTCACACCAGATATGGATCTCATAC ACGATCTTCACTTGGACTCGCTTGATCAGCTCGATCTTCTCCTCTT GTTGGAGGATCATTTCAATATGACGCTTGTAGATGATTTTGTAGT GACGCATCCAACGCTTCGCCGGGTTCAGATACAATTGTCACGAGA GGAAGAGAGAGGGACGAATATCATCGAGGTTGATGAAGAATATT GGAACGGCGTCGTCGAAGACAATATGGTGGCGAACCGGGCGCGA TATGAACAAGTGACAAAAGAACAAAAAGAAACGTTTTATCTGCA AAAGAGTTATCATGTCGATGGTTTCCGACAAGTGTTACACGAAGT TGTCTCGATACCTGAGACATATGAACGGAGCCAATTGCAGGCAGC TGTCGATGCCTTGATTGTACGCCATCCAATGTTACGGAGCTTCTTG AAGGTGCAAGAGGATCGTTTACAGTTCACAGTGTATTCAGAAAA GGCGTCATTCCGCTTGTTATCTGTGCCGACAGTTACTGAGGATCA ACGACAGAACTGGATTGAAAGAATGAAACAACAGTACTTAGAGG ACTTGATGGCATATTTCATTCATGATGTGTCTACGAACCGTATCG AACTATTTATCAACCACCATGTCGCAGATCAGGCATCGATGAACC TCTTGAAGCAGGATCTATCTGCCTTGCTTCAGGGCAAGGTATTAT GTCCTTTAGCTGTCGACTATTGGGATTACATCGATTACATCGATGC GAATATTGATCGAGCGGAGTCAGAAATCGAGCAAGTGAGTCATT CCGGATTCGCCGACGTCACAAGCGACGCGTTTGACGTCAACGAA GGTCGTCCGGTTCGATATCTATCGTTCCTGCTCAAGCGAGAAACA CCGGAAGAGTATATTGCTTATGCCAATTACATCATCTTAGGTGCC TTGGCAGCCGGACAATCACGACAACAGATGAGTGGTTCGACTATC GTCGATCTACGATCGTTTAACGGACTCGACATTAAGGGAGTCGTT GGAGACGTTCATACTACAATCCCACTCTGTCTTGAGCAGGGAGAG TCGTTCGAGACATTCAACCGGAAGTTCGACAGCTGGTATAAACAG TTCGAGTCTGGAATTAATTTTAATCATCTACTGTATCGCGACTATC CACATGTCCAGAGTGCACATCGTACGTTCGAGCATAACTTGGATG ACAATCTGAAAGTAAGCTCGAGCTTCCTCGGTGCAATACGAGAAC AAGAGATTCCGACGATGTTAGAAGAACTAAAAGCTTCACATACC ATTCTTCAGAATTTCTCGACACGTAAGCTCTATGCTTCCATCTTCT ATACAGGAAAGCAGTTAATCATCGTCCCACTCAGTCAACCAATGT TATCGGAAGACTTTATTACTAGACTAGGTGGTGAGATCCATCATG AAGACGAACCGAAATAA
chemotaxis protein MotB	motB	>LOFDPPFF_02284 Motility protein B ATGAAACGGAAAAAGAAGCCGCATGACGAACATATCTCCGAAGG TTGGCTGATTCCTTATGCCGATCTTCTGACGTTATTACTGGCCTTG TTCATCGTTCTGTTCGCTTCGAGTAACGTCGATGCCGTTAAGCTTA AAGCAATGTCCCAATCATTCAGCTCCGTCTTTAACGGCGGTTCCG GAATGATCACGAACAGTTCATTGTCGACCTCACAAGAAGAAGAA GATTCAAAAAAAACGGATGCCCGAACAAAGGCGCAAAGTTATGA AATCGCTGAACTTGAAAAAATCAAGGAAGAAGCAAATGACTACA TCAAACAACAGAAGCTTGAAAAAGACATCAAAGTCGAAGTGACG AATGAAGGACTGGTCTTCACGATCCGCGACCGTGCGCTCTTTTCC CCTGCCCAGGCCGAAGTGCGTGGCAATGCCGTTCAGATTGCCCAG GGGATGAGTAATTTACTCGTTAAAGCCGGTCAGCGCCAAATTCAG GTGTCCGGTCATACGGACAACATTCCGATCAACACGGCACAATAT CCGTCCAACTGGGAGCTGAGCACTGAGCGGGCGATCAGTTTCATG CGGGCACTCCAACGTAATTCGCAGCTTGCTCCTAAACGGTTTACC GTTAGTGGATACGGTGAATATCAACCGATCGCTTCCAACCAGACG GAAAGCGGTCGGAGTCAAAACCGCCGTGTCGAAGTATTGATCCG TCCGTTGATTGACATCAAAGCACAAAATGTTCTCGACGAGACGAA AGTCACACCATCATAA
chemotaxis	motA	>LOFDPPFF_02285 Chemotaxis protein PomA

protein MotA		ATGGATATCGTGTCGATTATTGGTATTATACTAGGCCTCATCACCC TAGTCGGAGGAATGATTTTAAAAGGGGCTTCGCCGGTCGCCCTCT TGAACCCGGCGGCACTTGTCATCATCTTTGCCGGAACCATTGCGG CCATCATGATTTCATTTCCGAAAGAGCGACTCAAAATCGTTCCTG CTTTATTTAAGGTCATCTTCTTTGAGCAAAAACTGATGACGAAAC AAACGTTGTTGCAACAGTTTTTAACACTTTCGACACAAGCTCGAA AAGAAGGGTTGTTGTCACTCGAAACAGCACTCGAAGAAGTGGAT AATGCCTTCATGCGCCGTGGTGTCATGATGGTCATCGACGGACAA CCGTCCGAATATGTCGAAGATGTCATGACCCGCGATCTCGAAAAC ATGACAGAACGCCATCACGCCAACGCCAACATCTTTACGCAAGCT GGTACATATGCGCCGACTCTTGGTGTACTCGGAGCCGTCATCGGA CTCGTCGCTGCCCTGTCCGACCTGTCGGACATCGAAAAATTGGGC CATGCGATTTCCGGTGCGTTCATCGCAACCCTGTTCGGGATTTTCA CGGGATATGTCCTCTGGTTCCCGTTCGCTACCAAACTCAAGCAAA AATCAGCCAATGAAATCCAACTGTATGAAATGATGATCGAAGGG ATTTTATCGATTCAGAATGGAGAGTCCCCTAAAAATCTGGAGGAT AAGCTACTTGTGTATCTGACACCGAAGGAGCGTGCGACGTATGAA ACGGAAAAAGAAGCCGCATGA
flagellar hook-associated protein 1 FlgK	flgK	>LOFDPPFF_02407 Flagellar basal-body rod protein FlgG ATGCAATCACTTTATACATCAGCCAGCACGATGGCTCAGCTCCAG AAGCAGCTCGATACGACGGGACATAATCTGGCGAATGCCAATAC GAACGGCTATAAACGTCGGGACTCTCAGTTTAATGAACTGTTGGT CCGCAATCTCAACAATCAGCCGGGCGGTCTTGTGACCGGACCGTT GACGACACCGGAAGGGCTGCGGCTCGGCGTCGGTGGATATGTCG CCAATGAAGCGACACGGTTTACGACAGGGACGTTCCAGAATACG GGACGGAAACTCGATGCTGCGCTCAGCAATCCACATCATTTCTTT GGTGTGATTGATGCGGACGGTGTGACGAAATTCACGCGGGACGG CAATTTTGAATTGTCACCGCAAGCGAACGGACAAGTTCTGTTGAC GGATGATGCCGGACGTTCTGTCATCAATCAGGCGAATGAGCCGAT TACGTTTCCGGATACGGCGACATCGATTGAACTGAACAAAGACG GCAACATCACGGGCATCTTGAACGGGGAACGACGGGTGCTCGCC CGGATTGGCGTCGCCGATATTCCGAACCACGGCGAATTGACGGAT GTTGGTGCCGGACTCTTCACGGCGACGGGACAATACCAGAATGC GGCAGGAAATCCGTTGACGGTCGGCACACTCGAGACGTCAAACG TCGACATGGGGACGGAAATGACGAACTTGACGCAGATTCAGCGG GCCTACCAGTTCAATTCCAAAGCCTTGACGACATCGGATCAGATG ATGGGAATCGTGACGTCGCTTAAGTAA
iron(III)-citrate import ABC transporter, permease protein	yfmD	>LOFDPPFF_02450 putative siderophore transport system permease protein YfhA ATGAACAGACTTCGTCAAAAACCATGGCTCGGTCTAGTCCTCATG TCACTCCTTGTCACCGTGCTCAGTTTCCTGTTGCTTGGCATCGGTT CCGTGTTTCTGAAGCCGGGTGAAATCGTCGCGGCTCTTCAAGGAG ACGGCGCCGGTTCCTTCATCGTCTGGAACTACCGGTTGCCGCGGA CGCTCCTCGCGTTACTCGCCGGCGGTTGTTTTGCCTTGTCCGGTGT CTTGTTACAGGCGATTATCCGCAATCCGCTCGTCTCACCGGATGT CATCGGGGTGACGAATGGGGCCGCGTTGTTCGCCGTCTTGACGAT TGCTTTGATTCCTGATGGTCCGCTTGTTTTGACACCGATTGCCGCC TTAATAGGAGCAACGCTTGTGATGGTCGCGTTGATGCTGCTGGCG GATCACGGGAAACTGCAAAACAGTTCCTTTGCCTTGCTCGGCATC GCCGTCAGTGCAATCTGTGCATCGGGAACGGAATACCTGTTGATC AAGTTTCCTCTCCAGACCAATGATTCGCTCGTCTGGCTCGCCGGC AGCATGTTCGGCAAAGGTTGGACGGAAGTGTACGTCCTGGCACC GGTCTTCCTGTTGCTTGGACTCGTCATCTGGTCCGGTCACCGGCAA CTCGACATCTTATCACTCAGTGAAGACGCAGCGATTGGTCTCGGA TTACGGATGAAGGGAACACGGTATGTGTTCCTCGCCTTTGCCGTC GCTTTGGCAGGTGTTGCGGTCGCAATGGTCGGGTCAATCGGTTTT

		CTTGGCCTCGTCGCCCCGCATATGGCACGGCGCTTGATCGGACAC CGGCATCATCTGTTGATTCCGATGGCTGTCCTCGTTGGGGGTGGA CTGCTTGTCGTTGCGGACGCGCTCGGACGCGGCATCCATCCGCCG CTTGAGATTCCGGCCGGATTAATCACGGCAATCATCGGTGTGCCG TACTTCCTGTATCTGTTGCGAAAAGAACGGGCGTGA
iron(III)-citrate import ABC transporter, permease protein	yfmE	>LOFDPPFF_02451 putative siderophore transport system permease protein YfiZ ATGATCCGACACATACGATTGATCCGCTTGCTCGTCGTACTCCTTG TCCTGATCGGACTCGGATCCTACCTCAGTCTGTTTCTCGGCGTCAC GACGATTCAACCGCTTGAAGCCATTCGGGAATGGTCATCCGGCAA CTTGTCGAAAGAGACACTGGTCTTGACGACACTCCGCTTGCCGCG GTTGTTACTCGGTTTATTACTCGGGGCAAACTTAGCCGTCGCCGG TGCCTTGATGCAGGCGGTCACACGTAATCCGTTGGCTTCGCCGCA AGTGTTCGGCGTCAACGCCGGGGCGTCGCTGTTTGTCGTCCTCGC TTTGTTGTTGTTTCCGGCACTTGGGACAGCGAATCTGGTCTATTTC GCCTTTTTCGGTGCAATGGTTGGCGGATTACTGGTCTTTTCGTTCG CCTCTGTCCGCGGCATGACGAGTCTGAAACTGGCCCTCGTCGGGA TGGCGATCCACTTGTTGCTGACGTCCTTGACGAAAGGGTTGATTT TGTTCAACGACCGGATCACCAACGTCCTGTACTGGTTATCCGGTT CAATCAGTGACAGTGGATGGATCGAAGTCCGGTTGATTTTACCCT GGTCGATCATCGGCTTGATCTTAGCCTTCAGCCTGGCCAAATCGC TGGCGATTTTCCAACTCGGTCAAGATGTGGCCGTCGGACTGGGGC AGAACATCACCCGGATTCGGATGCTGGCAGCCGTCGCTGTTGTCC TGCTGGCCGGGGTGACGGTCGCGGTCGCCGGAGCAATCGGCTTCA TCGGTCTGATGGTCCCGCATATCGTCCGGCGATTGGTCGGTGAGG ATTACCGCTATGTCTTACCGATTTCGGCGTTGTGCGGTGGTCTGTT GCTGACATATGCTGATGTCCTCGCCCGGTTCATCGCCTATCCGTAT GAATCACCGGTCGGGATCGTGACCGCGTTACTCGGAGCGCCGTTC TTTTTGTATTTAGCGAAACGGCAGACAAGGGGGATTGCCTAA
iron(III)-citrate import ABC transporter, iron(III)-citrate-binding protein	yfmC	>LOFDPPFF_02452 Fe(3+)-citrate-binding protein YfmC ATGTCACGTACACGCACATCATGGGCATTAGCCGTCTTGATGGTC AGTTGTCTGATGCTTGCGGCATGCGCCGGACAAGCAAAAGAAGA GACGAAACAGACGCATAAAGTCACGCACGAAGCAGGGACAACA AACGTTCCGGACAATCCGAAACGCGTCGTCGCCCTGGAATTCTCA TTCGTCGACGCGCTTGACGAACTGGGGATCGAACCGGTCGGCATC GCCCAAGAAAACAAAGACGATGTGTCGGGTCTGCTCGGCAAGAA GATTTCCTTTACGGAAGTCGGAACACGCCAGCAACCGAATCTCGA AGTCATCAGTTCGCTGAAACCGGACTTGATCATCGGTGACTTCAA CCGGCATAAAGGAATCTACAAACAGTTGCAGCAAATCGCACCGA CGATCATTTTAAAGAGCCGGAACGCGACGTATCAGGAAAACATC GCGTCGTTTAAGAGCATCGCGGAAGCGGTCGGTCAGACGGATAA GATGGATCAACGTCTCGAGTTACACGAAGAGCGTCTCGCAACAG CCAAACAAAAAGTCGATCCGAACGATCAACGTCAGATTATGGTC GGTGTCTTCCGGTCAGATTCGTTGACGGCACATGGCGAAACATCG TTTGACGGCGAATTGCTCGAAAAGATGGGGATTGATAATGCCATC ACGAAAACAGCGGAACCAACCGTGACGATCACACTGGAACAGAT CGTCAAATGGGATCCGGATGTCATCTTCATGGCAGAAGCCGATCC GAAGTTGCTTGATGAGTGGAAAAAGAATCCGCTGTGGAATCAAA TCACAGCCGTCAAAAAAGGGGAAGTCTACGAAGTCAATCGTGAC TTATGGACCCGTTACCGTGGACTCGACGCTGCGGAACAAATCGTC GATGAAGCCATTCAACTGCTGAATCAAACAAACAAGTAA
spermidine synthase [EC:2.5.1.16]	speE, SRM	>LOFDPPFF_02511 Polyamine aminopropyltransferase ATGGAACAAAAATTAAAGTTATGGTTCACGGAACACCAAACGGA AGATTACGGTATCACATTCCGTGTCAACCACGTTTATGAGAGCGA ACAAACGGAGTTTCAACGCCTGGAGATGGTTGAGACGGACGAGT

		TCGGTACGATGTTGTTACTTGACGGAATGGTCATGACAACAGATC GAGATGAGTTTGTATATCACGAAATGGTCGCACACGTTCCACTGT TCACACACCCGAATCCAAAATCGGTTCTGGTTGTTGGTGGAGGAG ACGGCGGCGTCATCCGCGAAGTGTTAAAACACCCATCAGTCGAA AAGGCTGTTCTTGTCGAAATCGACGGAAAAGTCATCGAATACTCG AAGAAATATCTACCAAACATCGCAGGTGGTCTCGACGACGCACG TGTTGAAGTCATCGTGGGAGACGGCTTCATGCATATCGCAGAAGC AGTCAATGAATATGATGTCATCATGGTTGACTCGACAGAACCTGT TGGTCCTGCCGTTAACCTGTTTACAAAAGGTTTCTACTCAGGAAT CTCAAAAGCATTAAAAGAAGACGGCATCTTCGTCGCACAGTCGG ATAACCCATGGTTCACACCAGACTTAATCCGTGACGTCCAACGCG ATGTCAAAGAAATCTTCCCAATCACGAAACTCTACATTGCCAACG TTCCGACTTACCCGAGCGGTCTGTGGACATTCACGATCGGATCGA AAAAACATGATCCTCTCGCTGTCGCACCAGAGCGTTTCCACGAGA TCGAAACGAAGTACTATACACCGGAACTTCACACAGCAGCATTCG CGCTACCGAAGTTCGTCAAAGATTTAACGATTTAA
agmatinase [EC:3.5.3.11]	speB	>LOFDPPFF_02512 Agmatinase ATGCGTTTTGATGAAGCTTATTCAGGTAAGGTATTTATCGCGAGT CAACCGACTCACGAAGATGCAAAAGGTGTCTTGTACGGCATGCC GATGGACTGGACGGTCAGTTTCCGTCCCGGGTCACGATTTGGTCC GGCCCGGATCCGTGAAGTGTCACTCGGACTCGAAGAATACAGTCC GTATCTCGACGGTGACATTGCGGATGCGAAATTGTTTGATGCCGG CGATATCCCGTTGCCGTTCGGCAATGCCCAAAAGTCACTCGACAT GATCGAAGAATACGTCGATTCGTTGCTGACGGCAGGAAAGTTTCC GCTTGGTATGGGGGGCGAACACCTCGTCACATGGCCGGTCGTCAA AGCCTTTGACAAACATTATGATGACTTTGTTGTGCTGCACTTTGAT GCACATACGGACTTACGCGATTCGTATGAAGGAGAACCGTTGTCG CACTCGACACCACTTAAAAAAATCGCAAACTTGATCGGACCGGA AAACTGTTATTCATTCGGCATTCGTTCAGGGATGAAAGAAGAGTT TGAATGGGCGAAGACGTCCGGTTACAACTTGTTTAAATACGAAAT CGTCGAACCGTTAAAAGCTATTTTACCGAAGCTTGCCGGTAAAAA GGTTTACGTGACGATCGATATCGATGTGCTCGATCCTTCGGCGGC ACCCGGAACCGGGACGCAGGAAATCGGTGGTGTGACGACAAAAG AATTACTTGAAGTCGTTCATATGATTGCACGTGCGGATGTCGACG TCATTGGAGCCGATTTGGTTGAAGTCTGTCCGGCGTATGATCAGT CTGACATGACAGCGATTGCGGCTGCCAAAGTCTTACGTGAAATGA TGATTGGGTTTATCAAGTAA
acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	ilvB, ilvG, ilvI	>LOFDPPFF_02646 Acetolactate synthase ATGACAGAAAAACAAAACAGTGAAAAAGAAAATATGGTACAGA AGAAAACAGGTGCCGATTTAGTCGTCGATACACTGATTGAACAA GGGGTCGACTATATTTTTGGTATTCCGGGAGCAAAGATTGACTCC GTCTTCAACGTCCTTCAAGATCGTGGACCGGAATTGATTGTCGCA CGCCACGAACAAAACGCCGCCTTCATGGCACAAGCCATCGGCCG CTTGACTGATAAACCGGGTGTGGTCCTCGTAACTTCCGGACCAGG GGCTTCGAACCTCGCAACCGGACTTGTGACGGCCAATTCGGAAGG TGACCCCGTTGTCGCGATTGCCGGTGCCGTGACACGTGCCGATCG TTTGAAACGGACCCATCAATCGATGGACAATCAAGCGCTCTTCAC ACCAATCACGAATTTCAGTGCCGAAGTTCAAGATGCAGACAACAT CCCGGAAGTCCTTTCGAATGCATTCCGGACTGCCGAAACAACATC CGGCGCTGCTTTCGTCAGCATTCCGCAAGACGTTGGTCTCAGTGA ATCAAACGTCACTTCCTTTAAAGCGGTCCCAACACCAAAACTCGG CATCGCACCCGAAGAATGGATCAACGAGACAGCAAATCTGATCG AAAAAGCACAATTGCCGGTCTTGTTACTCGGGATGCGTTCCAGTC AGCCCCATGTCGTCAAAGCCATTCGTGCACTGTTGAAACGCGTTT CGATTCCGGTCGTCCAGACATTCCAGGCAGCCGGAACATTGTCAC GGGAGCTCGAGTCGAATTTCTACGGACGTGTCGGTTTGTTCCGCA

		ATCAACCGGGAGATGCCTTGCTCGCTGAAGCCGATCTCGTGTTAG CTGTCGGATATGATCCGATCGGTTACGATCCGAAGTTCTGGAATC AACCTTCACACGAACGGACTTTGATTCACTTGGATCAAATGCGGG CTGAAATCGACCATTTCTATCGTCCGGATCGGGAACTTGTCGGGG ATGTCGCTGCAACAATCGACGCATTGGCTGATCGACTCAATCCGC TGAGCCTGCCAACCAGCTCGACGGAATTTTTACGCGGTTTACAAC AACGCCTCGAGGAGCGAGATATTCCACCGATTGTCAAGGATTCAC CGTTAACACATCCGCTGTATTTCATGAAAACCTTACGGGAACAAA TCGCTGACGATGTGACGGTTACGGTCGACGTCGGTTCGCACTACA TCTGGATGGCACGTCATTTCCGGTCTTACGAACCGCGTCACTTACT GTTCAGTAACGGGATGCAGACGTTAGGTGTCGCATTACCTTGGGC GATTGCCGCAACACTGGTTCGTCCAGGCAAAAAAGCCGTCTCGAT CTCAGGTGATGGTGGTTTCCTCTTCTCGGCGATGGAGCTTGAGAC AGCCGTCCGTTTGAATGCCCCGCTCGTCCATTTCGTTTGGCGCGAC AGCGGCTTTGATATGGTGGCTTTCCAACAAGAGATGAAATACAAA CGAAAATCCGGCACGTCGTTCGGTGAAGTGGATCTTGTGAAATAT GCTGAAAGCTTTGGTGCAAAAGGCTTGCGTGTCAATCATCCGTCT GAACTCGTCGCCGTCATGGAAGAAGCATGGCAAACAGAAGGTCC GGTCATCGTTGATGTTCCAATCGATTACAGCGATAACATTACACT CGGTAAAGAAGTACACTTGGATCAACTCAACTGA
acetolactate decarboxylase [EC:4.1.1.5]	alsD, budA, aldC	>LOFDPPFF_02647 Alpha-acetolactate decarboxylase ATGCAGCGTGAGGACACCTTACTTCAAATCTCGACGATGATGTCT TTGCTCGATGGTGTTTTTGAGAGCGAAACAAGTTATGCCTCCATT CTCGAAGGACATGACTTTGGAATCGGAACGTTTGATCACCTCGAT GGTGAAATGATTGGTTTTGACGGTTCCTTCTACCAACTCCGGTCA GACGGCAGCGCACGTCCTCTTGATCCGGAGACGACCACTCCCTTT TGTTCACTGACACGGTTCACGCCGGAACAGACGCTGTCCGTTGAT CAGGAAATGACAAAACAGGATTTTGAACAATGGTTGAGTGAACA ACTCGGTACAATCAACAGTTTTTATGCTGTCCGGATCGAAGGACA GTTTAGTGAAGTCAAGACACGGACGGTCGCCCGCCAAGAAAAAC CGTTCCGTCCGATTACGGAAGCCGTGGCCACGCAAAGTGCCCGGA CGTTCGAGCAGACGGAAGGCACACTGGCCGGCTATTACACGCCC CGGTTTGGTCACGGTATCGCAGTCGCCGGTTATCATCTCCACTTTA TCGACAAGGAACGAAGTGGCGGTGGCCACGTGTTTGACTATACG GTCAATCGCGTGACGGTCACGTTCGAAGAGAAACCGCGGCTCGA TCTTCGACTGCCGACGACAACTGCTTACCGCGAGGCGGATCTTGA AAGTCACGATATCGAACAAGAAATCAAAATCGCAGAAGGTTAA
pyrroloquinoline quinone biosynthesis protein G	pqqG	>LOFDPPFF_02669 hypothetical protein ATGGCGTTACTGCTTGCGCATCATCGTCCTGTCGCCCGGACCGTTT CCTGGGCCGGGGTGACAAACCTTGTCTGGACGTATGAAGAGCAG CAGACGATGCGGAAGATGTTGCGACGCTTCACGGGTGGGTTGCC GGAGCAACAAAAAGAAGCTTATCAAGTTCGTTCTCCGCTCTATTT TCCGCCGCAAGGCGATGTCTTGTTGATTCACGGCTTGTACGATCA AAATGTCCGATTGCGTCATGCGACGAATTACGCCGCCCGTTATCC AAAGCAGACGCATTTAAAAGTGTATCAATATGCCCATCAATTCCC GATTCGTCAAAAATTCGAAGTGACGGATGATGTCATCAACTGGAT GATGACGTGA
arginine decarboxylase [EC:4.1.1.19]	speA	>LOFDPPFF_02774 Arginine decarboxylase ATGAAAGGTCGGATGCCGATTGTTGAAGCACTGTATGCTCATGTA GAAAGGAAAGCTACTTCTTGGCACGTTCCCGGTCATAAAAACGG AACAGTACTAAACGGCTTACCTTCTTTTTTAGAATGGGATAAAAC AGAGTTGACTGGTTTAGATGATTTTCATCATCCTGAAGAAGCCAT CTACGAAGCAAAACTTTTGTTGCGTCAAATCTATGATGCCTCGGA TAGTCATTTTCTGGTGAATGGATCAACTGTCGGGAATTGGGCGAT GTTAGCGGCGGTTGCGAGTCGTGGAGACCGGATCTATGTGCAACG GAACTCGCATAAGTCTGTTTTTAATGCGTTGGAATGGTTGGGGTT

		ATCGCCCGTTTTAATGGAACCGGACTACCATGCAACAGGAATCAG CGGAAATGTTTCACGTGAAACATTAGAAGAGGCCTTGAAGCTGTA TCCTGGAGGAGTGGCAGTCTTTTTGACGTCACCCACCTATTATGG AGAAAGCGCCGAGATTGATAAATGGGTTCATTTGACGAAGTCGC ACGGGTTACCCTTACTCGTCGATGAAGCACATGGTGCACATTTTG GGGAAGCTTTTGGAGTTCGTTCTGCCTTTGAGTTAGGTGCAACCG CTGTTGTTCAATCTGCCCATAAGACTTTACCTGCATTGACGATGG GAGCTTGGATCCATGAACGTTTCACGGATGACGAACGAAGACGA CTAACACGAGCGCTTCAAGCCTTTCAAACGTCCAGTCCGTCCTAC TTGCTGATGGCTTCGCTTGATTTTGCACGTGATTACCGTCAACAGT TTACGGTTGAACAGATGTTGGAAATACGGAACAGCCATGAACAC TTTCACCAACGACTCAATCAACACACTGAGTTGGACGTATTTACG TTTGATGATTGGTCGCGGATGATTGTGTCCTGCCGCGGGTATTCC GGGAATCAAGTGTTGGCAGCATTGGCTAAGCAGGGTATAGATGC AGAGTTTGCTCTCGGGGAACATGTCGTTTGTATTTTACCGTTGCGC CTCTTACCGGAATCCGAATGTCATGCATGGATCGAACAAATCAAA CAGGCACTCGATATGATGAAAACAGAAGGAATTCCCGATAAAAG GTATATGGAACAACCTATTATGGGTAAAATAAAGGTATCATCACT TGCTTGTCCACTCGATCAACTGGAACGTACCGTGGCAGTCGAACG GTCTTTTGAAGAGGCAGTCGATTCTGTTTCACTTGAGACAATCATT CCATATCCTCCTGGAGTTCCACTTTTACTACGGGGTGAACGGGTG ACGCAAGCACATATCGAAATGATTAAGCAGTATACGACCACATC CGTCCATCTCCAAGGTGGGGAGCTTCTATATGAAGGGAAATTGCG TGTGATACAGGAAGGAATTACAGAATGA
alkaline phosphatase [EC:3.1.3.1]	phoA, phoB	>LOFDPPFF_02955 Alkaline phosphatase 4 ATGAAGAAAACATGGATCACGACAAGCGTACTGGGAATGACATT AGTGGCAGGTGTCACGGCGTATACATATGAAGCACCACGACACG TCGAGGCAAAACCACAGACGGAGTCGAAGAAAAAGGTCAAAAAT GTCATCATGATGATTCCGGACGGTTATTCTGCGTCATATGCAACA AATTATCGTTGGTACAACGGCGGTGACGAGACAGAACTGGATCG TCAGCTCAAGGGCATGATGCGGACATATTCCGCGAGTTCTAAAGT AACGGACTCTGCTGCGGCAGGAACGGCGATGGCAACGGGCACAA AAACGAACAACGGCACGATCGGGATGAATCCAAGTGGACAGGAA GTTGAATCAATCTTTGACCGGGCGGACCGTGTCGGCAAATCAACG GGACTGGTAGCGACATCTGCCATCACACATGCGACGCCGGCTGTC TTCGCTTCCCACGTCGCTTCACGTGCCAACGAAGCAGACATCGCA AAACAATACATGGATGAGATGAAAGTAGATGTCTTGCTTGGCGG CGGTCAAAAGTATTTCTTTGATAAGGAAAATGGTGGCGTACAAGA AGCAGGAAACCTCGTCAAAAAAGCGGAACGCGCCGGATATCAAT ATGCCGACTCGCTGGAAAGTCTTCAGGAGACCGATGGGCGAAAA GTGCTCGGCTTGTTTGCCGAGGAAGGAATGGCACCGGAACTCGAT CGAGAATTGACGCAACAACCAAGTTTGTCGACGATGACAAAAAA AGCAATTCAAACGCTGAATAAAGATAAAGAAGGATTTTTCCTGAT GGTGGAAGGCAGTCAGATTGATTGGGCGGGTCATGCACATGATG CTGCCTGGGCGATGAAGGATTCGGACGCCTTCCACAAAGCCGTAA AAGAAGCGATGCGTTTTGCGGCAAAAGATAAAAACACATTGGTC GTCGTAGCAGGCGATCATGAAACAGGCGGGATGACGGTTGGCGG TTATGATGAGTATGTGGCAAAGCCGGAAGTCTTGAAGAACGTCA AAGCAACCGGTGACCAGATGGTCCGTCAATTTAATGATGATTTGA CGAATATCGCGGAAATCGTCAAACAAGAAACATCATTTTATTTGA CTGCTCAAGAAGTCAAGACGCTCCAAACTGCTGATTCTAAAAAAC GTGTCATGCTGTTGAATGAAATGATCAGTAAGCGGGCCTATGTCG GTTGGACGACAACTGTTCATACAGGTGTAGATGTTCCGTTGTATG CATACGGTCCCCACAGCGATCAGTTTGCCGGTTTACATGACAATA CGGACTTACCCGGTTTAATTGCCAATGCGATGAAACTCAAGAAAT AA

acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	ilvB, ilvG, ilvI	>LOFDPPFF_02961 Acetolactate synthase ATGAACGCCGCTGAACGGTTCGTTGACTGTCTCGAAGCAGAAGGT GTGACACACATTTTCGGTGTGCCGGGGGAAGAGAACATTACGTTA CTCGAAGCGATCAGTAAATCAGACATCACCTTCGTGACGACACGT CATGAAACAAATGCGGCATTCATGGCCTCGATGTTCGGCCGATTG AGCGGACGCCCCGGCGTCTGCCTTTCGACGCTCGGACCCGGGGCA ACGAATATGATGACCGGTATCGCCAGTGCGACGATGGATCATTCT CCGGTCGTCGCGATTACTGGGCAAGGGGCGACGTGGCGGCAGCA TAAAGCTTCGCATCAGATGTTCGATCTGGTTGAGATGTACCAGCC GATCACAAAATCCAGCACATCGATCTCTTCCGGTGAAGTCATTTC AGAAGTCGTCCGCCAGGCGTTTGCTCAAGCTGCATCCGAAAAACC GGGCGCGACCCACATCTCCTTCCCGGAAGACATCGCTAAAGCTGA CGTCGATGCCAAAACTCCTTTGCTTGTGGATAGTGCTCCAACGTA TCTGCATCCGACCTCGGTCAAGGACAGTGAAGTCTTGCGTCAAAT GGAACAAGCGGAAAAACCTGTCGTGATTGCGGGATTCGGGATTA ATCGGAGCGGAGCGACGGATGCCTTTCGTCACTTCGTCGAACGTT TAGGTGCCCCCGTCGTCGAGACGATGATGGGAAAAGGAACGATT GCGTCCGATCATGAACTCGCTGCTCACACGATCGGTCTGCCAAAC GCTGATTATAATCAACGCATCATCGACCAAAGCGATTTAATCATT GCGATTGGTTATGACATTACGGAACTGCCGCCGTCGAAATGGAAC CCGAACCGGACACCGGTCCTCCACATCGACACGAATCAACATGA GGTGGACCAATATTATCCGGTCGTGGCCAATTTGATTGGTTCTTTG CCGGATACGTTACGGTTACTTGCCGAGGACGTGCCGAATCGTGCC TGGTCCGGTTGGCAACAAGACCGCGATCGATTACGAAAGGAAAT TCAGGCACCCTACTCGATGGCACTGCCGCTTCATCCTCAAAGCAT CGTCCGGGAACTGGAAAAGGCGACCGGTTCGGACGGGATGGTCT TTTCCGATGTCGGCGCGCACAAAGTTTGGCTCGGACGGCATTTTC AAACGACACGCCCGAATCAATTGTTCATTTCGAACGGCTTTTCCT CGATGGGGTACGGGTTATCAAGTGCCATCGCCGCGAAACTGCTTT ATCCGGACCGGCGTGTCCTCTGTGCGTCAGGTGACGGGGCCTTTT TAATGAATGGTCAGGATCTTGAGACGGCTGTTCGGCTGAAATTGC CGATCGTCGTCATCATCTGGCGCGACGGGACGTATGGACTGATCG AATGGAAACAACAGCAAGCTTACGGACGGGCCCCTTATATCGAA TTCGACAATCCGGATCTCGTTCAACTCGCTGTCGCCTTTGGCGCAC TTGGTCTGCGTGTCGGAGAACACGGCACACTGGCTGCTTGTCTCG AGCAAGCTTTCTTGAGTGACGGACCCGTTTTAATTGACTGTCCGG TCGATTACAGGGAGAATCTGAAGTTAAGTGACCGTTTACGAACTT ATGGAGGATGA
isochorismate pyruvate lyase [EC:4.2.99.21]	pchB	>LOFDPPFF_03070 Protein AroA(G) ATGGATCAACATGCAGAATTAAAACGCTTACGTGATGAACTCGAC CTGGTAAACGCAGAATTACTTGGATTAATCAATAAACGGGGCGA GATAGCGGTTGAAATCGGTAAAGTAAAACGGGCGCAAGGAATCG ATCGGTATGATCCGGTTCGTGAACGCCAGATGCTTGAATCGATTG CAGCAAGTAATCACGGTCCATTTGAAACAGGACGCCTACAGCAC GTATTTAAAGAAATTTTCAAAGCCTCTTTGGAACTGCAAGGAGAA GACCGGACACGCAAGTTGCTTGTGTCGCGTAAACAAAAGCCGAC GAATACCATCATCCGGATCGGAGATGACGTCATCGGTGATGGCTC GCAGCAGTTAATTGCCGGTCCTTGTGCCGTCGAAAGTGAGGAGCA GGTCTTTGAAGTGGCCGAGCAACTCGCGAAGCATGGGGTACGCTT CATGCGTGGTGGAGCTTACAAACCACGGACATCACCATACGATTT CCAGGGTCTCGGTTTAGAAGGATTGAAGATGCTAAAAAAGGCAG CTGATGCCCATGGTCTTCATGTCATTACAGAAATCATGACGCCGA GTGCAGTTGAGTCGGCTTTACCATACGTGGACATCATTCAAGTCG GTGCCCGCAATATGCAAAACTTCGATCTTTTGAAAGAAGTCGGCC GAACGGACAAACCGGTTCTGTTGAAACGTGGTTTGTCAGCGACGC TCGAAGAATTCATGTATGCAGCAGAGTACATCATGGCAAGCGGG

		AATGAGCAGGTCATCTTGTGTGAACGTGGTATTCGGACGTACGAG CGTGCGACACGAAACACATTGGATATCTCAGCTGTTCCGATTTTG AAGCAAGAAACACATTTGCCTGTCATGGTCGATGTAACGCATTCA ACGGGTCGTAAAGACCTGCTCCTGCCGACAGCGAAAGCGGCATA CGCAATCGGTGCAGATGCCGTCATGGTAGAAGTTCATCCGTTCCC TGCGCTTGCGCTCTCGGATGCGAACCAACAATTAGATTTTAATGA GTTTGATTCGTTCATCGAGAATCTGACTTCCACTTTTCCGGCACTA AACGTTCAATGA
two-component system, OmpR family, phosphate regulon sensor histidine kinase PhoR [EC:2.7.13.3]	phoR	>LOFDPPFF_03681 Alkaline phosphatase synthesis sensor protein PhoR ATGAATTTGCTAGACAATGCGATCCGTTATACGGAAACGGGCACG ATTCAGGTGCAGCTCAGGCAAGAGCCTAGCCATGTGGTTACGATC GTGGAAGACAGCGGGATCGGCATTCCCCCAGAGGAATTGCCTTCT ATTTTTGAGCGCTTTTATCGGGTGGAAAAATCGCGTTCCCGAGAA CATGGAGGTACCGGGTTAGGACTTGCTATCGTCAAGCAGCTGGTG GACATGCAGGGCGGAACGATTCAAGTATCCAGCGTGTTAGGAAA AGGCACTCGTTTCGAAATTACACTTCCGATTGGAGGGGATAGCCA GTGA
two-component system, chemotaxis family, protein-glutamate methylesterase /glutaminase	cheB	>LOFDPPFF_03931 Protein-glutamate methylesterase/protein-glutamine glutaminase GTGGATGTTCTTTTTGAATCGCTGCTTCCGCTCAAGGAGTTGAAG CGTCATATCGTGATCATGACCGGCATGGGATCGGACGGCGCCAA AGGGATGCTGGCTCTGAAAGAATCGGGAGCTGTAACCACGATTG CCGAATCGGAAGAAACCTGTATCGTCTACGGTATGCCCCGAGCAG CGGTCGAGCTTAAAGGTGTCATGCATGTGCTGAAGCAGCAAGAA ATTGCAGGCAAATTAATATCCGCAATCGGTTTATCGGCCTTATCTT AG

Example 8: Phosphate solubilization genome analysis

[00234] Using the genomic sequence obtained for CK1 and CK2 in Example 6, the genomes of these strains were analyzed for the presence and abundance of phosphate solubilization genes.

[00235] To obtain gene candidates for phosphate solubilization in the CK1, CK2 and CK3 strains, a combination of approaches was used to identify a relevant gene set (e.g., related to inorganic phosphate solubilization, phosphate solubilization organic, transport, regulatory genes, and production of organic acids). In those genes in which there was the possibility of building a hidden Markov model from Eggnog's database a similar approach to the identification of nitrogen fixation genes was used from Example 7. However, in most genes it was necessary to manually search for each representative sequence for each strain since the names and annotations vary greatly according to the database and according to the bacterial genus in which the sequences are to be searched.

[00236] For the manual search, representative sequences of *Klebsiella*, and *Bacillus* were searched in the Uniprot database, preferably choosing the sequences that were manually curated. Then, the crb-blast, **prokka, bowtie2, samtools, gffread and cuffinks programs were applied. Each gene sequence was searched in the files previously obtained in the genome annotation. Next, with these results, the ffn file** obtained from prokka was searched to create individual files with the nucleotide sequence of each gene found and prokka was used to obtain the gtf files of each gene, which was then used as input. Then, the **Bowtie2 program, samtools and gffread programs were used to map each sequence found against the**

fastq files directly from the sequencer in order to quantify the abundance of each gene. Finally, the program cuffinks was used to calculate the fragments per kilobase per million (FPKM), and thus provide an estimated abundance of each gene. This comparison is optimal for making comparisons with other genes of the same genome but cannot be used for estimates between different genomes. This pipeline was used individually for each gene and for each strain.

[00237] Results of the genome analysis are summarized in Table 29. Relative abundance of the phosphate solubilization genes in CK1 and CK2 is shown in Figures 8 and 9. Table 30 lists the gene names, enzymes, and protein sequences searched.

[00238] The presence of 39 genes related to phosphorus solubilization activity was studied in extremophile genomes. According to their function, the genes were divided into 5 different groups which comprise inorganic phosphorus solubilization, organic phosphorus mineralization, membrane transporters, regulatory genes, and synthesis of organic acids.

[00239] CK1 genome exhibited the presence of 27 genes linked to phosphorus solubilization and 17 genes were found in CK2 genome. CK1 showed distinct genes encoding for phosphatases, phytases and organic acids demonstrating its ability to solubilize organic and inorganic phosphate. CK2 had also allocated genes with different functions, however, the diversity of genes was lower than CK1. In addition, gene abundance or the copy number variation (CNV), was measured. The results showed that CK1 not only exhibited a greater gene diversity compared to CK2, but also a higher abundance.

[00240] It was concluded that CK1 has phosphate solubilization activity and is a better phosphate solubilizer bacterium than CK2.

Table 29: Presence (+) and absence (-) of phosphate solubilization genes

Gene	*Klebsiella aerogenes* CK1	*Bacillus cereus* CK2
pqqA	+	-
pqqB	+	-
pqqC	+	-
pqqD	+	-
gcd	+	-
gdh	-	+
ppa	-	-
ppx	-	+
aphA	+	-
appA	+	-
phnF	+	-
phnG	+	-
phnH	+	-
phnI	+	-
phnJ	+	-
phnK	+	-
phnL	+	-
phnM	+	-
phnN	+	-
phoA	+	++
pgpB/phoC	+	+
phoD	-	-
phoN	-	-

phyC	-	-
phnC	-	-
phnD	-	-
phnE	-	-
pstS	-	++
ugpB	+	+
phoP	-	+++
phoR	+	+
gspF	+	-
gspE	+	-
ppc	+	-
pyc	-	+
gltA	+	+
sucD	+	+
gad	+	-
mdh	+	+

Table 30: Phosphorus solubilization genes	
Gene Name	**FASTA protein sequence**
aphA	>sp|B5XXX7|APHA_KLEP3 Class B acid phosphatase OS=*Klebsiella* pneumoniae (strain 342) OX=507522 GN=aphA PE=3 SV=1 MRKLTLAFAAASLLFTLNSAVVARASTPQPLWVGTNVAQLAEQAPIHW VSVAQIENSLLGRPPMAVGFDIDDTVLFSSPGFWRGQKTFSPGSEDYLKN PQFWEKMNNGWDEFSMPKEVARQLIAMHVKRGDSIWFVTGRSQTKTET VSKTLQDDFLIPAANMNPVIFAGDKPGQNTKTQWLQAKQIKVFYGDSD NDITAAREAGARGIRVLRAANSSYKPLPMAGALGEEVIVNSEY
appA	>sp|P07102|PPA_ECOLI Periplasmic AppA protein OS=Escherichia coli (strain K12) OX=83333 GN=appA PE=1 SV=2 MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLM QDVTPDAWPTWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKG CPQSGQVAIIADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFN PLKTGVCQLDNANVTDAISRAGGSIADFTGHRQTAFRELERVLNFPQSNL CLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLTEIFLLQQAQ GMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIK TALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPD NTPPGGELVFERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGE VKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSL
gadA	>tr|C0LE03|C0LE03_PSEFL Putative gluconate dehydrogenase OS=Pseudomonas fluorescens OX=294 GN=gad PE=4 SV=1 MATVMKKVDAVIVGFGWTGAIMAKELTEAGLNVLALERGPMQDTYPD GNYPQVIDELTYSVRKKLFQDISKETVTIRHSVNDVALPNRQLGAFLPGN GVGGAGLHWSGVHFRVDPIELRMRSHYEERYGKNFIPKDMTIQDFGVSY EELEPFFDYAEKVFGTSGQAWTVKGQLVGDGKGGNPYAPDRSDHFPLE SQKNTYSAQLFQKAANEVGYKPYNLPSANTSGPYTNPYGAQMGPCNFC GFCSGYVCYMYSKASPNVNILPALKPLPNFELRPNSHVLRVNLDSSKTRA TGVTYVDGQGREIEQPADLVILGAFQFHNVRLMLLSGIGKPYDPITGEGV VGKNFAYQNMATIKAYFDKDVHTNNFIGAGGNGVAVDDFNADNFDHG PHGFVGGSPMWVNQAGSRPIAGTSNPPGTPAWGSAWKKATADYYTHQ VSMDAHGAHQSYRGNYLDLDPVYRDAYGLPLLRMTFDWQENDIKMNR FMVEKMGKIAEAMNPKAIALLGKKVGEHFNTASYQTTHLNGGAIMGTD PKTSALNRYLQSWDVHNVFVPGASAFPQGLGYNPTGLVAALTYWSARA IREQYLKNPGPLVQA
gcd	>sp|P15877|DHG_ECOLI Quinoprotein glucose dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=gcd PE=1 SV=3

	MAINNTGSRRLLVTLTALFAALCGLYLLIGGGWLVAIGGSWYYPIAGLV MLGVAWMLWRSKRAALWLYAALLLGTMIWGVWEVGFDFWALTPRSD ILVFFGIWLILPFVWRRLVIPASGAVAALVVALLISGGILTWAGFNDPQEI NGTLSADATPAEAISPVADQDWPAYGRNQEGQRFSPLKQINADNVHNL KEAWVFRTGDVKQPNDPGEITNEVTPIKVGDTLYLCTAHQRLFALDAAS GKEKWHYDPELKTNESFQHVTCRGVSYHEAKAETASPEVMADCPRRIIL PVNDGRLIAINAENGKLCETFANKGVLNLQSNMPDTKPGLYEPTSPPIITD KTIVMAGSVTDNFSTRETSGVIRGFDVNTGELLWAFDPGAKDPNAIPSDE HTFTFNSPNSWAPAAYDAKLDLVYLPMGVTTPDIWGGNRTPEQERYASS ILALNATTGKLAWSYQTVHHDLWDMDLPAQPTLADITVNGQKVPVIYA PAKTGNIFVLDRRNGELVVPAPEKPVPQGAAKGDYVTPTQPFSELSFRPT KDLSGADMWGATMFDQLVCRVMFHQMRYEGIFTPPSEQGTLVFPGNLG MFEWGGISVDPNREVAIANPMALPFVSKLIPRGPGNPMEQPKDAKGTGT ESGIQPQYGVPYGVTLNPFLSPFGLPCKQPAWGYISALDLKTNEVVWKK RIGTPQDSMPFPMPVPVPFNMGMPMLGGPISTAGNVLFIAATADNYLRA YNMSNGEKLWQGRLPAGGQATPMTYEVNGKQYVVISAGGHGSFGTKM GDYIVAYALPDDVK
gdhA	>sp|P10528|DHGA_BACME Glucose 1-dehydrogenase A OS=*Bacillus* megaterium OX=1404 GN=gdhA PE=3 SV=1 MYTDLKDKVVVITGGSTGLGRAMAVRFGQEEAKVVINYYNNEEEALDA KKEVEEAGGQAIIVQGDVTKEEDVVNLVQTAIKEFGTLDVMINNAGVEN PVPSHELSLDNWNKVIDTNLTGAFLGSREAIKYFVENDIKGNVINMSSVH EMIPWPLFVHYAASKGGMKLMTETLALEYAPKGIRVNNIGPGAMNTPIN AEKFADPEQRADVESMIPMGYIGKPEEVAAVAAFLASSQASYVTGITLFA DGGMTKYPSFQAGRG
gltA	>tr|A0A1Y0XB52|A0A1Y0XB52_BACAM Citrate synthase OS=*Bacillus* amyloliquefaciens OX=1390 GN=gltA PE=3 SV=1 MTATRGLEGVVATTSSVSSIIDDTLTYVGYDIDDLTENASFEEIIYLLWHL RLPNKTELAELKKQLAKEAAVPQEIIEHFKSYPLNNVHPMAALRTAISLL GLTDSEADVMNPEANYRKAIRLQAKVPGIVAAFSRIRKGLDPVEPKEEY GIAENFLYTLNGEEPSPIEVEAFNKALILHADHELNASTFTARVCVATLSD IYSGITAAIGALKGPLHGGANEAVMKMLTEIGEVENAEPYIRSKMEKKE KVMGFGHRVYKHGDPRAKHLKEMSKRLTNLTGESKWYDMSIRVEEIVT SEKKLPPNVDFYSASVYHSLGIDHDLFTPIFAVSRMSGWIAHILEQYDNN RLIRPRAEYTGPDKQTFVPIDERA
mdh	>tr|D8GYA5|D8GYA5_BACAI Malate dehydrogenase OS=*Bacillus* cereus var. anthracis (strain CI) OX=637380 GN=mdh1 PE=3 SV=1 MTIKRKKVSVIGAGFTGATTAFLLAQKELADVVLVDIPQLENPTKGKAL DMLEASPVQGFDANIIGTSDYADTADSDVVVITAGIARKPGMSRDDLVA TNSKIMKSITRDIAKHSPNAIIVVLTNPVDAMTYSVFKEAGFPKERVIGQS GVLDTARFRTFIAQELNLSVKDITGFVLGGHGDDMVPLVRYSYAGGIPLE TLIPKERLEAIVERTRKGGGEIVGLLGNGSAYYAPAASLVEMTEAILKDQ RRVLPAIAYLEGEYGYSDLYLGVPVILGGNGIEKIIELELLADEKEALDRS VESVRNVMKVLV
	>tr|C3SRV3|C3SRV3_ECOLX Malate dehydrogenase OS=Escherichia coli OX=562 GN=mdh PE=3 SV=1 MKVAVLGAAGGIGQALALLLKTQLPSGSELSLYDIAPVTPGVAVDLSHIP TAVKIKGFSGEDATPALEGADVVLISAGVARKPGMDRSDLFNVNAGIVK NLVQQVAKTCPKACIGIITNPVNTTVAIAAEVLKKAGVYDKNKLFGVTT LDIIRSNTFVAELKGKQPGEVEVPVIGGHSGVTILPLLSQVPGVSFTEQEV ADLTKRIQNAGTEVVEAKAGGGSATLSMGQAAARFGLSLVRALQGEQG VVECAYVEGDGQYARFFSQPLLLGKNGVEERKSIGTLSAFEQNALEGML DTLKKDIALGEEFVNK
phnC	>sp|Q81A96|PHNC_BACCR Phosphonates import ATP-binding protein PhnC OS=*Bacillus* cereus (strain ATCC 14579 / DSM 31 / CCUG 7414 / JCM 2152 /

	NBRC 15305 / NCIMB 9373 / NCTC 2599 / NRRL B-3711) OX=226900 GN=phnC PE=3 SV=2 MIEFRNVSKVYPNGTKGLNNINLKIQKGEFVIMVGLSGAGKSTLLKSVN RLHEITEGEIMIECESITAAKGKDLRRMRRDIGMIFQSFNLVKRSTVLKNV LAGRVGYHSTLRTTLGLFPKEDVELAFQALKRVNILEKAYARADELSGG QQQRVSIARALAQEAKIILADEPVASLDPLTTKQVLDDLKKINEDFGITTI VNLHSIALARQYATRIIGLHAGEIVFDGLVEAATDEKFAEIYGDVAQKSE LLEVAAK
phnD	>tr|A0A0C7KIY9|A0A0C7KIY9_KLEPN Phosphonate ABC transporter ATP-binding protein OS=*Klebsiella* pneumoniae OX=573 GN=phnC PE=4 SV=1 MNSSLAAVAETDFQPFTDPAAGRQRKVLSVRNLSKAYQAQHKVLDGISF DLHAGEMVGVIGRSGAGKSTLLHVLNGTHSASGGEILSYPEVGTPHDVS QLKGRALNAWRSHCGMIFQDFCLVPRLDVLTNVLLGRLSQTSTLKSLFK IFPAADRARAIALLEWMNMLPHALQRAENLSGGQMQRVAICRALMQNP GILLADEPVASLDPKNTQRIMDVLREISEQGISVMVNLHSVELVRAYCTR VIGVASGQLIFDDHPSRLTQDVLQRLYGDEVSQLH
	>tr|A0A6M0Q1I3|A0A6M0Q1I3_9BACI Phosphate/phosphite/phosphonate ABC transporter substrate-binding protein OS=*Bacillus* mesophilus OX=1808955 GN=phnD PE=3 SV=1 MKKLWVMMIIALFAVLAACGGGNDEVKEEEQVENTEEQTASEELEKLV VGVIPSLNQGNMQTAMDKLSKHFESELDIPVEITVYPDYQAVVQAMNY DEVNMAYFGPSTYIDANEQSGARAIMTQLIDGEPFYYSYIITHKDSPLTSI EDLVAQSKDLTFAFGDPSSTSGSLIPSIELKKQGVFTNQNEHQFDNLLYT GGHDATALAVENKQVDAGAIDSAIFDTLQANGKIGDNFKIIWQSEKLFQ YPWAVSKVVSDELVAKIQDAFLNVKDQEILDAFAATGFTVATDADYEAI REAKKEAK
phnE	>tr|A0A086IT87|A0A086IT87_KLEPN Phosphate-import protein PhnD OS=*Klebsiella* pneumoniae OX=573 GN=phnD PE=3 SV=1 MKKYMTGAVRLSAMVAGMMMAWQAAAAQPKELNLGILGGQNATQQI GDNQCVKAFLDKELNVDTKLRNSSDYSGVIQGLLGGKVDVVLSMSPSS YASVYLNNPKAVDIVGIAVDDKDQSRGYHSVVIVKADSPYKTLDDLKG KAFGFADPDSTSGYLIPNHAFKEKFGGNADNKYNNTFSSVTFSGGHEQDI LGVLNGQFAGAVTWASMVGDYNTGYTTGAFNRLIRMDHPDLMKQIRII WQSPLIPNGPILVSNALPADFKAKVVAAVKKLDTEDHACFIKAMGGTQH IGPGSVADFQQIIDMKRELVSAR
	>tr|W9BNE6|W9BNE6_KLEPN Phosphate-import permease protein PhnE OS=*Klebsiella* pneumoniae OX=573 GN=phnE_2 PE=3 SV=1 MKTTHTEFERYYQQVRSRQKRDAVCWSLLLLALYFAAGSAAEFNLLTI WHSLPHFFDYMAETIPPLSAGNLFADVQTKGSLAWWGYRLPIQLPLIWE TLQLALASTLVAVAIATVFAFLAANNAWSPAPVRFAIRVLVAFLRTMPE LAWAVIFVMAFGIGAIPGFLALMLHTVGSLTKLFYEAVESAQNKPVRGL AACGASPLQKIRFALWPQVKPLFLSYGFMRLEINFRSSTILGLVGAGGIG QELMTNIKLDRYDQVSITLLLIILVVSALDMLSGRLRLWVLEGKK
phnG	>tr|A0A0G8C4K6|A0A0G8C4K6_BACCE Phosphate-import permease protein PhnE OS=*Bacillus* cereus OX=1396 GN=phnE PE=3 SV=1 MNDVTIYSKSIPKPPSKLKHMLTAVLVILLLWGSSVQVDASLSKLVVGFP NMMDLLKEMVPPDWSYFQVITTAMLDTIRMAIIGTTLGAILAIPLALFAA SNVFTSTFLYSPARMILNFIRTIPDLLLAAIFVAIFGIGPLPGILALTFFSIGL VAKLLYESIESIDPGPLEAMTAVGANKVKWIVYGVIPQVKAHFVSYVLY TFEVNVRAAAVLGLVGAGGIGLYYDRTLGFLQYQQTASIIIYTLVVVLLI DYVSTLLREKL
phnJ	>tr|A0A2G0YHS1|A0A2G0YHS1_9PSED Phosphonate C-P lyase system protein PhnG OS=Pseudomonas sp. ICMP 8385 OX=1718920 GN=AO268_29955 PE=4 SV=1

	MNLSPRQHWIGVLARAQLNELQPHEAALKDAEYQLIRAPEIGMTLVRGR MGGNGAPFNVGEMTVTRCVVRLADGRTGYSYLAGRDKVHAELAALAD AHLQNTPPSPWLTDLISALAQAQARRRAQKEADTAATKVEFFTLVRGEN G
phoA	>tr|Q9XB36|Q9XB36_KLEAE C-P lyase subunit (Fragment) OS=*Klebsiella aerogenes* OX=548 GN=phnJ PE=4 SV=1 ADDTTNAVSIRQFFKRVTGVATTERTEDATLIQTRHRIPETPLTDDQILIFQ VPIPEPLRFIEPRETETRTMHALEEYGVMQVKLYEDIARFGHIATTYAYPV KVNGRYVMDPSPIPKFDNPKMHMMPALQLFGAG
	>sp|P00634|PPB_ECOLI Alkaline phosphatase OS=Escherichia coli (strain K12) OX=83333 GN=phoA PE=1 SV=1 MKQSTIALALLPLLFTPVTKARTPEMPVLENRAAQGDITAPGGARRLTG DQTAALRDSLSDKPAKNIILLIGDGMGDSEITAARNYAEGAGGFFKGIDA LPLTGQYTHYALNKKTGKPDYVTDSAASATAWSTGVKTYNGALGVDIH EKDHPTILEMAKAAGLATGNVSTAELQDATPAALVAHVTSRKCYGPSA TSEKCPGNALEKGGKGSITEQLLNARADVTLGGGAKTFAETATAGEWQ GKTLREQAQARGYQLVSDAASLNSVTEANQQKPLLGLFADGNMPVRW LGPKATYHGNIDKPAVTCTPNPQRNDSVPTLAQMTDKAIELLSKNEKGF FLQVEGASIDKQDHAANPCGQIGETVDLDEAVQRALEFAKKEGNTLVIV TADHAHASQIVAPDTKAPGLTQALNTKDGAVMVMSYGNSEEDSQEHTG SQLRIAAYGPHAANVVGLTDQTDLFYTMKAALGLK
phoB	>sp|P19406|PPB4_BACSU Alkaline phosphatase 4 OS=*Bacillus* subtilis (strain 168) OX=224308 GN=phoA PE=1 SV=4 MKKMSLFQNMKSKLLPIAAVSVLTAGIFAGAELQQTEKASAKKQDKAEI RNVIVMIGDGMGTPYIRAYRSMKNNGDTPNNPKLTEFDRNLTGMMMTH PDDPDYNITDSAAAGTALATGVKTYNNAIGVDKNGKKVKSVLEEAKQQ GKSTGLVATSEINHATPAAYGAHNESRKNMDQIANSYMDDKIKGKHKI DVLLGGGKSYFNRKDRNLTKEFKQAGYSYVTTKQALKKNKDQQVLGL FADGGLAKALDRDSKTPSLKDMTVSAIDRLNQNKKGFFLMVEGSQIDW AAHDNDTVGAMSEVKDFEQAYKAAIEFAKKDKHTLVIATADHTTGGFT IGANGEKNWHAEPILSAKKTPEFMAKKISEGKPVKDVLARYANLKVTSE EIKSVEAAAQADKSKGASKAIIKIFNTRSNSGWTSTDHTGEEVPVYAYGP GKEKFRGLINNTDQANIIFKILKTGK
phoD	>sp|P0AFJ5|PHOB_ECOLI Phosphate regulon transcriptional regulatory protein PhoB OS=Escherichia coli (strain K12) OX=83333 GN=phoB PE=1 SV=1 MARRILVVEDEAPIREMVCFVLEQNGFQPVEAEDYDSAVNQLNEPWPDL ILLDWMLPGGSGIQFIKHLKRESMTRDIPVVMLTARGEEEDRVRGLETG ADDYITKPFSPKELVARIKAVMRRISPMAVEEVIEMQGLSLDPTSHRVMA GEEPLEMGPTEFKLLHFFMTHPERVYSREQLLNHVWGTNVYVEDRTVD VHIRRLRKALEPGGHDRMVQTVRGTGYRFSTRF
	>sp|Q5NNZ8|ALPH_ZYMMO Alkaline phosphatase PhoD OS=Zymomonas mobilis subsp. mobilis (strain ATCC 31821 / ZM4 / CP4) OX=264203 GN=phoD PE=1 SV=1 MNSLLHHSFLKTVFSSLAIAIVTSSLSSVTIAATHPLDNHPKGEIAASSETA HNPWSGTRLIVAISVDQFSSDLFSEYRGRFRSGMKQLQNGVVYPMAYHS HAATETCPGHSVLLTGDHPARTGIIANNWYDFSVKRADKKVYCSEDPSL SADPQNYQPSVHYLKVPTLGDRMKKANPHSRVISVAGKDRAAIMMGGH MTDQIWFWSDNAYKTLADHKGEMPVTVKTVNEQVTRFMQQDEAPVM PSVCADHASALKIGNNRIIGLAPASRKAGDFKTFRVTPDYDRTTTDIAIGL IDELKLGHGNAPDLLTVSLSATDAVGHAYGTEGAEMCSQMAGLDDNIA RIIAALDSNGVPYVLVLTADHGGQDVPERAKLRGVETAQRVDPALSPDQ LSLRLAERFQLSHNQPLFFANEPQGDWYINRNLPEQTKAQLIQAAKSELS NHPQVAAVFTASELTHIPYPTRSPELWNLAERAKASFDPLRSGDLIVLLK PRVTPIAKPVSYVATHGSAWDYDRRVPIIFYTPHASGFEQPMPVETVDIM PSLAALLQIPLRKGEVDGRCLDLDPTEATTCPVK

phoN	>sp|P42251|PPBD_BACSU Alkaline phosphatase D OS=*Bacillus* subtilis (strain 168) OX=224308 GN=phoD PE=1 SV=3 MAYDSRFDEWVQKLKEESFQNNTFDRRKFIQGAGKIAGLSLGLTIAQSV GAFEVNAAPNFSSYPFTLGVASGDPLSDSVVLWTRLAPDPLNGGGMPKQ AVPVKWEVAKDEHFRKIVRKGTEMAKPSLAHSVHVEADGLEPNKVYY YRFKTGHELSPVGKTKTLPAPGANVPQMTFAFASCQQYEHGYYTAYKH MAKEKLDLVFHLGDYIYEYGPNEYVSKTGNVRTHNSAEIITLQDYRNRH AQYRSDANLKAAHAAFPWVVTWDDHEVENNYANKIPEKGQSVEAFVL RRAAAYQAYYEHMPLRISSLPNGPDMQLYRHFTYGNLASFNVLDTRQY RDDQANNDGNKPPSDESRNPNRTLLGKEQEQWLFNNLGSSTAHWNVLA QQIFFAKWNFGTSASPIYSMDSWDGYPAQRERVINFIKSKNLNNVVVLT GDVHASWASNLHVDFEKTSSKIFGAEFVGTSITSGGNGADKRADTDQIL KENPHIQFFNDYRGYVRCTVTPHQWKADYRVMPFVTEPGAAISTRASFV YQKDQTGLRKVSSTTIQGGVKQSDEVEEDRFFSHNKAHEKQMIKKRAKI TN
phoR	>sp|P26976|PHON_SALTY Non-specific acid phosphatase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=phoN PE=3 SV=1 MKSRYLVFFLPLIVAKYTSAETVQPFHSPEESVNSQFYLPPPPGNDDPAY RYDKEAYFKGYAIKGSPRWKQAAEDADVSVENIARIFSPVVGAKINPKD TPETWNMLKNLLTMGGYYATASAKKYYMRTRPFVLFNHSTCRPEDENT LRKNGSYPSGHTAYGTLLALVLSEARPERAQELARRGWEFGQSRVICGA HWQSDVDAGRYVGAVEFARLQTIPAFQKSLAKVREELNDKNNLLSKED HPKLNY
	>sp|P08400|PHOR_ECOLI Phosphate regulon sensor protein PhoR OS=Escherichia coli (strain K12) OX=83333 GN=phoR PE=1 SV=1 MLERLSWKRLVLELLLCCLPAFILGAFFGYLPWFLLASVTGLLIWHFWN LLRLSWWLWVDRSMTPPPGRGSWEPLLYGLHQMQLRNKKRRRELGNLI KRFRSGAESLPDAVVLTTEEGGIFWCNGLAQQILGLRWPEDNGQNILNL LRYPEFTQYLKTRDFSRPLNLVLNTGRHLEIRVMPYTHKQLLMVARDVT QMHQLEGARRNFFANVSHELRTPLTVLQGYLEMMNEQPLEGAVREKAL HTMREQTQRMEGLVKQLLTLSKIEAAPTHLLNEKVDVPMMLRVVEREA QTLSQKKQTFTFEIDNGLKVSGNEDQLRSAISNLVYNAVNHTPEGTHITV RWQRVPHGAEFSVEDNGPGIAPEHIPRLTERFYRVDKARSRQTGGSGLG LAIVKHAVNHHESRLNIESTVGKGTRFSFVIPERLIAKNSD
phoP	>sp|P23545|PHOR_BACSU Alkaline phosphatase synthesis sensor protein PhoR OS=*Bacillus* subtilis (strain 168) OX=224308 GN=phoR PE=1 SV=1 MNKYRVRLFSVFVVCMILVFCVLGLFLQQLFETSDQRKAEEHIEKEAKY LASLLDAGNLNNQANEKIIKDAGGALDVSASVIDTDGKVLYGSNGRSAD SQKVQALVSGHEGILSTTDNKLYYGLSLRSEGEKTGYVLLSASEKSDGL KGELWGMLTASLCTAFIVIVYFYSSMTSRYKRSIESATNVATELSKGNYD ARTYGGYIRRSDKLGHAMNSLAIDLMEMTRTQEMQRDRLLTVIENIGSG LIMIDGRGFINLVNRSYAKQFHINPNHMLRRLYHDAFEHEEVIQLVEDIF MTETKKCKLLRLPIKIERRYFEVDGVPIMGPDDEWKGIVLVFHDMTETK KLEQMRKDFVANVSHELKTPITSIKGFTETLLDGAMEDKEALSEFLSIILK ESERLQSLVQDLLDLSKIEQQNFTLSIETFEPAKMLGEIETLLKHKADEKG ISLHLNVPKDPQYVSGDPYRLKQVFLNLVNNALTYTPEGGSVAINVKPR EKDIQIEVADSGIGIQKEEIPRIFERFYRVDKDRSRNSGGTGLG LAIVKHLIEAHEGKIDVTSELGRGTVFTVTLKRAAEKSA
phyC	>sp|P13792|PHOP_BACSU Alkaline phosphatase synthesis transcriptional regulatory protein PhoP OS=*Bacillus* subtilis (strain 168) OX=224308 GN=phoP PE=1 SV=4 MNKKILVVDDEESIVTLLQYNLERSGYDVITASDGEEALKKAETEKPDLI VLDVMLPKLDGIEVCKQLRQQKLMFPILMLTAKDEEFDKVLGLELGAD

	DYMTKPFSPREVNARVKAILRRSEIAAPSSEMKNDEMEGQIVIGDLKILP DHYEAYFKESQLELTPKEFELLLYLGRHKGRVLTRDLLLSAVWNYDFAG DTRIVDVHISHLRDKIENNTKKPIYIKTIRGLGYKLEEPKMNE
	>tr|A0A119A2M7|A0A119A2M7_9PSED 3-phytase OS=Pseudomonas sp. TAD18 OX=1729583 GN=phyC PE=4 SV=1 MRFNCKPCLLPLLISLSAGHAQAATPVTAPTLKPWSATKAQALGWLAG DQRLAVSKREGVLLLDAQGKTLSHVPGAFASLDSRALGDQVLVASHDE KKQQVALFSLNPQSHEWLAPVYLPRRDYAVNGVCLYRDEASNIYLFTV GEEGKGEQWLVAADRKRLNQPRLVRSLPLPPEAGLCQVDDAAHQLFVN EQKVGWWAYPAHAEAQASRVPVAMIEPFGEVKQAAGAMVPVPGGML GLDPKAGELHLYQQQGKGWSPVARFPLKPLVEPEHLAVRQTPQGLDVW VQDADNNQLFEGRLSWNPVPVSVPPVLPVVKPSVQTDPVVSQGDAADD PAIWLHPHDLALSRVLGTNKKNGLEVYDLQGRRVQHLEVGRLNNVDVR PDFKLGTRTVDLAVATNRDHNSLSVFSIDRATGEVRAAGEVPTPLKDIYG LCLFKAPTGEIYSFANDKDGTFLQHRLSAKGEQVQGELVRQFKVATQPE GCVADDTHQRLFIGEEDVAVWALDARPEQPAALSSVINVGGPVHDDIEG LALYQGEKNSYLVISSQGNDSYVVLDAQPPYALRGAFRVGVNAEAGIDG ASETDGLEVTSANLGGPFTQGMLVVQDGRKRMPEHSQNYKYIPWADVA KTLNLP
ppa	>sp|O31097|PHYC_BACIU 3-phytase OS=*Bacillus* subtilis OX=1423 GN=phyC PE=1 SV=1 MNHSKTLLLTAAAGLMLTCGAVSSQAKHKLSDPYHFTVNAAAETEPVD TAGDAADDPAIWLDPKTPQNSKLITTNKKSGLVVYSLDGKMLHSYNTG KLNNVDIRYDFPLNGKKVDIAAASNRSEGKNTIEIYAIDGKNGTLQSMTD PDHPIATAINEVYGFTLYHSQKTGKYYAMVTGKEGEFEQYELKADKNG YISGKKVRAFKMNSQTEGMAADDEYGRLYIAEEDEAIWKFSAEPDGGS NGTVIDRADGRHLTRDIEGLTIYYAADGKGYLMASSQGNSSYAIYDRQG KNKYVADFRITDGPETDGTSDTDGIDVLGFGLGPEYPFGIFVAQDGENID HGQKANQNFKIVPWERIADQIGFRPLANEQVDPRKLTDRSGK
	>tr|A0A0H3GY84|A0A0H3GY84_KLEPH Inorganic pyrophosphatase OS=*Klebsiella* pneumoniae subsp. pneumoniae (strain HS11286) OX=1125630 GN=ppa PE=3 SV=1 MHLVKTILTAGLLLSAAAQAHNVLEFPQPENNPEEFYAVTEIPTGGIIKYE TDAKTGFIVADRFQSMPVAYPANYGSLTQSLAGDGDPLDVVFYTRAPM APGTLIKLRAIGVLKMIDGGEKDDKIIAVPASKIDPTYDDIKTISDLPKIEQ QRLEAFFRVYKELPEGRKRSSWPALMTPRPRSRRSNRPGRPGRRRTRNNI HRGRCPAPAAFAFTIPMAAKSHVTRHTTTLIPPYCILTQDEGDGCIVQPFH FLDPPPCLIPP
ppc	>sp|P19514|IPYR_BACP3 Inorganic pyrophosphatase OS=*Bacillus* sp. (strain PS3) OX=2334 GN=ppa PE=1 SV=2 MAFENKIVEAFIEIPTGSQNKYEFDKERGIFKLDRVLYSPMFYPAEYGYL QNTLALDGDPLDILVITTNPPFPGCVIDTRVIGYLNMVDSGEEDAKLIGVP VEDPRFDEVRSIEDLPQHKLKEIAHFFERYKDLQGKRTEIGTWEGPEAAA KLIDECIARYNEQK
ppx	>tr|A0A328LFZ7|A0A328LFZ7_9BACI Phosphoenolpyruvate carboxylase OS=*Bacillus* sp. SRB_336 OX=1969380 GN=ppc PE=3 SV=1 MSSELPAITPQNTQDPAGDTDLRRDVRRVSTLLGESLVRQHGPELLAMV EQVRLLTKESKEAARGETGTGPWSANDVAEQVREVLASLPLEQATDLV RAFAFYFHLANAAEQVHRVRSLRARAEEDGWLARTVAEIAEKAGAGAL QKVVNELDVRPIFTAHPTEASRRSVLDKVRKLSDILATPSAEGSSARSRQ DRQLAEIIDQMWQTDELRKVRPTPMDEARNAIYYLNNILTDAMPEVLTE LSGLLGAHGVTLPEDAAPLRFGSWIGGDRDGNPNVTADVTRDVLVLQN ANAVKISVAMVDELLSVLSNSSSLSGADAQLLESITVDLANLPGIAPRVL ELNAEEPYRLKLTCIKAKLLNTRRRVAADAHHEPGRDYASTAELLADLA LLETSLRNNSAALVADGALAAVRRAVASFGLHLATLDIREHADHHHDA VGQLLDRVGELPGPYAELDRAGRLQVLSRELASHRPLSGHPIKLDGAAD

	GTYDVFRVVRRALRTYGPDVVETYIISMTRGADDVLAPAVLAREAGLV QLTGDNRYAKIGFAPLLETVEELRASGEIVDRLLSDPSYRELVRLRGNVQ EIMLGYSDSNKESGVMTSQWEIHKTQRKLRDVAVKHGVNVRMFHGRG GSVGRGGGPTYDAILAQPNGVLEGAIK FTEQGEVISDKYSLPELARENLELSLAAVMQGSALHQAPRHTEDDLVRF GEVMEIVSGAAFASYRALIDDGDLPAYFLASTPVEQLGSLNIGSRPSKRP DSGSGLGGLRAIPWVFGWTQSRQIVPGWFGVGSGLKAAREAGREAELA EMLAHWHFFSSTISNVEMTLAKTDMDIAAHYVRTLVPESLAHLFATIRA EYDLTVAEIQRLTGEAELLDKQPLLKRSLNVRDQYLDPISYLQVELLRRV REAGIAKAEVDERLQRAMLITINGVAAGLRNTG
	>tr|W9BC06|W9BC06_KLEPN Exopolyphosphatase OS=*Klebsiella* pneumoniae OX=573 GN=ppx PE=3 SV=1 MPINDNTPRPQEFAAVDLGSNSFHMVIARVVDGAMQIIGRLKQRVHLAD GLDENSVLSEEAMTRGLNCLSLFAERLQGFSPSSVCIVGTHTLRQATNAA EFLKRAEKVIPYPIEIISGNEEARLIFMGVEHTQPERGRKLVIDIGGGSTEL VIGEDFEPRLVESRRMGCVSFSQAYFPGGVINKENFQRARLAAVQKLETL AWQFRIQGWTVALGASGTIKAAQEVLVAMGEKDGFITPERLEMLVNEL LKHKNFDALSLPGLSEDRKAVFAPGLAILCGVFDALAIKELRLSDGALRE GVLYEMEGRFRHQDIRSRTAQSLANQYNIDREQARRVLETTTQMLEQW QEQNPKLANPHLAALLKWAVMLHEVGLNINHSGMHRHSAYILQNSDLP GFNQEQQMLMATLVRYHRKAIKLDDLPRFTLFRKKQFLPLIQLLRLGVL LNNQRQATTTPPTLRLQTEAHHWTLTFPHNWFSQNALVLLDLEKEQQY WEGVPEWMLKIAEEEPDA
pqq	>tr|A0A0K6LY49|A0A0K6LY49_BACCE Exopolyphosphatase OS=*Bacillus* cereus OX=1396 GN=ppx PE=3 SV=1 MKEILKQQYAIIDIGSNTMRLVIYEKQNGGFYKEIENTKVVARLRNYLVD GVLIEEGIEVLLQTLFQFQESTRFHQLHHVLCVATATIRQAKNQEEIKKLV EGQTDFTLRVLSEYEEARYGYLAVMNSTSFSEGITVDIGGGSTEVTYFRN REILEYHSFPFGALSLKQQFIKDDIPTEEELEKLQTYLEYQFRTLPWLIDK KLPLIAIGGSARNLVKIHQNLICYPIAGVHLYKMKEEDIKNVKEELEALSF IELQKLEGLAKDRADTIVPAVEVFHTLVNVIEAPAFVLSRKGLREGVFYE ELTKDLGISYYPNVVEESLYLLSHEYEMDMEFVMQLIKHGRLICQQLEET GLISMSVEDWEVFHQAAKVFNIGKYIDEEASRLHTFYLLANKTIDGMMH KERVRLALIASYKSKMLFKQHLSPFEGWFDKNEQKKIRLLGAVLQFSAA LNIRQRSLVESISITESKEGLTFEIVCEQSALAEKVQAEKQKKQLERVLKT NIILLFKLKN
	>sp|P27503|PQQA_KLEPN Coenzyme PQQ synthesis protein A OS=*Klebsiella* pneumoniae OX=573 GN=pqqA PE=3 SV=1 MWKKPAFIDLRLGLEVTLYISNR
pqqA	>tr|A0A0D1XIK3|A0A0D1XIK3_ANEMI Pyrroloquinoline quinone (PQQ) biosynthesis protein C OS=Aneurini*bacillus* migulanus OX=47500 GN=AF333_24905 PE=4 SV=1 MAITSYEQIEEKIWDIVETEIIQGEFMQTLLAGEWTPAQVREFALQYSYYS RNFPRVLGAAIAAVEPEDDWWVPLVDNLWDEGGRGNPKSYHSRLYHSF MITAAPDVPTNEKYVPDYPVSPASKEAVNTFISFLRNATPLEAMASIGFG SELFAGKVMGLIGQGLEHPNYNRAQKLNTTFWTVHADHHEPRHYELCK NVLTRFTSSQDLEHMYRAGAYITRSEARFYDGLYERMKSV
pstS	>sp|P27503|PQQA_KLEPN Coenzyme PQQ synthesis protein A OS=*Klebsiella* pneumoniae OX=573 GN=pqqA PE=3 SV=1 MWKKPAFIDLRLGLEVTLYISNR
	>tr|A0A3S4JIM4|A0A3S4JIM4_KLEAE Phosphate-binding protein PstS OS=*Klebsiella aerogenes* OX=548 GN=pstS PE=3 SV=1 MNVMRTTVATVVAATLSMSAFSAFAAASLTGAGATFPAPVYAKWADT YQKETGNKVNYQGIGSSGGVKQIIANTVDFGASDAPLADDKLTQEGLFQ

	FPTVIGGVVLAVNLPGVKSGELVLDGKTLGDIYLGKIKKWDDEAIAKLN PGLKLPSQNIAVVRRADGSGTSFVFTSYLSKVNEEWKSKIGAGSTVNWP TGLGGKGNDGIAAFVQRLPGSIGYVEYAYAKQNNLAYTKLVSADGKPV SPTEDNFANAAKGVDWSKSFAQDLTNQKGENAWPITSTTFILVHKATNK PEQTAEVLKFFDWAYKNGGKEANALDYATLPEKRGRAGSRGMENQRQ RQQR
	>sp|P46338|PSTS_BACSU Phosphate-binding protein PstS OS=*Bacillus* subtilis (strain 168) OX=224308 GN=pstS PE=3 SV=1 MKKNKLVLMLLMAAFMMIAAACGNAGESKKSNSDSAKGEEKASGSLTI SGSSAMQPLVLAAAEKFMEENPDADIQVQAGGSGTGLSQVSEGAVQIGN SDVFAEEKEGIDAKALVDHQVAVVGMAAAVNPDAGVKDISKDELKKIF TGKIKNWKELGGKDQKITLVNRPDSSGTRATFVKYALDGAEPAEGITED SSNTVKKIIADTPGAIGYLAFSYLTDDKVTALSIDGVKPEAKNVATGEYPI WAYQHSYTKGEATGLAKEFLDYLKSEDIQKSIVTDQGYIPVTDMKVTRD ANGKQS
ugpB	>tr|W9BBW5|W9BBW5_KLEPN Glycerol-3-phosphate ABC transporter OS=*Klebsiella* pneumoniae OX=573 GN=ugpB PE=3 SV=1 MISLRHTALGLALSLAFAGQALAVTTIPFWHSMEGELGKEVDSLAQRFN AANPDYKIVPVYKGNYEQSLSAGIAAFRTGNAPAILQVYEVGTATMMAS KAIKPVYQVFSEAGIKFDESQFVPTVAGYYTDSKTGHLLSQPFNSSTPVL YYNKDAFKKAGLDPDQPPKTWQDLAAYTAKLKAAGMKCGYASGWQG WIQIENFSAWHGLPVATKNNGFDGTDAVLEFNKPEQVKHIALLEEMNK KGDFSYFGRKDESTEKFYNGDCAITTASSGSLADIRQYAKFNYGVGMMP YDADVKGAPQNAIIGGASLWVMQGKDKETYTGVAKFLDFLTKPENAAE WHQKTGYLPITTAAYDLTRQQGFYDKNPGADIATRQMLNKPPLPFTKGL RLGNMPQIRTIVDEELESVWTGKKTPQQALDSAVQRGNQLLRRFEQATK S
	>tr|A0A1B1L0E8|A0A1B1L0E8_BACTU sn-glycerol-3-phosphate-binding periplasmic protein UgpB OS=*Bacillus* thuringiensis OX=1428 GN=ugpB PE=3 SV=1 MSLVKKGAALLMAATMALSSAACSNSKTEGKPEALAKVAPVEKNGDK TVIRFWHAMGGKTQGVLDGLVADYNKSQNKYEIKAEFQGTYEESLTKF RTMSATKEAPALVQSSEITTKYMIDSKKITPIDSWIKKDKYDTSKLEKAIT NYYSVDGKMYSMPFNSSTPVLIYNKDAFAKAGLDPEKAPKTYAELQEA AKKLTIKEGGNVKQYGFSMLNYGWFFEELLATQGALYVDNENGRKDA AKKAVFNDKEGQKVFGMLDDLNKAGALGKYGASWDDIRAAFQSGQV AMYLDSSAGVRDLIDASKFNVGVSYIPYPEDSKQNGVVIGGASLWMTN MVSEETQQGAWDFMKYLTKPDVQAKWHTATGYFSINPDAYNEPLVKE QYEKYPQLKVTVDQLQATKQSPATQGALISVFPESRDAVVKALEAMYD GKNSKEALDEAAKATDRAISISARTSQK

Example 9: Additional Genomic Characterization of CK1 and CK2

[00241] Using the genomic sequence obtained for CK1 and CK2 in Example 6, the genomes of these strains were further analyzed for the presence of virulence genes (Table 31), osmotic stress-related genes (Table 32) and plant growth promoting genes (Tables 33, 35, and 46) using similar methods to Examples 7 and 8.

Table 31: Genome analysis of virulence genes

	***Klebsiella aerogenes* CK1**	***Bacillus cereus* CK2**
Victors	144	2
PATRIC_VF	117	2
VFDB	42	0

Table 32: Genome analysis of osmotic stress tolerance genes		
Strain	***Klebsiella aerogenes* CK1 gene count**	***Bacillus cereus* CK2 gene count**
Osmotic stress cluster	4	0
Choline uptake and conversion to betaine clusters	12	11
Universal stress protein family	7	1
Osmoregulation	4	1
EnvZ and OmpR regulon	4	0
Hyperosmotic potassium uptake	2	0

Table 33: Genome analysis of plant growth promoting genes CK1 and CK2		
Function	**CK1 *Klebsiella aerogenes***	**CK2 *Bacillus cereus***
Phosphate solubilization and mineralization	PRESENT	PRESENT
Nitrogen assimilation and reduction	PRESENT	PRESENT
Nitrogen fixation	MISSING	MISSING
Siderophore synthesis/Fe-uptake	PRESENT	PRESENT
L-tryptophane, indole synthesis	PRESENT	PRESENT
Auxin (Indole-3-Acetic acid) synthesis	INCOMPLETE	Detailed analysis required
ACC (1-Aminocyclopropane-1-Carboxylate)-deamination	MISSING	MISSING
Spermidine synthesis	PRESENT	PRESENT
Acetoin, Butanediol synthesis	PRESENT	PRESENT
Nitric oxide synthesis	MISSING	INCOMPLETE
Hydrogen cyanide synthesis	MISSING	MISSING
2,4-Diacetylphloroglucinol synthesis	MISSING	MISSING
Flagellar assembly	PRESENT	PRESENT

Table 35: *Klebsiella* genes involved in plant growth promoting features		
Enzyme name	**Gene name**	**FASTA gene sequence**
exopolyphosphatase [EC:3.6.1.11]	**ppx**	>ADJCKNHF_00078 Exopolyphosphatase ATGCCAATAAACGAAAAAACCCCTCGGCCGCAGGAGTTCGCTGC GGTCGACCTTGGTTCGAACAGTTTTCATATGGTGATCGCCCGTGT CGTCGACGGGGCAATGCAGATCATCGGTCGCCTGAAGCAGCGCG TCCACCTGGCCGATGGCCTGGATGAAAACTCGGTGTTGAGCGAAG AAGCGATTACTCGTGGGCTGAACTGCCTGTCGCTGTTTGCGGAAC GTCTGCAGGGATTCTCCCCTTCCAGCGTTTGTATCGTCGGGACGC ATACCCTGCGCCAGGCGGCTAACGCGGCGGATTTTCTCAAACGAG CGGAAAAAGTTATCCCTTATCCCATCGAAATAATCTCCGGTAACG AAGAAGCGCGTCTGATTTTTATGGGCGTCGAACATACGCAACCGG AGCGCGGCCGTAAGCTGGTTATCGACATCGGCGGCGGTTCGACTG AGCTCGTCATCGGCGAAGATTTCGAGCCCCGCCTGGTTGAAAGCC GACGTATGGGCTGCGTAAGCTTCTCGCAGGCCTATTTCGCCGGCG GCGTTATCAATAAAGAAAACTTCCAGCGCGCGCGCCTGGCGGCG GTGCAGAAACTGGAAACCCTGGCCTGGCAGTTCCGTATTCAGGGG TGGAACGTGGCGCTGGGCGCCTCTGGCACCATCAAAGCCGCGCA CGAAGTGCTGGTCGCCATGGGGGAGAAAGACGGCTTCATTACCC CGGAACGTCTTGAAATGCTGGTCAGTGAGCTTCTGAAGAATAAAA ACTTCGACTCATTAAGCCTGCCGGGATTGTCGGAGGACCGCAAAG

		CGGTATTCGCCCCGGGTCTGGCGATTTTGTGCGGGGTATTCGACG CGCTGGCGATCAAAGAACTGCGCCTGTCCGACGGCGCCCTGCGCG AAGGCGTGTTGTACGAGATGGAAGGTCGCTTCCGCCACCAGGAT ATTCGCAGCCGTACGGCCCAGAGCCTGGCGAACCAGTACAATATC GATCGCGAACAGGCGCGCCGGGTACTGGAGACTACCACTCAGAT GCTGGAACAGTGGCAGGAGCAAAACCCGAAACTGGCTAACCCGC ATCTGTCTGCCCTGCTGAAGTGGGCGGTAATGCTACATGAAGTGG GGCTGAACATTAACCACAGCGGCATGCATCGCCACTCTGCCTATA TCCTGCAAAATAGCGATCTGCCGGGCTTTAATCAGGAGCAGCAGA CGCTGATGGCCACGCTGGTGCGCTATCACCGCAAAGCTATCAAGC TTGATGATTTGCCGCGTTTTACCTTGTTCAAGAAAAAACAGTTCTT GCCGCTGATCCAACTACTGCGTCTGGGCGTATTACTGAACAATCA GCGTCAGGCGACCACTACGCCGCCAAAACTGACATTGAAGACAG AAGCCAACCACTGGACGTTAATTTTCCCGCATGACTGGTTTAGCC AGAATGCGTTGGTGCTGCTGGATCTGGAAAAAGAGCAACAGTAC TGGGAAGGCGTGCCGGAATGGCTGCTGAAAATTACTGAAGAAGA AGCGTAA
indolepyruvate decarboxylase [EC:4.1.1.74]	**ipdC**	>ADJCKNHF_00151 Indole-3-pyruvate decarboxylase ATGCAACCGACTTACACCATTGGCGATTATCTGCTGGATCGTCTC GTAGATTGTGGTATCGATCGCCTGTTCGGCGTACCTGGTGATTAC AACTTACAGTTTCTCGATCACGTGATAGCCCATCAAGATTTGGGA TGGGTCGGCTGTGCTAACGAACTGAACGCGGCCTACGCCGCAGA CGGCTATGCGCGTATAAAAGGCGCTGGCGCGCTGCTAACCACCTA CGGCGTAGGGGAGTTAAGCGCGTTGAATGGGGTGGCCGGTAGTT ATGCGGAACATATCCCGGTGCTGCATATTGTGGGCGCCCCTTCCA CTGGCGCGCAGCAGCGCGGTGAACTCCTGCACCATACGCTCGGCG ATGGCGATTTCACCCATTTCTCGCGGATGAGCGAACAAATTACCT GTACTCAGGCGACGCTAACGGCGGGCAACGCCTGTCATGAAATT GACCGGGTATTAAGCGACATGCTGACCCACCACCGCCCAGGGTAT CTGATGCTGCCTGCCGACGTGGCGAAAGCCCGTGCGGTGCCGCCG GCCCGCGCGCTGGTCATTAAGGGCCCGGCGGCCGATGAAAACCA GCTTGCCGGCTTTCGCGAGCACGCGGCCAAATTGTTGCGCAGCAG TCGCCGCGTATCGCTGCTGGCGGATTTTCTCGCTCAGCGTTACGGT CTGCAAAACACACTACAGCAGTGGGTTAAGTCCGCGCCTATTACC CACGCCACCATGCTGATGGGGAAAGGGCTATTTGACGAACAAGG CTCAGGTTTTGCCGGGACCTATAGCGGGATCGCCAGCGCGCCGCA GACTCGCGAGGCGATGGAAAGCGCCGATGCCATCATCTGCGTGG GTACGCGCTTTACCGATACGATTACCGCCGGCTTTACCCATCATTT GCCAACGGAGAAAACCATCGAAATCCAGCCGTTCGCCGCGCGGG TTGGCGATCACTGGTTCAGCCGGATCCCGATGGATCAGGCGCTGG CGGCACTCATTGACGTTTCTGGCAAGCTGTCCGCCGAATGGAGCG CGCCAGATATCATCGCGCCCGACGCTTCCGGCGCGCCGCAGGGG AATCTGACGCAGAAAAGCTTCTGGAGTACGGTCGAGAAACAGCT GCGGCCGGGCGACATTATTCTTGCCGACCAGGGGACCTCGGCATT CGGCATCGCCTCATTAAAACTTCCCTCCCAGGCGACGCTGCTGGT GCAGCCGCTATGGGGCTCAATCGGCTTTACGCTACCTGCCGCCTA CGGCGCACAGACAGCCGCCGCGGACAGAAGGGTGGTATTAATCA TTGGCGATGGCGCCGCCCAGCTCACTATCCAGGAGATGAGCTCAA TGCTGCGCGATAAGCAAAAGCTGTTAATTTTGCTGTTGAATAATG AGGGCTACACCGTCGAGCGCGCGATTCACGGGCCAGAACAGCGC TACAACGATATCGCATTGTGGGACTGGAGCCGCTTCCCCGATGCT TTTGCGCCGGATACGCCTTCCCGCTGTTGGCGGGTAACGCAAACC GGCGAATTGGCGGAGGCGATGGCCGATAGCATTAATTCCGATAA GTTAACGATGGTCGAAGTCATGCTGCCGAAAATGGATATTCCTGA TTTCTTACGCGCGGTCACCCAGGCGCTGGAAAATCGCAACAACCG CGGCTAA

polyketide synthase	**Atu3672**	>ADJCKNHF_00178 3-oxoacyl-[acyl-carrier-protein] synthase 1 ATGAAACGTGCAGTGATTACTGGCTTGGGCATCGTTTCCAGCATC GGTAATAACCAGCAGGAAGTCCTGGCATCTCTGCGTGAAGGACG TTCAGGGATCACTTTCTCTCAGGAGCTGAAGGATTCAGGAATGCG TAGCCACGTGTGGGGCAACGTCAAACTGGATACCACGGGCCTCAT TGACCGCAAAGTAGTTCGCTTTATGAGCGATGCATCTATCTATGC TTATCTGTCCATGGAGCAGGCGGTAGCCGACGCAGGTCTGGCGCC GGAAGCATACCAGAACAACCCGCGTGTCGGCCTGATTGCAGGTTC CGGCGGCGGCTCCCCGAAATTCCAGGTCTTCGGCGCCGATGCCAT GCGTAGCCCGCGTGGTCTGAAAGCCGTGGGCCCATACGTTGTGAC TAAAGCGATGGCTTCCGGCGTATCTGCCTGCCTCGCCACGCCGTT TAAAATCCACGGCGTCAACTACTCTATTAGCTCCGCTTGCGCCAC TTCCGCACACTGCATCGGTAACGCGGTAGAACAGATTCAGCTGGG CAAACAGGACATCGTCTTTGCCGGCGGCGGCGAAGAGCTGTGCT GGGAAATGGCTTGTGAATTCGACGCCATGGGCGCGCTGTCCACTA AATACAACGATTCTCCGGACAAAGCGTCCCGTACCTATGATGCGA ACCGCGACGGTTTCGTTATCGCGGGCGGCGGCGGCATGGTCGTGG TGGAAGAGCTGGAACACGCGCTGGCGCGCGGCGCGCATATCTAT GCGGAAATCGTCGGTTACGGCGCGACTTCCGATGGCGCGGACAT GGTTGCTCCATCTGGCGAAGGCGCAGTGCGCTGCATGCAGATGGC GATGCACGGCGTTGATACCCCGATCGACTACCTGAACTCCCACGG CACTTCGACTCCGGTAGGCGACGTGAAAGAGTTGGGCGCTATCCG CGAAGTCTTCGGCGACAACAGCCCGGCTATCTCCGCCACCAAAGC GATGACCGGCCACTCTCTGGGCGCCGCAGGCGTACAGGAAGCCA TCTACTCTCTGCTGATGCTGGAGCACGGTTTTATCGCGCCAAGCA TCAACATTGAAGAGATGGACGAGCAGGCTGCCGGCCTTAACATC GTCACCAAGCCGACCGATGCTCAGTTGACCACCGTGATGTCCAAC AGCTTCGGCTTCGGCGGCACCAACGCGACCCTGGTTATGCGTAAA TACAACGCCTAA
tryptophan synthase alpha chain [EC:4.2.1.20]	**trpA**	>ADJCKNHF_00747 Tryptophan synthase alpha chain ATGGAACGTTACGAGACGCTATTTGCACAGTTAAAAAACCGCCA GGAAGGCGCCTTTGTTCCCTTCGTCACCCTCGGCGATCCGGGGCC GGAACAGTCGCTGAAAATCATCGATGCGCTGATTGAAGCCGGCG CCGATGCGCTGGAACTGGGGATCCCCTTCTCCGACCCGCTGGCCG ACGGCCCGACGATTCAGGGCGCCACATTGCGCGCTTTTGCCGCCG GCGTTACCCCGGCGCAGTGCTTCGAGATGCTGGCGGCGATCCGCC ACAAGCATCCGACCATTCCGATCGGCCTGTTGATGTACGCGAACC TGGTGTTCAGCCCGGGGATTGATGAGTTCTACGCCGAATGCGCGC GTGTCGGCGTGGATTCCGTGCTGGTCGCCGACGTGCCGGTCGAAG AGTCCGCCCCGTTCCGTCAGGCAGCGCTGCGCCATAACATTGCGC CGATTTTCATCTGCCCGCCAAATGCCGATGACGATTTACTGCGCC AGATTGCCTCCTATGGCCGCGGCTATACCTACCTGCTATCGCGCG CTGGCGTGACAGGCGCGGAAAACCGCGCCGCGCTGCCGCTGCAT CATCTGATTGAAAAATTGGCGGAATATAACGCCGCGCCGCCGCTG CAGGGCTTTGGTATCTCGGCGCCGGAGCAGGTTTCGGCCGCTATT GACGCCGGTGCCGCCGGGGCAATATCCGGCTCGGCCATCGTCAA GATCATCGAGCGCAACCTTGAACAGCCGCAAAAAATGCTCGAAG AGCTAAAAACCTTCGTACAGAGTCTGAAAGCGGCGACCAAAACC GCCTGA
tryptophan synthase beta chain [EC:4.2.1.20]	**trpB**	>ADJCKNHF_00748 Tryptophan synthase beta chain ATGAGCACTTTACTGAACCCGTATTTCGGCGAATTCGGCGGTATG TACGTTCCGCAGATCCTGATGCCCGCCCTGCGCCAGCTGGAAGAG GCTTTCGTCAGCGCGCAAAAAGATCCTGAGTTTCAGGCCGAATTC ACCGACCTGCTGAAAAACTACGCGGGCCGCCCGACGGCGCTGAC CAAATGCCGCAATCTGACCGAAGGCACCCGCACCACGCTGTACCT CAAGCGTGAAGATCTGCTCCACGGCGGCGCGCACAAAACCAACC

		AGGTGCTGGGCCAGGCGCTACTGGCCAAACGTATGGGTAAAACG GAAATTATCGCCGAAACCGGCGCCGGCCAACACGGCGTCGCCTC GGCGCTGGCCAGCGCCCTGCTCGGTCTGAAATGCCGCATCTATAT GGGCGCCAAAGACGTCGAGCGGCAGTCGCCGAACGTGTTCCGCA TGCGCCTGATGGGTGCGGAAGTCATTCCAGTGCACAGCGGTTCCG CCACCCTGAAAGATGCCTGTAACGAAGCGCTGCGCGACTGGTCCG GCAGCTACGAGAAGGCGCACTACATGCTCGGCACCGCCGCTGGC CCGCACCCATTCCCGACTATCGTGCGTGAATTCCAGCGCATGATC GGCGAAGAAACCAAAGCGCAGATCCTTGAGAAAGAAGGACGCCT GCCGGACGCGGTGATCGCCTGCGTTGGCGGTGGTTCTAACGCCAT CGGCATGTTCGCTGATTTCATTGATGAATCCCGCGTTGGCCTGATT GGCGTCGAGCCTGCCGGCCACGGTATCGAAACCGGCGAGCACGG CGCGCCGCTGAAGCATGGTCGCGTCGGCATTTATTTCGGCATGAA GTCGCCGATGATGCAAACCTCCGACGGGCAGATTGAAGAATCTTA TTCTATCTCCGCCGGGCTGGATTTCCCGTCAGTGGGGCCTCAGCA TGCGTTCCTTAATAGCACCGGGCGCGCTGAGTATGTGTCAATTAC CGACAACGAAGCGCTGGATGCCTTTAAAGCGCTCTCCCGCCATGA AGGCATCATTCCGGCGCTGGAGTCGTCGCACGCTCTGGCGCACGC GCTGAAGATGATGCGCGAGAATCCGGATAAAGAGCAGCTGCTGG TGGTTAACCTGTCCGGCCGCGGCGATAAAGACATCTTCACCGTAC ACGACATTTTGAAAGCGCGAGGGGAAATCTGA
indole-3-glycerol phosphate synthase [EC:4.1.1.48]	**trpC**	>ADJCKNHF_00749 Tryptophan biosynthesis protein TrpCF ATGCAGACCGTTTTAGCAAAAATCGTTGCCGACAAAGCGATTTGG GTAGAAGCCCGCAAACAACAACAACCGTTAGCCAGTTTTCAGAA TGACATTGTGCCGTCCGAACGCCATTTTTACGATGCGCTGGCCGG CGCCCGCACCGCTTTTATTCTCGAGTGCAAAAAGGCGTCGCCGTC GAAGGGACTGATTCGGGAAGATTTCGACCCGGCGACCATCGCCG GGGTTTATAAGCACTACGCCTCGGCAATTTCGGTACTGTGCGATG AGAAATATTTTCAGGGCAGCTTTGATTTTCTGCCGATCGTCAGCA AAGTCGCGCCGCAGCCGATTCTGTGTAAAGACTTCACCATCGACC CTTACCAGATTTATCTCGCGCGTTACTACCAGGCCGATGCCTGCCT GCTGATGCTTTCGGTGCTCGATGACGATCAATATCGCCAGCTCGC CGCCGTCGCCCACAGTCTCAATATGGGCGTCCTGACCGAGGTCAG CAATGAAGAGGAGCTGGAGCGCGCGATTGCGCTGAAGGCCAAAG TCGTCGGCATTAACAACCGCGATCTGCGCGATATGTCGATTGATC TGAACCGCACGCGGCAATTGGCGCCGCGTCTCGGCCCGGATGTCA CCGTGATCAGCGAATCCGGAATCCATACCTATGGCGAAGTCCGCG AGCTTAGCCACTTCGCCAACGGCTTCCTGATTGGCTCGGCGCTGA TGGAACAACCGGACCTCAGCGCTGCGGTGAAGCGCGTGCTGTTA GGTGAGAACAAGGTCTGCGGCCTGACTCGTCCGCAGGATGCGCA AGTCGCCTGGGAGGCGGGCGCCATCTACGGCGGCCTGATTTTCGT CGATAGTTCGCCGCGTGCCGTTAACGATCAGCAGGCACAGGCGGT AATGGCCGCCGCGCCGCTTAGCTACGTTGGCGTGTTCCGTGATGC AGCCGTTGAAGAGGTCGTCACCCGCGCGACCAAATTGAAACTCG CCGCGGTCCAGCTTCATGGGAGCGAAGATCAGGCCTGGATTGATG CCCTGCGCGCGGCGCTGCCGGAGCAGATCCAAATCTGGAAGGCG CTGAGCGTCGGCGAAAGTTTACCGCCGCGCAACCTGAACCATGTG ACCAGGTATGTCTTTGACAACGGTCAGGGCGGGAGCGGTCAACG TTTCGACTGGTCGCTGCTGCAGGGCCAGGACCTGCGTAACGTGAT GCTGGCAGGCGGCCTCAGCGCCGATAACTGCGTAGAAGCCGCGA AAAGCGGCTGTGCCGGACTCGATTTCAACTCAGGCGTAGAGTCGC AGCCGGGAATAAAAGAGGCAAGCCTGGTGGCTGCCGTTTTCCAG ACGCTGCGCGCATATTAA
anthranilate phosphoribosyltransferase	**trpD**	>ADJCKNHF_00750 Bifunctional protein TrpGD ATGGCCGACATCCTGCTGCTCGATAATATCGACTCCTTTACCTATA ACCTCGCCGACCAGCTGCGGGCTAACGGCCACAACGTGGTTATTT

[EC:2.4.2.18]		ATCGTAATACCGTACCGGCACAATCGCTGATTGAACGTATCGGCA CCATGGATAATCCGGTGCTGATGCTCTCTCCGGGGCCGGGAACCC CAAGCGAAGCCGGCTGCATGCCCGAGCTGCTGACCCGCCTGCGC GGCAAGTTACCGATTATCGGTATCTGCCTCGGCCACCAGGCCATC GTGGAAGCCTACGGCGGCTATGTCGGCCAGGCGGGAGAAATCCT TCACGGCAAAGCGTCAAGCATTGAGCATGACGGCCAGGCGATGT TCGCCGGTCTCGCCAACCCGCTGCCGGTGGCCCGCTACCATTCTC TTGTCGGCAGCAATATTCCGGCCGGGCTCACCATTAACGCCAATT TCAACGGTATGGTGATGGCGGTTCGCCACGACGCCGATCGCGTCT GCGGCTTCCAGTTCCATCCGGAATCGATTCTGACTACCCAAGGAG CGCTACTGCTGGAGCAAACGCTGGCATGGGCGCTGCAGAAACTG GAGCAGACCAATGTCGTACAGCCGATTCTGGAAAAACTGTACCA GGCCGAGACGCTGAGCCAGCAGGAGAGCCACGTGCTGTTTTCCG CCGTCGTGCGCGGCGAAGTGAAGCCGGAACAGCTGGCCGCCGCG CTGGTAAGCATGAAAGTGCGCGGCGAACAACCACAGGAAATTGC CGGCGCCGCTACCGCGCTGCTGGAAAACGCCGCGCCGTTCCCGCG CCCGGATTATCAGTTTGCCGATATCGTCGGTACCGGCGGCGATGG CAGCAACAGTATCAATATCTCAACCGCCAGCGCCTTTGTCGCCGC CGCCTGCGGTTTAAAAGTGGCGAAACACGGTAACCGCAGCGTCTC CAGTAAATCGGGTTCGTCCGACCTGCTGGCCGCGTTTGGCATCAA CCTGGATATGAATGCCGATAAATCGCGCGCCGCGCTGGATGAACT GGGCGTCTGCTTTCTGTTCGCGCCGAAATACCACACCGGTTTCCG CCACGCGATGCCGGTCCGCCAGCAGTTGAAAACGCGCACCCTGTT TAACGTGTTGGGGCCGCTTATCAACCCGGCGCACCCGCCGCTGGC GTTGATTGGCGTCTACAGCCCGGAACTGGTGTTGCCGATTGCAGA AACCTTGCGCGTACTCGGTTATCAACGCGCCGCGGTGGTACACAG CGGCGGCATGGACGAAGTCTCGTTGCATGCGCCGACCGTGGTCGC CGAACTCAATAACGGCGAAATCCAGAGCTATCAGCTGACCGCCG CCGACTTCGGCCTGACGCCTTATCATCAGGAGCAACTGGCCGGCG GCACGCCGGAAGAAAACCGTGACATTCTCACGCGCTTGCTACAA GGTAAAGGTGAAGCCGCTCATGAAGCCGCCGTGGCCGCCAACGT CGCCATGTTGATGCGTTTACACGGGCATGAAGACCTGAAAGCCAA CGCCCGGCAGGTACTGGATGTGCTGCACAGCGGAGCGGCCTATG ACAGAGTGACCGCATTAGCGGCAAGAGGGTAA
anthranilate synthase component I [EC:4.1.3.27]	**trpE**	>ADJCKNHF_00751 Anthranilate synthase component 1 ATGCAAACATCAAAACCAGCGCTCGAGCTTCTCACCAGCGACGCC ATCTATCGCGAAAACCCGACGGCGTTATTCCATCAATTATGCGGC GCGCGTCCGGCAACCTTGCTGCTGGAATCGGCCGACATCGATAGT AAAGACGATTTAAAAAGCCTGCTGCTGGTCGATAGCGCCCTGCGC ATTACCGCTCTTGGCAATACCGTCACTGTCCAGGCGCTTTCAGCG AACGGCGCCGCGCTGCTTGAACTGCTGGATAACGCATTGCCGTCC GGCATTGAGAATCTGCGCCAGCCGAACAGCCGGGTACTCACCTTC CCACCGGTTAGCGCCCTGCTGGATGAAGACGCTCGCCTGTGTTCG TTATCGGTGTTCGATGCGTTTCGTCTGTTACAGGATTTGGTCAGCG TCCCGCAGGCCGAGCGCGAAGCGATGTTCTTCGGCGGCCTGTTCG CTTACGACCTGGTGGCCGGTTTTGAGGATTTACCACCGCTCAATA CCGATACCGCCTGCCCGGATTACTGTTTCTACCTGGCGGAGACGC TGCTGGTCATCGATCACCAGACCAAAAGCACCCGCATTCAGGCGA GCCTGTTCACGCCGCTGGAGAATGAGAAACAGCGTCTTCTGCAAC GTATCGCCCAGCTTCGCCAGCAGTTAAATGAACCGCCCGCGCCGC TGCCGGTGACAACGGTTGCCGAAATGCGCTGCGACGTCGATCAG AGCGATGAAGAGTACGGCGCCGTGGTGCGCAAAATGCAGCGCGC CATTCGCGCGGGCGAAATTTTCCAGGTCGTGCCGTCGCGCCGCTT CTCCCTCCCCTGCCCGTCGCCGCTGGCCTCGTACGATGTGCTGAA AAAGAGCAATCCCAGCCCGTATATGTTCTTTATGCAGGATAACGA TTTCACCCTGTTCGGCGCATCGCCGGAAAGCTCGCTGAAATACGA

		CGCCGTCAGCCGCCAGATTGAGATCTACCCCATTGCCGGCACCCG TCCGCGCGGCCGCCGCGCCGATGGTTCGCTGGATCGCGATCTCGA TAGCCGTATTGAGCTGGAGATGCGTACCGACCACAAAGAACTTTC TGAACATCTGATGCTGGTCGACCTGGCCCGTAACGATCTGGCCCG CATCTGTACCCCGGGTAGCCGCTACGTGGCGGATTTAACCAAAGT CGATCGCTACTCCTTTGTGATGCATCTGGTTTCCCGCGTGGTCGGC GAACTGCGCCGCGATCTTGATGTCCTGCACGCCTACCGCGCCTGC ATGAATATGGGCACCCTTAGCGGCGCGCCGAAAGTTCGCGCCATG CAGCTAATCGCCGCCGCGGAAGGCAAGCGTCGCGGTAGCTACGG CGGCGCGGTCGGCTACTTTACCGCCCATGGCGACCTCGATACCTG CATCGTGATCCGCTCAGCCTACGTTGAGGATGGCATTGCTACCGT GCAGGCGGGCGCCGGTATCGTGCTCGATTCCGTTCCGCAATCCGA GGCGGATGAAACCCGTAATAAAGCTCGCGCCGTGCTGCGCGCCA TTGCTCAGGCCCACCACGCGAAGGAGACTTTCTAA
alkaline phosphatase [EC:3.1.3.1]	**phoA, phoB**	>ADJCKNHF_00859 Primary amine oxidase ATGGCAAACGGCTTGATGTTTTCCCCTCGTAAAACCGCGCTGGCG CTGGCTGTCGCGGTGGTTTGCGCCTGGCAATCACCGGTCTTCGCT CACGGTAGCGAAGCGCACATGGTGCCGTTGGATAAAACGCTGCA GGCGTTCGGCGCCGATGTGCAGTGGGATGACTACGCGCAAATGTT CACCCTGATAAAAGACGGCGCTTACGTCAAAGTAAAACCCGGCG CCAAAACGGCGATCGTCAACGGTAACCCCCTTGATCTACAGGTGC CGGTAGTAATGAAGGAAGGTAAAGCCTGGGTCTCCGATACCTTTA TCAACGATGTATTCCAGTCCGGTCTCGATCAGACCTTCCAGGTAG AAAAACGCCCTCACCCGTTAAATTCGCTCTCGGCGGCGGAAATCG GTGAAGCAGTGACCATTGTTAAAGCCGCGCCGGAGTTCCAGCCG AATACCCGCTTTACTGAGATTTCCTTACACGAGCCGGACAAGGCG GCTGTATGGGCCTTTGCCCTGCAGGGAACGCCCGTTGATGCACCC CGCACCGCCGATGTGGTGATGCTCGATGGCAAACATGTCATTGAA GCCGTCGTCGATCTGCAAAACAAAAAAATCCTCTCATGGACGCCG ATTAAAGGCGCCCACGGGATGGTGCTGCTTGATGACTTCGTCAGC GTGCAGAACATTATCAATGCCAGCAGCGAGTTCGCTGAGGTGCTG AAAAAGCACGGTATTACCGATCCCAGTAAGGTGGTCACCACCCC GCTCACCGTCGGCTACTTTGATGGCAAAGATGGCCTGCAGCAGGA TGCACGTCTGCTGAAAGTCGTCAGTTATCTGGATACCGGCGACGG CAACTACTGGGCGCACCCGATTGAAAACCTGGTGGCGGTGGTCG ACCTTGAAGCGAAGAAAATCATCAAAATCGAAGAAGGCCCGGTG CTCCCGGTACCGATGGAGCCCCGTTCTTACGATGGTCGCGACCGC AACGCCCCGGCGGTGAAACCGCTGGAGATAACCGAACCGGAAGG CAAAAACTACACGATCACCGGCGATACCATTCACTGGCGGAACT GGGATTTTCATCTGCGCCTGAACTCGCGCGTCGGGCCCATTCTCTC GACGGTGACTTACAACGATAACGGCACAAAACGCCAGGTAATGT ATGAAGGTTCCCTCGGCGGGATGATCGTCCCCTACGGCGACCCTG ACGTCGGCTGGTATTTCAAAGCCTATCTGGACTCCGGCGATTACG GCATGGGCACCCTAACATCGCCTATTGTTCGCGGTAAAGATGCGC CGTCAAATGCAGTACTGCTGGACGAAACTATCGCCGATTACACCG GCAAACCGACCACTATTCCAGGCGCGGTCGCCATATTCGAACGCT ATGCCGGGCCAGAATATAAGCACCTGGAAATGGGCAAGCCCAAC GTCAGCACCGAGCGCAGGGAACTGGTGGTGCGCTGGATCAGTAC CGTCGGGAACTATGATTATATCTTTGACTGGGTGTTCCACGACAA TGGCACCATCGGTATCGATGCCGGCGCCACCGGCATTGAAGCCGT TAAAGGCGTGAAGGCGAAGACCATGCACGACCCCAGCGCCAAAG AGGATACCCGCTACGGGACGCTGATCGACCATAATATTGTCGGCA CCACCCACCAGCATATTTATAATTTCCGCCTCGATCTCGACGTGG ACGGCGAAAACAACACCCTGGTGGCGATGGATCCTGAAGTGAAG CCAAACACCGCCGGCGGCCCGCGCACCAGCACCATGCAGGTGAA TCAGTACACAATCGATAGCGAGCAGAAAGCGGCGCAGAAATTCG

		ACCCTGGCACTATCCGCCTGCTGAGCAACACCAGCAAAGAGAAC CGCATGGGTAACCCGGTCTCTTACCAGATTATCCCTTATGCCGGC GGCACGCATCCGGCGGCGACCGGCGCGAAGTTCGCCCCGGACGA GTGGATATATCATCGTCTGAGCTTTATGGATAAACAGCTGTGGGT GACGCGTTACCACCCGACAGAGCGTTATCCGGAAGGGAAATACC CTAACCGTTCCGCCCAGGATACCGGCTTAGGCCAGTACGCGAAGG ATGATGAGTCGCTGACAAACCACGACGACGTCGTGTGGATCACC ACCGGCACCACCCACGTCGCGCGCGCCGAAGAGTGGCCAATTAT GCCGACCGAGTGGGCGCACGCGCTGCTCAAGCCGTGGAACTTCTT TGACGAAACCCCAACGCTTGGCGAGAAGAAAAAGTAA
pfam01011	**pfam01011**	>ADJCKNHF_00899 Quinate/shikimate dehydrogenase (quinone) ATGGCTACAGGCAACGTGCCGCGCGGATTCCCCCGGATCCTGCAG TGGCTACTCGCCGGACTGATGTTAATCATCGGTCTGGCAATCGGC ATTTTAGGCGCCAAACTGGCAAGCGTCGGCGGCACCTGGTATTTC GCCATTATGGGACTGGTGATGGTTATCGCCTCCCTGCTTATTTTCC GCAATCGGCGCGGCGGCATCGTTCTTTATGCCGTCGCCTTCGCGG CTTCCATTGTTTGGGCTATCAGCGACGCCGGCTGGACCTACTGGC CGCTGTTCTCACGCCTGTTTGCGCTTGGCGTTCTGGCTTTTCTGTG CGCCATTGTTTGGCCTTTTCTTTCCAGCGCACCGGCAAAAAAAGG CGCGGCCTTCGCCCTCGCGGGCGTGCTGGCCGTGGCACTGCTGGT CAGTTTTGGTTGGATGTTTAAATCCCAGCCGCTGGTCAGCGCCAG CGAAGCGGTGCCGGTAAAACCGGTACAGCCAGGTGAAGAACAAA AGAACTGGCAGCACTGGGGTAATACCACTCACGGCGACCGTTTCG CCGCGTTGGATCAGATCAATAAAAACAATATCAACCAGCTACAG GTTGCCTGGATTGCCCATACCGGCGATATTCCGCAGAGTAACGGT TCCGGTGCGGAAGACCAGAATACGCCGCTGCAGATTGGCGATAC GCTTTATGTTTGTACGCCATATAGCAAAGTCCTGGCGCTGGATGT CGATAGCGGCAAAGAAAAATGGCGCTACGACTCGAAAGCGACGG CGCCTAACTGGCAACGTTGCCGCGGTTTAGGCTACTACGAAGATA GCCAGGCGCAGGCTAATGCCGTGGCCGGGACTCAGCCTGCCGCCT GTGCCCGCCGCCTGTTCCTGCCGACTACCGATGCGCGCCTGATCG CAATCGATGCCGATACCGGTAAAGCCTGTGAAGCATTTGGTGAAC ACGGTACCGTCGATCTCAGCGTCGGCATGGGGGAAATCAAACCT GGTTATTATCAGCAGACCTCTACCCCGCTGGTGGCCGGTAACCTT GTTGTCGTTGGTGGTCGCATCGCGGATAACTACTCCACCGGTGAA CCGCCGGGTGTAGTTCGCGCTTTTGACGTGCATACCGGTAAACTG GCCTGGGCCTGGGATCCGGGTAACCCGCAGCTGACCGGCGTACC GCCGGAAGGACAAACCTACACACGCGGGACGCCGAACGTCTGGT CCGCGATGTCTTACGATGCCAAACTGAATCTCATTTATCTGCCAA CCGGTAACGCCACGCCAGATTTCTTCGGCGGCGAACGTACGGCAC TGGATGATAAATACAGCTCATCAATCGTTGCGGTCGATGCCGCCA CCGGTAAAGTGCGCTGGCATTTCCAGACCACCCATCACGATCTGT GGGATTTCGACCTGCCTTCGCAACCACTGCTGTACGATCTGCCGG ACGGTAAAGGCGGTACGACGCCGGTACTGGTGCAAACCAGCAAG CAGGGCATGATCTTCATGCTTAACCGCGCGACGGGTGAACCGGTG GCGAAAGTGGAAGAACGCCCTGTCCCGGCCGGCAACGTCAAAGG TGAACGCTACTCGCCGACGCAGCCCTACTCCGTCGGCATGCCGAT GATCGGCAACGAAACGTTGAAAGAATCGGATATGTGGGGCGCCA CCCCGGTTGACCTGCTGCTGTGCCGTATTCAGTTCAAAGAGATGC GCCATCAGGGTGTCTTTACACCGCCGGGTGAAGACCGCTCCTTGC AGTATCCGGGCTCGCTTGGCGGAATGAACTGGGGCAGCGTGTCG GTCGATCCGAATAACGGCCTGATGTTCGTCAATGACATGCGCCTT GGACTGGCTAACTACATGGTACCGCGAGCGAAAGTGGCTAAAGA TGCCAGCGGTATCGAAATGGGTATCGTACCGATGGAAGGTACGC CGTATGGCGCAATGCGCGAGCGTTTCCTGTCGCCGCTGGGCATCC CCTGCCAGAAGCCGCCGTTCGGTACCATGTCGGCGGTTGATCTGA

		AAAGCGGTAAGCTGGTCTGGCAGGTTCCGGTAGGTACGGTAGAA GATACCGGTCCGCTGGGTATCCGCATGCATATGCCGATCCCTATC GGCATGCCAACGCTGGGAGCTTCGCTGTCTACCCAGTCTGGCCTG CTGTTCTTCGCCGGCACCCAGGATTTCTATCTGCGCGCCTTTGATA CCGCCAACGGCAAAGAGATTTGGAAATCTCGCCTGCCGGTGGGC AGCCAATCCGGCCCGATGACCTACGTTTCACCGAAAACCGGTAAG CAGTACATCATTATCAACGCCGGCGGCGCGCCAGTCTCCGGAT CGCGGCGATTACATCATCGCTTACGCTTTAGCGGATAAGCAGTAA
nitrate reductase gamma subunit [EC:1.7.5.1 1.7.99.-]	**narI, narV**	>ADJCKNHF_00973 Respiratory nitrate reductase 2 gamma chain ATGATACAGTACTTAAACGTCTTCTTTTACGATATCTACCCTTATC TCTGCGGCACCGTGTTCCTGGTGGGCAGTTGGCTGCGCTATGACT ACGGGCAGTATACCTGGCGCGCGTCATCCAGCCAGATGCTCGATA AACGGGGCATGGTGCTGTGGTCGAACTTATTCCATATCGGCATCC TCGGCATTTTCTTCGGCCACTTCTTCGGGATGCTGACGCCGCACTG GGTCTATTCATGGTTTCTGCCGATGTCGCAGAAACAGGTGATGGC GATGGTGCTGGGCGGTGTCTGCGGCGTACTGACCCTGGTCGGCGG TATTGGCCTGCTGGCGCGCCGCCTGACCAACCCGCGCATTCGCGC CACCTCCACCACTGCGGATATTCTGATCCTGTGCATTCTGCTGATT CAGTGCGCGCTGGGGCTGACGACCATCCCGTTCTCCGCCCAGCAT CCGGACGGCAGCGAAATGCTGAAACTGGTGGATTGGGCGCAGGC GGTAGTCACCTTCCACGGCGGCGCATCGGCGCATCTGGACGGCGT CGCGTGGGTGTATCGCGTCCATCTGGTGCTGGGAATGACTATCTT CCTTATCTTCCCGTTCACCCGGCTGGTTCACGTCTGGAGCGCGCCG ATAGAGTATTTCACCCGCCGCTACCAGGTGGTGCGCTCCCGGCGC TGA
nitrate reductase molybdenum cofactor assembly chaperone NarJ/NarW	**narJ, narW**	>ADJCKNHF_00974 putative nitrate reductase molybdenum cofactor assembly chaperone NarW ATGCGGATCCTCAAAGTCATTGCTCTGTTGCTGGAGTATCCCGAC GACGCGCTGTGGGATAACCGCGAGGAGGCGCTGGCGCTGGTCAG CGCCGATGCGCCTGCCCTGACGCCGTTTGTTAGGCGATTACTGGC GGCGCCGCTGCTCGACCGCCAGGCCGAATGGTGTGAGGTATTTGA ACGCGGTCGCGCCACCTCGCTGTTGCTGTTTGAACACGTTCACGC CGAATCACGCGATCGCGGCCAGGCGATGGTCGATCTGATGAACC AGTATGAACAGGCGGGCCTGCAGATCGATTGTCGCGAACTGCCG GACCACCTGCCTTTATATCTTGAATACCTCAGCATTCTCCCATTAG CCGATGCCCGTGAAGGACTGCAGAACGTCGCGCCTATTCTGGCGT TGCTCGGTGGACGCTTAAAGCAGCGCGAATGCGATTACTATCAAC TCTTTGACACCCTTCTTGCGCTGGCGGATAGCCCACTCAATAGTG ACAGTGTCACCAGGCAGGTAGCGAGTGAGAAGCGTGACGACACC CGCCAGGCGCTGGATGCGGTGTGGGAAGAGGAACAGGTGAAGTT TATTGAAGATAATGCAACCGCTTGCGATAGCTCGCCGATGCAAGC TTATCAACGACGCTTTAGCCAGGATGTGGCGCCGCAGTACGTCGA CATCCGCGCCGGAGGCCCGAAATGA
nitrate reductase / nitrite oxidoreductase, beta subunit [EC:1.7.5.1 1.7.99.-]	**narY, narH, nxrB**	>ADJCKNHF_00975 Respiratory nitrate reductase 2 beta chain ATGAAAATACGTTCACAAGTCGGAATGGTGCTGAATCTGGATAA ATGCATCGGATGCCATACCTGCTCCGTCACCTGTAAAAACGTCTG GAGCAGCCGCGAAGGGATGGAATATGCGTGGTTCAACAACGTGG AAACCAAGCCAGGTATTGGTTACCCCAAAAACTGGGAAGATCAG GACGAGTGGCAAGGCGGCTGGATCCGCGGTATCAGCGGCAAGCT TACTCCGCGTCTGGGCAACCGCGTCAGCGTGTTGTCGAAGATTTT CGCCAACCCGGTGCTGCCGCAGATTGACGATTATTACGAACCCTT TACCTACGATTATCAGCACCTGCACAACGCGCCGGAGGGCAAAT ACTTGCCTACCGCCCGCCCGCGTTCGCTGATTAGCGGCGAACGGA TGGATAAGATCACCTGGGGGCCAAACTGGGAGGAACTGCTCGGC GGCGAGTTTGAAAAACGCGCCAAAGACCGTAACTTCGAAGCGAT GCAAAAAGAGATGTACGGCCAGTTTGAAAACACCTTCATGATGT

		ATCTGCCGCGTCTTTGCGAACATTGCCTCAATCCGAGCTGCGTAG CGACCTGCCCAAGCGGCGCCATCTATAAGCGTGAAGAAGACGGT ATCGTGCTGATCGACCAGGATAAATGCCGCGGCTGGCGGATGTGC ATCAGCGGTTGTCCGTACAAAAAAATCTACTTTAATTGGAAGAGC GGCAAATCGGAAAAATGCATCTTCTGCTATCCGCGTATTGAGTCC GGGCAACCGACAGTCTGTTCAGAAACCTGCGTTGGCCGCATCCGC TACCTTGGCGTGCTGCTGTACGACGCGGACCGTATCGAAGAAGCG GCCAGCACTGAACATGAAACCGACCTCTACGAGCGCCAGTGTGA TGTGTTCCTCAACCCCAACGATCCGGCGGTCATCGAAGAGGCGTT GAAACAGGGTATTCCACATAACGTGATCGACGCCGCGCAGAAAT CACCGGTGTATAAACTGGCGATGGACTGGAAGCTGGCGCTGCCG CTGCACCCGGAATACCGCACCTTACCGATGGTCTGGTACGTGCCG CCGCTGTCGCCGATTCAGTCGGTCGCCGACGCTGGCGGCCTGCCG AGTAACGGTAACGTCCTGCCGGCGGTAGAAAGCCTGCGTATACC GGTACAGTATCTGGCGAACCTGCTGAGCGCCGGTGATACCGGCCC GGTCTTGCGCGCGTTAAAACGCATGATGGCGATGCGCCATTACAA ACGTTCGCAAACCGTCGAAGGCGTGACCGATACCCGTGCGATTGA AGAAGTGGGCCTCAGCGTCGAACAGGTGGAAGAGATGTATCGCT ACCTGGCGATCGCCAATTATGAAGACCGCTTCGTGATCCCCACCA GCCACCGCGAACTGGCGGAGGACGCCTTCCCTGAACGCAACGGC TGCGGTTTTACCTTCGGCGATGGTTGCCATGGTTCTGATACTAAAT TCAACCTGTTCAACAGTCGTCGCATCGACGCTATTGACGTCGGAG ATGTTCGTCGACATGGGGAGGGAGAGTAA
nitrate reductase / nitrite oxidoreductase, alpha subunit [EC:1.7.5.1 1.7.99.-]	**narG, narZ, nxrA**	>ADJCKNHF_00976 Respiratory nitrate reductase 2 alpha chain ATGAGTAAATTACTGGATCGCTTTCGCTACTTTAAGCAGAAACGC GAGACCTTTGCCAACGGCCACGGTCAGGTCTACGACAATAACCGT GACTGGGAAGATAGCTACCGGCAACGCTGGCAATTCGACAAAAT TGTCCGCTCCACGCACGGTGTGAACTGTACCGGCTCCTGTAGCTG GAAAATTTATGTCAAAAACGGTCTGGTCACCTGGGAAACCCAGC AGACCGATTATCCGCGCACCCGACCGGACCTGCCAAATCACGAA CCGCGCGGCTGTCCGCGCGGCGCCAGCTACTCCTGGTATCTCTAC AGCGCCAACCGCCTGAAGTACCCGCTGGCGCGCAAACGGCTGAT TGAGCTGTGGCGCGAAGCACTTACACAGCATCCCGACCCGGTACA GGCCTGGGATAGCATCATGCAGGACCCCCTGAAAACCCGCAGCT ACAAACAAATCCGCGGTAAAGGCGGTTTTGTTCGCTCCAGTTGGA AAGAGTTAAATCAACTGATCGCCGCAGCTAACGTCTGGACCATCA AAAACTACGGTCCGGACCGCGTCGCGGGCTTTTCGCCGATCCCGG CGATGTCGATGGTTTCCTACGCCGCGGGTACCCGCTATTTATCGTT GATCGGCGGCACCTGCCTGAGCTTTTATGACTGGTACTGCGATTT ACCCCCCGCCTCGCCGATGACCTGGGGCGAACAGACCGACGTGC CGGAATCCGCCGACTGGTATAACTCCAGCTACATTATTGCCTGGG GTTCAAACGTCCCGCAGACCCGAACCCCGGACGCGCACTTCTTCA CCGAAGTGCGCTACAAGGGCACCAAAACCATCGCCATTACTCCG GATTATTCGGAAGTCGCCAAGCTCTGCGACCAGTGGCTGGCGCCG AAGCAAGGTACCGACAGCGCGCTGGCGATGGCGATGGGCCACGT GATCCTCAAAACCTTCCACCTCGATAACCCAAGCGATTACTTTCT CAACTACTGCCGTACCTATACCGATATGCCGATGCTGGTAATGCT CGACCGTCGTGACGACGGCAGCTATGCGCCTGGCCGTATGCTGCG CGCCGCCGACCTGCTTGACGGGCTGGGAGAAAGTAATAACCCGG AATGGAAAACCGTCGCCTATAACGCCGAAGGCGAGCTGGTCGCG CCGAACGGATCCATCGGCTTTCGTTGGGGCGAAAAAGGCAAATG GAATCTCGAACAACAGGCTAACGGCCGGGACGTCGAATTAAAAT TGTCGCTGCTGGATATGCACGATAGCGTGGTGTCGGTCGGTTTCC CCTACTTCGGCGGCAACGAAAACCCGCATTTCCGCAGCGTGAAGC AGGAGCCGGTAACGCTTCATCAGCTGCCAGCTAAACAGCTACCGT TGGCCAATGGTGAGAGCGCTTTGGTGGTGAGCGTGTATGACCTGG

		TGCTGGCTAACTACGGTCTGGATCGCGGTCTTGGCGATGCCAATG CCGCGCGCGACTTCGCGGATGTCAAAGCCTATACCCCGGCATGGG CCGAGCAGATCACCGGCGTGCCGCGTCAACATATCGAACAAATC GCCCGCGAGTTCGCCGATACGGCGCATAAAACCCATGGCCGTTCG ATGATTATCCTCGGCGCCGGTGTGAACCACTGGTACCACATGGAT ATGAACTACCGCGGGATGATCAACATGCTGGTGTTCTGCGGCTGC GTCGGTCAGAGCGGCGGTGGCTGGTCGCACTATGTCGGCCAGGA GAAACTGCGCCCGCAGACCGGCTGGCTGCCGCTGGCGTTCGCGCT GGACTGGACTCGTCCGCCGCGGCAGATGAACAGTACCTCTTATTT CTACAACCACGCCAGCCAATGGCGCTACGAAAAACTGACCGCTC AGGAGCTGCTGTCGCCGCTGGCCGACGCCAGCAAATTCAGCGGC CATATGATTGACTTCAACGTTCGCGCCGAGCGCATGGGCTGGCTG CCGTCCGCGCCGCAGCTTAACGTTAATCCGCTGAGCATCAGGCAG CAGGCCGAGGCCGCCGGGCTGTCACCGGCCGATTTCACTGTCCAG TCGTTAAAAGCAGGCGATATTCGCTTTGCCGCCGAGCAGCCGGAT AGCGGCAACAACCACCCGCGCAACCTGTTTATCTGGCGTTCGAAC CTGCTGGGTTCGTCCGGTAAGGGCCATGAGTACATGCTCAAGTAC CTGCTCGGTACCGATAACGGTATTCAGGGCGAGGAATTTGGCTCC ACCGCTGACGTGAAGCCGGAGGAAGTCGAGTGGCAGACCGCGGC GATCGAGGGCAAACTTGATCTACTGGTGACCCTCGATTTCCGCAT GTCCAGTACCTGCCTGTTCTCCGATATCGTCCTGCCGACCGCCACC TGGTATGAAAAAGACGATATGAACACCTCAGACATGCACCCGTTT ATCCACCCCCTTTCCGCCGCCGTCGACCCGGCCTGGGAGGCGAAA AGCGACTGGGAAATCTACAAGGACATCGCCAAAAGTTTCTCTGA AGTGTGCGTCGGCCACCTTGATAAAGAGACCGATGTGGTACTGGT ACCGCTGCAGCATGACTCTCCGGCGGAGCTGTCACAGCCGTTCGA AGTCCTCGACTGGCGCAAGGGCGAATGCGATCTCATTCCAGGCAA AACCGCGCCGTCAATTGCGCTGGTTGAACGTGACTACCCGGCCAC CTGGGAACGCTTCACCTCGCTGGGGCCGTTACTCGATAAGCTCGG CAACGGCGGTAAAGGCATTTCGTGGAATACGCAAAGCGAGGTCG ACTTCCTCGGCAAACTTAACTACGTCAAGCCAGACGGTCCGGCCA AAGGCCGTCCGCGTATCGACAGCGCTATCGACGCCAGTGAAGTC ATCTTAAGCCTGGCGCCGGAAACCAACGGCCAGGTGGCGGTGAA AGCCTGGCAAGCGCTGGGAGAATTTACCGGCCGCGACCACACTC ATCTGGCGCTGAATAAAGAGGATGAGAAAATCCGCTTCCGCGAT ATTCAGGCGCAGCCGCGCAAGATCATCTCCAGCCCAACGTGGTCT GGTCTGGAAAGCGAACATGTCTCCTATAATGCCGGTTATACCAAC GTTCACGAACTGATCCCGTGGCGTACCCTCTCCGGGCGGCAACAG CTGTATCAGGATCATCCCTGGATGCGCGCCTTCGGCGAGAGTCTC GTGGCCTATCGCCCACCGATCGATACGCGCAGCGTCAGCCAGATG AAGGAAGTGCCGCCAAACGGCTTCCCAGAAAAAGCGCTGAACTT CCTGACCCCGCATCAGAAATGGGGTATCCACTCGACCTATAGCGA AAACCTGCTGATGCTGACGTTGTCGCGCGGCGGGCCCATCGTCTG GCTAAGCGAAACCGACGCAAAAGAACTGGGGATTGAAGATAACG ACTGGATCGAAGCCTTCAACGCCAACGGCGCCCTCACCGCGCGTG CGGTGGTGAGCCAGCGCGTGCCGCCGGGCATGACCATGATGTATC ACGCTCAGGAACGCATTATGAACATTCCAGGTTCGGAGGTGACCG GTCGCCGGGGCGGCATCCACAACTCCGTGACCCGCGTCTGTCCTA AACCCACGCATATGATTGGCGGCTATGCCCAACTGGCTTACGGCT TTAACTACTACGGCACCGTCGGCTCCAACCGCGACGAGTTCATTA TGATCCGCAAAATGAAAAATATTGACTGGCTGGATGGCGAAGGT CGTGACCAGGTACAGGAGGCGAAGAAATGA

pyrroloquinoline quinone biosynthesis protein PqqF	**pqqF**	>ADJCKNHF_01048 hypothetical protein ATGACCACCGCCACCCGCATCGTGGAACTGGCAGGCGGGATTCG CGCAACGCTGGTTCATCAGCCGCAGGCGACGCGTGCTGCGGCGTT GGTTAAGGTGGGTGCCGGAAGCCATCACGAAACCGATGCCCTGC CGGGGCTGGCCCATTTACTGGAACATTTGCTGTTTCGCGGCAGCC AGCGCTATCACGCAGACGAGCGATTAATGGCGTGGATCCAACGC CAGGGCGGCAGCGTCAACGCCACCACCCTTGCCCGCCACAGCGC CTATTTCTTCGAGGTCGCCGCCAGTAGTCTGGCCGAGGGCATCAC CCGTCTACGGGATACGCTCCAGGCGCCGCTGCTGTCGCCTGAAGA TATCCGTCAGGAACTGGCGGTCATCGATGCGGAAAACCGGCTTAT CCAGCAGCACGATCCCTCCCGCCGTGAAGCCGCAGCCCGTCACGC GATGGCGGCGCCCGCGGCTTTTCGCCGTTTTCAGGTCGGCAGCAT GGATTCTCTGGGCGGAAACTTGCCTGCGCTGCAGGTTGCGCTCGG CGAGTTTCATCAGCGCTATTATGTCGCCAGCCATCTGCAGCTATG GCTTCAGGGGCCGCAGTCGCTTGATGAATTAGCCGCATTGGCCCA TTTTTTTGCCGCGGGATTCCCTGGCGGCCTGCCGCCGGAAAGCCC GCCGTCTGCGTATTTTAGCAACAATGTGGATCTTCAACTGGCCGT TGAAGACCAACCGGCGGTATGGCGTTGTCCGCTCATTGCAGTAAG TGACAACGTCACTACTTTTCGTGAATTCTTACTGGATGAAGCGCC CGGCAGCCTGCTGGCCGGGCTACGTGAATGCGGGCTCGCGGACG ATGTCGCGCTGAACTGGCTTTACCAGGATGAACGCGTCGGCTGGC TGGCGCTGGTATTTACCAGCGACCATCCCGACGCCATCCAGCAGC ATCTCGAGCGATGGCTGCAGGCATTGCGCCACACCTCGCCTGAAC AGCAGTTGCACTATTACAGGCTGGCGCAGAGGCGTTTTAACGCAC TCACCCCGCTCGAACAGTTACGTCAGCGGGCATTGGGTTTTGCGC CCGATTCCCCGCCCATCGACTTTGCCCGTTTCTGCGCCAGCTTGCT GACGGCGCCAGCCTCTTCGCTGGTGTGCCGCAAAATAGCGGCTGG CGATGGCGTGGCAACCCAGGGCTTTACCTTGCCGCTCGGCCGCAG GCAACCACGGACAGTCGTGATTGATCCGCTGGCATTTAGCTTCTA TCCGCAGGCGGCGACCACGGCAGCGCCTGACCTGCCGCCAACGA CCAGCCCGCTGCTGCATGTCATTGCAGATAATCAAACGCCAACGC TGATCGTTCGCAAGCCATTCTATAGCGTGCTTAGTCAGGCGCAGG GGATGGCGATAAGCCAGCAGCTCCGTCCCTTGCTCGCGCAACTTC GCCATGCTGGCGGCAGCGGCGAGTGGCAAACGGTGGACGGCAAC TGGCAGCTTACCCTACAGCTACCGGAATCCGGCGGCGTAGCGGA GCGCGTCGTCACCGCACTTATGCGCCGATTAGCCCAACCCGCTCC GGGGACGACGGTCGCACCTGAAACCATTGCGATTCGCCAGCTACT GCAACAATTACCTGAACATCTGACTATCGCCCGGGCGCAAGAGG GTTGGCTGGCGGCGATGGTGGGCGGCAGCGGCAATCTGGCGCAG CAGGTTGCCCGTCAGTTGACGCTGCTCAATACCCCGATCAACGCC GAGCTTCACTCTTCGGCGGGCTGTCGCCGCGGTATTCAGCGTATT CCCCACGCCAGCTCGGATAACGCGCTATTAGTTTTTATTCCATTGC CCGAGGGGGCATCGCTGGCCGCGCTGCAACTGCTGGCGCTACTTT GCGAGCCGCAATTCTTCCAGCGTCTGCGGGTCGAACAGCAGATTG GCTACGTGGTGAGCTGCCGTTATCAGCGGATCGCCGATCGCGATG GCCTGCTGCTGGCGCTGCAGTCGCCAGATCGTTCCATCAGTAACC TGCTACGCTGCTGTAAAACCTTTCTCCGCCAGTTAACGCTGGGTG GGCAAGCTGAGTTCAGTCAGTTACAACACCAGTTGGCTGAGCAGC ACGGTCTGCCGCAGGACGCCAGCGCCACCGCACTCTCCGCCCTGC ACCAGCGCTATCATCTACCGGTAGCCACGCCGCAGAACGTTAACG ACCTACAGCTGGACGAGGTCATCGCGCTATGGCGTGAGATAACTC GCCGTCGCCGCAGCTGGCGAATCCTGTATAGCGCGCCGACGACGT CCGCCACTTAA
PqqA peptide cyclase [EC:1.21.98.4	**pqqA**	>ADJCKNHF_01049 PqqA peptide cyclase GTGAGCCAGAATAAACCCGCCGTTAATCCGCCGCTGTGGCTACTG GCGGAGCTGACCTATCGCTGTCCGTTGCAGTGCCCCTACTGCTCT

]		AACCCGCTGGACTTTGCTCAGCAGGAGAAAGAACTCACCACCGA ACAGTGGATTGAGGTCTTTCGCCAGGCGCGGGCCATGGGTAGCGT GCAGATGGGTTTCTCCGGCGGCGAACCGCTGACGCGCAAAGATCT GCCGGAGCTTATCCGCGCCGCGCGCGACCTCGGTTTTTACACCAA TCTGATTACGTCAGGCATTGGGCTCACCGAGAGCAAACTCGACGC CTTCAGCGAGGCCGGGCTGGATCATATCCAGATTAGCTTCCAGGC CAGCGATGAAGTGCTTAACGCGGCGCTGGCGGGCAACAAAAAAG CGTTCCAGCAGAAGCTGGCGATGGCGAAAGCGGTAAAAGCACGC GACTACCCGATGGTGCTGAACTTTGTCCTCCATCGCCACAATATC GACCAGATCGATAAAATCATCGAGCTGTGTATCGAGCTGGAAGC GGATGATGTTGAGCTCGCCACCTGCCAGTTTTACGGCTGGGCGTT CCTCAATCGTCAGGGGTTACTGCCGACCCGCGAACAGATCGCCCG AGCTGAACAGGTCGTTGCTGATTACCGCCATAAAATGGCGGCTAA CGGTAATCTGACCAATCTGCTCTTTGTCACCCCGGACTACTACGA AGAACGCCCTAAAGGCTGTATGGGCGGCTGGGGCTCGATATTCCT CAGCGTGACCCCGGAAGGCACCGCGCTGCCGTGTCACAGCGCGC GCCAGTTACCGGTCGAGTTCCCATCGGTGCTGGAGCAGAGCCTGG AATCGATCTGGTATGACTCGTTTGGCTTCAACCGCTACCGCGGCT TCGACTGGATGCCGGAGCCGTGCCGTTCCTGTGATGAAAAAGAG AAAGATTTCGGCGGCTGCCGCTGTCAGGCCTTTATGCTGACCGGC AATGCCGATAACGCTGACCCGGTGTGCAGCAAATCGCCGCACCA CCATAAAATCCTTGAAGCGCGGCGCGAAGCGGCCTGTAGCGACA TCAAAATCAGCCAGCTGCAGTTCCGTAACCGCACCCGTTCACAGC TGATCTATAAAACCCGGGAATTGTGA
pyrroloquinoline quinone biosynthesis protein D	**pqqD**	>ADJCKNHF_01050 PqqA binding protein ATGCAAAAAAGCGCAATCATCGCCTTTCGTCGCGGCTACCGCCTG CAGTGGGAAGCTGCTCAGGATAGCCACGTGATCCTCTATCCGGAA GGAATGGCGAAACTAAATGAGACCGCCGCCGCGATCCTCGAACT GGTCGATGGTCAACGCGACGCGGCAAAAATAATCGCCGAACTCA ACGCCCGTTTCCCGGAAGCCGGCGGCGTCGATGACGACGTCATCG AATTCCTGCAGATAGCTTACCAACAGAAGTGGATTATCTTCCGTG AGCCAGAATAA
pyrroloquinoline-quinone synthase [EC:1.3.3.11]	**pqqC**	>ADJCKNHF_01051 Pyrroloquinoline-quinone synthase ATGCAGATTCGCGAAACCCTATCGCCACAGGCGTTTGAACAAGCG CTACGGGAAAAAGGCGCCTACTACCATATCCATCATCCGTACCAT ATTGCGATGCATAACGGCGAGGCCAGCCGCGAACAAATCCAGGG CTGGGTGGCGAACCGTTTTTACTACCAGACCAATATCCCGCTAAA AGACGCGGCGATTATGGCAAACTGCCCCGATCCACACACCCGAC GCAAATGGGTGCAGCGGATCCTCGACCACGATGGCAGTAACGGC CAGGAAGGCGGTATTGAAGCCTGGCTGCAGTTGGGTGAAGCCGT GGGGCTAAGCCGTGATGAGTTACTCAGCGAGCGCCACGTGCTGCC CGGGGTGCGTTTTGCCGTCGACGCCTACGTTAATTTTGCCCGGCG GGCCAACTGGCAGGAAGCGGCGTGCAGTTCGCTGACCGAACTGT TTGCCCCGCAAATCCATCAGTCGCGCCTCGACAGCTGGCCGCAGC ACTACCCATGGATCAAAGAAGAAGGCTATTTCTACTTCCGCAGCC GCTTAAGCCAGGCCAATCGCGACGTCGAACATGGGCTGGAGCTG GCGAAGATCTACTGCGATAGCGCGGAAAAGCAGAACCGGATGCT GGAGATCCTGCAGTTTAAGCTCGACATTCTGTGGTCGATGCTGGA TGCCATGACCATGGCCTATGCGTTGCAGCGCCCGCCCTATCATAC GGTCACCGACAAGGCGGCCTGGCACACGACCCGACTGGTATAA
pyrroloquinoline quinone biosynthesis protein B	**pqqB**	>ADJCKNHF_01052 Coenzyme PQQ synthesis protein B ATGTTTATAAAAGTCCTCGGTTCCGCCGCTGGCGGAGGTTTTCCG CAGTGGAATTGTAACTGCGCCAACTGTCAGGGGCTGCGCAATGGC ACAATTCAGGCCACCGCCCGCACCCAGTCTTCGATTATCGTTAGC GATAACGGCAAAGAGTGGGTGCTGTGTAACGCCTCTCCGGATATC AGCCAGCAAATTGCCCACACGCCAGAGTTAAACAAACAAGGCGT

		GCTGCGCGGCACGCATATTGGCGGCATTATCCTTACCGATAGCCA GATTGACCATACTACCGGGCTGCTGAGCCTACGCGAAGGGTGTCC CCATCAGGTCTGGTGCACGCCGGAGGTACATGAGGATCTCAGCAC GGGTTTTCCCATTTTTACTATGTTACGGCACTGGAACGGCGGCCT GATTCACCATCCTGTCACCCCGCTGAATAGTTTTACCGTTGACGCC TGTCCCGACCTGCAGTTTACCGCCGTCCCCATCGCCAGCAATGCG CCGCCCTACTCGCCGTTTCGCGATAGGCCGCTGCCGGGCCATAAC GTGGCGCTGTTTATCGAAAACCGCCGCAACGGCCAGACGCTATTC TATGCGCCGGGGCTTGGCGAACCGGACGAAGCGCTCTTGCCGTGG CTGAAAAAAGCGGACTGTCTGCTGATTGACGGCACCGTATGGCA GGATAATGAACTGCAGGCTGCCGGCGTCGGGCGCAATACCGGTC GTGATATGGGCCATCTGGCGCTTGGCGATGAACACGGCATGATGG CGCTGCTGGCCTCACTCCCGGCGAAGCGCAAGATTCTGATTCATA TCAACAATACTAATCCAATCCTTAACGAGCAGTCGCCGCAGCGTA ACGCCCTGACGCAACAGGGAATTGAAGTGAGCTGGGACGGAATG CCTATCACGCTTCAGGACTAA
pfam13353	**pfam13353**	>ADJCKNHF_01563 Anaerobic sulfatase-maturating enzyme ATGAAAAAAAGCACCACCATTCCATTAACGCCATTACAGAACCA GGGGCGCTATCTGCCCGCCTATAAACGCCGCTATCACATGATGGC GAAACCCAGCGGCTCCACCTGCAACCTGGACTGTCAATACTGTTT TTATCTGCATAAAGAGCAGCTTTTACATCAGCCGCACGACAAAGG AATGAGCGACGAGGTACTGGAGAATTTCATTCGTCAGTACATCCA AAGCCAGGACGGCGAAGAGATTATTTTCTCCTGGCAGGGCGGCG AGCCAACCCTGATGGGACTGGAGTTTTTCGAAAAGGTCGTTGAGC TGCAAAAAAAAATATCAGCCGAAGCACCAGCGCATTGAGAACGAT CTGCAGACCAATGGCGTGCTGATTAACGATAAGTGGGCCGCCTTC TTGAAGGCGCATAACTTCCTGGTCGGGGTATCGATCGATGGCCCG CGCGAGATCCACGATCGCTTCCGCGTGACGCGCAGCGGCAAGCC GACCTTCGATAAGGTTATGGAAGGGATCGCGGCGCTGAAGCGCC ACGGCGTGCCGTTCAACGCGCTGGCAGTCGTTAACCGGGTGAATG CCCGTTTCCCGCGCGAGGTATATCGTTTTCTTACCCGCGAACTCGG CGCCACCTATATCCAGTTTACGCCCTGCGTAGAGGCCGCCGAGTT TAAAACTACCGCGCCGCAGTTCTGGCGCGAAGAGACGATCCCCAT CACCGGCAGCCGCCGGGCGAAACCGGGGGATCTGGATTCAATCG TCACCGACTGGTCGGTGGATCCGGACGATTGGGGGCATTTTCTGA CCGAAGCTTTTGATGAGTGGGTGACCTGTGATCTGGGCCGCGTGC AGGTAAATTTGTTCGAAACCGCCGTGGTGCAGACTATGGGGCTTC CATCCCAGTTATGCATCACCGCGCCGTTTTGCGGCAAGGCGCTGG CGATTGAGAAAAACGGCGACGTCTACTCCTGCGATCACTACGTCT ACCCGGAATATAAGCTTGGCAATATTAAGGCGCATAAGCTGGCG CATATGGTCTTTTCCGAGCGGCAGAAAGTGTTTGGCATGGGCAAG AAAGAGACGCTGCCCGCCTACTGCAAAAGCTGCCCGCATCTGAAT TTATGCTGGGGCGAATGCCCGAAAAACCGCATCGTGCGCGCCCCG GACGGCGAAGAAGGGCTCAATTATTTGTGTCCCGGCTTTCGCCAT TTTTACGCGACGGTTAAACCGACGCTTGAGAAAATTGCCGCCATG CTGAAGTAG
pfam13186	**pfam13186**	>ADJCKNHF_01571 Anaerobic sulfatase-maturating enzyme ATGAAACACAGCACCACCGTGCCTGTTAACGCATTACCTTCGGCA GAAAAGTACGCGGGTAACGGCCCCGCCTACCAACGTCGCTTTCAT GTGATGGCGAAACCCAGCGGCTCCGCCTGTAATCTCGATTGTAGC TACTGCTTTTACCTGCACAAAGAACACTTACTCCAGCAGGAAAAG CGCAGCTACATGAGCGATGAAACGCTGGAAAACTTTATCCGCCA GTACATCGATGGACAGGATGGCGAACAGGTGGTCTTCTCCTGGCA GGGCGGCGAACCGACCCTAATGGGACTGGAGTTTTTCCACAAAGT GGTGAAATTCCAACAGCAATATAAAAAGCCCGGCCAGCGGATCG AAAACGATCTGCAAACCAACGGTATCCTGATTAACGATGCCTGGG

		CTGAATTCCTCAAAACGAATCATTTCCTTGTCGGCCTGTCGATTGA CGGCCCGCGAGAGTTGCACGACCGTTATCGCATCACCCGCAGCGG CAAACCGACATTTGATAAAGTGATGGCCGGCGTCGACGCCCTGA AGCGCCACGGCGTTCCATTCAATGCGCTGGTGACCATCAACCGTA CCAACGCCCGTTTCCCATTAGAGGTTTACCGCTTTGTTACCCGCGA ACTGGGGGCGACCTATGTGCAGTTTAACCCCTGCGTCGAACCGGT GGACTTTACCCAGACCGCGCCCCATTTCTGGCGTGATGACACTAT CCCCACCGTCGGCAGCCGCCGCGCGCGCCCCGGCGATTTAGACTC CATCGTCACCGACTGGTCGGTCGACCCGGACGACTGGGGACGCTT CCTGATAGCCACCTTCGAAGAGTGGGTGAACAACGATCTTGGCCG CGTACAGGTCAATCTGTTCGAAACCGCCGTCGCCCAGATGATGGG TCTGCCGGCGCAAATTTGCACCACCGCGGAGTTTTGCGGCAAAGG ACTCGCGGTCGAGAAAAACGGCGATGTTTTCTCCTGCGATCACTA CGTCTATCCGGAGTATCAAATCGGCAATATCGCCGATAACAGCCT GGCGCGAATGGCTTTCTCCGAACGTCAGCAGGCTTTCGGTATGGG TAAATGCGACACGCTGCCCCAGCAGTGCAAGCAGTGCCCTTACCT GAAGCTTTGCCACGGCGAGTGCCCGAAAAACCGTCTGGTGCTCAC TACCGACGGCGAAGCCGGTTTGAACTATCTCTGCCCGGGCATTAA AGCCTTTTTCAACTATGCCGAGCCGATTCTGGCGGGCATCGTCAC GCTGGTGAAACGCGATTTTAAAGGAGTTAGCCGATGA
agmatinase [EC:3.5.3.11]	**speB**	>ADJCKNHF_01700 Agmatinase ATGAGCACTTTAGGTCATCAATACGATAACTCCCTGGTATCCAAC GCCTTTGGTTTCCTGCGTCTGCCGATGAACTTTATGCCGTATGAAA GCGATGCGGATTGGGTCATCACCGGCGTGCCGTTTGATATGGCGA CCTCCGGGCGCGCGGGCGGCCGTCATGGCCCGGCAGCGATCCGTC AGGTGTCAACCAACCTCGCCTGGGAGCACAACCGTTTCCCATGGA ACTTCGACATGCGCGAACGCCTGAACGTCGTGGACTGCGGCGATC TGGTCTACGCCTTCGGCGACGCCCGCGAAATGAGCGAGAAACTG CAGGCGCACGCGGAGAAACTGCTGGCGGCCGGTAAACGCATGCT CTCCTTCGGCGGCGACCATTTCGTCACCCTGCCGCTGCTGCGCGC CCACGCCAAGCATTTCGGTAAAATGGCGCTGGTACACTTCGATGC CCACACCGATACCTACGCCAACGGCTGTGAATTCGACCACGGCAC CATGTTCTACACCGCGCCGAACGAAGGGCTTATCGATCCGAACCA CTCCGTGCAGATCGGTATTCGTACCGAATTCGATAAAGATAACGG TTTTACCGTGCTTGATGCGGGCCAGGTTAACGACCGCAGCGTCGA TGACATCATCGCTCAGGTGAAGCAGATCGTCGGCGATATGCCGGT GTACCTGACCTTCGATATCGACTGCCTGGATCCGGCATTTGCGCC AGGTACTGGTACGCCGGTGATCGGTGGACTCACCTCCGACCGTGC GATCAAACTGGTGCGCGGCCTGAAGGATCTGAACATCGTCGGGA TGGACGTGGTTGAAGTCGCCCCGGCCTATGACCAGTCCGAAATCA CCGCCCTGGCGGCGGCGACTCTGGCGCTGGAGATGCTTTATATTC AGGCGGCGAAGAAAGGCGACTAA
pyrroloquinoline quinone biosynthesis protein PqqF	**pqqF**	>ADJCKNHF_01868 Protease 3 ATGCCCCGCAGTTTATGGTTCAAAGTTCTTGTTGTAGTGGTCGCCC TTTGGGCGCCGTTAAGTCAGGCAGACACCGGATGGCAACCGATTC AGGAAACCATCCGTAAAAGCGAAAAAGATCCCCGTCACTATCAG GCTATTCGCCTGCAAAACGGCATGGTCGTGCTGCTGGTATCCGAT CCGCAGGCGGTAAAATCGCTGTCGGCGCTGGTGGTGCCGGTGGGT TCATTACAGGATCCGGCCGACCATCAAGGGCTGGCGCACTATCTC GAGCATATGACCTTAATGGGCTCGCAGAAGTACCCGCAGCCTGAC AGTCTTGCTGAATTCCTCAAAATGCACGGCGGCAGTCATAATGCC AGCACGGCGCCGTATCGCACCGCGTTCTACCTTGAAGTGGAAAAC GATGCTCTCAACGGCGCTGTCGATCGGCTGGCCGATGCCATTGCC GCGCCGCTGCTGGATAAAAAATATGCCGAACGCGAACGTAACGC GGTCAACGCCGAATTGACTATGGCGCGTACCCGGGACGGGATGC GCATGGCGCAGGTGAGCGCCGAAACCATCAACCCTGCGCATCCG

		GCTTCACAATTCTCCGGCGGTAACCTCGATACACTGAGCGATAAG CCTGGCAGCCCGGTGCTTGATGCGCTACACGCTTTCCGCGACCGC TGGTACTCGGCAAACCTGATGAAGGCAGTTATCTACAGCAATAAG CCGCTGCCTGAGTTGGCAAGCATTGCCGCCGCGACCTACGGGCGG GTGCCTAATCATGACATCAGCAAGCCGGAGATTACCGTACCGGTC GTGACCGATGCGCAGAAGGGCATTGTGATTCACTACGTGCCGGCG ATGCCGCGTAAGGTGCTGCGCGTTGAATTCCGCATCGATAACAAC AGCGCTCAGTTCCGCAGCAAGACCGATGAGCTGGTGACCTATATG ATTGGCAACCGCAGCCCCGGCACTTTATCCGACTGGCTGCAGAAG CAGGGGCTGGCGGAAGGGATTCGCGCGGATTCCGATCCGGCGGT CAACGGTAATAGCGGCGTGCTGGCGATCTCCGCTACCCTCACCGA TAAAGGCCTGGCGCACCGCGATGAAGTTACCGCCGCTATTTTCAG CTACCTGAATTTGCTGCGTACACAGGGTATTGATAAGCGCTACTT TGATGAATTAGCCCACGTGCTGGAGCTCGATTTCCGTTATCCGTC GATTAACCGCGATATGGATTATGTGGAGTGGTTGGCCGATACCAT GATTCGCGTGCCGGTAGAGCACGTACTGGACGTGGTTAATATCGC CGACCGCTATGATGCCCAGGCGATCAAAGACCGTCTGGCGATGAT GACCCCGCAAAATGCGCGTATCTGGTACATCAGCCCGAATGAGCC GCACAACAAAACCGCTTATTTCGTCAACGCGCCGTACCAGGTCGA TAAAATTAGCGCCCGGACCTTCACCGACTGGCAGCAAAAATCTGC GGCCATCAAGCTGCAGCTGCCGACGCTGAACCCGTATATTCCGGA TGATTTCACGCTGATTAAGAGCGATAAGGCCTACCCGCATCCGGA GCTTATCGTCGATGAGCCGACGCTGCGCGTGGTGTACGCGCCAAG CCAGTACTTTGCCAGTGAACCGAAGGCCGACGTCTCGCTGGTGCT ACGTAACCCGCAGGCGATGGACAGCGCGCCGTCAGGTGATGT TCGCGTTGAATGATTACCTGGCCGGTATCGCCCTCGATCAGCTTA GCAATCAGGCCGCGGTAGGCGGGATAAGCTTCTCGACCGGCGCC AACAACGGTCTGATGGTTAATGCCAACGGCTATACCCAGCGTCTG CCGCAGCTCTTTACCGCGCTGCTGGACGGCTACTTTAGCTATACG CCGACCGAAGAGCAGCTTGAGCAAGCGAAGTCCTGGTATGCCCA GATGATGGATTCGGCGGACAAAGGCAAAGCCTATGACCAGGCGA TTATGCCGATTCAGATGCTGTCGCAGGTACCCTATTTTGAGCGTA AAACACGTCGCGATTTACTACCGTCAATCACTCTGAAAGAGGTGA TCAACTACCGCGATAACCTGAAAGCAAGAGGGCGGCCGGAGCTG CTGGTCATCGGTAACATGAGCGCCAGACAGTCCACCGATCTAGCC CGCCAGATCCAAAAACAGCTTGGCGCCGATGGCAACGAGTGGTG TCGCAACAAAGACGTGCTGATCGACAGCAAACAGCTGGCGATGT TTGAGAAAGCAGGCAGCAGCACCGACTCCGCGCTGGCGGCGGTT TTCGCGCCGCCAAATGTCGATGAATACAGCAGCATGGCCGCCAGT TCGCTGTTAGGGCAGATTATTCAGCCCTGGTTCTACAACCAGTTA CGTACTGAAGAACAACTCGGCTATGCGGTATTCGCCTTCTCAATG AATGTGGGCCGCCAGTGGGGGATGGGCTTCCTGCTACAGAGCAG CGATAAACAGCCGGCCTTCCTCTGGCAGCGCTTCCAGGCCTTCTT CCCGACGGCGGAAGCCAAACTGCGGGCGATGAAACCGGAAGAGT TTGCCCAGATCCAGCAGGCGGCGATTAGCCAGATGCTGCAGGCG CCGCAAACGTTGAGCGAAGAAGCATCAAAGCTGAGCAAAGATTT CGATCGCGGTAATATGCGCTTCGATTCACGTGATAAAGTAGTGGC TCAGATGAAACTGCTGACGCCGCAAAAACTTGCCGACTTCTTCCA TCAGACGGTGGTGGATCCGCAAGGCATGGCACTGTTATCCCAGGT TTCCGGCAGCCAGAACGGCAAGACGGAATACGCCGCCCCTGAAG GCGGTAAGGTATGGGAAAGCGTCAGCGCATTGCAAAAATCCTTA CCCCTGATGCGAGAGAATGAATGA
alkaline phosphatase [EC:3.1.3.1]	**phoA, phoB**	>ADJCKNHF_02213 Alkaline phosphatase GTGAAATTATCTGCCCTCTTTATTGCCCTGTTACCGCTGCTGGCTC CCCCGGTTATTCATGCGCAAACCACTTCTTCGCCGGTGCTGGAAA ATCGCGCGGCGCAGGGCGATATCACGACCCCAGGCGGGGCGCGC

		CGTTTAACGGGCGATCAGACCGAAGCGCTGCGCGCTTCGTTAATC AATAAGCCGGCGAAAAATATTATTTTGCTCATTGGCGATGGCATG GGTGATTCAGAAATTACCGCCGCACGAAATTATGCCGAAGGCGC CGGCGGTTTCTTTAAAGGTATTGATGCCCTGCCGCTGACGGGCCA ATACACCCATTATTCTCTGGATAAAAAAACCGGCAAGCCGGATTA CGTGACGGATTCCGCCGCGTCGGCAACCGCGTGGACCACCGGCGT GAAAAGCTATAACGGCGCGCTGGGCGTTGATATCCACGAAAAAG ATCATCAGACCATCCTTGAGCTGGCGAAAGCCGCGGGTCTTGCCA CCGGCAATGTCTCGACGGCTGAACTGCAGGATGCGACGCCGGCG GCGCAGGTGGCGCATGTGACCTCGCGTAAATGCTATGGCCCTGGC GTGACCAGCGAAAAATGCGCCAGCAACGCGCTGGAAAAAGGCGG CAAGGGCTCTATCACCGAACAACTGCTGAATGCCCGTCCGGATGT CTCTTTAGGCGGCGGGGCGAAGACCTTTGCTGAAACGGCGACCGC AGGGGAGTGGCAGGGGAAAACCCTGCATGAGCAGGCGGTCGCTC GCGGCTATCAGATTGTGACCGACGCCGCTTCACTCGCCGCTATCA GCGAAGCAAATCAGGGTAAACCGCTGCTCGGTCTGTTCTCCGACG GCAATATGCCGGTGCGGTGGGAAGGCCCGAAAGCCTCTTATCAC GGCAATATCGACAAACCGCCGGTAACCTGTACGCCAAACCCGAA ACGCGATGCTTCCGTACCGACGCTGGCGCAGATGACCGAAAAAG CGATTGATCTCCTGAGCCGCAACGAGAAAGGTTTCTTCCTGCAGG TTGAGGGGGCGTCTATCGATAAACAGGACCACGCGGCAAACCCT TGCGGCCAGATTGGCGAAACCGTCGACCTCGATGAAGCGGTACA GAAAGCGCTGGAATTTGCCAAAAAAGAGGGCAATACCCTGGTGA TCGTCACCGCCGATCACGCCCACTCCAGCCAGATTATCCCGGCAG ACACGAAAGCGCCGGGCCTGACCCAGGCGCTGACGACCAAAGAT GGCGCGGTAATGGTGATGAGCTATGGCAACTCTGAAGAAGAGTC GATGGAGCACACCGGCACCCAACTGCGTATTGCCGCGTACGGAC CGCATGCGGGCAACGTGGTGGGTCTCACCGACCAGACCGATCTGT TTTACACCATGAAAGACGCGCTGGGCCTGAAATAA
two-component system, OmpR family, phosphate regulon sensor histidine kinase PhoR [EC:2.7.13.3]	**phoR**	>ADJCKNHF_02227 Phosphate regulon sensor protein PhoR GTGCTGGAACGGCTGTCATGGAAAAGGCTGGCGCTTGAGCTTTTC TTATGTTGTATCCCGGCCCTGATCCTCGGGGCGTTTTTCGGTCATC TGCCGTGGTTTTTACTGGCGGCGGTGACCGGATTGCTTATTTGGC ATTTCTGGAATTTGTTACGTCTGTCGTGGTGGCTGTGGGTCGATCG CAGTATGACGCCGCCGCCGGGAAGCGGCAGTTGGGAACCGCTGC TGTATGGTCTGCATCAAATGCAGATGCGTAATAAAAAACGTCGCC GCGAGCTGGGGAGCCTCATCAAGCGCTTTCGCAGCGGGGCGGAA TCCTTACCCGATGCGGTGGTGCTGACCACCGAAGAGGGCGCCATC TTCTGGTGTAACGGCCTGGCGCAACAAATCCTTAATCTACGCTGG CCGGACGATAGCGGGCAGAATATCCTCAACCTGCTGCGCTACCCA GAGTTTGCTAACTATCTGAAAAACCGTGATTTCACCAAGCCCCTT AATCTGGTGCTCAATAACGCCCGTCATCTGGAAATTCGCGTGATG CCTTATAGCGATAAACAGTGGTTGATGGTGGCGCGCGATGTCACG CAAATGCACCAGTTGGAAGGCGCGCGGCGCAACTTTTTCGCCAAC GTCAGCCACGAGCTGCGCACGCCGCTCACCGTACTGCAGGGTTAT CTCGAGATGATGCAGGAGCAGGTGCTGGAAGGGCCGACGCGGGA AAAAGCGCTGCATACCATGCGTGAGCAAACGCAGCGGATGGAAG GGTTGGTGAAGCAGTTGCTGACGCTCTCGCGTATTGAAGCCGCGC CGGTGCTGGCGATGAATGATAAAATCGACGTCCCGATGATGCTGC GGGTGGTTGAGCGCGAGGCGCAAACCCTCAGCCAGGGTAAGCAT CAGCTGCACTTTAGCGTCGATGAAACGCTCCAGGTGATGGGCAAC GAAGAGCAGTTGCGCAGCGCGATTTCCAATCTGGTGTACAACGCC GTTAACCATACGCCAGCGGGAACTGAGATTCACGTCAGCTGGCA GCGGGCGCCACACGGCGCGCTGTTCAGCGTTGAAGACAACGGTC CGGGCATTGCGCCTGAACATTTACCCCGGCTAACCGAGCGGTTCT ACCGCGTCGACAAGGCGCGCTCCCGGCAAACCGGCGGCAGCGGT

		TTAGGGCTGGCTATCGTGAAACATGCGGTTAGCCATCACGAAAGC CGGCTGGAAATCGAAAGTACGGTCGGGAAGGGAACACGCTTTAG CTTCCTGCTGCCGGAACGTTTAATTGCCAAAAATGGCGCCTGA
Pyoverdine chromophore precursor synthetase PvdL	**pvdL**	>ADJCKNHF_02461 Enterobactin synthase component F ATGAGTACACGTTTACCGCTGGTTGCGGCGCAGCCGGGAATTTGG ATGGCTGAACGCCTCTCCACGCTACCCGGCGCCTGGAGCGTTGCC CACTATGTTGAACTGCGCGGCAATCTTGATCCGGCGCTGCTGAGT AAGGCGATCGTCGCCGGGCTTAAGCAGGCCGATACCCTGAGCAT GCGCTTTTGCGAAGATAATGGCGAAGCGTGGCAGTGGGTTGATG ACGCGCGCGAGTTTGCCGAGCCGCAAAGCGTTGACCTGCGCCAG CAGGCCGATCCGCATATGTCCGCGCTGACGCTGATGCAAAGCGAT CTCGGGCAGAATCTGCGCGTCGACAGCGGTAATCCGCTGGTCTGC CATCAGCTCATGCGCGTTGGCGACGACTGCTGGTACTGGTATCAG CGCTATCACCATTTACTGGTCGATGGTTTTAGTTTCCCGGCCATTA CCCGCCAGATCGCCGCTATTTATCGTGCCTGGCAACGCGGCGAAG AGACGCCGGATTCACCGTTTACGCCGTTCGCCGAAGTGGTGGAAG AGTATCAGCGCTACTACGGCAGCGAGGCGTGGCAGCGCGATAAA GCCTTCTGGCAGGCGCAGCGTCAGGCGTTGCCGTCTCCGGCCTCG CTATCAGACGCGCCGCTGGCCGGGCGGGCGACCAGCAGCGATAT CTGGCGCCTGAAACTGGAGGCCGATCCGGCTGTCTTCAGCCAGCT CGCGGCCAGCGCGCCGCAGTGCCAGCGCGCCGATCTGGCGTTGG CGCTGACGACGTTGTGGCTGGGGCGGTTGTGCGGCCGAATGGATT ACGCGGCTGGCTTTATCTTTATGCGCCGCATGGGATCGGCGGCGC TGACCGCCACCGGCCCGGTACTCAACGTACTGCCGCTGGCGGTGA ATATCGACGCGCAGGAGACGCTGGCGCAACTGGCGACGCGTCTC TCCGGACAACTGAAAAAAATGCGTCGCCATCAGCGCTACGATGC CGAGCAAATTGTCCGCGATAGCGGTAAAGCGGCGGGCGACGAAC CGCTGTTTGGCCCGGTGCTGAACATCAAAGTCTTTGATTACCAGT TGGATATCGACGACGTGCAGGCGCAGACGCATACCCTCGCCACC GGCCCGGTGAATGACCTCGAGCTGGCACTGTTCCCGGACGAACGC GGCGGTCTGTCGCTGGAGATCCTCGCCAATAAAGCGCGTTATGAT GAGGCGACGCTGAACCGCCACGTGTCGCGGCTGACCGCGCTGCT GGCGCAGTTCGCCGCCAACCCGGCGCTACGCTGCGGCGAGGCGG AGATGCTGTCGGCGGAAGAAGGCGCGCAGCTGGCATTGATCAAC AATACCGCGATGCCGCTGCCGACCACTACCCTCAGCGCACTGGTG GCGGAACAGGCGCGGAAAACGCCGGATGCCCCGGCGCTGGCGGA TGCCAACTGGCGCTTTAGCTACCGCGAAATGCGCCAGCAGGTGGT GGCGCTGGCCAACCTGCTGCGGCAACGCGGCGTGAAGCCGGGGG ATAGCGTGGCGGTTGCCTTACCGCGCTCGGTGTTCCTGACGCTGG CGCTGCACGGCATTGTCGAAGCCGGCGCCGCCTGGCTGCCGCTGG ACACCGGCTACCCGGATGACCGTCTGCGGATGATGCTGGAAGAT GCGCGGCCATCGCTGCTGATTACCTCTGACGATCAACTGGCCCGT TTTAGCGATATTCCGGGACTGACCAGCTTGTGTTATGAGCAGCCG CTGGCTGCTGAAGATGATACGCCGCTGGCGCTGTCAAAACCGGA ACATACCGCGTATATCATCTTCACCTCCGGTTCCACCGGGCGGCC GAAAGGGGTGATGGTCGGGCAGACCGCCATCGTGAACCGCCTGC TGTGGATGCAAAATCACTATCCGTTAACCGCCGCCGATGTGGTGG CGCAGAAGACGCCGTGCAGCTTTGATGTCTCGGTATGGGAGTTCT GGTGGCCGTTTATGACCGGCGCCCAGCTGGTGATGGCGGCGCCGG AGGCGCATCGCGATCCACAGGCGATGCAGCGGTTCTTCACGGATT ATGGCGTGACCACCACCCACTTTGTTCCGTCGATGCTGGCGGCGT TTGTCGCCTCGCTGGATAGCGATAATGTGTCTTCCTGCCGGACGC TAAAACGCGTTTTCTGTAGCGGCGAAGCGCTGCCGACGGAACTGT GTCGCGAATGGGAGCGCTTAACCGGCGCGCCATTGCATAACCTGT ACGGGCCGACGGAAGCGGCGGTGGATGTCAGCTGGTATCCCGCC TGCGGGCCAGAGCTGGCGGCGGTAACCGGCAACAGCGTGCCTAT

		CGGCTGGCCGGTATGGAACACCGGATTACGTATTCTTGATGCTGC GATGCGCCCTGTGCCGCCGGGCGTGGCGGGTGATTTGTACTTAAC GGGCATTCAGCTGGCACAGGGATATATGGGGCGCCCTGATCTCAC CGCCAGCCGCTTTATTGCCGACCCGTTTGCCCCCGGCGAGCGCAT GTACCGCACCGGCGATGTGGCGCGCTGGCTGGATAACGGGGCGG TAGAGTATCTTGGCCGCAGCGACGATCAGTTGAAAATTCGCGGCC AGCGCATTGAGCTTGGCGAGATCGACCGGGTGATGGCGGCGCTG CCGGACGTCGCGCAGGCGGTGTGCCACGCCTGCGTCTTCAATCAG GCGGCGGCCACCGGCGGCGATGCCCGCCAGCTCGTCGGTTATCTG GTGAGCGAGTCCGACCAGCCGCTGGACGTGGCGGCGCTGAAGGC GCGTCTTAGCGAACAGCTGCCGCCGCACATGGTGCCGGTGGTGTT AATCCAGCTGGAATCCTTCCCGCTCAGCGCCAACGGTAAGCTGGA TCGTAAAGCGCTACCGCTCCCCTCCTTAAGCAGCGAGCGCAGCGG TCGCCCGCCGCAATCGGCTACCGAAATGGCCGTTGCCGCGGCGTT CAGCCAGCTACTGGGCTGCGAGGTAAATGACATCGACGCCGATTT CTTCGCCCTCGGTGGCCATTCGCTGCTGGCGATGCGGCTGGCGGC GCAGCTTAGCCGCGAGCTGGCGCGGCAGGTGACGCCGGGGCAGG TGATGGTCGCTTCGACCGTCGGCAAGCTGAGCGCGCTGCTGGCTT CCGACCTGAGCGACGAGCAGGCGCAGCGCCTGGGCTTCGATGCG CTGTTGCCGCTGCGCGAGAGCGACGGTCCGACGCTGTTCTGCTTC CATCCGGCCTCCGGTTTTGCCTGGCAGTTCAGCGTGCTGGCGCGT TATCTTAACCCGCGCTGGTCAATTACCGGTATTCAGTCGCCGCGT CCGACGGGGCCGATGGCTTCCGCCGCCAACCTCGACGAAGTCTGC GAGCACCATCTGCGCACGCTTTTAGCGCAGCAGCCGCATGGGCCT TACTATCTGTTTGGTTATTCGCTCGGCGGAACGCTGGCGCAGGGG ATTGCCGCCCGTTTACGCCAGCGCGGCGAAGAGGTGGCGTTCCTC GGCCTGCTGGATACCTGGCCGCCGGAGACGCAAAACTGGGCGGA GAAAGAGGCGAACGGTCTGGATCCCGAAGTGCTGGCGGAAATCG CCCGCGAGCGCGAAGCGTTTCTCGCCGCTCAGCAGGGGCAGGCTT CCGGCGAGCTGTTCAGCGCGATCGAAGGTAACTACGCCGATGCG GTGCGCCTGTTGACGACCGCGCACAGCGCGAAGTTTGACGGCAA GGCAACGCTATTTGTGGCGGAGAAAACGCGCCAGAAAGGGATGG ATCCGCAGGTCGCATGGGGGCCATGGGTTGGCGAGCTGGAGGTG TTCAGCCAGAACTGCGCCCACGTCGAGATTATCTCGCCGCAGGCC TTTGAAGCGATAGGCCCGGTAGTGCGGGAGATTCTGGGGTAA
salicylate biosynthesis isochorismate synthase [EC:5.4.4.2]	**pchA**	>ADJCKNHF_02468 Isochorismate synthase EntC ATGGAAACGTCACTGGCTGAGGATGTACAGGAAAAAACGCAGAC CCTGTCGCCGCAAAGCTTCTTCTTTATGTCGCCGTACCGCAGCTTC AGTACCACCGGCTGTTTTAGCCGTTTTTCCCAGCCTGCCGTCGGCG GTGATTCGCTGAACGGCGAGTTCCAGCAGAAAATGGCGGCCGCTT TTGCCGAAGCCCGTGCGGCGGGGATCCGCAAGCCGGTCATGGTC GGGGCGATTCCGTTCGACACCAATCAGCCTTCCGAGCTCTATATT CCCGAACGTTGGGAAACCTTCTCCCGTACCGACAAACAGCAGTCC GCGCGTTACGCGGCGCCGCTCAAAGCTATGGATGTTGTCGATCGT CAGGAGATCCCGGAACAGGACGAGTTTTTGGCGATGGTGGAACG CGCCGCCGCGCTGACGGCGACTCCGGAAGTCGACAAAGTGGTGC TCTCAAGGCTGATTGATATTACGACCCGCGACCGGGTCGATAGCG GCGCGCTGCTGGAGCGGCTGATCGCCCAGAACCCGGCGAGCTTTA ACTTCCATGTTCCACTCTCCAATGGTGATGTGCTGCTGGGCGCCA GCCCGGAACTGCTGCTGCGTAAAGAAGGGCTGCACTTCAGTTCGC TGCCGCTGGCCGGCTCCGCCCGCCGCCAGCCTGACGATGTGCTGG ACCGGGAAGCGGGTAACAAGCTACTGGCGTCGGGCAAAGATCGC CATGAGCACGAGCTGGTGACGCAGGCGATGAAGAGCGTGCTTGG CCCTCGCAGCAGTCATCTGTCGCTACCGGAGTCGCCGCAGCTGAT TACCACCCCGACGCTCTGGCATCTGGCGACGCCGATCGAAGGTAC GGCGCTGGCGGAAGAAAACGCCATGTCGCTGGCCTGCCTACTGC

		ACCCGACCCCGGCGCTGAGCGGCTTCCCGCACCAGGTGGCGAAG CGGCTGATTGCCGAGCTCGAACCGTTCGATCGCCAACTGTTTGGC GGCATTGTCGGCTGGTGCGATGACGAAGGCAACGGCGAATGGGT GGTGACCATCCGCTGCGCGCGCTTACATCAACGCTCGCTACGCCT GTTTGCCGGCGCGGGTATCGTCCCGGCCTCTTCGCCGCTGGGCGA ATGGCGTGAAACCGGCGTCAAACTCACCACCATGCTCAACGTATT TGGCTTGAATTAA
Pyoverdine chromophore precursor synthetase PvdL	**pvdL**	>ADJCKNHF_02469 Enterobactin synthase component E ATGATTGCATTTACCCGTTGGCCGGAAGAGTTTGCGGCCCGCTAT CGTCAAAAAGGCTACTGGCAGGATCTGCCGTTAACCAATCTGATT ACTCGTCATGCGGACAATGACGCCGTGGCGATTATCGACGGCGA GCGGCAGATTAGCTACCGCCAGTTTAACCAACTGGTGGATAACCT CGCGTCCTCCCTGCAGCATCAGGGACTCAAGCGCGGAGAAACCG CGCTGGTGCAGCTTGGCAACGTCGCCGAGTTCTACATTACTTTCTT TGCGCTGCTGCGCATCGGCGTCGCACCGGTTAACGCTTTGTTTAG CCATCAGCGCAGCGAACTTAACGCCTATGCCGCGCAGATTAAACC GGTGCTGCTGATTGCCGATCGCGAGCACGCGCTGTTTGCTGACGA TAGCTTTCTCCATGGTTTTATCGCTGAGCATCCTTCGCTGCGCGTC GCGCTGCTGCGTAACGATGGCGGCGAGCGCGACCTGGCAACGGA AATTAGCCGCACGGCGGATAACTTTGTCGCCAATCCGACGCCGGC TGACGAAGTGGCTTTTTTCCAGCTCTCCGGCGGCAGCACCGGGAC GCCGAAGCTTATTCCGCGAACCCATAACGATTACGACTACAGTAT CCGCCGCAGCAACGAGATCTGCGGTATTAACGCCGACACGCGCT ATCTCAACGCGCTGCCGGCGGCGCACAACTATGCGATGAGCTCGC CGGGATCGCTGGGCGTCTTTCTCGCCGGCGGCCGGGTGATCCTCG CCGCTGACCCGAACGCCACGTTGTGTTTCCCGCTGATCGAAAAAC ATCAGATTAACGTCGCGTCGCTGGTGCCGCCGGCGGTCAGCCTGT GGCTGCAGGCTATTCATGAATGGGGCAGCAACGCGCAACTGCAA TCGCTGAAGCTGCTGCAGGTTGGCGGAGCGCGCCTGTCCGCGACG CTCGCCGCGCGTATCCCGGCGGAAATCGGCTGCCAGCTGCAGCAG GTGTTCGGCATGGCGGAAGGGCTGGTTAACTACACCCGCCTCAAC GATAGCCCGCAGCGGATTATCAACACCCAGGGTTGCCCGATGTGT CCTGACGACGAAGTGTGGGTGGCGGATGCCGACGGTAACCCGCT GCCGCGCGGCGAAGTGGGCCGTCTGATGACCCGCGGCCCTTATAC CTTCCGCGGCTATTACAACAGCCCGCAACATAACGCTGAAGCCTT TGATGCCGATGGATTTTACTGCTCCGGCGATCTGATTTCGATCGAT GAAGATGGCTATATCACCGTCCAGGGCCGGGAAAAAGATCAGAT CAACCGCGGTGGCGAGAAGATCGCCGCTGAAGAGATAGAAAACC TGCTGCTGCGCCATGAGGCGGTGATCCACGCCGCGCTGGTTAGCA TTGAAGACAATCTGCTGGGCGAGAAGAGCTGCGCTTATCTGGTGG TGACATCGCCGCTGCGCGCCGTCGCGGTGCGCCGCTTCCTGCGCG AGCAGGGCGTGGCGGAATTTAAATTGCCGGATCGCGTGGAGTGC GTTGCCGCGCTGCCGCTGACGCCGGTGGGCAAAGTCGATAAAAA ACAATTACGTCAGTGGCTGGCCGAAGGCAAGCTGGGCTGA
Pyoverdine chromophore precursor synthetase PvdL	**pvdL**	>ADJCKNHF_02470 Enterobactin synthase component B ATGGCAATCCCCAAATTACAGGCTTACGCGCTGCCGGAAGCCAGC GATATTCCGGCCAACAAAGTTAACTGGGCCTTTGAGCCGTCGCGC GCCGCGCTGCTGATCCATGATATGCAGGAGTATTTCCTCAACTTC TGGGGCGAAAACAGCGCGATGATGGAAAAAGTGGTGGCCAATAT CGCCGCCCTGCGCGACTTCTGCAAACAAAACGGCATTCCGGTGTA CTACACCGCCCAGCCGAAAGAGCAGAGCGATGAAGACCGCGCCC TGCTGAATGATATGTGGGGGCCGGGGTTGACTCGCTCGCCGGAAC AGCAGCAGGTGATTGCCGCGCTGGCGCCGGATGAGCAGGATACG GTGCTGGTGAAATGGCGCTACAGCGCGTTTCATCGCTCACCGCTT GAAGAGATGCTGAAAGAGACCGGCCGCGACCAGCTGATCATCAC CGGCGTTTACGCCCATATCGGCTGTATGACCACCGCCACCGACGC

		TTTTATGCGCGATATCAAACCGTTCTTTGTCGCCGACGCGCTGGC AGATTTCAGCCGCGAAGAGCATTTGATGGCGCTGAAATACGTCGC CGGCCGTTCTGGACGCGTGGTGATGACCGAAGAATTGTTGCCGCT GCCGGCCTCCAAAGCGGCGCTGCGCGCGCTAATTCTGCCGCTGCT CGACGAATCCGACGAACCGCTGGATGATGAAAACCTGATCGACT ACGGTCTGGATTCGGTGCGTATGATGGCGCTGGCCGCCCGCTGGC GCAAAGTACACGGCGATATCGACTTCGTGATGCTGGCGAAAAAC CCGACCATCGACGCCTGGTGGGCGCTGCTCTCCCGCGAGGTGAAA TAA
acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	**ilvB, ilvG, ilvI**	>ADJCKNHF_02673 Acetolactate synthase isozyme 1 large subunit ATGGCAAGTTCGGGCACCACATCAAACACAATGCGCTTTACCGGC GCGCAGCTGGTTGTTCATTTACTGGAACGCCAGGGTATCACTATG GTCAGCGGCATTCCGGGCGGCTCCATCCTGCCTATCTATGATGCC TTGAGCCAAAGCACGCAGATCCGCCACATCCTGGCGCGCCACGA GCAGGGGGCGGGTTTTATCGCTCAGGGGATGGCGCGTACCGAAG GTAAACCCGCAGTCTGCATGGCCTGTAGCGGCCCTGGCGCCACCA ACCTGATTACCGCCATCGCCGATGCCCGCCTCGATTCTATTCCGCT GGTCTGCATCACCGGGCAGGTTCCGGCCTCAATGATCGGCACCGA TGCCTTCCAGGAAGTCGATACCTACGGCATCTCTATCCCCATCAC CAAGCATAACTACCTGGTGCGCGACATCGCCGAGCTGCCGCAGGT GATGAGCGACGCCTTCCGTATTGCCCAGTCCGGGCGCCCCGGGCC GGTGTGGATAGATATTCCTAAGGACGTACAGGCGGCAACCATTG AACTGGAAACGCTGCCGGAGCCAGGCGAGCGCGCCCCGGCACCA GCATTCGCGCCTGAAAGCGTGCGTGAAGCGGCGGCAATGATCAA CGCGGCGAAACGCCCGGTACTGTATCTGGGCGGCGGCGTGATTA ACGCGCCTGAGCCGATTCGGGACCTGGCGGAAAAAGCCAACCTG CCGACCACCATGACCTTAATGGCGCTGGGTATGTTGCCGAAGGCG CATCCTTTGTCGCTGGGCATGCTGGGGATGCACGGCGCGCGCAGC ACTAACTTTATTCTGCAAGAAGCTGATTTACTGATTGTTTTAGGCG CGCGTTTTGATGACCGGGCGATTGGCAAGACCGAGCAGTTCTGCC CGAACGCGAAGATTATTCACGTCGATATCGACCGCTCTGAGCTTG GCAAAATTAAGCAACCGCACGTAGCGATTCAGGGCGATGTGGCG GAGGTCTTAGCCCAGCTTATTCCGCAGATTGAGGCGCAGCCGCGT GATGAGTGGCGCCAGCTGGTGGCTGATTTACAAAGAGAATTCCCC TGCGCCATCCCGCAGGAAAGCGATCCGCTCTCCCATTACGGCCTG ATTAACGCCGTGGCCGCCTGCGTTGATGATGAGGCGATCATCACC ACCGATGTGGGTCAGCATCAGATGTGGACGGCGCAGGCCTATCC GCTCAACCGTCCGCGCCAGTGGCTGACTTCCGGCGGTCTCGGCAC CATGGGCTTCGGCCTGCCGGCGGCCATCGGCGCGGCGCTGGCCAA TCCGCAGCGTAAGGTTATTTGTTTCTCCGGTGACGGCAGCCTGAT GATGAATATTCAGGAGATGGCCACCGCTGCCGAAAATCAGCTGG ATGTAAAAATTATCCTGATGAACAACGAAGCGCTGGGGCTGGTG CATCAGCAGCAGAGCCTGTTCTATCAGCAGGGCGTCTTCGCCGCG ACCTATCCGGGGATGATTAACTTTATGCATATAGCTGCCGGTTTT GGTCTGCAAACCTGTGATTTAAATAACGAATCCGATCCGCAGGCG GCGCTGCAGGCGATTATCAACCGCCCAGGTCCGGCGTTGATCCAC GTGCGTATCGACGCGCAGCAAAAAGTGTATCCGATGGTACCGCC GGGTGCGGCCAATACTGAGATGGTGGGGGAATAA
acetolactate synthase I/III small subunit [EC:2.2.1.6]	**ilvH, ilvN**	>ADJCKNHF_02674 Acetolactate synthase isozyme 1 small subunit ATGCAAAAGCAACACGATAACGTCATTCTGGAACTCACCGTCCGC AACCACCCAGGTGTGATGACCCACGTCTGCGGGCTATTTGCCCGG CGCGCGTTTAACGTTGAAGGCATTCTCTGCTTGCCGATCCAGGGC AGCGAGTACAGCCGCATCTGGCTGCTGGTAAATGATGACCAGCG GCTGGGGCAGATGATTAGCCAGATTGAAAAGCTGGAAGATGTCA CCAATGTGGCGCGTAACCAGTCCGATCCCACCATGTTTAACAAAA TTGCGGTGTTCTTCGAATAG

ferredoxin-nitrate reductase [EC:1.7.7.2]	**nasB**	>ADJCKNHF_03005 Nitrite reductase [NAD(P)H] ATGAGCAAAGTCAGAATCGCTATTATCGGTAACGGCATGGTCGGC CATCGCTTTATCGAAGAGCTTCTTGATAAGGCGCCTGCCGGACAA TTCGACATTACCGTGTTCTGTGAAGAGCCGCGTATCGCCTATGAC CGTGTCCACCTGTCGTCTTACTTCTCCCATCACACTGCGGAAGAG CTGTCGCTGGTACGCGAAGGTTTCTATGAGAAACACGGCGTCAAG GTACTGGTCGGCGAACGCGCGATTACCATCAACCGTCAGGAAAA GGTGATCCACTCCAGCGCTGGCCGTACCGTTTTCTACGACAAGCT GATTATGGCGACTGGCTCATACCCGTGGATCCCGCCCATTAAAGG CGCGGAAACCCAGGATTGCTTCGTCTATCGTACTATTGAAGATCT TAACGCCATCGAATCCTGCGCCCGTCGCAGCAAACGCGGCGCGGT GGTCGGCGGCGGTCTGCTCGGCCTGGAAGCGGCTGGCGCGCTGA AAAATCTCGGCGTGGAAACCCACGTGATCGAGTTTGCGCCGATGC TGATGGCCGAGCAGCTCGACCAGATGGGCGGCGAGCAGCTGAAG CGTAAGATTGAAAGCATGGGCGTGAAGGTTCACACCAGCAAAAA TACCAAAGAGATCGTTCAGCAGGGCACCGAGGCACGCAAAACGA TGCGCTTCGCCGACGGTAGCGAACTGCAGGTCGATTTCATCGTCT TCTCTACCGGTATCCGTCCGCGCGACAAGCTGGCTACCCAGTGCG GTCTCGCCGTCGCCCAACGCGGCGGCATCATGGTCAACGATAGCT GCCAGACCTCCGATCCGGATATCTACGCTATCGGCGAATGCGCCA GCTGGAATAACCGCGTATACGGTCTTGTCGCCCCGGGCTACAAAA TGGCGCAGGTTACCGTTGACCATATCCTCGGCAACGACAATCTGT TCACCGGCGCCGACCTCAGCGCCAAGCTGAAGCTGCTCGGCGTGG ACGTTGGCGGTATCGGCGACGCCCACGGGCGCACGCCGGGCGCG CGTAGCTACGTCTATCTCGACGAAAGCAAAGAGGTCTACAAACG GCTCATTGTCAGCGAAGATAACAAAACCCTGCTTGGCGCGGTACT GGTCGGCGACACCAGCGATTACGGCAACCTGCTGCAGCTGGTGCT GAATGCCATCGAGCTGCCGGAAAACCCGGATTCGCTGATCCTCCC GGCCCACGCCGGCAGCGGCAAGCCGTCCATCGGCGTGGATAAAC TGCCGGACAGCGCGCAGATTTGTTCCTGCTTCGACGTCAGCAAAG GCGACCTGATCGCCGCTATCAATAAAGGCTGCCACACCGTGGCGG CGCTGAAAGCGGAAACCAAAGCCGGAACCGGCTGCGGCGGCTGT ATTCCGCTGGTGACGCAGGTGCTCAACGCCGAGCTGGCGAAACA GGGTATCGAAGTGAACAACAATCTGTGTGAGCACTTCGCCTACTC TCGCCAGGAGCTGTTCCACCTGATCCGCGTCGAAGGCATCAAAAC CTTCGACGAACTGCTGGAAAAACATGGTCAGGGCTACGGCTGTG AAGTCTGTAAGCCGACCGTCGGTTCCCTGCTGGCCTCCTGCTGGA ATGAGTACATCCTCAAACCACAGCACACGCCGCTGCAGGACACC AACGATAACTTCCTCGCCAACATCCAGAAAGATGGCACCTACTCG GTTATCCCGCGCTCCGCAGGCGGCGAAATTACGCCAGAAGGCCTG GTTGCCGTCGGTCGCATCGCGCGCGAATTTAATCTGTATACCAAA ATCACCGGCTCCCAGCGTATCGGCCTGTTCGGCGCGCAAAAAGAC GATCTGCCGGAAATCTGGCGTCAACTGATTGAAGCCGGCTTCGAA ACCGGCCATGCCTACGCCAAAGCGTTACGTATGGCGAAAACCTGC GTCGGCAGTACCTGGTGCCGCTACGGCGTCGGCGATAGCGTCGGC TTCGGCGTAGAACTGGAAAACCGCTATAAAGGTATCCGTACCCCG CACAAAATGAAGTTCGGCGTCTCCGGTTGTACCCGTGAATGCGCG GAAGCCCAGGGTAAAGACGTTGGGATCATCGCCACCGAGAAAGG CTGGAACCTGTACGTGTGCGGTAACGGCGGGATGAAACCACGCC ACGCCGATCTGCTGGCCGCGGACCTCGATCGCGATACGCTCATCA AATATCTCGACCGCTTTATGATGTTCTACATCCGCACCGCCGATA AGCTTACCCGTACCGCGCCGTGGCTGGACAACATGGAAGGCGGT ATCGACTATCTGCGCAGCGTCATCATCGACGATAAGCTGGGCCTG AACGATCACCTTGAAGAAGAGCTGGCTCGCCTGCGCGCCGCTTTT GCCTGCGAATGGACCGAGACCGTCAATAACCCGGCGGCGCAGAC GCGCTTCAAACACTTTATCAACAGCGATCAGCGCGACCCGAACGT

		TCAGGTGGTGCCGGAACGTGACCAGCATCGCCCGGCCACGCCCTA TGAGCGCATCCCGGTCACGCTGGTGGAGGAAAACGTATGA
chemotaxis protein MotA	**motA**	>ADJCKNHF_03338 Motility protein A GTGCTAGTGATATTGGGTTATCTCGTGGTCCTGGGAGCGGTATTT GGCGGCTATTTACTGGTGGGCGGCCACCTTGGCGCGCTGTACCAG CCGGCGGAATTCCTGATTATCGGCGGCGCCGGCATCGGCGCGTTT ATCGTCGGCAACAACGGAAAGGCCATCAAATCCACGCTGCGGGC CTTGCCCAAAATGGTACGTCGCTCCAAATACAGCAAGGCGCTGTA TATGGATCTGATGGCGTTGCTGTTCCTGCTGCTCGCAAAATCCCGT CAACAGGGAATGCTGTCGCTTGAGTTCGATATCGACAATCCTCAG GAAAGTGAAATTTTCGCTAATTATCCGCGCATCCTTGCCGATAAC CATCTGGTGGAGTTCATAACCGATTATTTACGCCTGATGGTGAGC GGCAACATGAATGCTTTTGAAATTGAAGCGCTGATGGACGAAGA GATCGAAACCTTCGAACAGGAGAGCGAAGTGCCCGCCGGCAGCC TGGCGATGGTCGGCGACTCTCTGCCGGCATTTGGTATTGTCGCGG CGGTAATGGGGGTGGTGCACGCGCTGGCCTCGGCGGACCGTCCG GCGGCAGAGCTCGGGGCGCTTATCGCCAACGCGATGGTGGGGAC TTTCCTCGGCATTCTGCTGGCCTATGGATTTATCTCGCCGCTGTCG ACGCTGCTGCGGCAAAAAAGCGCCGAGACGGTCAAGATGATGCA GTGCATCAAGGTGACATTGCTCTCCAGCCTCAACGGCTACGCGCC GCAAATCGCCGTCGAATTTGGCCGCAAAACGTTATACACCACCGA GCGCCCGTCGTTTGTCGAGCTTGAAGAACACGTACGCCAGGTGAA AGCGCCTGCCGCGCAGGCGACGGAAAGCGAAGAAGCATGA
chemotaxis protein MotB	**motB**	>ADJCKNHF_03339 Motility protein B ATGAAGCATAATCACCCGGTGGTTCTGGTCAGAAAGCGCAAATC ACACCAGCCAGCCCATCACGGCGGTTCGTGGAAGATTGCCTATGC CGATTTTATGACGGCGATGATGGCCTTCTTCCTTGTGATGTGGCTG CTGGCGATCGCCAGCCCGCAGGAGCTGACGCAAATAGCCGAATA TTTCCGTACGCCGCTGAAAGTCGCCCTCACCAGCGGCGATAAAAG CAGCTCGGAAAGCAGCCCGATCCCCGGCGGCGGCGAAGACCCGA CCCGTGAAGTCGGGTTAGTCAGCAAGCAGATCAATACCGCGGAT AAACGTGCCGAAGAGCTACGGCTAAACAAACTGCGTGACAAGCT CGATCAGTTGATTGAGTCAGACCCGCGCCTGAAGGCGCTACGTCC GCATCTGCTGATCAACATGATGGACGAAGGACTGCGCATTCAGAT TATCGATAGCCAGAATCGGCCGATGTTTAAAACCGGTAGCGCTCA GGTGGAAAGCTATATGCGCGATATCCTGCGAGCGATTGCGCCAAT CCTCAATGATTTGCCGAACAAGATAAGCCTCGCCGGGCATACCGA TGACATCCCCTACGCCAGCGGCGAACGTGGTTACAGCAATTGGGA ACTGTCGGCGGATCGCGCCAACGCCTCGCGCCGCGAGCTGATCGC CGGCGGGCTGGCGGAAGGGAAGGTGCTGCGGGTGGTTGGTATGG CGGCGACCATGAGCCTGAAACAGCACGGCGCCGATGATGCCATC AACCGCCGCATTACCGTACTGGTGCTTAACAAAGAGACCCAGCA GAGCATTGAGCATGAAAATGGCGAAAGCAATGCGCTGGAGATTA GCCAGCCGGATACGCTGCCAAAGCTGGTCGCGCCCGCGCCGGTTA ACCGCGATTCACACCCTGAGGTGACCCCATGA
two-component system, chemotaxis family, sensor kinase CheA [EC:2.7.13.3]	**cheA**	>ADJCKNHF_03340 Chemotaxis protein CheA ATGAGCATGGATATTAGCGCTTTTTATCAGACTTTTTTTGATGAAG CAGATGAGCTGCTGGCAGACATGGAGCAACACCTGCTGGAGCTG GATCCGCAGGCCCCCGATATCGAACCGCTAAACGCTATTTTTCGC GCGGCGCACTCGATCAAAGGCGGCGCGGCGACGTTTGGCTTTTCC GTATTGCAGGAAACCACCCATCTGCTGGAGAACCTGCTCGACGGC GCCCGGCGCGAGGAGATGCGCTTGAGCACCGAAATTATCAATCT GTTTCTGGAAACCAAAGATATTATGCAGGAGCAACTGGACGCCTA TAAAACCTCGCAGCAGCCTGACGCTGAGAGCTTTGACTATATCTG CCAGGCGCTGCGGCAGCTGGCGCTGGAAGCGCAGCAGCAGGACG CGCCAGCCGCGCCGCCCGTCGTGGCCCAGCCTGCGCCGACGGCCG

		TCGCCGGCGGTATGCGCGTGAGTTTAACCGGGCTTAAAGCCAATG AAATTCCGCTGATGCTGGAAGAGCTTGGCAATCTCGGCGAGGTAC ATGATCCGCAGCAAACTGACAATAGCCTTGAGGTGACCCTGCTGA CCACCGCCAGCGAAGAAGATATTTGCGCGGTGCTCTGTTTCGTTC TTGAGCCGGAACAGATCAGCTTTACCACGCCGCCAACCACTGCCG CTAAACCATTGCCATCGGCCGAAGTTGTGCCGCCGCCGGTCGCCC AACCGCAGCCTGCTGTCGTCGAGCCGCCGAAAGCGCCGAGAGCG AAGGCCAGCGAATCGACCAGTATTCGCGTGGCGGTAGAGAAAGT TGACCAGTTGATTAACCTCGTCGGCGAACTGGTGATCACCCAGTC CATGCTGGCGCAGCGCTCAGGTAACCTGGATCCGGTGACCCATGG CGATCTGCTCAACAGCATGAGCCAGCTGGAACGTAACGCTCGCG ACCTGCAGGAATCGGTGATGTCGATTCGCATGATGCCGATGGAAT ATGTATTCAGCCGCTACCCGCGGCTCGTGCGCGACCTGGCCGGCA AGCTCAATAAGCAGGTGGAACTGACGCTGCAGGGCAGCTCCACC GAACTTGATAAGAGCCTGATCGAGCGCATTATCGACCCGTTAACC CACCTGGTGCGCAATAGCCTCGACCACGGTATTGAAGATCCGCAA ACCCGTCTGGCGGCAGGTAAGTCTGAGGTGGGCAATCTGATTCTT TCCGCTGAACATCAGGGCGGCAATATCTGCATCGAAGTGATCGAT GACGGCGCCGGGCTCAATCGCGAAAAAATTCTCGCCAAAGCGGC GGCGCAGGGGCTGGCGGTCAGCGACAGCATGAGTGATGAAGAGG TCGGAATGCTTATTTTTGCGCCGGGCTTTTCGACCGCGGAACAGG TGACCGACGTCTCTGGCCGCGGCGTCGGCATGGACGTCGTGAAAC GGAACATCCAGGAGATGGGCGGGCACGTTGAAATCCATTCCCGC GCGGGCAAAGGGACCTCGATTCGTATTTTGCTGCCGCTGACGCTC GCTATCCTCGACGGCATGTCGGTCAAGGTCAATGAAGAGGTCTTT ATTCTGCCGCTCAACGCGGTCATGGAATCGCTGCAACCGCAGGCC GAAGACCTGCATCCGATGGCCGGCGGCGAGCGGATGCTGCAGGT TCGCGGCGAGTATCTACCGCTGGTGGAGCTCTACCGGGTGTTTGA TGTCGCCGGGGCGAAAACCGAGGCCACTCAGGGCATCGTGGTGA TTCTGCAAAGCGCCGGCCGCCGCTATGCGCTGCTGGTGGATCAGC TGATCGGCCAGCACCAGGTGGTGGTGAAAAACCTGGAAAGCAAT TACCGCAAAGTGCCGGGAATTTCCGCGGCGACGATCCTCGGTGAC GGCAGCGTGGCGCTGATCGTCGACGTGTCGGCGCTGCAAATGCTC AATCGGGAAAAGCTGCTGAGCGCAGCGGCCGCATAA
purine-binding chemotaxis protein CheW	**cheW**	>ADJCKNHF_03341 Chemotaxis protein CheW ATGGCAGGATTAGCAACCGTCAGCAAATTGGCTGGCGAAACGGT AGGTCAGGAGTTTTTAATCTTTACCCTCGGCAATGAAGAATACGG CATCGATATTCTGAAAGTGCAGGAGATCCGCGGCTATGACCAGGT GACGCGTATCGCCAACACCCCGGATTTCATCAAAGGCGTCACCAA TCTGCGCGGGGTGATCGTGCCGATTATCGACCTGCGGGTAAAATT CGCCCAGCAGGGCGTCTCTTATGATGAAAACACGGTGGTTATCGT GCTTAACTTCGGCCAGCGGGTGGTGGGGATTGTGGTCGACGGCGT CTCTGACGTGTTGTCTCTCACCGCCGAACAGATCCGCCCGGCGCC GGAATTCGCGGTAACGCTGGCGACCGAGTATCTCACCGGTCTTGG CGCGCTCGGCGAGCGTATGTTGATTCTCGTCGATATCGAAAAGCT GCTCAGCAGCGAAGAGATGGCGCTGGTCGATAACGTCGCCAAAA GCCACTAA
chemotaxis protein methyltransferase CheR [EC:2.1.1.80]	**cheR**	>ADJCKNHF_03344 Chemotaxis protein methyltransferase ATGAAGCAGACGACATCAACCGCGGCGCGTGAAAGCGGATCGGC GCTGGCGCAGATGGTTCAGCGTCTGCCGCTCTCCGACGCGCATTT TCGCCGCATCAGCCAGCTTATCTATCAGCGTGCCGGGATCGTGCT GGCGGCGCATAAGCGCGAGATGGTGTACAACCGGCTGGTGCGCC GTTTGCGTCTGCTGGGCATTCATGATTTCGGCGACTACCTGGCGCT GCTGGAAAGCGACCCGCACAGCGCCGAGTGGCAGGCGTTTATCA ATGCGCTGACCACCAACCTGACCGCCTTTTTTCGCGAGGCGCACC ACTTTCCGATTCTGGCGGAGCATGCGCGCTCGCGTCCCGGGAACT

		ATAGCGTGTGGAGCACCGCCGCCTCGACCGGCGAAGAACCTTATT CCATCGCCATTACGCTCGGTGATGCGCTCGGGGAACGTGCGGGCA GTTGCCAGGTCTGGGCCAGCGATATTGACACCCAGGTGCTGGAGA AAGCGGAAGCAGGGATTTATCGCCATGAAGATCTGCGCACTCTG ACGCCAATCCAGATGCAGCGTTATTTTCTGCGCGGCACCGGGCCG CATCAGGGGCTGGTGCGCGTGCGTCAGGAGCTGGCGGCGCGGGT CAACTTCCAGCCGCTGAATCTGCTGGCGGCGGAGTGGGCGCTGCC GGGGCCGTTCGACGCGATTTTTTGCCGCAACGTGATGATCTATTT CGATAAACCGACGCAGGAACGCATCCTGCGCCGCTTTGTCCCCTT GCTTAAACCGGGGGGGCTGTTGTTTGCCGGTCACTCCGAGAATTT CAGCCAGATCAGCCGGGATTTCTACCTGCGTGGACAGACCGTGTA TGGGCTGGCCAAGGAGAAGTAA
two-component system, chemotaxis family, protein-glutamate methylesterase/glutaminase	**cheB**	>ADJCKNHF_03345 Protein-glutamate methylesterase/protein-glutamine glutaminase ATGAGTAAAATCAGAGTGTTATGTGTTGATGATTCGGCCCTGATG CGCCAGTTGATGACCGAGATCGTCAATGGCCACGCCGATATGGA GATGGTGGCGGTGGCCCCGGACCCGCTGGTCGCACGGGATCTGAT CAAAAAATTTAACCCACAGGTGCTGACGCTGGACGTCGAAATGC CGCGCATGGACGGCCTCGATTTCCTCGAAAAGCTGATGCGCCTGC GGCCGATGCCGGTGGTGATGGTTTCATCGCTGACCGGTAAAGGTT CGGAAATTACCCTGCGCGCGCTGGAGCTGGGGGCGGTGGATTTCG TCACCAAACCGCAGCTCGGGATCCGCGAAGGCATGCTGGCTTACA GCGAACTGATAGGCGAAAAGATCCGTACCGCCGCACGGGCGCGG CTACCGCAGCGCGCCAATGACCAGCCGCCGGCCATTTTAAGCCAC GGACCGCTGCTGAGCAGCGAGAAGCTGATCGCCATTGGCGCTTCC ACCGGCGGCACCGAAGCGATCCGTCAGGTGCTACAACCGTTGCC GGCCACCAGTCCGGCGCTGCTGATCACCCAGCATATGCCGCCGGG ATTTACCCGCTCGTTTGCCGAACGGTTGAATAAGCTGTGCCAGAT CACGGTGAAAGAGGCGGAAGAGGGCGAACGCGTGCTCCCGGGAC ACGCCTATATTGCGCCTGGGGATCGCCATCTGGAGCTGGCGCGTA GCGGCGCTAACTATCAGGTCAAGCTGCACGACGGCCCGGCGGTA AATCGCCATCGTCCCTCGGTGGATGTGCTGTTTCGTTCGGTGGCCC GCCACGCCGGGCGCAATGCGGTGGGGGTGATCCTCACCGGCATG GGCAACGACGGCGCGCAGGGGATGCTGGAGATGCATCGCGCCGG GGCCTATACCCTGGCGCAGAGTGAGGCGAGCTGCGTGGTGTTCGG CATGCCGCGCGAGGCCATCGCCAGCGGCGGGGTCAACGAAGTGG TTGAACTGGAGCGCATGAGCCAACGCATGCTGGCGCAGATAGCC GGCGGCCAGGCGCTGCGAATTTAA
two-component system, chemotaxis family, chemotaxis protein CheY	**cheY**	>ADJCKNHF_03346 Chemotaxis protein CheY ATGGCAGATAAGAATCTCCGTTTTCTGGTCGTCGACGACTTTTCC ACCATGCGTCGTATCATCAGAAATTTGCTTAAAGAGCTCGGCTTC AACAACGTCGAAGAGGCGGAAGATGGCGCGGACGCGCTAAATAA GCTGCGAGCCAGCAGCTTTGATTTCGTGGTCTCCGACTGGAACAT GCCTAACGTTGACGGCCTGGAGCTGCTGCAGACCATTCGTGCCGA TGCCGCGCTGGCGGCGATGCCGGTATTGATGGTGACGGCGGAAG CGAAAAAAGAAAATATTATTGCCGCCGCGCAGGCAGGCGCCAGC GGTTATGTGGTGAAACCTTTTACGGCGGCGACGCTGGAAGAAAA GCTCAACAAGATTTTTGAAAAATTGGGCATGTAA

flagellar biosynthetic protein FlhB	**flhB**	>ADJCKNHF_03348 Flagellar biosynthetic protein FlhB TTGGCGGAAGACAGCGATCTGGAAAAAAGCGAGGCCCCCACCGC CCACCGGTTGGAGAAGGCGCGTGAAGAGGGCCAGATCCCGCGCT CGCGCGAGCTGACCTCGGTACTCATGCTGGTGGCCGGGCTCGCCA TTATCCTGATGTCCGGCAGCAATATCACTCGCCAACTGGCGGAAA TGCTGACGCAGGGCCTGCACTTTGACCACGGGATGGTCAGCAATG ACAAACAAATGCTGCGCCAGCTGGGAATGCTGCTGCGTCAGGCG GTGCTGGCATTGCTGCCGGTAATGGCCGGGCTGGTGCTGGTGGCG CTGGCCGCGCCGATGCTGCTTGGCGGCATTTTATTCAGCACCAAG TCGCTCAAATTCGATCTTAAACGGCTGAATCCGCTTTCCGGTCTG AAACGCATGTTCTCCACCCAGGTGCTGGCGGAGCTGTTAAAAGGG ATCCTCAAAGCCACGCTGGTCGGTTGGGTAACCGGGCTGTACCTA TGGCACAACTGGGCGGCGATGCTGCATCTGATGACCCAACAGCC GCTCGACGCGTTGGCCAATGCGCTGCAGATGATCCTCTATTGCGG ATTTCTGGTGGTGCTCGGATTGACGCCGATGGTGGCGTTTGACGT TTTTTATCAGCTGTGGAGCCACTTCAAAAAGCTGAAGATGACCAA ACAGGATATCCGCGACGAATTCAAAGATCAGGAAGGCGACCCGC ATGTTAAAGGGCGGATCCGTCAACAGCAGCGGGCGATTGCCCAG CGGCGGATGATGGCCGATGTGCCGAAAGCGGACGTGATAGTCAC TAACCCGACCCACTATGCCGTGGCGTTGCAGTACAACGATAAAAA AATGAGCGCGCCGAAGGTGTTGGCTAAAGGGGCGGGGGAGATTG CGCTGCGCATTCGCGAACTGGGAGCGCAACACCGTATTCCGATGC TTGAAGCGCCGCCGCTGGCCCGCGCGCTCTATCGCCATAGCGAGA TTGGCCAGCATATTCCCGCCACCCTCTATGCCGCGGTCGCCGAAG TGCTGGCCTGGGTTTATCAGCTGCGCCGCTGGCGGCGCGAGGGCG GCCTGATCCCGAAAAAACCTCAACGTTTACCGGTGCCGGAAGCAC TGGATTTTGCAAAAGAGAGTGACTCTGATGGCTAA
flagellar biosynthesis protein FlhA	**flhA**	>ADJCKNHF_03349 Flagellar biosynthesis protein FlhA ATGGCTAATTTGGCCTCCCTGCTGCGTTTGCCGGGGAATGTTAAA GATACGCAATGGCAGGTTCTGGCCGGCCCGATCCTGATCCTGCTG ATTTTGTCGATGATGGTGCTGCCGCTGCCGGCGTTTATCCTCGACC TGCTTTTTACTTTCAATATCGCGTTGTCGATCATGGTGCTGCTGGT GGCGATGTTTACCCAGCGCACGCTGGACTTCGCCGCGTTTCCGAC CATTCTGCTGTTCTCGACGCTGCTGCGCCTGTCGCTCAACGTCGCC TCGACGCGCATCATTTTGATGGAAGGGCACACCGGGGCCGCCGCC GCGGGGCGGGTCGTGGAGGCCTTCGGTCACTTCCTGGTCGGCGGT AATTTCGCCATCGGTATCGTGGTGTTTATCATCCTCGTGCTGATCA ACTTCATGGTTATCACCAAAGGCGCCGGGCGTATCGCCGAAGTGG GGGCGCGTTTCGTACTCGACGGCATGCCGGGTAAGCAAATGGCG ATCGATGCCGACATGAACGCCGGGCTTATCGGTGAAGAAGAGGC GAAAAAACGCCGCGCGGAAGTCACGCAGGAAGCCGATTTCTACG GCTCGATGGACGGCGCCAGCAAGTTTGTTCGCGGCGATGCCATCG CCGGGCTAATGATTATGGTGATTAACGTGGTCGGCGGACTGCTGG TCGGCGTGGTGCAGCACGGTATGGAGCTGGGGGCGGCGGCGGAA AGCTACACCTTGTTGACCATCGGCGACGGGCTGGTGGCGCAAATC CCGGCGCTGGTGATCTCTACCGCCGCCGGGGTCATCGTGACCCGG GTGGCGACCGATCAGGATGTCGGCGAACAGATGGTCGGCCAGCT ATTCAATAACCCAAAGGTCATGCTGCTGTGTGCCGCGGTACTTGG GCTGCTGGGGCTGGTGCCGGGGATGCCGAACCTGGTCTTCCTGCT GTTTACCGCCGCGCTGCTCGGGCTGGCCTGGTGGCTGCGCGGGCG CGAAAAACAGGCGCCGAAAGCCGCCGACGAACCCATCGTGCAGG AGAATACCCAGGCCGCGGAAGCCAGTTGGGCCGATGTCCAGTTG GAAGATCCGCTGGGCATGGAAGTGGGTTACCGGCTGATTCCGATG GTCGATTTTCAGCAAAATGGCGAGCTGTTGGGGCGTATCCGCGGT ATCCGCAAGAAATTCGCCCAGGAGATGGGCTATCTGCCGCCGGTG GTGCATATCCGCGATAACCTCGAACTGGCGCCCGCCCGCTACCGC

		ATTCTGATGAAAGGCGTGGAAATCGGCAGCGGCGAAGCGCAGCC TGGGCGCTGGCTGGCGATCAACCCCGGCAACGCTATCGGCGAGCT GGCGGGGGATAAAACTATCGATCCGGCCTTCGGTCTGGAGGCGG TGTGGATTGATAGCGCGTTGCGCGAGCAGGCGCAAATTCAGGGCT ATACGGTGGTGGAGGCCAGTACGGTGGTGGCGACCCATCTCAAC CACCTCATCGGCCAGTTCGCCAGCGAACTGTTTGGCCGCCAGGAG ACGCAGCAGCTACTCGACCGTGTGTCGCAGGAGATGCCGAAGCT GACCGAAGATTTCGTACCGGGCGTGGTATCGCTGACCACGCTGCA TAAGGTGTTGCAGAATCTGCTGGCCGAGCGGGTATCGATCCGCGA TATGCGTACCATTATCGAGACGCTGGCGGAACATGCGCCGACGCA AAGCGATCCTTACGAGCTGACCACCGTCGTGCGCGTGGCGCTGGG GCGGGCGATTGCCCAGCAGTGGTTCCCTGGCAATGGTGAAATTCA GGTTATCGGCCTGGATACCCAACTGGAACGACTGCTGCTGCAGGC GCTGCAGGGCGGCGGCGGTCTCGAACCGGGGCTTGCCGACCGCC TGCTGGAGCAGGCGCGGCAGGCGCTGCAGCGCCAGGAGATGCTC AGCGCGCCGCCGGTGCTGCTGGTTAACCACGCGCTGCGCCCGCTA CTGGCGCGCTTCCTGCGCCGTAGCCTGCCGCAGATGGCGGTGCTT TCCAACCTGGAGATCAACGACGATCGCCAGATTCGCATGACCTCA ACCATTGGAGCGGCCTGA
flagella synthesis protein FlgN	**flgN**	>ADJCKNHF_03351 Flagella synthesis protein FlgN ATGGACAGATTACGCACTCTGCTGGATAAACTGGCGGAAACCCTG CGGGCGCTGGATGACGTGCTGGCGCAAGAGCAACAATTGCTTTGT GCGGATGAACTGCCCGGCGTGGCGCTGCAGCGCGTCACCGATAG CAAGAGTCAACTGCTGGCGACGGTGGCCTGGCTTGAACAACAGC GCCCGGCGCTGGAAGCCAACCTTGCGCTACGCGCGCCTTACCCCG GCCATGAAAGCTTCAGCGAACGCTGGCGGCAGATCCAGCAGTTA AGCCAGAGCCTGCGTGAAAAGAATCAGCATAACGGCCTGTTGCT CAATCAACAGATCGCCCATAACCAGCAGGCGCTGGCAATTCTTAG CAAGAATAATAAATCGCTGTACGGGCCGGACGGTCAGTCGCGCG CCGCCAGTCTGCTGGGCCGTAAAATCGGCGTCTGA
negative regulator of flagellin synthesis FlgM	**flgM**	>ADJCKNHF_03352 Negative regulator of flagellin synthesis ATGAGTATCGATCGCACCCAGCGGTTACAGCCGGTTTCCACGGTG CAGCCGCGTGAAACCCCGGCCGACAACCCGCTTCAGCCGCGCAA GGCCACCGCGGCGGAAACCGCCGTTAGCGCCACCAAAGTGAAAC TGAGCGATGCGCAGGCGCGGCTGATGCAGCCCGGCACCCAGGAT ATTGATATGAACCGGGTCGAGGCTATCAAACAGGCGATTCGTAGC GGCGAACTGAAAATGGACGCGGGCAAAATCGCCGACGCCCTGCT GCAGGATGCGCACAACGATATCCAGCGCCTTGCCGGTAGCAAAA CAGATAAGGCCTGA
flagellar basal-body rod protein FlgB	**flgB**	>ADJCKNHF_03354 Flagellar basal body rod protein FlgB ATGCTCGACAAACTGGACGCTGCTCTGCGTTTTGGCCAGGAGGCG CTGAACCTGCGCGCCCAGCGCCAGGAAATACTGGCCGCCAATATC GCCAACGCAGACACGCCGGGCTATCAGGCGCGGGATATCGATTT CGCCAGCCAACTGAATAAAGTCCTGCAACAGGGGCGGGTAAACG GCAACGGCATGGCGCTGAACCTGACGGCGGCGCGTCATATTCCG GCGCAGACCATGCAGCCGCCGGAGCTGGATCTGCTGTTCCGGGTG CCGGACCAGCCGTCGATGGACGGCAACACGGTGGACATGGATCG TGAACGCACCAACTTCGCTGACAACAGCCTGAAATATCAGACCG ACCTGACGCTGCTCAACGGTCAGATCAAAGGGATGATGTCGGTGC TGCAACAAGGATAA
flagellar basal-body rod protein FlgC	**flgC**	>ADJCKNHF_03355 Flagellar basal-body rod protein FlgC ATGTCTTTACTCAATATTTTTGATATCTCCGGCTCGGCGCTCTCGG CCCAGTCACAGCGGATGAATGTCAGCGCCAGCAATATGGCCAAC GCCGATAGCGTCACCGGCCCGGATGGCGAACCCTATCGCGCGAA GCAGGTGGTGTTCGAAGTGGCCGCGGCACCAGGGCAGCAGACAG GCGGCGTGCGCGTCTCGCAGGTGGTCGATGACCCGGCGCCCGCGC

		GGATGGTTTATCAACCGGGTAATCCGCTGGCCGATGCTAAGGGTT ATGTACGGATGCCGAACGTCGATGTGGTAAGCGAAATGGTTAAC ACCATCTCCGCCTCCCGCAGCTATCAGGCCAACGTCGAAGTGCTC AACACCACTAAGTCGATGATGATGAAAACCCTGACGTTGGGTCA GTAA
flagellar basal-body rod modification protein FlgD	**flgD**	>ADJCKNHF_03356 Basal-body rod modification protein FlgD ATGGCTATTGCCGCAACCACCAATGAATCGACCAACAACGCGGTT CTTGATTCCGCCAGCAAAAGCAGCACCAGCCAGGATCTGCATAAC AGCTTCCTGACGTTGCTGGTGGCGCAGTTGAAAAATCAGGACCCG ACCAACCCGATGCAGAACAACGAGCTGACCTCGCAGCTGGCGCA GATTAATACCGTACAGGGCATCGAAAAACTCAACACCACCCTTGG CGCGATCTCCGGGCAGATCAACAGCAACCAGTCGCTGCAGGCCA GCGCGCTGATCGGCCACGGCGTGATGGTACCGGGTAATAACATTC TGGTCGGCAGCAAAGAAGGCCAGGTCAGCACCACGCCGTTTGGC GTCGAACTGGAGCGCGCCGCCGATCAGGTCACGGCAACCATCAC CAACGCCAACGGCCAGGTGGTGCGGACCATTGAGATTGGCGGCC TCACCGCCGGGGTGCACGCCTTCACCTGGGACGGCTCGCTGGATG ATGGTACCGCCGCGCCGGACGGCGCCTATAAAGTGGCGATTAAC GCCAAGGGCAACGGCGAGCAGCTGGTGGCGCGTAGCCTGCATTT CGGCATGGTTAACGGTGTGATTAACGACAGCAACGGCGCGAAGC TGGATCTCGGCCTGGCCGGTAACGCCAGCCTCGAAGAAGTGCGG CAGATCCTGTAA
flagellar hook protein FlgE	**flgE**	>ADJCKNHF_03357 Flagellar hook protein FlgE ATGGCCTTTTCTCAGGCAGTCAGCGGCTTAAATGCGGCGGCCACC AATCTCGACGTGATTGGCAACAATATCGCTAACTCCGCGACCGCG GGTTTTAAATCCGGCAGCGTGTCGTTCGCCGATATGTTCGCCGGT TCGCAGGTCGGGCTGGGGGTTAAAGTTTCCGGGATCACCCAGAAC TTTAAAGGCGGCACCACTACCGGCACCAGCCGCGCGCTGGATGTG GCGATTAACGGCAACGGCTTCTTCCGCATGCAGGATAAAGACGG CGGTATTTTCTATACCCGCAACGGCCAGTTTAAGCTGGACGAAAA CCGCAATCTGACCAATATGCAGGGGCTGCAGCTGACCGGCTATCC GGCCGCCGGCACGCCGCCGACCATTCAACAGGGCGCCAACCCGG TACCGCTGAGCATTCCGGAAGGAATGATGAACGCCAAAGCGTCG ACTTCCGGCGAAATGGTCGCCAATCTGAAGTCGACGCATAAAGTG CCGGAGAACAAGACCTTCGACCCGGCGAAGCAGGACAGCTATAA CTACGTCAACACCATCACCGCCTACGATTCGCTGGGTAACGCCCA CAACATCAACGCCTATTTCGTGAAAACCGACGATAACAAATGGC AGGTCTATACCCAGGACGGCAGCGCGGCTGCGGTCAGCGCGGGC ACCATGGAGTTCAATACCAGCGGCAACCTGGTCAGCGTTAACGGC CAGGCGGGCGAGTTCAGCATGACCATTCCGATGAGCGCGAAAGA CGGCGCCCCGGCGCAGAACTTCACGCTCAGCTTCGCCGGTAGTAT GCAGCAGAACGTCGGTAGCGATTCGGTGAGTAAAGTGGCGCAGG ATGGTTATGCCGCCGGTGAATACACCAACTTCCAGATTAACGATG ACGGTACCGTCGTCGGTATCTATTCCAACCAACAGACCCAGGTCC TGGGGCAGATTGTGATGGCCAACTTCTCCAACCCGGAAGGGCTGG CGTCGCAGGGCGATAACGTCTGGCAGGAGACCGGCGCCTCCGGC CAGCCACGGGTGGGACTCTCCGGCGGCGGCGGTTTTGGCAAGCTG ACCAGCGGCGCGCTGGAGTCTTCCAACGTCGACCTGAGCCAGGA GCTGGTGAACATGATTGTCGCCCAGCGTAACTATCAGTCCAACGC CCAGACCATCAAGACGCAGGATTCGATCCTGCAGACGCTGGTCA GCCTGCGCTAA
flagellar hook protein FlgE	**flgE**	>ADJCKNHF_03358 Flagellar basal-body rod protein FlgF ATGGATCACGCGATTTATACCGCGATGGGCGCCGCGCGCCAGAC GCTGGAGCGACAGTCGATTACCGCCAACAATCTCGCCAACGCCTC GACGCCGGGCTTTCGCGCCCAGCTCGCCGCGCTGCGCGCGGTGCC GGTTGACGGGCCGAGCCTCGCCACCCGCACGCTGGTGGCGGCCTC

		GACGCCGGGCGCCGATATGAGCCAGGGGGCGCTGAACTACACCG GGCGCCCGCTGGACGTGGCGCTGCAGCAGGACGGTTTTCTGGCGC TCAGCCTGCCGGGCGGCGGCGAAGCCTATACCCGCAACGGCAGC ATTCAGGTTTCGGCTAACGGTCAGTTGACGGTGCAGGGAATGCCG CTGCAGGGCGACGGCGGGCCGATTGAGGTACCGCCATCGGCGGA AATCACTATCGCGGCCGACGGCACCATTTCGGCGCTGAATCCCGG CGACCCGCCGAACACCATCGCGCAGATTGGCCGCCTGAAGCTGGT GAAAGCTGATGCGCGCGAAGTGATGCGCGGCGATGACGGCCTGT TCCGCCTGACCCCGGAAACCCAGCAGCGCCGCGGCAATCTGTTGG CCAACGACCCGCAGGTGCGGGTCATGCCGGGCGTGCTGGAGGGC AGTAACGTCAAGCCGATGGAGACCATGGTCGATATGATCGCCAA CGCCCGTCGCTTTGAAATGCAAATGAAGGTCATCCACAGCGTGGA TGAGAACGAACAGCGGGCGAACTCTCTGCTGTCAGTAAGCTGA
flagellar hook-associated protein 1 FlgK	**flgK**	>ADJCKNHF_03359 Flagellar basal-body rod protein FlgG ATGATTCCCTCTTTATGGATTGCGAAAACCGGTCTTGATGCGCAG CAGACCAATATGGACGTGATCGCCAACAACCTGGCGAACGTCAG CACCAACGGTTTTAAACGCCAGCGCGCGGTGTTTGAAGATCTGCT GTATCAGACCATGCGCCAGCCGGGGGCGCAGTCCTCCGAGCAGA CCACGCTGCCTTCCGGCCTGCAGATCGGTACCGGCGTGCGCCCGG TCGCCACCGAGCGTCTGCATAGCCAGGGCAACCTGTCGCAGACCA ACAACAGCAAAGACGTGGCGATTAAAGGCCAGGGCTTCTTCCAG GTGCTGCTGCCGGACGGCAGCCAGGCTTACACCCGCGACGGCTCG TTCCAGATCGATCAGAACGGCCAACTGGTGACCGCCAGCGGCTTC CAGGTGCAGCCGGCGATCACCATACCGGCCAACGCGTTGACCATT ACCATCGCCCGCGATGGCATCGTGAGCGTCACCCAGCAGGGTCA GACCGCCGCCCAGCAGGTCGGGCAACTGACGTTAACCACCTTTAT TAACGACAGCGGCCTCGAAAGCGTGGGCGAGAACCTGTACCAGG AAACTGAAAGCTCCGGCGCGCCGAATGAGAGCACGCCGGGCCTG AACGGCGCCGGTATGCTCTACCAGGGTTATGTCGAGACCTCTAAC GTCAACGTGGCGGAAGAGCTCGTTAATATGATCCAGACCCAGCG CGCCTATGAGATCAACAGCAAAGCGGTTTCGACGTCGGATCAGAT GCTGCAGAAACTGACCCAGCTGTAA
flagellar hook-associated protein 1 FlgK	**flgK**	>ADJCKNHF_03363 Flagellar hook-associated protein 1 ATGTCCAATAGCTTAATCAATACGGCGATGAGCGGACTGAATGCG GCGCAGGTGGCGCTCAGTACCGTCAGCAACAATATCTCTAACTAC AACGTGGCGGGTTATAACCGGCAGACGGCGATTCTGGCCCAAAA CGGCGGCCTGGCCACCATGAACGGTTTTATCGGTAACGGCGTGAC CGTGACCAGCGTGAACCGCGAATATAACCAGTTCATCACCAACCA GTTGCGCGGCGCGCAGAGCGCGGCCGGTTCGCAGAACGCCTACT ACGAAAAGATTTCGCAGATCGATAATCTGCTGGCCAGCAAAACC AATACCCTGTCGGGGAGCCTGCAGGATTTTTTCACCAATTTGCAG AACCTGGTGAGCAACGCCGGCGACGACGCGGCGCGCCAGACGGT GCTGGGCAAGGCTAACGGCCTGGTTAACCAGTTTAATAATACCGA TAAATATCTGCGCGACATGGATAGCGGCGTTAATCAGCAAATTAA CGACACCGCCCAGCAGATTAACAGCTATAGCCAGCAGATTGCCC GTCTTAACGATGAGATTACCCGCCTGCGCGGCAGCGCCAGCGGCG AACCGAACGCGCTGCTCGATCAGCGCGATCAGCTGGTCAGCGAA CTCAACCAACTGGTGGGCGTTCAGGTAACCCAGCAGGACGGCGA CGCCTATACCGTCTCCTTCGCCAACGGCCTGACCCTGGTGCAGGG CAACAACAGCTATCAGGTGGAAGCGATCCCTTCCAGCAGCGACC CTTCGCGCCTGACTCTCGGCTATAACCGCGGCAGCGGCGCCAACG AAGTGCCGGAAGGGCAGATCACCAGCGGCAGCCTGAGCGGCGTA CTGCGTTTTCGCAGCGAGACGCTGGACGGCGTGCGCAATCAGCTC GGCCAACTGGCGCTGGCGATGGCCGATAGCTTTAACCAGCAACA CCGCGAGGGCTTCGATCTCAACGGTGAGCAGGGGGGCGATTTCTT CAGCTTCAGCGGCGCGCGGGTGGTTGATAACACGCGCAATACCG

		GCGATGCCTCGCTGTCGGTGTCGTATACCGATACCAGCAAGGTAA AAGCCAACGATTACCGCGTAGAGTATGACGGCGCCAACTGGCAG GTCAGCCGTCTGCCGGACAACGTCAAAGTCAACGCCACCGCCGGT AAAGATGCAGCCGGTAACCCGACGCTGAGCTTTGATGGTCTCGAA GTCAGTATTGATGGCAACCCGCAGCAGAAAGATAGCTTTACGGTG AAGCCGGTCAGCGACGTGGCGGGCAACCTGAAAGTGGCGATTAC CGATTCAGCGAAAATCGCCGCCGCCGGTAAAGATGACAGCGGCC GCGGCGATAACGATAACGCTAAAAAACTGCTCGATCTGCAGACC AAAAACCTGGTGGATGGCAAAGCGACGCTTAGCGGCGCCTACGC CGGGATCGTCAGCGGCGTGGGCAACCAGACCGCCGCCGCGAAGG TGAGCAGCGAATCGCAGTCCAGTATCGTCACCCAACTGGCCCGTC AACAGCAGTCGCTCTCCGGGGTAAACCTCGACGAAGAGTATGGC GAGCTCCTGCGTTTCCAGCAGTACTACATGGCGAACGCGCAGGTG ATCCAGACCGCCAGCTCGCTGTTCGACGCGCTGCTGAATATTCGT TGA
flagellar biosynthetic protein FliR	**fliR**	>ADJCKNHF_03381 Flagellar biosynthetic protein FliR GTGATCCCCTTTGACAGCGCCCAGCTTAGCGAATGGCTCAGCCAG TATTTCTGGCCGCTGCTGCGTATTCTGGCCCTCATCAGCACCGCGC CGGTGCTGAGTGAAAAGCAGATAAGCAAAAAGGTGAAAATCGGT CTCGGCGGCCTGATTGCGATACTGATCGCCCCAACGCTGCCCATC AACGCGATCCCCATTATCTCTGCTGCCGGTTTATGGCTGGCGATTC AGCAGATCCTGATCGGCGCGGCGCTGGGGCTAACGATGCAGCTG GCTTTCGCCGCGGTACGCCTCGCCGGCGAAGTCATCGGCATGCAG ATGGGGCTATCGTTCGCCACCTTCTTCGACCCCAGCGGCGGCCCC AATATGCCGGTGCTGGCGCGGCTGCTTAACCTGCTGGCAATGCTG CTGTTTTTAAGCTTTGACGGCCACCTGTGGCTGATCTCGCTGCTGG CCGACAGTTTCCATACCCTGCCGATCCAGAGCCAGCCGCTGAACG GCAACGGTTTCCTCGCGCTCGCCCAACTGGGTTCCTTAATCTTTAT CAACGGCATGATGCTGGCGTTACCGCTGATTTGTCTGTTGCTCAC GCTCAATATCGCCCTGGGTCTGCTCAACCGTATGACGCCGCAGCT ATCGGTATTCGTGATCGGTTTCCCGGTGACCATGACCTTTGGCATT ATGACCCTCGGCATGATGATGCCGATGCTGGCCCCCTTCTGCGAA CACCTGTTTGGCGAGATGTTCGATCGCCTGGCGGCCGTTATCGGC GGTATGACGTTTTAA

flagellar biosynthetic protein FliQ	**fliQ**	>ADJCKNHF_03382 Flagellar biosynthetic protein FliQ ATGACGCCGGAATCCGTGATGGCCATTGGCACCGAAGCGATGAA GGTCGCCCTGGCGCTGGCCGCCCCGCTGCTGCTGGCGGCGCTAAT CAGCGGGCTGGTGGTCAGCCTGCTGCAGGCCGCCACCCAGATTAA CGAGATGACCCTATCGTTCATCCCCAAAATTCTCGCGGTAGTGGC GACGATTATTATCGCCGGACCGTGGATGCTGAACCTGCTGCTGGA CTATATGCGCACATTATTCAGCAACCTGCCTAATATTATTGGCTA G
flagellar biosynthetic protein FliP	**fliP**	>ADJCKNHF_03383 Flagellar biosynthetic protein FliP ATGTTCCCTACTCTGTTCGCTTGCCTTCGCCGTCGGGCGCCGTGGC TCGCCGCCGCGTTACTGCTGCTGAGCCCTGCCGCCTTCGCACAGC TGCCGGGGCTTATCAGTCAGCCGCTGGCCAACGGCGGCCAGAGCT GGTCGCTGCCGGTACAGACGCTGGTGCTGTTGACCTCGCTGACCT TCCTGCCGGCGATGCTGCTGATGATGACCAGTTTTACCCGCATCA TCATCGTACTGGGTCTGCTGCGTAACGCGCTGGGCACGCCTTCCG CGCCGCCGAACCAGGTGATGCTCGGGCTGGCGCTGTTCCTGACCT TCTTTATCATGTCGCCGGTGTTCGACAAGGTCTATCAGGAGGCGT ACCTGCCCTTCAGCCAGGACAAGATCGGCCTTGATACGGCGCTGG ATAAAGGCGCGCAGCCGCTGCGCGAATTTATGCTGCGCCAGACCC GCGAAAGCGATCTGGCGCTGTACGCTCGTTTGGCCAACCAGCCGC CGCTGGCCGGGCCGGAGGCGGTACCGATGCGTATTCTACTGCCCG CCTACGTCACCAGCGAACTGAAAACCTCCTTCCAGATTGGTTTTA CGGTGTTTATTCCGTTCCTGATTATCGATTTAGTGGTCGCCAGCGT GCTGATGGCGCTGGGGATGATGATGGTGCCGCCGGCGACGATCTC GCTGCCGTTTAAGCTAATGCTTTTTGTGCTGGTGGATGGCTGGCA GCTGCTGCTGGGCTCGCTGGCGCAGAGCTTCTATTCCTGA
flagellar motor switch protein FliM	**fliM**	>ADJCKNHF_03385 Flagellar motor switch protein FliN ATGAGTGATCCTAAGCAACCGTCTGGCGCAGGAAAGGAATCCGT AGACGATCTGTGGGCTGATGCGCTTAATGAACAACAGTCGTCTGA GAAATCCAGCGCCACCACCGATGGGGTGTTCAAATCGCTGGAGG CCCAGGATGCGCTCGGCAGCCTGCAGGATATCGATCTGATCCTCG ATATTCCGGTGAAGCTGACCGTTGAACTGGGGCGCACCAAAATG ACGATTAAAGAGCTGCTGCGCCTGTCGCAGGGATCGGTTGTCGCG CTGGATGGCCTGGCGGGCGAACCGCTGGATATCCTGATCAACGGC TATCTGATAGCCCAGGGCGAAGTGGTGGTGGTGGCCGATAAATTC GGTGTACGCATTACCGATATCATTACCCCGTCCGAACGTATGCGT CGGTTGAGCCGCTAA
flagellar motor switch protein FliM	**fliM**	>ADJCKNHF_03386 Flagellar motor switch protein FliM ATGGGCGATAGCATTCTTTCACAGGCAGAGATCGACGCCTTGCTC AACGGCGACAACACGGGCGACGAGCCCGAGACGGTTGTCGGCGG TAAAGAGAGCGAGGTTAAGCCTTACGATCCGAATACCCAGCGCC

		GCGTGGTGCGTGAACGCCTGCAGGCGCTGGAAATTATCAACGAG CGTTTTGCCCGGCAGTTCCGCATGGGATTGTTCAACCTGTTGCGCC GCAGCCCGGACATCACCGTCGGGCCGATTAAAATTCAGCCGTATC ACGAGTTTGCCCGCAACCTGCCGGTGCCGACCAACCTTAATCTGG TACACCTGAACCCGCTGCGCGGCACGGCGCTGTTTGTCTTCGCGC CGAGCCTGGTGTTTATCGCCGTCGATAACCTGTTCGGCGGCGACG GGCGTTTCCCGACCAAGGTCGAAGGCCGAGAATTCACGCCCACC GAACAGCGGGTCATCAAACGCATGCTGCGCCTGGCGCTGGACGC CTACGGCGACGCATGGAGCGCAATCTATAAGATTGACGTCGAAT ACGTGCGTGCGGAAATGCAGGTCAAATTCACCAACATCACCACCT CGCCGAACGATATCGTGGTGACCACGCCGTTCCAGGTGGAGATTG GCGCGCTAAGCGGTGAATTCAATATCTGTATTCCTTTCGCCATGA TTGAGCCGCTGCGTGAACTGCTGACCAATCCGCCGCTGGAGAATT CCCGCCAGGAAGATAGCCAGTGGCGCGAAACGTTGGTCAAGCAG GTGCAGCACTCTGAGCTGGAGCTGATTGCCAACTTCGTCGATATC CCGATGCGCTTATCGAAAATACTTAAGCTGCAGCCAGGCGACGTT TTACCGATAGATAAACCGGATCGCATTATCGCCCATGTCGACGGC GTGCCGGTGCTGACCAGCCAATATGGCACCTTAAACGGGCAGTAC GCCCTTCGTGTTGAACACTTGATTAACCCTATTTTGAATGCTCTGA GTGAGGAACAGCCCAATGAGTGA
flagellar hook-length control protein FliK	**fliK**	>ADJCKNHF_03388 hypothetical protein ATGAATCTCAATGCTTTGCCCGCCCTTAGCCTACCCGGCGACGCC AGCGCCCTGGCGGATCTGGCGCTCGATGACGCTCAGCTGTCATCT GCCTTTGCGCAACTGCTTGGCGCGCGCTTCACGCCCGCGCAAAGC GGCACGCTGCCGCCGGCGGCGCTGAGCGCCGACGATGAAAGCGC CCCGCCGCTAAGCCGTAACCAGCTTAACCAGCTGCTGGCCGCGCT TGGCGAACGCGGCACGCTGCTGGGCAATGCGCTACCGGCATCGG CGGAAAACGCCGTCGACACAACAGCGAAAAAAGAGGATACGCGC CCGGATACGCCACCGCTCAGCGAGGCGAAAACTTTAGATCCGGC GACGCTGCAGGCACTGTACGCCATGCTGCCGGCGGCAATCGTCGC CCCGCCGCCGCAGACCGCGCTACCGCAGGCTCAACCAGCTGCGA CCAGCGGCGATAAAACCGCGCTCCACATCGGCAACGCGGCGACT CAGCATGTCGCGAACCTGCCGGAAGCCGAACCGGCGGCGAAGCC GCAGCCGGGCACGGATCCCCTTAGCGGGCAAAATCTGCCTTCTCC TGTTGTGCAGACCGCGACCACGCCGCAGCACGATATGGCCGAAC CTCCGGCGGAGAATACTCCGGCGCAGCCAGCCGCCGTCGCTTTCG CCGCCGCCAGCCCCAGCCAGAGCGCCACGCCCGCCAGTGCGCTG GTAACCGCGCCGCCGACGCCGCAGCTTAATGCCCAGCTCGGCAGC CCGGAATGGCAGCAGGCGCTGAGCCAGCAGGTGCTGATGTTCCA CCGCAACGGCCAGCAGAGCGCCGAACTGCGCCTGCATCCGCAAG AGCTGGGGGCGCTGCAGATCACCCTGCAGCTCGACGATAAACAG GCGCAGCTGCACATCACTTCCGCACACGGTCAGGTACGCGCGGCG GTCGAGGCGGCTATGCCGCAGCTACGTCACGCGCTGGCTGAGAG CGGAATCAACCTCGGTCAGAGCAGCGTTGGCGGCGAGGCGACGC CGCAGTGGCAGCAGCAAAACGGTAACGGTGAAGGCCGCGCCAGC TACGCTGAACGCCATGGCGGCGGCAGCGATGCCGCGCCGATTGA GCCAGTCAGCGCCCCGGCAGCCCTGCAGCGAATGGCCAACCAGC TCAACGGCGTCGATATTTTCGCCTGA
flagellar FliJ protein	**fliJ**	>ADJCKNHF_03389 Flagellar FliJ protein ATGAAAGCACAGTCCCCTTTGATTACCCTGCGCAATCTGGCCCAG GAGGCCGTCGAACAGGCGGCGCAGCGTTTGGGCCAGGCGCGCCA GGCGCAACAGGCCGCCGAGCAACAGCTGACGATGCTGCTGAACT ATCAGGACGAGTACCGGCAAAAGCTCAACAGCACCCTTTCTGGC GGCATGGAAAGCTCGCGCTGGCAGAACTACCAGCAGTTCATTGCC ACCCTCGAACAGGCTATCGAACAACAGCGCCAGCAGCTTCTGCA GTGGGGGCAAAAGGTGGATCACGCCGTGAAGCAGTGGCAGGACC

		ATCAGCAGCGGCTGAACGCCTACGATACCCTGCACACGCGCGCG CAAAACGCCGAGCTGCAGTTGGAAAACAAACGCAATCAAAAATT GATGGATGAGTTCGCGCAACGCAGTACACAAAGGAATACCGCTT CATGA
flagellum-specific ATP synthase [EC:7.4.2.8]	**fliI**	>ADJCKNHF_03390 Flagellum-specific ATP synthase ATGACCGCCCGTCTCGGCCGCTGGCTGAATTCGCTTGAAGCGCTG GAGCAGCGTATCGCCCGAACGCCGACCGTACGACGCTATGGTCGT CTGACCCGCGCCACCGGTCTGGTGCTGGAGGCCACCGGCCTGCAG CTGCCGCTCGGCGCAACCTGCCTTATCGAGCGCGACGGCGGGGGC GGCGTGCAGGAAGTGGAAAGCGAAGTGGTCGGCTTTAACGATCA GCGGCTGTATCTGATGCCGCTGGAAGAGGTCGAAGGAATCGTGC CAGGGGCGAGAGTTTACGCCCGCAGCGCGGCGGACGGCCAGCAC GCCGGTAAACAACTGCCGTTGGGCCCGGCGCTGCTGGGACGCGT GCTCGACGGCGGCGCCAGGCCGCTTGATGGCCTGCCCGCGCCGG AAACCGGCTATCGCGCGCCGCTGATTACCGCGCCGTTTAACCCGC TGCAGCGTACCCCTATCGAGCAGGTGCTGGACGTCGGCGTACGCA CCATTAACGGCCTGCTGACCGTTGGGCGCGGCCAACGTATGGGGC TGTTCGCCGGCTCCGGCGTCGGTAAAAGCGTGCTGCTGGGCATGA TGGCGCGCTACACCCAGGCCGACGTTATCGTCGTCGGCCTGATCG GCGAACGCGGCCGGGAAGTCAAAGACTTTATCGAGAATATTCTC GGCGCCGAAGGCCGCGCGCGTTCAGTGGTGATCGCCGCCCCGGC GGACGTATCGCCGCTGCTGCGCATGCAGGGCGCCGCTTACGCCAC CCGCATCGCCGAAGATTTTCGCGATCGCGGCCAGCACGTGCTGCT GATCATGGATTCGCTCACCCGCTATGCGATGGCGCAGCGAGAAAT CGCGCTGGCGATCGGCGAACCGCCTGCAACCAAAGGCTATCCGC CATCGGTATTCGCCAAACTGCCGGCGCTGGTTGAACGCGCGGGCA ACGGTATCAGCGGCGGCGGTTCGATCACCGCCTTCTATACCGTAC TCACCGAAGGGGACGATCAGCAGGATCCGATCGCCGATTCGGCG CGCGCGATCCTCGATGGTCACGTGGTGCTGTCCCGACGTCTGGCG GAGGCCGGTCACTACCCGGCCATCGATATTGAAGCCTCGATCAGC CGCGCGATGACGTCACTTATCGATGACGAACATTATCGCCGGGTA CGCACCTTTAAACAGATGCTGGCCAGCTTCCAGCGCAACCGCGAT TTAATAAGCGTCGGCGCCTATGCCGCCGGTAGCGACCCGCTGCTG GATAAAGCCATTACCCTGTATCCGCAAATGGAGACCTATCTGCAG CAGGGAATTTTCGAGCGCTGCGGTTATGACGAAGCCTGTCTGCAG CTACAGCAGCTGATTGTTTAA
flagellar assembly protein FliH	**fliH**	>ADJCKNHF_03391 Flagellar assembly protein FliH ATGTCTGATCGCATTAATTCCATGCCCTGGCAGCCCTGGTCACTC AACGACCTCGGCGACGCGGCGCCAGCTTTTGAACCGCCGCTACCG ACGTTGGATAACGAAGCCTTGCAGCCTGACGCTCAGGCGGAACT GCAGCAGCAGCTTGCCGCCCTGCGCCTGCAGGCCGAGCAGCAAG GTCAGCAATCCGGTTATGCCGATGGCCAGCAAAAAGGCTATGAA GCCGGATTTCAGCAGGGACTTGAGGAGGGCCGCCAGCAGGGGCT GCTGGAAGCACAGCAGCAGCAACAGCCGCTGACCGACCACTGGC AGCAGCTGGTGAGCGAGTTTCAGCACACCCTTGATGCGCTCGATT CGGTCATCGCCTCACGCCTGATGCAGCTGGCGCTAACCGCCGCGA AACAGGTGCTTGGCCAGCCGCCGGTCTGCGACGGCACTGCCCTGC TGACGCAAATTCAACAGTTGATCCAGCAAGAACCGATGTTCAACG GCAAGCCGCAGCTGCGCGTACACCCGCAAGATTATGAGCGCGTT GAGCAGCAGTTAGGCACCACCCTCAGCCTGCACGGCTGGCGGTTG CTGGCGGATGGCGATCTGCATCCCGGCGGCTGTAAGGTCAGCGCC GAGGAGGGCGATCTCGACGCCAGTCTCGCCACCCGCTGGCACGA ATTGTGTCGCCTCGCCGCGCCGGGAGATCTGTGA
flagellar motor switch protein FliG	**fliG**	>ADJCKNHF_03392 Flagellar motor switch protein FliG ATGAGCCTGACCGGAACCGATAAAAGCGCCATTTTACTGATGACG CTGGGCGAAGACCGCGCGGCGGAGGTGCTCAAGCACCTCTCCTCC

		CGCGAAGTCCAGCTTTTGAGCGGCACCATGGCCGGCATGAGCCA GGTCTCGCATAAACAGCTCGGCGAGATCCTGTCTGAATTTGAAGA CGATGCCGAACAGTTCGCCGCCCTGAGCGTCAACGCCAGCGACTA TTTGCGTTCGGTGCTGGTGAAAGCGCTGGGCGAAGAGCGTGCCGC CAGCCTGCTGGAGGATATTCTCGAATCCCGCGAAACCACCTCCGG GATGGAAACGCTCAACTTTATGGAGCCGCAGAGCGCCGCCGACC TGATCCGCGATGAACACCCGCAGATCATCGCCACCATCCTGGTAC ATCTCAAGCGCGGCCAGGCGGCGGATATTCTGGCGCAGTTCGATG AGCGCCTGCGCAACGACGTAATGCTGCGTATCGCCACCTTCGGCG GCGTGCAGCCGGCGGCGCTGGCGGAGTTGACCGAAGTACTCAAC AACCTGCTCGACGGCCAGAACCTCAAGCGCAGCAAAATGGGCGG AGTGCGTACCGCCGCCGAGATTATCAACCTGATGAAAACCCAGC AGGAAGAAGCCGTTATCGACGCGATGCGCGAATACGATGGCGAG CTGGCGCAGAAGATCATCGACGAGATGTTCCTGTTCGAAAACCTG GTGGAGGTCGACGATCGCAGTATCCAGCGCCTGCTGCAGGACGT GGACAGCGAATCGCTGCTGATTGCTCTGAAGGGCGCCGAGCAGC CGCTGCGCGAGAAGTTCCTCAAAAACATGTCCCAGCGCGCGGCC GATATTCTGCGCGACGATCTCGCCAACCGTGGGCCGGTGCGCATG TCGCAGGTGGAAAACGAACAGAAAGCGATTCTGCTGATAGTCAG ACGGCTGGCGGAGAGCGGCGAAATGATTATTGGCGGCGGCGAGG ACACCTATGTCTGA
flagellar M-ring protein FliF	**fliF**	>ADJCKNHF_03393 Flagellar M-ring protein ATGAGTGCCTCGTTATCCGCCGGCGAAAGCCGCGACAACGGCCTG CAGGCCATCTGGAGCCGTCTGCGCGCCAATCCAAAAATACCGCTG CTGGTGGCCGCCTCCGCCGCTATCGCCATTATCGTCGCGCTGCTG CTGTGGGCGAAAAGCCCGGATTATCGCGTGCTGTACAGCAATCTG AACGATCGCGACGGCGGCGCTATCGTCACCCAACTGACGCAGAT GAACATCCCCTACCGCTTCGCCGAGAATGGCGCGGCGCTGATGAT CCCGGCGGAGAAAGTGCATGAAACCCGTCTGCGTCTTGCGCAGC AGGGGCTGCCGAAGGGCGGCGCCGTTGGCTTCGAACTGCTGGAT CAGGAAAAATTCGGCATCAGCCAGTTCAGCGAACAGATTAACTA TCAGCGCGCTCTTGAAGGCGAACTCTCACGCACTATCGAGTCGCT GGGGCCGGTGCAGAATGCGCGGGTGCACCTGGCGCTGCCGAAGC CCTCGCTGTTCGTCCGCGAGCAAAAGTACCCTTCCGCTTCTGTCAC CCTGACGCTGCAGCCGGGCCGTGCGCTGGATGATGGCCAAATCA ACGCTATCGTCTATATGGTATCGAGTAGCGTCGCCGGCCTGCCGG CTGGCAACGTCACCGTGGTCGATCAGGCCGGACGCCTGCTGACGC AGTCTGACGGCACCGGGCGCGACCTCAACGCCTCGCAGCTGAAA TATGCCAGCGAAGTGGAAAGCGGCTATCAGCGACGCATTGAAAC GATCCTGGCGCCGGTGGTCGGCAGCGCCAACGTCCGCGCTCAGGT GACCGCACAGATCGATTTCGCCTCCCGCGAGCAGACCGACGAAC AGTACCAGCCGAACCAGCAGCCCGATAAAGCGGCGATCCGTTCG CAGCAAACCAGCAGCAACGAGCAAATCGGCGGACCGCAGGTGGG CGGCGTTCCTGGGGCGTTATCCAACCAGCCGAGCGCGCCGGCCAC CGCGCCGATTGAAACCGCTAAACCGGCGGCCAATAACGCCAGCA ACGCGACCAACACCCGTAGCGCCGCGGCCAACAGCGGCCCGTTA AGCACCCGACGCGACGCCACCACCAACTACGAACTCGATCGCAC CATCCGCCATACCCAACAAAAAGCCGGGACGGTGGAGCGTCTGT CGGTCGCCGTGGTGGTGAACTACAGCCTCAACGCCGACGGCAAA GCGCAGCCGATGAGTAAAGAACAACTGGCGCAGATTGAAGCTCT GGTGCGCGAAGCGATGGGCTACTCCAGCAGCCGCGGCGATAGCC TACAGGTGGTCAATACGCCATTTACCGACAATCAGATGACCGGCG GCGAGCTGCCGTTCTGGCAGAGCCAGGCGTTTATCGATTTGCTGC TCGAACTGGGACGTTATCTGCTGGTGCTGCTGGTCGGCTGGGTAT TGTGGCGCAAGCTGATTAAGCCACAGCTGCAGCAGCGTCAGGCC GCACAGCAAGCCGCGGTCGCCGCCGCCAGCGCGCCGGTCGCTAA

		AGCGAACGACAGCCATAAACCAAGCAATGAGGAGCTGGCGCTGC GCCGTAAATCGCAGCAGCGCGTCAGCGCAGAAGTCCAGAGCCAG CGCATCCGCGAACTGGCGGATAAAGATCCGCGGGTCGTCGCTCTG GTAATCCGCCAATGGATGAGTAACGAACTATGA
flagellar hook-basal body complex protein FliE	**fliE**	>ADJCKNHF_03394 Flagellar hook-basal body complex protein FliE ATGGCGATTCAGGGTATTGAAGGCGTACTGCAACAGATGCAGGC GATGGCGATTCAGGCGGGAAATAACGGGCAGAATAGCGTACCGC AGGGAGTCAGTTTTGCCAGTGAATTGACCGCCGCGCTGGGTAAAA TCAGCGATACCCAGCAGGCCGCGCGTCAACAGGCGCAAAACTTC GAGCTGGGCGTGCCGGGTATCAGCCTGAATGATGTGATGGTCGAT TTACAGAAATCTTCAGTTTCGTTGCAGATGGGCGTGCAGGTGCGC AATAAGCTGGTGGCGGCCTATCAGGACATTATGAATATGCCGGTT TAG
flagellar protein FliT	**fliT**	>ADJCKNHF_03398 Flagellar protein FliT ATGGAACGCCAACAGCAGCTTTTAGCCGCCTATCAGCAGATCCAT ACCCTGAGCAGCCAGATGATTGCCCTGGCGCGCGCCGGGCAATG GGAAGCGCTGGTGGAAATGCAGTTTGCCTACGTGACGGCGGTCG AGAAAACCGCCGAATTTACCGGCAAAGCGGGGCCATCGCTGGCT CTGCAAGAGATGCTCAACGCTAAGTTGAAGCAGATTATCGACAAT GAGGGAGTACTGAAAGGGCTATTGCAACAGCGGATGGAACAATT AAAAACGCTGATCGATCAATCCACCCGCCAGAACGCGGTCAACA ACGCTTACGGCCAGTTCGACGATCGTTCGCTCCTGCTTGGCGAAC TGCAGTCCGATAACGTGGTCGCCATTAAGAGCAAAAGCGAAGAA TTACAATAA
flagellar protein FliS	**fliS**	>ADJCKNHF_03399 Flagellar secretion chaperone FliS ATGTATAACCGTAGCGGCACGCAAGCCTACGCACAGGTCAGTCTG GAAAGCAGCGCGATGAGCGCCAGTCCGCACCAGTTAATCGTAAT GTTGTTCGACGGGGCGCTTAACGCCCTGCTTCGCGCACGCATCCT GATGAATCAGGGGGATATCGCCGGTAAAGGCCTGGCGCTGTCGA AGGCAATCAACATCATCGACAACGGGTTGAAAAGCGGCCTCGAC CACCAGCAAGGCGGCGAAATCGCCGATAATCTGGCGGCGCTGTA CGATTATATGAAGCGACGCCTAATGCAGGCCAACCTGCATAATGA CGAAGCGGCGATCGTCGAAGTGGTCAAGCTGCTGGAGAATATCG CCGATGCCTGGCGACAAATTGGGCCAAACTATCAACCTGCTCAGG GTACATTGTGA
flagellar hook-associated protein 2	**fliD**	>ADJCKNHF_03400 Flagellar hook-associated protein 2 ATGGCATCGATCAGTTCCTTAGGCATCGGCTCAGGACTCGACCTC AACGGTTTACTGGACAAACTCAGCAAGGCGGAACAACAGCGTCT GACGCCGTATACCACTCAGCAAACCAGCTATAACGCGCAGCTAA CGGCTTACGGCACGTTAAAAAGCTCGCTGGAAAAATTCGATAACC TGAGCAAGGAGCTGGCTAAGCCGGAGTTTTTCAACAGCACCACC GCCACCAAGCACGACCAGTTCACCATCACCACCACCAATAAGGC GGTGCCGGGCAACTATAGCGTTGAAGTGCAGAAGCTGGCGCAGC CGCAAACCCTGACCACCCAGGCGACAATTACCGACCAACAAGAG AAACTTGGAACCGCCGGCAACAGCGACCGCTCTATTACGATCACC GCCGGCGACCCGCCAAAAGAAACCACGATTCCGCTGAGCGACGA CCAGACCTCGCTGCTGGAGATGCGCGATGCCATCAACGGCGCTAA AGCCGGCGTCACCGCCAGCATCATGCGCGTCGGCGACAATGACT ATCAGCTGGCGCTGAGCTCCTCCACCACCGGCGAAAAAAACACC GTGTCGGTGCAGGTCAATAACGACGATAAACTCGGCGCTATCCTC AACTACGACAGCAATAGCAAAAGCGGCGCGATGAAGCAGACCGT TGCCGGACAGGATGCGGAGATTATCGTCAACGGCACCAAAATTA AGCGCAGCACCAACTCGATTGCCGATGCGCTGCAGGGCGTCACC ATCGACCTGAAAACCACCACCAAAGCTGGCGAACCGCAAAACCT GGTGATCGGCATCGATAAAAGCGGCACCGCCGACAAAATCAAAG AGTGGGTGGATAATTATAATTCGCTGCTCGACACCTTCGGCTCGC

		TGACCAAATACACCCCGGTGAAAAGCGGTGAAGCGCAAAGCGCC AAGAACGGCGCGCTGCTGGGCGATAACACCCTGCGCGGCATTCA GTCATCGATTAAAAGCGCGCTCAGCGCCGCTCAGGACAACCCGG AGCTGAAAGGCCTTGGCAACCTCGGGATCTCAACCAATCCCAAA ACCGGCAAGCTTGAAGTCGACAGCACCAAGCTCAATAAAGCGCT CGACGAGAAACCGGATCAGGTCGCCAACTTCTTCGCCGGCAACG GCAAAGACACCGGGATGGCCACCGAAATCCATAATGAAATCCAG AACTATATTAAAGCGGGCGGCATCATCGAGAACTCGACCAAAAG CATCAACACCAATCTCGATCGCCTGAATATCCAGATCGACACTGT TTCCGACAGCATCCAGAACACTATCGATCGCTATAAACAACAGTT TGTTCAGTTGGATACCATGATGTCCAAGCTGAGCAGCACGGGTAA CTACTTACAACAGCAGTTCTCGTCCCAGTAA
flagellar hook-associated protein 3 FlgL	**flgL**	>ADJCKNHF_03401 Flagellin ATGGCACAAGTAATTAATACCAACAGCCTGTCGCTGATGGCGCAA AACAACCTGAACAAATCCCAGTCTTCCCTGGGCACGGCGATTGAG CGTCTGTCTTCCGGTCTGCGCATCAACAGCGCCAAGGACGATGCC GCGGGTCAGGCGATCTCCAACCGTTTTACCGCTAACATCAAAGGC CTGACTCAGGCTTCCCGTAACGCTAACGACGGTATCTCCCTGGCG CAGACCACCGAAGGCGCGCTGAATGAAGTCAACGATAACCTGCA GAACATCCGTCGTCTGACTGTGCAGGCGCAGAACGGTTCTAACTC TTCCAGCGACCTGCAGTCCATCCAGGATGAAATCACCCAGCGTCT GTCTGAAATTGACCGAATTTCTCAGCAAACCGATTTCAACGGTGT GAAAGTACTGAGTAGCAATCAGAAGCTGACTATTCAGGTTGGCG CTAATGATAATGAAACGATTGACATCGACCTGAAAGATATCAATA AAAGCACTCTAAATTTAGATACCTTCTCTGTGGCATTCGGCGTCA ATAAGGGGGATGTCGGTAAAACTGCTGTTGCTGCAAATGATTCCA TTCAACTGGATAAAACAGTAACAATCGCTGCCGGGCAAAAAGCA AATTCTAAAGACGTTACTGGTTATGTTAAAGATGATAAGGGTGAT ATTTATGCTCGTACTGGCGCTACAGAGTATTACAAAGTAGAAAGC ATTGACAAAGATGGAACAGCAACTTTTGCAGCGGCACCGGCAGC ACCATCTGGTACGACTAAAGCAGTAACCGAAGGTAAGATTTCTGT TAAGGCAACCGATAATGCAGATAAAGATTTAGCTAATACTTTCGC GTACACGGGTACAGAGAAAGGTGCTCCTAAATATGTGATTAAAG ATACTAGTGGCGCGACTGACCGTTATTACGCGGCTACTTTTGATG CCGATGGTAAAGTGGTTCGCGGCAACGAGCTCAGTTCAACTCCTG CTACTGAAGATCCGCTTGAAGCATTAGACAAAGCCCTGTCCCAGG TAGACCAACTGCGCTCCTCCCTGGGTGCGGTACAGAACCGTTTCG ATTCTGTTATCAACAACCTGAACAGCACCGTGAACAACCTGTCCG CGTCCCAGTCCCGTATTCAGGATGCTGACTACGCGACCGAAGTGT CCAACATGAGCCGCGCGAACATCCTGCAGCAGGCGGGTACCTCC GTGCTGGCGCAGGCTAACCAGTCGACTCAGAACGTCCTGTCTCTG CTGCGTTAA
ferredoxin-nitrate reductase [EC:1.7.7.2]	**nasB**	>ADJCKNHF_03579 Nitric oxide reductase FlRd-NAD(+) reductase ATGCGGCGACTGGTAATTATCGGCAACGGTATGGCGGCAACCCG GCTGGCAGAGAAGCTGGCGGCGCGCGCGCAGGGGCGTTTCATCA TCACGCTACTCGGCGATGAACCGCAGCCGGCCTACAACCGCATTC AGCTCTCGCCGGTACTCGGCGGGGAAAAAACGGCGTCGCAAATC CAACTGCTGCCGACGGAGTGGTACGCCCAGCATGGTGTCCGCGTG CGGCTTGGCGAGGCGGTCAGCGAAGTGGATGTCGCGGGGCGGAG GCTGCGCGTCGGCGGCGACTGGCTGGAATGGGATGAACTGGTGTT CGCCACCGGGTCGCAGCCGTTTATCCCGTCGCTGCCGGGTATTGA GCGCCCGCAGGTATTCGCCTTTCGCACCCTGGCGGATGTTAAAGA CATTCTGGCAATCCCCGGCCCGGCGGTGGTAATCGGCGGTGGCGT ACTGGGCGTGGAGGCCGCGGCGGCGCTGCGCCGTCACGGTGGGG AAGTGACGCTACTCCATCGCGGTAGCGGTTTGATGGAGCCGCTTA CCGATGCTTTTGCCGCGGAACAGTTAAAACAACAGCTTGAGGCAC

		GCGGCATCCGCTGCGAGCTGGAGAGCCGAATTGCCGCTATTGACG AGCAGCATGTGCTGCTGGAAGACGGGCGCGCTTTTGCCGCCAGCC GGGTGGTGTTGGCCACCGGCGTGCGGCCGGATATCCGTCTGGCGA CGCGCAGCGGCGTAGCCTGCCAGCGGGGGATTATCGTCGACCGC CGGATGGCGACCTCGCTGCCGGGGATCAGCGCTATCGGCGAGTGT TGTGAGATTGACGGCCAAACCTGGGGACTGGTGGCTCCCTGCTTG CGCCAGGCCGATGTATTAGTTGAACGCCTGTGCGGGGCTCCCGGC GAAGAATTCAGCTGGCAGGACGGCGGCACCCGGCTGAAGGTCAC CGGCATCGACTTTTTTAGCGCCGGCGAACAGCGGGCCGGCGAGC AGGACCAGATCTACAGCAGTTGGGACCCCATCGATCGCCACTACC GTCGCCTGCTGATCCGCGATGGCAGGTTGCACGGCGTGCTGCTGC TGGGCGACTGCCAGCAGGCGGCGCCGCTTACCGCGCTGCTCGGCA GCGATAGGTCCCCTTCAGTGGAGTGGCTTTTTGACCCTTCTATAAC GCAGCCGCGGGCTGCAGGAAAAATGACGATGACTAAACCTGTAT TAGTGCTGGTCGGACACGGCATGGTCGGCCACCATTTTCTTGAGC AATGCGTGAGCCGGAACCTGCACCAGCAGTACCGTATCGTGGTTT TTGGCGAAGAGCGCTATGCCGCCTATGACCGGGTTCATCTCTCGG AATATTTCGCCGGGCGCAGCGCAGAGTCGCTATCGCTGGTAGAGG GAGACTTTTTTAGCCAGTACGGCATTGAGCTGCGGCCAGGAGAGA CGATCGCGGAAATCGATCGTCCGGCGCGAATCGTGCGCGATGCCC ACGGCCATGAAACCCATTGGGATAAGCTGGTGCTGGCGACCGGC TCCTATCCCTTCGTGCCGCCAATCCCCGGTAACGATGAAGAAGGC TGCTTCGTCTATCGTACGCTTGACGATCTTGACCGCATTGCCGCCC GCGCCGCCACTGCGCAGAGCGGGGTGGTCATTGGAGGCGGGCTG TTGGGGCTGGAAGCCGCCAACGCGTTAAAACAGTTGGGGCTTAA GACCCATGTGGTGGAGTTCGCCGCCAACCTGATGGCGGTGCAGCT GGATAACGGCGGCGCGGCGATGCTGCGGGAGAAAATTCTCGATC TTGAGGTTGGCGTGCACACCAGCAAAGCGACGACGGCGATAGTG CGCACCGCCGACGGGCTGCAGCTTAACTTCGCCGATGGCGGCACG CTGCAGACCGATATGGTGGTCTTTTCCGCCGGGATCCGCCCGCAG GATGCGCTGGCGCGCGGCGCAGGCCTGGCAATCGGCGAACGCGG CGGTATCGGTATCGATGACCACTGCCGGACCTCGGACGCAGATAT ATTGGCGATTGGCGAATGCGCGCTGTGGGACAACAAAATTTATGG TCTGGTAGCGCCGGGCTACCACATGGCGCGCACCGCGGCGGCGC AGTTGGCTGGTGAAGCGGCCCGCTTTAGCGGCGCCGATATGAGCA CCAAACTCAAACTGCTCGGCGTGGATGTAGCGTCGTTTGGCGATG CTCACGGACGTACAGCTGGTTGCCAGAGCTATCAATGGACCGATG GTCCGCGGCAGATCTACAAAAAGATCGTTGTCAGCGCTGATGGCA AAACGCTGCTGGGCGGCGTATTGGTGGGCGATGCCGGTGACTAC GCGACGCTGTTGCAGATGATGCTGAACGGCATGGCGCTACCGTCT CGTCCGGAAAGTCTGATCCTCCCGGCCATGGATGGGGCCACGACG AAAGCGCTGGGGGTGGCGGCGCTGCCGGATAGCGCGCAGATTTG CTCTTGCCATAACGTCAGTAAGGGAGACATTTGCCAGGCGGTCAG CGCCGGAGCGGGCGATATGGCGGCGATAAAAAGCTGCACTAAAG CGGCGACCGGCTGCGGAGGCTGTAGCGCGCTGGTCAAACAGGTG ATGGAACACCAGCTTACCGGGCAGGGCGTCGAGGTTAAAAAAGA TATCTGCGAGCATTTTCCGTGGTCGCGACAGGAGATCTATCATCT GGTACGAGTCAACCACATCCATACCTTCGATCAGCTCATTAGCCG TTACGGGCAGGGCCACGGCTGTGAAGTGTGTAAACCGCTGGTGG CGTCGGTACTGGCCTCCTGCTGGAATGAGTATCTGCTGAAACCGG CGCATTTGCCGCTGCAGGACACCAACGATCGCTACTTCGCCAATA TTCAGAAAGACGGCACTTACTCGGTGGTGCCGCGGATGGCCGCA GGCGAAGTGACACCGGATGGGCTTATCGCTATCGGCCAGATCGCC AAACGTTACCAGCTGTACAGTAAAGTGACCGGAGGACAGCGTAT CGACCTGTTTGGCGCGCGGCTGGAGCAACTGCCGGACATCTGGCG CGAACTGGCGGCGGCGGGATTTGAAACCGGACACGCCTACGGCA

		AATCATTACGCACGGTAAAATCCTGCGTCGGCTCGACCTGGTGCC GCTATGGGGTTCAGGATTCAACGGGGCTGGCGGTAAGGCTTGAA CATCGTTACAAGGGGCTGCGCGCGCCGCATAAAATCAAAATGGC GGTCTCGGGCTGTACCCGCGAATGTGCCGAAGCGCAAGGTAAAG ACATTGGGGTTATTGCGACTGAAAAGGGCTGGAATCTTTACGTCT GCGGCAACGGCGGGATGAAACCGCGCCATGCGGACCTCTTTGCG AGTGACCTTGATGACGCCAGCCTAATCCGTACCGTCGATCGGTTG TTGATGTTTTATATTCGCACCGCCGACCGCCTGCAGCGCACCAGT AGCTGGATGGATAACCTTGAAGGCGGCGTGGCGTATCTACGCGA GGTGATCTTGCACGATAGTCTCGGTATCGGCGATGAGCTGGAGCA GGAGATGGCGCGGGTGGTGGATAGCTACCAGTGCGAATGGCAGA CCACCCTGAACGACCCACAGCGGCTGGCGCTATTTCGTTCCTACG TTAACAGCGATGAGGCCGATGAGGCGGTGCAGCGGCAAATCCTG CGCGGTCAGCCGCAGCTGGTGGCGCCGCAAGGGATTGGGCAACC GGCCCTGCCGTCGCGGCCGTGGCAGGCGATCTGCGATCTGGACGC GATCCCGCCGCAGGCGGGGATCGGCGCGCGCCTCGGCGAGCGGC AGATTGCGCTGTTCCGCTTCGGCGAGCAAGTTTATGCGCTGGATA ACCAGGAACCCGGCAGCGAGGCCAACGTGTTATCGCGCGGCATT TTAGGCGACGCGGGCGGCGAGCCGATCGTTATTTCGCCGCTGTAT AAACAGCGGATTCGCTTGCGAGATGGTCGCTTGTACGACAGCGGC GAGCCGTCGGTGCGCGCGTGGCCGGTGAAGATCGAACAGGGCAA AGTGTGGGTCGGCAACCAGGCATTGCTGCTGCGCGCGGAGGCGA GCTGA
ferredoxin-nitrate reductase [EC:1.7.7.2]	**nasB**	>ADJCKNHF_03580 Nitrate reductase ATGAGCGAAACCCGAACCACCTGTCCATACTGCGGCGTCGGCTGC GGAGTTATCGCCCGCGTTGAACCCAGTGGAACCGTCACGGTTCGC GGCGATGAAAACCATCCCGCTAACTTTGGCCGCTTGTGCGTAAAA GGGGCAGCGCTTGGGGAAACGACCTCGCTTAGCGGGCGGTTATT ACACCCTGAAGTCGATGGCCGGGCGGTCGGCTGGCCGCAGGCGC TGGCGGAGGCGGGTTCACGTCTGCGCGACATTATTGAGCGCTACG GCCCGCAGGCGGTGGCGTTTTACGCTTCCGGTCAGCTGTTAACTG AGGATTATTACGCCGCCAACAAGTTGATGAAGGGCTTTATCGGCG CCGCCAATATCGATACGAATTCGCGGTTATGTATGTCATCGGCGG TCACCGGCTATAAGCGGGCGCTCGGCGCGGACGTCGTGCCGTGTA GCTATGAAGATGTCGAGCAGAGCGATCTGGTGGTGCTGGTGGGCT CCAACGCCGCCTGGGCGCATCCGGTTCTCTATCAGCGGTTGGTGC AGGCGAAACGCGATAATCCGCGGTTGCGGATCGTGGTGGTGGAT CCGCGACGCACCGCGACCTGTGATATTGCCGACGATCATCTGGCG TTGGCGCCCGGTAGCGATGGCGGGCTATTTGTCGGCCTGCTAAAT GCCATTGCCGCCAGCGGTGGAATGGCGGCGGGTTTTCGCGACCAG CGGCAGGCGCTGACCATCGCCGCGCAGTGGAGCGTGGAAAAAGC GGCCGCTTTCTGCGGCCTGGCGCCGGAGCAAGTGGCTCGCTTTTA TCGTGATTTTATCGCTGCACCGCGCGCCATCACGCTGTACACCAT GGGAATTAATCAGTCCGCCAGCGGCAGCGATAAGTGCAACGCGA TTATCAATGTCCATCTTGCCAGCGGGAAGTTTGCCCGCCGCGGCT GCGGGCCGTTTTCGCTGACCGGTCAACCCAACGCCATGGGCGGGC GTGAAGTGGGGGGGCTGGCGACGATGCTGGCGGCGCATATGAAT TTTGAGCCGCAGGACCTGCAGCGATTAGCGCGCTTTTGGGGCAGC GAGCGACTGGCGCAGACGCCGGGACTAACCGCCGTCGAACTCTT CGCCGCGATTGGACGCGGCGAGGTCAAAGCGGTGTGGATTATGG GGACCAATCCGGTGGTCTCACTGCCCGATAGCCACGCGGTGAGCC AGGCGCTGTCCAGGTGTCCGCTGGTGATGGTCTCCGATGTCGCCG CCAATACCGATACGGGGCGCTTTGCCCATATCCGCTTTCCGGCGC TGGCATGGGGCGAAAAAAACGGTACCGTGACCAACTCGGAGCGG CGGATTTCGCGTCAGCGGGCTTTTTTGCCGCCGCCGGGGGAGGCG AAAGCCGACTGGTGGATCATTTCCCGTCTCGCCGCCGAATTAGGT

		TATGCCCGAGCTTTTTCATGGCAACATCCGCATGAGGTATTTTGTG AACACGCGGCGCTCTCAGGGTTTGAAAATGACGGTCAGCGGGCG TTTGATATTGGCGGGCTGGCGGACCTCAGCCGGGAGGCGTGGGAT GCCCTGACACCGGTGCGCTGGCCGGTGAGCCGCAGCGCCGCGCC CTGGCGGTTAACGGAGGGCTGGCACGGCGACGGCAGGTTGCGGA TGGTGCCGGTGTCGCCGCAGCCGACCCGGGCGCAGACCGAGGCA TTTTATCCATTAATCCTCAATAGCGGACGTATTCGCGATCAGTGG CATACCATGACCCGCACCGGCGAAATACCGCGGTTGATGCAGCA CATTGCCGAACCAGTCGTCGAGGTGGCGCCTGCCGATGCGCGTCG TTTTCAATTACGTGAGGGAGAACTGGCTCGCGTCTGGTCGCGCCA CGGCGTGATGATTGCGAAGGTGATAGTCAGCGAAGGGCAGCGCG CCGGTTCGCTCTTTGTGCCGATGCACTGGAATAATCAGTTTGCCC GCCAGGGACGGGTCAATAATTTACTGGCGGCGGTCACCGATCCGC ATTCCGGGCAGCCGGAGAGCAAGCAGTCGGCGGTGGCGATAGCG CCGTGGCGGCCGGCGTGGCAAGGGGAGCTATTATCTCGCGAGCC CTTAGCGTTGCCATCCTCGCTGCACTGGCGGCGACGGGCGGTGGT AGGGCTTAGCCATTTGTCGCTGGCCGCGGATACCGGCCCGCAAAG CTGGCTGACCGAGTGGTGTCGCAAGCAGGGATGGCAGTTGCAAA TTGCCGAGGGCGGCGGGCTGTGGAACCTACTGGCATGGCACGAC GGGCAATTGATGCTCGGCTGCTGGAGCGATATTAAGCCGCCGCAA ATCGATGCTGAATGGCTGTATACGGCGTTTCGGACGCCGCCGCAG ACCGCCGGCCTACGCCATGCGTTGCTCAGCGGCCGTAAGGGTGGC GACAGCGCGCCGCGTGGGCAGACTATCTGTAGTTGCTTTAGTATC GGCGAGCGGCAGATCGGCGAGGCTATTGCCGGCGGCTGCGTCAG CGTAGAGGCGCTTGGCGCGAAGCTCAAGTGCGGCACCAACTGTG GTTCCTGTATTCCGGAACTCAAAGCGCTGCTGGCGGCAAATCAAA CCCGAACGCCGGTTTGA
MFS transporter, NNP family, nitrate/nitrite transporter	**narK, nasA, NRT, nrtP**	>ADJCKNHF_03584 Nitrate/nitrite transporter NarK ATGAGTCAATCTTCAATCCCGGAGAAGGCTAGCAGCTCAGTCATC ACCGACTGGCGTCCTGAAGATCCTGAGTTTTGGCAACAGCGCGGC CACCGTGTGGCGAGCCGCAATTTATGGATCTCCGTTCCCTGTCTTT TACTGGCGTTCTGCGTCTGGATGTTGTTTAGCGCCGTCGCGGTAA ACCTCAATAAAGTGGGTTTTCAGTTCACTACCGATCAGCTGTTTAT GTTGACCGCATTGCCAGCGCTTTCCGGCGCGCTGCTGCGCGTACC TTATGCCTTTATGGTCCCGCTGTTCGGCGGCCGCCGCTGGACGGC GTTCAGTACCGGTATCATGATTATTCCGTGCGTTTGGCTGGGCTTT GCGGTACAGGATACTTCCACGCCGTTTAGCGTGTTCGTGATTATC TCTCTGCTGTGCGGCTTTGCCGGCGCTAACTTTGCTTCCAGTATGG CGAACATCAGCTTCTTCTTCCCGAAAGAGAAGCAGGGCGGCGCG CTGGGGGTTAACGGCGGCCTTGGTAACATGGGCGTCAGCGTGATG CAGCTGGTTGCGCCGCTGGTAGTCTCGATTTCTATTTTTGCCGTTT TTGGCGGTAGCGGTAGCGAGCAGCCGGATGGCTCAATGCTGTATC TGGAAAACGCCGCGTGGATCTGGGTGCCATTCCTGATCATCTTTA CCCTGGCCGCGTGGTTCTTTATGAACGATCTGTCGGCCTCAAAAG CGTCGCTGAGCGAACAGTTGCCGGTACTTAAACGCCTGCATCTGT GGATTATGGCGCTGCTGTATCTGGCGACCTTTGGTTCCTTTATCGG TTTCTCCGCCGGGTTTGCGATGCTGTCAAAAACCCAGTTCCCGGA CGTGCAGATCCTGCACTATGCCTTCTTCGGTCCGTTTATTGGCGCG CTGGCGCGTTCGATGGGCGGGGCGATTTCCGACCGTCTCGGCGGG ACCCGCGTGACGCTGGTGAACTTCGTGGTGATGGCTATTTTCTGC GCGTTACTGTTCCTGACCCTGCCAACCAATGGTCAGGGCGGCAAC TTCATCGCCTTCTTCGCGGTATTTATGGTGCTGTTCCTGACCGCCG GGCTGGGCAGCGCCTCTACCTTCCAGATGATTTCCGTGATCTTCC GTAAGCTTACGATGGACCGCGTGAAAGCGCAGGGCGGCAGCGAA GCGCAAGCGATGCGTGAAGCGGCGACGGATACCGCCGCGGCGTT GGGCTTTATTTCGGCGATTGGCGCGATCGGTGGTTTCTTTATTCCG

		AAAGCGTTCGGTATTTCGCTGGATCTGACCGGCTCGCCGGCCGGG GCAATGAAAGTCTTCCTCGTTTTCTATATTGCCTGCGTAGTAATCA CCTGGGCGGTATACGGCCGTAAACAGAAATAA
nitrate reductase, catalytic subunit	**nasC**	>ADJCKNHF_03585 Respiratory nitrate reductase 1 alpha chain ATGAGTAAATTTCTGGACCGGTTTCGCTACTTCAAACAGAAGGGT GAAACCTTTGCCGATGGGCACGGCCAGCTTCTTAAAACCAACCGG GATTGGGAGGATGGATACCGCCAGCGTTGGCAGCATGACAAAAT CGTGCGTTCCACTCACGGTGTGAACTGCACCGGCTCATGCAGCTG GAAAATTTATGTCAAAAATGGCCTGGTCACCTGGGAAACCCAGC AAACTGATTACCCGCGTACCCGCCCCGATCTGCCGAACCATGAAC CACGCGGCTGCCCGCGCGGCGCCAGCTACTCCTGGTATCTGTACA GCGCTAACCGCCTGAAATATCCGCTGATGCGTAAGCGTCTGATGA AGATGTGGCGTGAAGCGAAAGTTCAGCATAGCGATCCGGTTGAG GCATGGGCTTCAATTATTGAAGATGCCGATAAAGCGAAAAGCTTT AAACAGGCCCGCGGTCGCGGCGGTTTTGTTCGTTCTTCATGGAAA GAAGTGAACGAACTGATTGCCGCTTCAAACGTCTATACCGTCAAA ACTTACGGTCCAGACCGCGTGGCAGGCTTTTCGCCGATCCCGGCG ATGTCGATGGTTTCCTATGCGTCCGGCGCCCGTTACCTGTCGCTGA TTGGCGGTACCTGTCTGAGCTTCTACGACTGGTACTGCGACCTGC CGCCAGCCTCGCCGATGACCTGGGGCGAACAGACCGATGTGCCG GAATCTGCCGACTGGTATAACTCCAGCTACATCATCGCCTGGGGC TCCAACGTCCCGCAGACCCGTACCCCGGACGCGCATTTCTTTACC GAAGTTCGCTACAAAGGGACCAAAACCGTGGCGATTACTCCGGA CTATGCCGAAATCGCCAAGCTCTGCGATCTGTGGCTGGCGCCGAA GCAGGGTACCGATGCCGCGATGGCGCTGGCGATGGGCCACGTCA TGCTGCGTGAGTTCCACCTCGATAAACCGAGCCAGTACTTCACCG ATTACGTACGTCGCTACACCGACATGCCGATGCTGGTCATGCTCG AAGAGCGCGACGGCTACTATGCCGCTGGCCGTATGCTGCGCGCTG CCGACCTGGTTGACTCCCTGGGCCAGGAGCAGAATCCGGAATGG AAAACCGTCGCCTTTGACGAGAAGGGCGAAATGACCGTACCTAA CGGTTCTCTGGGTTTCCGCTGGGGCGACAAAGGCAAGTGGAACCT CGAACAGCGCGATGGTAAAACCGGCGAAGAAATTGAGCTGCGCC TGAGCCTGCTTGGCAGCCATGATGATATCGCCAACGTCGGTTTCC CATACTTTGGCGGCGAAGGTTCCGAGCATTTCAACAAAGTCGACC TCGAAAACATTCTGCTGCACAAACTGCCGGTAAAACGCCTGCAGA TGGCCGATGGTTCCACCGCGCTGGTGACTACCGTTTATGACCTGA CCATGGCGAACTACGGCCTGGAACGCGGTCTGAACGATGAAAAC TGCGCGACCAGCTACGATGACGTCAAGGCGTACACTCCGGCCTGG GCAGAAAAAATCACCGGCGTATCCCGCGCGCACATCATCCGTACC GCGCGCGAATTTGCCGATAACGCCGATAAGACCCATGGCCGCTCG ATGATTATCGTCGGTGCGGGCCTGAACCACTGGTTCCATCTGGAC ATGAACTACCGCGGGCTGATCAACATGCTGATCTTCTGCGGCTGC GTTGGCCAGAGCGGCGGCGGTTGGGCGCACTACGTTGGTCAGGA AAAACTGCGTCCGCAGACCGGCTGGCAGCCGCTGGCGTTCGGCCT TGACTGGCAGCGTCCGGCACGCCACATGAACAGTACATCGTACTT CTATAACCACTCCAGCCAGTGGCGCTATGAAACCGTCACCGCGCA GGAACTGCTGTCGCCGATGGCGGATAAATCCCGCTACAGCGGAC ATCTGATCGACTTCAACGTGCGCGCTGAGCGTATGGGCTGGCTGC CGTCGGCGCCGCAGCTGGGCGTGAACCCGCTGCGTATTGCTGACG AAGCGAAGAAAGCCGGCATGACGCCGGTCGATTACACCGTGAAA TCGCTGAAAGAGGGGTCTATTCGCTTTGCGGCCGAGCAGCCGGAG AACGGTAAAAACCATCCCCGTAACCTGTTTATCTGGCGTTCCAAC CTGCTGGGCTCCTCCGGTAAAGGCCATGAATATATGCTCAAGTAC CTGCTGGGTACCGAGAACGGTATTCAGGGCAAAGACCTTGGCAA GCAGGGCGGCGTGAAGCCGGAAGAAGTCGAATGGCGGGATAACG GTCTCGACGGCAAACTGGATCTGGTCGTCACGCTCGACTTCCGTC

		TGTCGAGCACCTGTCTGTACTCCGACATCGTACTGCCGACCGCAA CCTGGTACGAAAAAGACGATATGAATACCTCGGATATGCATCCGT TTATTCACCCGCTGTCTGCCGCCGTTGACCCGGCCTGGGAATCCA AAAGCGACTGGGACATCTATAAAGGTATCGCTAAGAAATTCTCTG AAGTCTGCGTAGGCCACCTCGGCAAAGAAACCGACGTCGTGACG CTGCCGATTCAGCACGATTCCGCCGCGGAAATGGCGCAGCCGTTT GACGTTAAAGACTGGAAAAAAGGCGAATGTGACCTGATCCCAGG TAAAACCGCGCCGCATATTATTCCGGTCGAGCGTGATTATCCGGC GACCTACGAGCGTTTCACCTCTATCGGCCCGCTGCTGGAAACCAT CGGCAACGGCGGTAAAGGTATCGCCTGGAATACCCAGAGCGAGA TGGACCTGCTGCGTAAGCTCAACTACACCAAGGCGGAAGGCCCG GCGAAAGGCCAGCCGAAGCTGGAGACCGCTATTGACGCCGCTGA GATGATCCTCACCCTGGCGCCGGAAACTAACGGTCAGGTAGCCGT GAAGGCGTGGAAAGCGCTGAGCGAATTTACCGGCCGCGACCATG CGCATCTGGCGCTGAACAAAGAAGACGAGAAGATCCGTTTTCGC GATATCCAGGCGCAGCCGCGTAAGATCATCTCCAGCCCGACCTGG TCTGGCCTGGAAGACGAACATGTCTCCTATAACGCCGGTTATACC AACGTTCACGAGCTGATCCCATGGCGTACGCTGTCCGGCCGTCAG TCGCTGTATCAGGATCACCAGTGGATGCGCGACTTTGGCGAAAGC CTGCTGGTCTATCGTCCGCCGATTGACACCCGTTCGGTGAAAGCG GTGATGGGCGAGAAGTCCAACGGCAATAAGGAGAAGGCGCTGAA CTTCCTGACGCCGCACCAGAAGTGGGGGATTCACTCTACTTATAG CGATAACCTGCTGATGCTGACTCTGTCGCGCGGCGGGCCGATCGT CTGGATGAGCGAAGCGGATGCGAAAGATCTGGGTATCGAGGATA ACGACTGGATCGAAGTCTTCAACGCCAACGGCGCCCTGACGGCG CGTGCGGTAGTGAGCCAGCGCGTACCGGCAGGAATGACCATGAT GTACCACGCGCAGGAACGTATCGTTAACCTGCCGGGTTCTGAAGT TACCGGTCAGCGCGGGGGGATCCACAACTCGGTTACCCGTATTAC GCCAAAACCGACCCATATGATCGGCGGCTACGGCCACCTGGCGT ACGGCTTTAACTACTATGGCACCGTCGGTTCCAACCGCGATGAGT TTGTTGTGGTACGTAAGATGAAGAACATTAACTGGTTAGACGGCG AAGGTAATGACCAGGTACAGGAGAGCGTAAAATGA
nitrate reductase / nitrite oxidoreductase, beta subunit [EC:1.7.5.1 1.7.99.-]	**narY, narH, nxrB**	>ADJCKNHF_03586 Respiratory nitrate reductase 1 beta chain ATGAAAATTCGTTCACAAGTCGGCATGGTGCTGAATCTCGATAAA TGCATCGGCTGTCACACCTGCTCCGTAACCTGCAAAAACGTCTGG ACCAGTCGTGAAGGGATGGAGTACGCCTGGTTTAACAACGTAGA AAGTAAGCCGGGCGTCGGTTTCCCGAACGACTGGGAAAACCAGG AAAAATGGAAAGGCGGCTGGATCCGTAAAATCAACGGTAAACTG CAGCCGCGCATGGGCAACCGCGCGATGCTGCTGGGTAAAATCTTC GCCAACCCGCATCTGCCGGGAATCGATGATTACTACGAGCCGTTT GATTTTGACTACCAGAATCTGCATAACGCGCCGGAAAGCAAACAT CAGCCGATCGCTCGTCCGCGTTCGCTGATTACCGGCCAGCGGATG GACAAAATTACCAGCGGCCCGAACTGGGAAGAGATCCTCGGCGG CGAGTTTGAAAAACGCGCCAAAGACCAGAACTTCGAAAACATGC AGAAGGCGATGTACGGCCAGTTCGAAAACACCTTCATGATGTATC TGCCGCGCTTATGCGAGCACTGCCTGAACCCGGCGTGCGTCGCGA CCTGCCCGAGCGGTGCCATCTATAAGCGTGAAGAAGACGGTATTG TCCTGATCGACCAGGATAAGTGCCGCGGCTGGCGTATGTGCATCA CCGGCTGCCCGTACAAGAAGATCTATTTCAACTGGAAGAGCGGG AAATCCGAGAAATGCATCTTCTGCTACCCGCGTATTGAATCCGGG ATGCCGACGGTGTGCTCCGAAACCTGTGTGGGACGTATTCGCTAT CTCGGTGTCCTGCTCTACGACGCGGACGCGATTGAAAACGCAGCC AGCACCGAGAACGAGAAAGATCTGTATCAGCGTCAACTGGACGT CTTCCTCGATCCTAACGATCCAAAAGTGATTGAACAGGCATTAAA AGATGGTGTACCGCAGGGCGTAATTGAAGCCGCGCAGCAGTCGC CGGTTTACAAAATGGCGATGGACTGGAAGCTGGCGCTGCCGCTGC

		ACCCGGAATATCGCACCTTGCCAATGGTCTGGTACGTGCCGCCGC TGTCGCCGATTCAGTCCGCCGCCGATGCGGGCGAACTGGGTAGCA ACGGGATCCTGCCGGATGTAGAAAGCCTGCGTATTCCAGTCCAGT ATCTGGCGAACCTGCTGACCGCGGGCGATACCCAGCCTGTACTGC TGGCGCTGAAACGTATGCTGGCGATGCGCCACTTCAAACGTGCGG AAACCGTCGACGGCATCGTCGATACCCGCGCGCTGGAAGAGGTC GGGCTGAGCGAAGCGCAGGCGCAGGAGATGTACCGTTATCTGGC TATCGCCAACTACGAAGATCGTTTCGTGGTGCCGAGCAGCCATCG CGAACAGGCTCGCGATGCCTTCCCGGAGAAGAGCGGTTGCGGCTT TACCTTCGGCGATGGTTGCCACGGCTCTGACAGCGAATTCAACCT GTTTAACAGCCGTCGCATTGACGCCATTGACGTTACCAGCAAAAC GGAGCCGCACGCATGA
nitrate reductase molybdenum cofactor assembly chaperone NarJ/NarW	**narJ/narW**	>ADJCKNHF_03587 Nitrate reductase molybdenum cofactor assembly chaperone NarJ ATGATTGAACTCGTGATTGTGTCGCGTCTGCTCGAATACCCTGAC GCTGCCTTATGGCAGCATCAGCAGGAGATGTTCGAGGCTCTCGCG TCATCGGAAAAACTCGCCAAAGAAGATGCCCAGGCGCTGGGCGT TTTCCTGCGCGATTTAGTCGCTCAGGATCCGCTGGACGCCCAATC GGCGTATAGCGAGCTGTTTGACCGCGGCCGCGCCACCTCGCTGCT GCTGTTTGAACATGTTCACGGCGAGTCCCGCGATCGCGGGCAGGC GATGGTCGACCTGATGGCGCAGTACGAGCGCCACGGTCTGCTGCT GGATAGCCATGAGCTGCCGGATCACCTGCCGCTGTACCTTGAGTA TCTGGCGCAGTTGCCGGAAGAGGAAGCGCTTGGCGGCCTGCGGG ACGTTGCGCCAATCCTTGGCCTGCTCAGCGCGCGTCTGCAACAGC GCGAGAGCCGCTATGCGGTGTTGTTCGAGCTGCTGTTGAAGCTTG CCAATACTCAGGTCGATAGCCAGAAAGTGGCGGAGAAGATTGCC GACGAGGCCCGCGACGATACACCGCAGGCGCTGGATGCCGTCTG GGAAGAAGAGCAGGTCAAATTCTTTGCCGACCAGGGCTGCGGCG AGTCGGAAATCTCCGCTCACCAGCGCCGTTTTGCCGGAGCCGTGG CCCCGCAATATTTGAATATCTCTAACGGAGGACAGCACTAA
nitrate reductase gamma subunit [EC:1.7.5.1 1.7.99.-]	**narI, narV**	>ADJCKNHF_03588 Respiratory nitrate reductase 1 gamma chain ATGCACTTCCTGAATATGTTCTTCTTTGACATCTATCCGTACATTG CGGGTTCAGTGTTTCTTATTGGCAGCTGGCTGCGCTACGACTACG GCCAGTACACCTGGCGCGCTGCCTCCAGTCAGATGCTGGATCGTA AAGGGATGAACCTGGCGTCAAACCTGTTCCATATCGGGATCCTGG GTATTTTTGCCGGTCACTTCCTCGGTATGCTGACCCCGCACTGGAT GTATGAGTCCTTCCTGCCGATCGACGTGAAGCAGAAAATGGCGAT GTTTGCCGGCGGGGCGTGCGGCGTGATGACGTTGGTCGGCGGTTT ACTGCTGCTCAAGCGCCGTCTGCTGAGCCCGCGCGTTCGTGCTAC CACCACCACAGCGGATATCCTGATCCTCTCGTTGCTGATGGTGCA ATGCGCGCTGGGTCTGCTGACCATTCCATTCTCCGCCCAGCATAT GGACGGTAGCGAAATGATGAAACTGGTCGGCTGGGCGCAGTCGG TGGTGACCTTCCACGGCGGAGCTTCGCAGCATCTCGATGGCGTAG CTTTTGTCTTCCGAGTTCACCTGGTGCTGGGGATGACGCTGTTCCT GCTGTTCCCGTTCTCGCGCCTGGTTCACATCTGGAGCGCGCCGGT CGAGTACCTGACGCGCAAATACCAGATTGTGCGCGCGCGTCGCTA G
acetolactate synthase, catabolic	**alsS**	>ADJCKNHF_03736 Acetolactate synthase, catabolic ATGGACAAACAGTATCCGCAGCGCCAGTGGGCGCACGGCGCCGA TCTGGTCGTCAGCCAACTGGAAGCGCAAGGCGTACGGCAGGTCTT CGGGATCCCCGGCGCTAAAATCGATAAGGTTTTCGACTCGTTGCT GGACTCCTCAATCCGCATTATTCCGGTACGTCACGAGGCCAACGC CGCCTTTATGGCCGCCGCGGTCGGGCGCATTACCGGCAAAGCGGG CGTCGCGCTGGTGACCTCCGGACCCGGTTGTTCCAACCTGATAAC CGGGATGGCCACCGCCAATAGCGAAGGCGACCCGGTGGTGGCGC TGGGCGGCGCGGTCAAACGCGCGGATAAAGCCAAACAGGTACAC

		CAGAGTATGGACACGGTGGCGATGTTCAGCCCGGTCACCAAATA CGCGGTAGAAGTGACCTCGCCGGATGCGCTGGCGGAAGTGGTTTC TAACGCTTTTCGCGCCGCCGAGCAGGGTCGCCCGGGCAGCGCCTT CGTCAGTCTGCCGCAGGATGTGGTCGATGGTCCGGTGACCGGCAA AGTCCTACCCGCCAGCAGCGCGCCGCAGATGGGCGCCGCGCCTG ACGAGGCAATCAATCAGGTTGCGAAGTTGATTGCCCAGGCGAAG AATCCGGTGTTCCTGCTTGGATTAATGGCCAGCCAGACGGAAAAC AGCGCCGCGCTGCATCGTTTGCTGGAAACCAGCCATATTCCGGTC ACCAGCACCTATCAGGCCGCCGGGGCGGTCAATCAGGATAACTTC TCGCGCTTCGCCGGGCGCGTCGGGCTGTTTAACAATCAGGCCGGT GACCGCTTATTGCAACTGGCCGACCTGGTTATCTGCATCGGCTAT AGCCCGGTGGAATACGAACCGGCGATGTGGAACAGCGGCAACGC GACGCTGGTCCACATCGACGTACTGCCCGCCTATGAAGAGCGTAA CTACACGCCGGATGTCGAGCTGGTGGGCGACATCGCCGGCACGCT GAACAAGCTGGCGCAAAATATCGATCATCGGCTGGTGCTCTCGCC GCAGGCCGCTGAAATCCTCCACGACCGCCAGCATCAACGCGAAC TGCTTGACCGCCGCGGAGCGCAGTTGAATCAGTTTGCCCTGCACC CGCTGCGCATCGTTCGCGCCATGCAGGATATCGTCAACAGCGACG TCACGCTGACGGTCGATATGGGGAGCTTCCATATCTGGATCGCCC GCTATCTCTACAGCTTCCGCGCCCGTCAGGTGATGATCTCCAACG GTCAGCAGACCATGGGCGTCGCCCTGCCGTGGGCCATCGGGGCCT GGCTGGTCAATCCGCAGCGCAAAGTGGTCTCGGTCTCCGGCGATG GCGGTTTTCTGCAATCCAGCATGGAGCTGGAAACGGCGGTCCGCC TGAAAGCCAACATCCTGCATCTTATCTGGGTCGATAACGGCTACA ACATGGTCGCTATCCAGGAAGAGAAAAAATATCAACGCCTGTCC GGCGTCGAGTTCGGTCCTATGGATTTTAAAGCCTATGCCGAATCC TTCGGCGCGAAAGGGTTTGCGGTGGAAAGCGCTGAGGCGCTGGA GCCGACGCTACGCGCGGCGATGGACGTCGACGGCCCGGCGGTGG TCGCCATCCCCGTGGATTACCGTGATAACCCGCTGCTGATGGGCC AGCTACACCTGAGTCAAATTCTTTAA
acetolactate decarboxylase [EC:4.1.1.5]	**alsD, budA, aldC**	>ADJCKNHF_03737 Alpha-acetolactate decarboxylase ATGAATCATGCTTCAGATTGCACCTGCGAAGAGAGTCTGTGTGAA ACGCTACGCGCGTTTTCCGCTCAGCATCCCGATAGCGTGCTGTAT CAAACTTCGCTGATGAGCGCCCTGCTCAGCGGCGTCTACGAAGGT ACCACCACCATTGCGGACCTGCTGAAGCACGGTGATTTCGGGCTC GGCACTTTTAATGAACTCGACGGCGAGCTGATCGCGTTTAGCAGC CAGGTTTATCAACTGCGTGCCGACGGCAGCGCGCGTAAAGCGCGT CCGGAACAGAAAACGCCGTTTGCGGTGATGACCTGGTTTCAGCCG CAGTACCGTAAAACCTTTGACCATCCGGTCAGCCGCCAGCAGCTG CATGAGGTTATTGACCAGCAAATTCCTTCCGACAATCTGTTCTGC GCGCTGCGAATCGATGGTCATTTCCGCCACGCCCATACCCGCACC GTGCCTCGTCAGACGCCGCCCTACCGGGCGATGACCGACGTGCTC GACGATCAGCCGGTTTTCCGCTTTAACCAGCGTGACGGCGTACTG GTCGGTTTTCGGACCCCCCAGCATATGCAGGGAATTAACGTCGCC GGCTATCACGAACACTTCATTACCGATGACCGCCAGGGCGGCGGC CACCTGCTGGACTACCAGCTCGACCATGGGGTATTGACCTTCGGC GAAATTCATAAGCTGATGATCGACCTTCCCGCCGACAGCGCGTTC CTGCAGGCCAATTTGCATCCCGATAATCTCGATGCCGCCATCCGT TCAGTAGAAAGTTAG
quinoprotein glucose dehydrogenase [EC:1.1.5.2]	**gcd**	>ADJCKNHF_03828 Quinoprotein glucose dehydrogenase ATGGCAGAAACAAAATCTCAACAATCACGGTTACTTGTCACGCTG ACGGCGCTGTTTGCCGCCTTCTGTGGCCTGTATCTGTTAATCGGTG GGGTATGGCTGGCCGCTATTGGCGGTTCCTGGTACTACCCTATCG CAGGCCTGGTGATGCTGGCCGTCACCGTTATGCTGTTCCGCGGCA AGCGCGCTGCGCTGTGGCTGTACGCCGCCCTGCTGCTGGCAACCA TGATTTGGGGGGTATGGGAAGTCGGTTTCGACTTCTGGGCGCTGA

		CGCCGCGTAGCGACATCCTGGTCTTCTTCGGCATCTGGCTGATTCT GCCATTTGTCTGGCGTCGTCTGCCGGTCCCTTCCGCCGGTGCCGTT GGCGGTCTGGTTATCGCCCTGCTGATTAGCGGCGGGATCCTGACC TGGGCCGGTTTCAACGATCCGCAGGAAGTGAACGGTACGCTGAG CGCTGACGCGACGCCGGCTGCGCCGATTTCTACCGTCGCCGATAG CGACTGGCCGGCTTATGGCCGCAACCAGGAAGGCCAGCGTTATTC ACCGCTGAAGCAAATTAATACCGATAACGTGAAGAACCTGAAGG AAGCCTGGGTATTCCGCACCGGCGACCTGAAGCAGCCGAACGAT CCGGGTGAAATCACTAACGAAGTGACGCCGATTAAAGTTGGCGA CATGCTGTATCTGTGTACCGCGCACCAGCGTCTGTTCGCGCTTGA CGCGGCCACCGGTAAAGAGAAGTGGCATTTTGACCCGCAGCTGA ACGCCGATCCGTCGTTCCAGCACGTGACCTGCCGTGGCGTCTCCT ATCATGAAGCCAAAGCAGATAACGCGCCTGCCGACGTCGTCGCC GACTGCCCGCGCCGTATTATTCTGCCGGTCAACGATGGCCGTCTG TTCGCGGTGAACGCCGACAACGGTAAGCTGTGCGAAACCTTTGCC AACAAAGGCATTCTCAACCTGCAAACCAATATGCCGGTAACCAC GCCGGGTATGTATGAACCGACGTCGCCGCCGATTATCACCGATAA GACTATCGTCATTGCCGGCGCGGTAACCGATAACTTCTCAACCCG CGAGCCATCAGGCGTAATCCGCGGCTTTGATGTGAATACCGGTAA ACTGCTGTGGGCCTTCGACCCGGGTGCGAAAGACCCTAATGCGAT CCCGAGCGATGAGCATCACTTCACACTCAATTCACCTAACTCCTG GGCGCCTGCCGCCTATGACGCGAAGCTGGATTTAGTCTATCTGCC GATGGGCGTTACCACGCCGGATATCTGGGGCGGCAATCGCACGC CGGAACAGGAACGTTACGCCAGCTCTATCGTAGCGCTGAACGCA ACCACCGGGAAACTGGCATGGAGCTACCAAACCGTACACCACGA TCTGTGGGATATGGATATGCCGTCGCAGCCGACGCTGGCCGACAT TGATGTGAACGGTAAAACCGTGCCGGTGATTTACGCTCCGGCCAA AACCGGCAACATCTTCGTGCTGGATCGCCGTAATGGCGAACTGGT GGTCCCGGCGCCGGAAAAACCGGTTCCGCAAGGTGCGGCGAAAG GCGATTATGTTGCTAAAACCCAGCCGTTCTCCGAGCTGAGCTTCC GTCCGAAGAAAGACCTGACCGGCGCAGATATGTGGGGCGCCACC ATGTTTGACCAACTGGTGTGCCGCGTTATCTTCCATCAGATGCGCT ATGAAGGTATCTTCACTCCACCGTCTGAACAGGGCACGCTGGTCT TCCCGGGGAACCTGGGGATGTTTGAATGGGGCGGTATCTCCGTCG ATCCAAACCGTCAGGTGGCTATCGCCAACCCGATGGCGCTGCCGT TCGTCTCTAAATTGATCCCACGCGGCCCGGGCAACCCGATGGAAC CGCCAAAAGACGCGAAAGGCTCTGGTACCGAGTCCGGCGTTCAG CCGCAGTATGGCGTCCCGTTCGGCGTCACGCTGAACCCGTTCCTG TCGCCGTTTGGCCTGCCGTGTAAACAACCGGCATGGGGTTATATC TCGGCGCTGGATCTGAAGACCAACGAAGTAGTGTGGAAAAAACG CATCGGTACGCCGCAGGATAGTCTGCCGTTCCCGCTGCCTGTCCC GCTGCCATTCAATATGGGTATGCCGATGCTGGGCGGACCGATCTC AACCGCCGGTAACGTGCTGTTTATCGCCGCCACCGCCGATAACTA CCTGCGCGCTTACAACATGAGTAATGGTGAAAAACTGTGGCAGG CGCGTCTGCCTGCAGGTGGCCAGGCGACGCCGATGACCTATGAA GTGAATGGCAAGCAGTACGTTGTCATCTCTGCCGGCGGTCATGGC TCGTTCGGTACTAAAATGGGCGACTACATCGTTGCCTATGCGTTA CCGGATGACGCGAAATAA
spermidine synthase [EC:2.5.1.16]	**speE, SRM**	>ADJCKNHF_03833 Polyamine aminopropyltransferase ATGGCCGAGAGTAATCAGTGGCATGAGACGCTGCACGACCATTTT GGTCAATATTTTACCGTTGATAACGTACTGTACCATGAGAAGACC GATCATCAGGATTTAATCATCTTCGAAAATGCGGCATTTGGCCGC GTGATGGCGCTTGATGGCGTGGTGCAAACCACCGAGCGCGATGA GTTTATTTACCATGAAATGATGACCCACGTTCCGCTGCTGGCCCA TGGTCACGCAAAGCACGTGCTGATCATCGGCGGCGGCGATGGCG CGATGCTGCGTGAAGTCTCCCGCCACCAACATATCGAAACCATTA

		CCATGGTGGAAATCGACGCCGGAGTGGTATCGTTCTGCCGTCAGT ACCTTCCAAACCATAACGCCGGCGCCTATGACGACCCGCGCTTTA CGCTGGTGATTGATGACGGCGTGAACTTCGTCAACCAAACGTCAC AAACTTTTGATGTCATTATCTCCGACTGTACTGACCCGATCGGCCC CGGTGAGAGCCTGTTTACCTCGGCGTTTTATGCTGGCTGTAAACG TTGCCTGAACCCCGGCGGAATTTTCGTTGCCCAGAACGGCGTAAG CTTCCTGCAGCAGGATGAAGCGGTAGGCAGCCATCGCAAACTCA GCCACTATTTCACCGATGTCAGCTTCTACCAGGCGGCGATCCCGA CCTACTATGGCGGTATCATGACCTTTGCCTGGGCGACCGATAATG AAGCCCTGCGTCATTTGTCGACGGAAATTATTCAGGCCCGCTTCC ATAGCGCCGGGCTGAAATGCCGTTATTACAATCCGGCAATTCATA CCGCGGCTTTCGCGCTACCGCAATACCTGCTGGATGCGCTGACCG CCAGCTAA
S-adenosylmethionine decarboxylase [EC:4.1.1.50]	**speH, speD, AMD1**	>ADJCKNHF_03834 S-adenosylmethionine decarboxylase proenzyme TTGAAAAAGCTTAAGCTGCACGGCTTCAACAACCTGACTAAAAGC CTGAGTTTTTGTATTTACGATATCTGCTACGCTAAAACCGCCGAA GAGCGCGATGGCTATATAGCCTATATCGATGAACTCTATAATGCC AATCGCCTGACGGAAATCCTCTCCGAGACCTGTTCAATCATTGGC GCCAACATACTCAACATCGCACGCCAGGATTATGAACCGCAGGG CGCAAGCGTCACCATTTTGGTTAGCGAAGAGCCTATCGATCCGCA GCTTATCGATCAGAGCGAGCATCCGGGCCCGCTGCCTGAGACCGT GGTCGCACATCTCGATAAAAGCCACATCTGCGTGCATACCTATCC GGAAAGCCATCCGGAAGGCGGTCTGTGCACCTTCCGCGCCGATAT TGAAGTCTCCACCTGTGGAGTGATTTCACCGCTGAAGGCACTGAA CTACCTGATTCACCAACTGGAATCCGATATCGTAACCATTGATTA TCGCGTGCGTGGTTTCACCCGTGATATCAACGGTATGAAGCATTT TATCGATCATGAAATCAACTCTATTCAGAACTTCATGTCAGAAGA TATGAAGTCGCTCTATGACATGGTGGACGTGAACGTCTATCAGGA AAATATGTTCCATACCAAAATGATGCTGAAAGAGTTCGATCTGAA ACACTACATGTTCCACACCAAACCGGAAGAGTTAAGCGAACAAG AGCGCAAGGTGATTACCGACCTGCTGTGGAAAGAGATGCGGGAA ATTTATTACGCCCGCAATATCCCTGCGGTGTAA
acetolactate synthase I/III small subunit [EC:2.2.1.6]	**ilvH, ilvN**	>ADJCKNHF_03878 Acetolactate synthase isozyme 3 small subunit ATGCGCCGGATATTATCTGTATTACTGGAGAACGAATCGGGAGCA TTATCCCGGGTGATCGGCCTCTTTTCGCAGCGCGGCTACAATATT GAAAGCCTGACGGTAGCGCCAACCGACGATCCGACGTTGTCCCG CATGACCATCCAGACGGTGGGCGACGAAAAAGCCATTGAGCAGA TCGAAAAGCAATTACATAAGCTGGTGGACGTGCTGCGGGTCAGC GAACTGGGTCAGGGCTCCCACGTCGAACGTGAAATCATGCTGGTG AAAGTGCAGGCCAGCGGTTATGGCCGCGAAGAGGTGAAACGCAA CACCGAGATCTTCCGCGGGCAGATCATTGACGTCACGCCATCTAT TTATACCGTGCAGTTGGCCGGAACCAGCGATAAGCTGGATGCGTT CCTGGCTTCTTTACGCGATGTCGCGCGCATTGTTGAAGTGGCGCG ATCCGGAGTAGTCGGCCTGTCGCGCGGCGATAAAATCATGCGCTA A
acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	**ilvB, ilvG, ilvI**	>ADJCKNHF_03879 Acetolactate synthase isozyme 3 large subunit ATGGAGATGTTGTCAGGAGCCGAGATGGTCGTCCAATCGCTTGTC GATCAGGGCGTCAAGCAAGTATTCGGCTATCCCGGAGGCGCGGT CCTCGATATCTATGATGCATTACATACCCTCGGCGGCATTGACCA TGTGCTGGTCCGCCATGAGCAGGCGGCGGTGCATATGGCCGACG GACTGGCGCGCGCAACCGGCGAAGTCGGGGTGGTGCTGGTGACC TCCGGCCCGGGAGCGACTAACGCTATTACCGGCATTGCAACGGCT TACATGGATTCTATTCCGCTGGTCATTCTTTCCGGGCAGGTCGCCA CCTCGCTGATTGGCTACGATGCCTTCCAGGAGTGCGATATGGTCG GTATCTCGCGCCCGGTGGTTAAACACAGCTTCCTCGTGAAACAGA CTGAAGATATCCCCGGGATTTTAAAGAAAGCCTTCTGGCTGGCGG

		CCAGCGGCCGACCGGGGCCGGTAGTGGTCGATTTGCCGAAGGAT ATTCTCAATCCGGCGAAAAAGCTGCCTTATGTTTGGCCGGATGCG GTCAGCATGCGTTCCTATAACCCGACAACCAGCGGTCATAAAGGG CAGATCAAACGTGCGTTGCAAACGCTGGTGGCGGCGAAAAAACC GGTCGTGTACGTTGGCGGCGGGGCAATCAATTCGCAGTGCGAAG CACAGCTGCGTACGCTGGTCGAAAAGCTGAAGCTACCGGTGGTCT CTTCATTAATGGGTTTAGGCGCTTTTCCGGCGACTCATCAGCAGG CGCTGGGGATGTTGGGGATGCACGGTACCTATGAAGCCAACATG ACCATGCATCATTCCGACGTTATTTTTGCAGTCGGCGTCCGCTTTG ACGATCGCACCACCAACAATTTGGCTAAGTATTGCCCGAACGCCA CGGTGCTGCATATTGATATCGATCCCACGTCGATCTCCAAAACCG TCCCGGCAGATGTGCCGATCGTCGGCGACGCGCGCCAGGTGCTTG ACCAGATGTTTGATCTGCTTGAGCAGGAAGAGAGCCAGCAACCG CTGGATGAGATCCGCGACTGGTGGCAGCAGATCGAACAGTGGCG TTCCCGTCACTGTCTGCAATACGACACGCAAAGCGGCAAGATCAA ACCGCAGGCGGTGATTGAGGCTATCTGGCGCCTGACCAATGGTGA TGCTTACGTGACTTCCGACGTTGGACAGCATCAGATGTTCGCCGC GCTCTATTATCCATTCGATAAACCACGGCGTTGGATTAACTCCGG CGGCCTCGGCACGATGGGCTTTGGCCTGCCAGCGGCACTGGGCGT GAAGATGGCGCTACCGCAAGAAACCGTGATCTGCGTGACCGGCG ATGGCAGCATCCAGATGAACATTCAGGAGCTTTCCACCGCCCTGC AGTATGAACTGCCGGTGCTGGTGCTGAACCTGAATAACCGCTACC TCGGAATGGTAAAGCAGTGGCAGGATATGCTCTATTCTGGCCGCC ATTCGCAGTCCTATATGGAATCGCTGCCGGACTTCGTTCGCGTCG CCGAGGCTTATGGCCACGTTGGTATTCGTATCAGCGAGCCGCAAG AGCTGGAAGCGAAGCTGGCGGAAGCCCTGGAGCAGGTGCGTAAT AATCGTCTGGTGTTCGTTGATGTTACGGTTGATGGCAGCGAGCAT GTTTATCCCATGCAGATCCGCGGCGGCGGCATGGACGAAATGTGG TTGAGCAAAACGGAGAGAACCTGA
inorganic pyrophosphatase [EC:3.6.1.1]	**ppa**	>ADJCKNHF_04028 Inorganic pyrophosphatase ATGAGCTTACTCAACGTACCTGCGGGCAAAGAGCTGCCGGAAGA CATCTACGTCGTTATCGAAATCCCAGCTAACGCAGACCCAATCAA ATACGAAGTTGACAAAGAGAGCGGCGCACTGTTCGTTGACCGTTT CATGTCCACTGCGATGTTCTATCCGTGCAACTACGGCTACATCAA CCACACCCTGTCCCTGGACGGCGACCCGGTTGACGTGCTGGTCCC GACTCCGTACCCGCTGCAACCAGGCTCAGTTATCCGCTGCCGTCC GGTTGGCGTACTGAAAATGACCGACGAATCCGGTGAAGATGCCA AGCTGGTTGCGGTACCGCACACCAAGCTGAGCAAAGAATACGAT CACATCAAAGATGTGAACGACCTGCCGGAACTGCTGAAAGCCCA GATCACTCACTTCTTCGAGCACTACAAAGATCTGGAAAAAGGCAA GTGGGTTAAAGTCGACGGTTGGGACAACGCTGAAGCGGCTAAAG CTGAAATCGTTGCTTCCTTCGAGCGCGCTAAACAGAAGTAA
hydrogen cyanide synthase HcnB [EC:1.4.99.5]	**hcnB**	>ADJCKNHF_04202 Hydrogen cyanide synthase subunit HcnB ATGAACACGCTGCGCTGTGACATTTTAATCCTCGGCGCCGGCCCC GCAGGGGTGGCGGCCGCGCTCTCCGCCGCCGCCTGCGATAAACA GGTGATTATTCTCGACGATAATCCCGCCCCTGGCGGGCAAATCTG GCGTGCCGGTCCGCAGGCGACGCAGCCCGCCCTGGCCCGGCACT ACCGCGACGCCATCGCCGCGTCTGCCGCCATCCGGTTAGTGAACG GCGCGCGGCTGATTGCCCGCCCCTCCGCGTACAGTGTGCTGTTTG AAACCGCCGACGGCGGTGGTGTGGTTTACTGGCAGAAACTGATCC TCTGCTGCGGCGCGCGCGAGCTGTCGCTGCCCTTTCCCGGTTGGA CCTTACCCGGCGTGACCGGCGCGGGCGGCCTGCAGGCGCAAATC AAACAGGGCCTTGCGCTGAAAGGAGAAAAGGTGGTGATTGCCGG CAGCGGTCCGCTACTGCTGGCGGTGGCGGATACGGTGAACAAGG CCGGAGGCGAAGTGACGAATATCATTGAGCAAGCGCCGCTACCG GCACTGCTGCGCTTCGCCGGTGGGCTGTGGCGCTGGCCGCAGAAG

		CTGCGCCAGTTAGCGATGCTGGCTCCGAAAGGCTATCTTAGCGGC ACGCAGGTGATCCGCGCTCACGGCACAACGCGGCTGGAAGCCGT TACGTTGCGCCAGCGCGGCGACGAGCGAACTATCGCCTGCGATCG GCTGGCTATCGGCTACGGGCTGATACCCAATATCGAGACGGCGCT GCTGTTTGGCTGCGCCACGGCGCAGGAGGCGATACAGGTTAACC GCTGGCAGCAGACCAGCATCGCGGATATCTACGCCGCCGGCGAG TGCACCGGTTTCGGCGGTAGCGAACTGGCGCTGGCGGAGGGCGA AATCGCCGGTTTTGCCGCCGCCGGGGCCAGCCATCAAGCGCAGGC GTTATTTGCCCGCCGCGCCCGCTGGCAGCGCTTCGCCGACGCCAT AAACCGCGCCTTCCGGCTGGCGGAATCTTTGAAAAACGCGGCGA CGCCGGAGAGCCTGCTGTGCCGCTGCGAGGATGTGCGCTGCGGC GATGTGGCGGCAGCCGGAGGCTGGCCGCAGGCCAAACTTACCCA GCGCTGCGGAATGGGCGCCTGTCAGGGGCGCACCTGCGCCGCCA GCGCCCGCTGGTTATATGGCTGGCCGCTGCCGCAGCCGAGAGAAC CGCTGGCCCCTGCCCGCGCGGAAACGCTTATTGCCCTCGCCAGGT TGAGCGCCGAGCCGTAA
hydrogen cyanide synthase HcnA [EC:1.4.99.5]	**hcnA**	>ADJCKNHF_04203 hypothetical protein ATGAATGCCACGCTCACTATCATCGTTGATGGCGAAGCGCTGACG GTGCCGGAAGGGATCAGCGTGGCGGCGGCGCTGGCGTTGACCGG CGACCCCACCACCCGCCAGGCGGTTAACGGCGGCCTCCGCGCGCC GTTTTGCGGCATGGGCGTCTGCCAGGAGTGCCGGGTCACCGTCGA TGGCCTACGGGTGCTGGCCTGCCAGACCCTGTGCCGGTCCGATAT GCAAATAGAAAGGAGCCGCGATGAACACGCTGCGCTGTGA
hydrogen cyanide synthase HcnC [EC:1.4.99.5]	**hcnC**	>ADJCKNHF_04204 Glycine oxidase GTGAAGCAGTGCGACGTCATCGTGATCGGCGCCGGGATCATCGG CGCCGCCTGCGCGTGGCAGCTGGCGAAGCGGGGGCAGAGCGTGA CGCTTATCGATGACGGTCAGCCTGGCGCGACGGCGGCCGGTATGG GCCATCTGGTTTGCATGGATGACGACCCCGCCGAGCTTGCATTAT CGGCATGGTCGCTGGAACGCTGGCGCGCTATCACGCCACGGATGC CCGACAATTGCGCCTGGCGCGGCTGCGGTACGCTGTGGCTGGCGG AAAGCGAAGAAGAGATGGCCGGGGCTGGCGACAAACAGCGGCG GATGGCCGGCCATCAGGTGCACAGCGAACTCCAGACCCCGCAGC AGATCGCCGGGCGCGAGCCGCTGCTGCGCGACGGGCTGGCCGGC GGCCTGTGGGTGCCAGGCGATGGCATCGTCTACGCGCCGAACGTC GCCCGCTGGCTGATTACCGATGCCGGAAACCATCTTACCTGCCTG CGCGATAGCGTACAGACGATTGACGAGCCGCAGGTGCTGCTCGC CAGCGGCAAACGGCTACAGGCGCGGGCGATCGTGGTGGCCTGCG GCCTTGAAGCTAACGCGCTGTTAGCGGAAAACTGGCTGCGACCG AAAAAAGGCCAACTGGCGATTACCGATCGCTATGGGCCGCAGGT GCATCACCAGCTGGTTGAGCTGGGTTATGGCGCCAGCGCCCACGG CGGCGGCACCTCGGTGGCGTTTAACCTTCAGCCGCGGCCAACCGG CCAGCTGCTAATTGGCTCTTCGCGTCAGTTTGATAACCGCGAGCG CGAGTTGGATCTGCCCTTGCTGGCGCAGATGCTCGATCGCGCCCG CCACTTCGTGCCGGCGCTGGCGACGTTGAATATCATCCGCTGCTG GAGCGGCCTGCGCGCCGCCTCTCCGGATGGCAATCCGTTGATCGG CCCGCACCCCACCCGCCGTGGTTTATGGCTAGCGCTGGGTCATGA AGGGCTGGGCGTCACCACTGCCCCGGCCTCGGCTGAACTGCTGGC GGCGCAGATCCTCGATGAACGCTGCCCATTGGCTCCCGACGCCTG GCTCCCGGCTCGTTTATCTCAACAGGAGGCGATCGCATGA
acetolactate synthase I/III small subunit [EC:2.2.1.6]	**ilvH, ilvN**	>ADJCKNHF_04581 Acetolactate synthase isozyme 2 small subunit ATGATGCAACATCAGGTCGCTTTACAGGCTCGCTTCAACCCCGAA ACCTTAGAACGCGTGCTGCGCGTGGTGCGCCATCGCGGTTTTCAA ATTTGCTCAATGAATATGGAAACCGCGTCGGATGCGCAAAACATA AATATCGAGCTGACCGTTGCCAGCCAGCGGCCCGTCGAATTACTG TTTAGTCAGTTACGCAAACTGGTCGACGTCGCCTGCGTCGAGATC CAGCAACCCACATCACAACAAATCCGCGCCTGA

acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	**ilvB, ilvG, ilvI**	>ADJCKNHF_04582 Acetolactate synthase isozyme 2 large subunit ATGAACGGGGCGCAGTGGGTGGTACATGCTTTGCGAACACAGGG GGTCGACACGGTATTTGGCTATCCGGGTGGCGCGATTATGCCGGT TTACGATGCTTTGTATGACGGCGGCGTGGAACACCTGCTGTGTCG GCACGAGCAAGGCGCCGCAATGGCCGCCATCGGTTATGCCCGCG CGACCGGCAAAACTGGTGTTTGCATCGCCACTTCCGGTCCTGGCG CCACCAACCTGATCACCGGTTTGGCTGACGCGTTACTTGATTCTGT ACCTGTTGTCGCCATCACCGGTCAAGTGGCGGCGCCGTTTATCGG CACCGATGCTTTTCAGGAAGTGGACGTTCTCGGTTTGTCGCTGGC CTGCACCAAACACAGTTTCCTCGTGCAGTCGTTGGAAGAGCTGCC GCGCGTCATTGCGGAAGCTTTCCAGGTGGCAAACTCAGGCCGTCC TGGCCCGGTACTGGTTGATATTCCAAAAGATATCCAGTTGGCTAA AGGCGAATTAGATCCGCATTTCTCCACCGTCCCTGATGATGTTGA GTTCCCGCACACACAAGTCGAGCAGGCGTTAGCGATGCTTGCGCA GTCCCACAAGCCAATGCTGTACGTGGGTGGCGGTGTTGGAATGGC ACAGGCGGTACCGGCCGTGCGCGAATTTCTGGCGGTGACGCAGA TGCCGGTAACCTGCACTCTGAAAGGGTTGGGCGCCGTCGCCGCGG ATTATCCGTATTACCTTGGCATGCTGGGTATGCACGGAACCAAGG CAGCAAACCTGGCGGTGCAGGAGTGCGATTTATTAATCGCCGTCG GCGCCCGTTTTGATGACCGGGTTACCGGCAAGCTGAATACCTTTG CCCCGCACGCCAAAGTAATCCATATGGATATTGACCCGGCCGAGC TGAACAAACTGCGCCAGGCGCACGTCGCCTTAACCGGAGATTTAA ACGCCATGCTGCCGGCGTTGCAGCAGCCGTTGGCCATCGATGCGT GGCGCGAGCGCAACGCGCAGCTGCGCGCGGAGCACGCCTGGCGT TACGATCATCCCGGCGAGGCAATCTACGCGCCGCTGTTGCTCAAG CAGCTTTCCGATCGCAAACCGGCGGATTGCGTCGTGACGACCGAT GTCGGCCAGCACCAAATGTGGTCGGCCCAGCACATGACCTATACC CGCCCGGAAAACTTCATCACTTCCAGCGGCCTCGGCACCATGGGT TTTGGTCTGCCGGCAGCCGTTGGCGCGCAGGTGGCTCGCCCGGAC GATACGGTTATCTGTATCTCCGGCGATGGCTCTTTCATGATGAAC GTGCAGGAGCTGGGCACCGTTAAGCGCAAGCAATTACCGTTGAA AATCGTGCTGCTGGATAACCAACGTTTAGGCATGGTTCGCCAGTG GCAGCAGCTGTTTTTCCAGGAGCGTTACAGCGAAACCACGCTTAC CGATAATCCTGATTTTCTTACGCTGGCCAGCGCTTTTGGCATTCCA GGCCAGCACATCACCCGTAAAGACCAGGTTGAAGCGGCACTCGA CACCATGCTTTCGAGCCAGGGGCCATACCTGCTTCATGTCTCAAT CGATGAACTTGAGAATGTCTGGCCGTTGGTGCCGCCCGGCGCCAG TAATGCAGAAATGCTGGAGAAATTATCATGA

Example 10: CK1 pathogenicity analysis

[00242] CK1 was grown on agar plates in the presence of different antibiotics and enzyme inhibitor combinations to detect carbapenemase enzymes and evaluate CK1's pathogenicity.

[00243] CK1 was tested using the agar diffusion method with DCM kits (Britannia) according to manufacturer's protocol. Briefly, Cultures were grown at 30°C for 10 hours. The results showed a circular inhibition zone in the discs of the DCM kit, which indicated that CK1 is not a producer of carbapenemase type *Klebsiella* pneumoniae, carbapenemase (KPC), metallo-beta-lactamases (MLB), and Oxacillinase (Oxa). The results showed a lack of carbapenemase functionality and lack of pathogenicity in CK1 (FIG. 10).

Example 11: Characterization of antibiotic resistance and sensitivity

[00244] CK1 and CK2 were grown on agar plates in the presence of different antibiotics and in different concentrations to evaluate their antibiotic resistance capacity. Cultures were grown at 30°C for 24 hours. Results are shown in Table 34 and 35 (R: resistant; S: sensitive).

Table 34: Bacterial Resistance to Antibiotics

	Tetracycline			**Kanamycin**			**Gentamicin**			**Streptomycin**			**Ampicillin**		
Concentration µg/ml	5	10	15	10	25	50	10	25	50	25	50	75	50	75	100
CK1 *Klebsiella aerogenes*	R	R	R	R	S	S	R	S	S	R	S	S	R	R	R
CK2 *Bacillus cereus*	S	S	S	R	S	S	R	S	S	S	S	S	S	S	S

	Chloramphenicol			**Vancomycin**			**Carbenicillin**			**Cephalexin**		
Concentration µg/ml	2	10	50	0.5	2	4	100	250	500	1	2.5	5
CK1 *Klebsiella aerogenes*	R	R	S	R	R	R	S	S	S	S	S	S
CK2 *Bacillus cereus*	S	S	S	R	R	S	R	R	S	R	R	R

[00245] CK1 and CK2 were further tested using the agar diffusion method with DCM kits (Britannia) according to manufacturer's protocol for their resistance to following antibiotics and combinations were tested using the agar diffusion method: Ciprofloxacina, Amicacina, cefepime, Tazatobatam-Piperacilina, Ceftolozane-Tazobactam, Meropenem, Meropenem-Tazobactam, Meropenem-EDTA, Meropenem-boronic acid, and Meropenem-cloxacilina.

[00246] CK1 and CK2 did not show resistance to any these antibiotics.

Example 12: Effects of CK1 and CK2 on fungal growth

[00247] Bacterial strains CK1 and CK2 were tested for their ability to inhibit the growth of phytopathogenic fungi by employing a dual culture assay on PDA plates. 10 µl of bacterial cell suspension (10^8-10^9 CFU/mL) grown previously in LB medium was placed on one side of the Petri dishes, leaving 1 cm from the margin or alternatively as four microdroplets at each end of the Petri dish. Bradyrhizobium was used as a control. Once the moisture from the inoculum was absorbed by the culture medium, a mycelial disk (6 mm) of the phytopathogen (Fusarium sp. and Sclerotinia Sclerotium) was placed at a distance of 70 mm from the bacterial culture or alternatively the phytopathogen was placed in the middle of the four microdroplets corresponding to the bacterial culture. Plates with sterile distilled water (instead of bacterial suspension) and antagonist fungus served as control. The plates were incubated at 28±2 °C in the dark, and the percentage of inhibition (PI) was registered daily for 220 h. The PI was calculated according to Shrivastava et al. (P. Shrivastava, R. Kumar, M.S. Yandigeri, In vitro biocontrol activity of halotolerant Streptomyces aureofaciens K20: a potent antagonist against Macrophomina phaseolina (Tassi) Goid, Saudi J. Biol. Sci. 24 (2017) 192–199, https://doi.org/10.1016/j.sjbs.2015.12.004.) as follows: %PI = (C - T) /C × 100 where 'C' is the colony growth of M. phaseolina in control plates, and T is the colony growth of the pathogen in dual-culture plates.

[00248] Results are shown in FIG. 11 and FIG. 12. Each bacteria and bacteria combination was differentially effective against each fungus. The assays revealed CK1 and CK2 bacteria were able to

inhibit fungal growth. In general, CK1, CK2 and CK1 + CK2 mix were all more effective long term in inhibiting fungal growth as compared to the commercial *Bradyrhizobium* product

Example 13: Ammonia and nitrate production and total nitrogen quantification in soybean plants

Ammonia and nitrate production

[00249] *Methodology*:

[00250] The ability to synthase ammonia and nitrate was evaluated in CK1, CK2, CK1 + CK2, the diazotrophic bacterium *Gluconacetobacter* PAL5 (a universal free nitrogen fixer) and *Bradyrizobium*. All the strains were cultured in ECO culture medium (see the composition below) at 200 rpm for 24h. After the incubation time, the commercials ab83360 – Ammonia Assay Kit and Abnova™ Nitrate/Nitrite Colorimetric Assay Kit were used to assay the abilities of bacteria to synthetize Ammonia and Nitrate.

[00251] *Ammonia detection*

[00252] For the ammonia detection, the strains (previously grow in ECO medium) were centrifugated at 10,000 rpm for 10 min and washed in cold PBS buffer. Then, the cells were resuspended in 100 µL of Assay Buffer (part of the kit) and homogenized quickly by pipetting up and down a few times. The samples were centrifugated for 5 min at 4°C at 13,000 rpm in order to remove any insoluble material. The supernatants were transferred to a clean tube and kept on ice. Finally, the supernatants were mixed with 50 µL of the reaction mix (commercialized in the kit) and incubated at 37°C for 60 minutes (in the incubation the samples were protected from light). After the incubation, the optical density was measured at 570 nm. The production was calculated introducing the OD values obtained in a standard curve ammonia (µM).

[00253] ECO composition (g/L): 3 glucose, 5 $NH_4H_2PO_4$ and 3 yeast extract PBS buffer composition (g/L): 8 NaCl, 0.2 KCl, 1.15 Na_2HPO_4, 0.2 KH_2PO_4

[00254] *Nitrate detection*

[00255] For the Nitrate detection, 80 µL of each bacteria (previously grow in ECO medium) was mixed with: 10 µL of the Enzyme Cofactor Mixture and 10 µL of the Nitrate Reductase. The samples were covered and incubated at room temperature for one hour. After the incubation time, 50 µL of Griess Reagent R1 and 50 µL of Griess Reagent R2 were added to each sample. Once the color to development appeared after an incubation of 10 minutes at room temperature, the absorbance was read at 540 nm. The production was calculated introducing the OD values obtained in a standard curve Nitrate (µM).

[00256] Results:

Table 36. Ammonia and Nitrate quantification using commercial kits

	***Klebsiella aerogenes* CK1**	***Bacillus cereus* CK2**	***Klebsiella aerogenes* CK1 + *Bacillus cereus* CK2**	***Gluconacetobacter PAL5***	***Bradyrhizobium***
Ammonia (µM)	89.3	82.76	117.63	58.7	24.42
Nitrate (µM)	129. 07	108.7	145.0	114.22	70.56

[00257] Conclusion: Extremophiles microorganism were able to synthetize Ammonia and Nitrate at the same concentrations as the universal *Gluconacetobacter* PAL5. Also, this ability was stimulated when the strains CK1 and CK2 were combined.

[00258] Regarding to *Bradyrizobium*, the strain did not show the ability to synthetize ammonium and nitrate under laboratory conditions. That's because this type of bacteria needs to establish a symbiotic relationship with the plant to fix the nitrogen.

Total quantification of Nitrogen in 40- days Soybean plants

[00259] *Methodology:*

[00260] Soybean seeds were mixed with the products Extremia A, CK2 + stabilizer, Extremia MIX, and *Bradyrizobium* (the preparation of the products was already described in Example 3, please noticed that CK2+ stabilizer was prepared as well as Extremia A) using a dose of 5 kg/mL for Extremia A and CK2 + stabilizer. The commercial dose for Bradyrizobium was 0.9 kg/mL. Soybean seeds inoculated with regular water instead of biological products were used as controls. The seeds were sown in pots with fertile soil under greenhouse conditions, with an approximate temperature of 30-33 °C for 40 days. After 40 days, whole plants (leaves, roots, and stems) were dried at 80°C for 48 hours and the total nitrogen content (%) was calculated using the Kjeldahl method.

[00261] *Kjeldahl method*

[00262] 0.5 g of dried soybean tissues were introduced into a Kjeldahl tube and mixed with 5 g of catalyst regent (CuSO4 + K2SO4). Then, 10 mL of H2SO4 (concentrated) was carefully added to the Kjeldahl tube and the regents (without the soybean samples were used as a blank. The samples were placed in a Kjeldahl digester and heated for approximately 90 minutes, until no release of white fumes was observed. The distillation was carried out using a Büchi automatic distiller (in the presence of NaOH) and the samples were collected in 60 mL of 4% boric acid + indicators (cresol bromine green and methyl red). Finally, a titration of the distilled samples was arrived out with H2SO4 (0.0601 N) until the color change from light blue to red. This assay was performed in duplicate. The results were expressed as a percentage (w/w).

[00263] Results

Table 37: Total Nitrogen quantification in 40-days soybean plants inoculated with extremophiles by Kjeldahl method

	Extremia A	***Bacillus cereus* CK2 + stabilizer**	**Extremia MIX**	***Bradyrizobium***	**Control**
Nitrogen (%)	3.2 ± 0.01 **c**	2.82 ± 0.001 **a**	3.15 ± 0.01 **c**	3.17 ± 0.02 **c**	3.0 ± 0.01 **b**

[00264] The values reported in the table are the averages ±standard error. Different letters indicate significant differences among means ($p < 0.05$) according to Tukey's HSD test.

[00265] *Conclusion*: At 40 days, the products Extremia A, MIX and *Bradyrizobium* significantly enhance the total content of nitrogen in soybean plants compared to control. Additionally, these results

showed that the application of Extremia A and Mix in soybean seeds improve the nitrogen content as well as the application of commercial products (*Bradyrizobium*).

[00266] As it has been reported, *Bradyrizobium* is a biological Nitrogen fixer that has the ability to establish a symbiosis with leguminous plants (such as soybean) by the formation of nodules in roots. This symbiosis allows the conversion of the atmospheric nitrogen (N2) into ammonium (NH4+) and make it assimilable for the plant.

[00267] Extremophiles bacteria showed a different mechanism to enhance the Nitrogen uptake that does not involve biological fixation (please, see Example 7 in the genome this pathway is absent). The products improve the nitrogen content in the plant, leaving a greater amount of nitrate and ammonium (Table 37) available for plants assimilation.

[00268] In this assay, *Gluconacetobacter* PAL5 was not tested because leguminous plants are not commonly inoculated with this product.

Example 14: Organic acids production

Organic Acids Production

[00269] *Methodology:*

[00270] The organic acids production was detected in the supernatant of the following strains: CK1, CK2, CK1 + CK2, *E. coli*, and *Bradyrizobium*. The bacteria CK1, CK2, CK1 + CK2 and *E. coli* were cultured in Luria Bertani (LB) medium overnight at 30°C, 200 rpm. Regarding to *Bradyrizobium*, this strain was cultures in Yeast-Mannitol liquid medium for 48h at 30°C, 200rpm. After the incubation time, the cells were washed twice with a 0.85% (w/v) physiological solution. Then, 200 µL of each bacteria were cultured in 20 mL of NBRIP culture medium (with tricalcium phosphate (Ca3(PO4)2) as an insoluble phosphate source) and incubated at 30°C, 150 rpm for 5 days. Due to the presence of suspended particles of insoluble $Ca_3(PO_4)_2$ in the supernatant, the broths were centrifuged at 13,000 rpm for 10 min to obtain a clear supernatant. Triplicate aliquots of the supernatant (100 µl) were transferred into clean, dry, acid washed test tubes and the determination of five organic acids were carried out by High Performance Liquid Chromatography (HPLC). The experiment was performed using a C18 column (250 × 4.6 mm) and the parameters were set as follows: solvent 20% methanol and 80% deionized sterilized H2O; flow rate 0.8 ml/min; temperature 40°C; UV detector 210 nm and injection Autoclaved un-inoculated medium and E. coli inoculated media served as negative controls.

[00271] LB composition (g/L): 10 yeast extract, 5 NaCl and 10 tripteine. pH = 7

[00272] Yeast-Mannitol medium composition (g/L): 5 mannitol, 0.5 yeast extract, 0.5 K2HPO4, 0.2 MgSO4 7 H2O, 0.1 NaCl, FeCl3 6 H20 (one drop of 10% solution), MnSO4 (one drop of 10% solution), 5 mL Congo Red (0,5 g + 200 mL). pH 6.5-6.8

[00273] NBRIP composition (g/L): 10 Glucose, 5 Ca3(PO4)2, 5 $MgCl_2 \cdot 6H_2O$, 0.25 MgSO4 7 H2O, 0.2 KCl, 0.1 (NH4)2SO4. The pH of the NBRIP medium is adjusted to 6.75 ± 0.25 before sterilization (autoclave 121°C, 1 atm, during 15 min).

[00274] *Results:*

Table 38. Organic Acids Production quantified by HPLC					
Organic Acids (mg/L)	***Klebsiella aerogenes* CK1**	***Bacillus cereus* CK2**	***Klebsiella aerogenes* CK1 + *Bacillus cereus* CK2**	***E. coli***	***Bradyrizobium***
Lactic Acid	163.33	43.05	134.34	<5	33.45
Acetic Acid	205.23	<5	189.44	<5	39.62
Citric Acid	595.54	61.56	374.14	<5	24.83
Malic Acid	195.43	143.55	168.45	<5	354.46
Succinic Acid	198.26	<5	95.19	<5	16.52

[00275] *Conclusion*: These results are complemented with Example 8, where the organic acids genes were already described.

Inorganic phosphate detection:

[00276] *Methodology:*

[00277] The inorganic phosphate was evaluated in the supernatant of the following strains: CK1, CK2, CK1 + CK2, *E. coli*, and *Bradyrizobium*. The bacteria CK1, CK2, CK1 + CK2 and *E. coli* were cultured in NBRIP culture medium (see the composition above) at 200 rpm for 24h. Then, the bacteria were **centrifugated at 10,000 rpm for 10 min, and 10 µl of the supernatant was analyzed for phosphate content** using a commercial kit EnzChek® Phosphate Assay Kit (E-6646). For which, the supernatant was mixed with a reaction mix, prepared as follows:

[00278] 740 µL of dH2O

[00279] 50 µL 20X reaction buffer

[00280] 200 µL MESG substrate solution

[00281] 10 µL purine nucleoside phosphorylase

[00282] 10 µL experimental enzyme

[00283] Then, the samples were preincubated for 10 minutes at 22°C. Finally, the absorbance was reded at 360 nm as a function of time for both the experimental reaction and the control reaction. The production was calculated introducing the OD values obtained in a standard curve phosphate (mmolar).

[00284] Results:

Table 39. Inorganic phosphate quantification with a commercial kit					
	***Klebsiella aerogenes* CK1**	***Bacillus cereus* CK2**	***Klebsiella aerogenes* CK1 + *Bacillus cereus* CK2**	***E. coli***	***Bradyrizobium***
Inorganic Phosphate (mmol/UFC)	0.47	0.85	3.2	0.078	0.074

[00285] Conclusion: Extremophilic microorganisms were able to solubilize inorganic phosphate both individually and in combination. According to the genetic analysis of phosphate solubilization (example

8), we would expect that CK1 be a better phosphate solubilizer than CK2 due to the greater genetic diversity exhibited. However, CK2 showed a greater inorganic phosphate ability (Table 39) in the quantification with the commercial kit.

[00286] When the extremophiles were grown together this ability highly increased. This effect could be explained due to the different genomic and biochemical features exhibited by CK1 and CK2. Potentially, CK2 highly expressed the gene gdh which encodes a "glutamate dehydrogenase" (this gene is absent in CK1). In addition, CK1 could have the ability to express the gene gcd, encoding for a "glucose dehydrogenase" (absent in CK2 genome). The implication of both genes has been largely described in phosphate solubilization process. Therefore, it could be hypothesized that a beneficial trait between both strains could be responsible for the grater phosphate solubilization process.

[00287] Regarding to *Bradyrizobium*, the strain showed the ability to solubilize inorganic phosphate at similar concentrations as *E. coli* (the strain used as negative control).

Example: 15: Evaluation of soybean-seed treatments in the control of *Fusarium tucumaniae* in greenhouse trials

Methodology

[00288] The trial was planted on February 24, 2022, in the Phytopathology laboratory of the EEAOC, Las Talitas, Tucumán, Argentina. The soybean variety used was DM 5958. The design experiment was completely randomized with four repetitions (FIG. 14). Each experimental unit consisted of a plastic pot (10 cm diameter x 13 cm) with 100 g of the sterile substrate (Grow Mix Multipro) sown with 6 soybean seeds. Those treatments that included the pathogen were inoculated at the time of sowing with 15 g of sorghum inoculated with F. tucumaniae. The trial included 10 treatments (Table 40).

[00289] The parameters evaluated were the following:

[00290] Plant emergence at 7, 10, 14, and 20 days after sowing

[00291] Severity at the root (scale from 1 to 5)

[00292] Fresh weight (g)

[00293] The results obtained from the tests were statistically analyzed using the Infostat program (Di Renzo et al., 2008). The emergence parameter of plants was evaluated using mixed generalized linear models (MLGM) and a test comparison of means (LSD, α=0.05). The root severity and fresh weight parameters were statistically evaluated with general and mixed linear models and a mean comparison test (LSD, α=0.05).

Table 40: Treatments and doses of seed treatments applied in the greenhouse trials.

System: soybean/*Fusarium tucumaniae*	
Treatments	**Doses (ml/100 kg seeds)**
1- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	500
2- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	300
3- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2	500
4- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2	300
5- *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	500

6- *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	300
7-Control no pathogen	-
8-Control pathogen	-
9-Control biofungicide (Rizoderma)	300

[00294] *Results*

[00295] The results of the greenhouse trials against *F. tucumaniae* in soybeans are presented in Tables 41 and 42.

[00296] For the variable plant emergence (Table 41), no significant differences were observed between the treatments evaluated at 7 days after sowing (dds) (P= 0.3811). No significant differences were observed between the evaluated treatments at 10 and 14 days (P=0.5599 and P=0.4722). The control without pathogen presented an emergence value of 75.0% at 10 days and 79.2% at 14 days and the pathogen control showed a value of 66.7% and 62.5% respectively. Among treatments inoculated with *F. tucumaniae*, the one that presented the highest values of emergence on both dates was treatment 10 (91.7%) followed by treatment 5 (79.2%) and treatment 4 (75.0%). At 20 days, no significant differences were observed among evaluated treatments (P=0.3277). Among the treatments inoculated with the pathogen that presented the highest emergence values, could be highlighted treatment 10 (91.7%) followed by treatments 5 (79.2%) and 4 (75.0%) (Figure 15).

Table 41. Average of plants number and emergence (%) in soybean (DM 5958) infected with *F. tucumaniae* in a greenhouse trial.

System: soybean/*Fusarium tucumaniae*	**Emergence**							
	7 days		10 days		14 days		20 days	
Treatments	N°	%	N°	%	N°	%	N°	%
1- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	3.7	62.5	4.25	70.8	4.50	75	4.25	70.8
2- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	4	66.7	4.25	70.8	4.25	70.8	4.25	70.8
3- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2	3	50	3.50	58.3	3.50	58.3	3.25	54.2
4- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2	4.25	70.8	4.50	75	4.50	75	4.50	75
5- *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	4	66.7	4.75	79.2	4.75	79.2	4.75	79.2
6- *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	4	66.7	4	66.7	4.25	70.8	4	66.7
7-Control no pathogen	4.50	75	4.50	75	4.75	79.2	4.75	79.2
8-Control pathogen	3.50	58.3	4	66.7	3.75	62.5	3.75	62.5
9-Control biofungicide (Rizoderma)	4	66.7	4	66.7	4	66.7	3.75	62.5
10-Control chemical (Acronis: pyraclostrobin + methylthiophanate)	5.50	91.7	5.50	91.7	5.50	91.7	5.50	91.7
P-value	0.3811		0.5599		0.4722		0.3277	
*Means in each column followed by the same letter do not differ significantly (LSD, P < 0.05).								

[00297] Regarding the root severity, the pathogen control presented values of 2.21. All seed treatments inoculated with the pathogen were statistically different (P<0.0001) from the pathogen control, being the treatments 10, 9, 6, 2, 4, and 5 the ones that presented the lowest values (Table 42). For the fresh weight measurement, no treatment was statistically different from the pathogen control (7.8 g) (P= 0.0810) (Table 42).

Table 42: Root severity and fresh weight in soybean (DM 5958) infected with F. tucumaniae in a greenhouse trial.

System: Soybean/*Fusarium tucumaniae*		
Treatments	**Severity**	**Weight (g)**
1- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	1.23 B	9.3
2- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	0.68 CD	9.5
3- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2	0.96 BC	6.4
4- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2	0.73 BCD	10.3
5- *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	0.80 BCD	9.2
6- *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	0.65 CD	10
7-Control no pathogen	0.43 D	9.2
8-Control pathogen	2.21 A	7.8
9-Control biofungicide (Rizoderma)	0.65 CD	8.1
10-Control chemical (Acronis: pyraclostrobin + methylthiophanate)	0.41 D	12.9
P-value	<0.0001	0.0810
*Means in each column followed by the same letter do not differ significantly (LSD, P < 0.05).		

[00298] *Conclusions*

[00299] Inoculations with *F. tucumaniae* under controlled conditions were effective in the test carried out on soybeans (DM5958). However, the values of plant emergence in soybean were not affected when inoculated with *F. tucumaniae*.

[00300] The pathogen control presented the highest severity value in the roots. The rest of the treatments were statistically different (P<0.0001) from the pathogen control.

[00301] The fresh weight of soybean plants was affected by the presence *of F. tucumaniae*. In addition, the rest of the evaluated treatments were not statistically different from the pathogen control (P= 0.0810).

[00302] Bibliography

[00303] Di Rienzo J.A., Casanoves F., Balzarini M.G., Gonzalez L., Tablada M., Robledo C.W. 2008. InfoStat, versión 2008, Grupo InfoStat, FCA, Universidad Nacional de Córdoba, Argentina.

Example 16: Evaluation of soybean-seed treatments in the control of Macrophomina phaseolina in greenhouse trials

[00304] The trial was planted on February 1, 2022, in the Phytopathology laboratory of the EEAOC, Las Talitas, Tucumán, Argentina. The soybean variety used was M6410 IPRO. The design experiment was completely randomized with four repetitions (FIG. 16). Each experimental unit consisted of a plastic pot (12 x 16 x 5 cm) with 700 g of sterile sand sown with 20 soybean seeds. Those treatments that included

the pathogen were inoculated at the time of sowing with 2.5% p/p of rice inoculated with *M. phaseolina*. The trial included 10 treatments (Table 43).

[00305] The parameters evaluated were the following:

[00306] Plant emergence at 3, 6, and 10 days after sowing

[00307] Plant height (cm)

[00308] Fresh weight (g)

[00309] Severity at the root (scale from 1 to 5)

[00310] The results obtained from the tests were statistically analyzed using the Infostat program (Di Renzo et al., 2008). The emergence parameter of plants was evaluated by means of mixed generalized linear models (MLGM) and a test comparison of means (LSD, α=0.05). The plant height, root severity, and fresh weight parameters were statistically evaluated with general and mixed linear models and a mean comparison test (LSD, α=0.05).

Table 43: Treatments and doses of seed treatments applied in the greenhouse trials.

System: soybean/*Macrophomina phaseolina*	
Treatments	**Doses (mL/100Kg of seeds)**
1- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	500
2- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	300
3- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2	500
4- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2	300
5- *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	500
6- *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	300
7-Control no pathogen	-
8-Control pathogen	-
9-Control biofungicide (Rizoderma)	300
10-Control chemical (Acronis: pyraclostrobin + methylthiophanate)	100

[00311] *Results*

[00312] The results of the greenhouse trials against *M. phaseolina* in soybeans are presented in Tables 44 and 45.

[00313] For the plant emergence measurement (Table 44), no significant differences were observed among the evaluated treatments at 3 days after sowing (dds) ($P > 0.9999$).

[00314] At 6 dds, significant differences were shown among the treatments ($P<0.0001$). The control without pathogen presented an emergence value of 87.50% being statistically different from the rest of the treatments except for treatment 10 (Acronis) which presented a value of 77.50%. The highest emergence values obtained belonged to treatment 10 (77.50%) followed by treatments 1, 2, and 3 with an emergency of 42.50%. At 10 days, the seed treatments that presented the highest emergency values were treatment 10 (75.00%) followed by treatments 3, 5, and 9 (55.00%), presenting statistical differences compared to the pathogen control (28.35%) (Figure 17).

Table 44: Average of plants number and emergence (%) in soybean (M6410 IPRO) infected with *M. phaseolina* in a greenhouse trial.

System: soybean/*Macrophomina phaseolina*	**Emergence**					
Treatments	N°	%	N°	%	N°	%
1- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	2.75	13.75	8.50 B	42.50	10.33 C	51.65
2- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	2.50	12.50	8.50 B	42.50	9 CD	45
3- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2	3.25	16.25	8.50 B	42.50	11 C	55
4- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2	0.75	3.75	5 C	25	7.66 CD	38.30
5- *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	1.75	8.75	7 BC	35	11 C	55
6- *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	0.75	3.75	7.25 BC	36.25	8.25 CD	41.25
7-Control no pathogen	13.25	66.25	17.50 A	87.50	18.5 A	92.50
8-Control pathogen	1.50	7.50	7.50 BC	37.50	5.67 D	28.35
9-Control biofungicide (Rizoderma)	0	0	6.50 BC	32.50	11 C	55
10-Control chemical (Acronis: pyraclostrobin + methylthiophanate)	3.25	16.25	15.50 A	77.50	15 B	75
P-value	>0.9999		<0.0001		<0.0001	
*Means in each column followed by the same letter do not differ significantly (LSD, P < 0.05).						

[00315] Regarding the root severity, the pathogen control presented values of 7.33%. All the seed treatments inoculated with the pathogen were statistically different (P<0.0001) from the pathogen control, except for treatment 2 (6.03%) (Table 45).

[00316] For the fresh weight measurement, no treatment was statistically different from the pathogen control (7.63 g), except for the treatment 10 (19.43 g) and the control without the pathogen (30.07 g) (P<0.0001) (Table 45).

[00317] Regarding the stem length, statistical differences were obtained among the treatments (P<0.0001) (Table 45). Treatment 1 (11.9 cm) statistically differed from the pathogen control (P<0.0001) that showed a plant-length average of 14.37 cm.

[00318] Treatments that presented length values higher than the pathogen control were numbers 5 (15.60 cm) and 10 (16.66 cm).

Table 45: Root severity, fresh weight, and length measurements in soybean (M6410 IPRO) infected with *M. phaseolina* in a greenhouse trial.

System: Soybean/*Macrophomina phaseolina*			
Treatments	**Severity (%)**	**Weight (g)**	**Length (cm)**
1- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	3.33 B	10.67 C	11.19 D
2- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	6.03 A	10.53 C	11.66 CD
3- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2	1.67 BC	11.53 C	12.21 BCD
4- *Klebsiella aerogenes* CK1+ *Bacillus cereus* CK2	1 BC	7.70 C	12.18 BCD
5- *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	0.83 BC	11.35 C	15.60 AB

6- *Bacillus cereus* CK2+ *Exiguobacterium undeae* CK3	2.12 BC	7.18 C	14.25 ABC
7-Control no pathogen	0 C	30.07 A	14.34 ABC
8-Control pathogen	7.33 A	7.63 C	14.37 ABC
9-Control biofungicide (Rizoderma)	1.85 BC	11.95 C	14 BCD
10-Control chemical (Acronis: pyraclostrobin + methylthiophanate)	1.95 BC	19.43 B	16.66 A
P-value	<0.0001	<0.0001	0.0002
*Means in each column followed by the same letter do not differ significantly (LSD, P < 0.05).			

[00319] *Conclusions*

[00320] In greenhouse trials, infections performed on soybeans (M6410 IPRO) with *M. phaseolina* were effective in causing a reduction in the plant emergence values. Seed treatments evaluated were effective in increasing the emergence values, being treatment 10 the one that presented the highest values, followed by treatments 9, 5, and 3.

[00321] Regarding the severity measurement, the pathogen control showed the highest values, while all seed treatments were statistically different (P<0.0001) from the pathogen control, except for treatment 2.

[00322] Infections with *M. phaseolina* reduced the fresh weight and the treatments were not statistically different from the pathogen control, except for treatment 10 (19.43 g) and the control without pathogen (30.07 g) (P< 0.0001).

[00323] Infections with *M. phaseolina* affected plants' length but no statistical differences were observed compared to controls. The treatments that presented length values greater than the pathogen control (14.37 cm) were treatment 5 (15.60 cm) and treatment 10 (16.66 cm).

[00324] Bibliography

[00325] Di Rienzo J.A., Casanoves F., Balzarini M.G., Gonzalez L., Tablada M., Robledo C.W. 2008. InfoStat, versión 2008, Grupo InfoStat, FCA, Universidad Nacional de Córdoba, Argentina.

Example 17: CK2 Strain Species Determination

[00326] A partial nucleotide sequence of the 16S rRNA gene (1288 nt) was obtained from the whole genome sequencing of CK2 strain and was used to search for similar sequences in the nucleotide collection (nr/nt) database from NCBI using BLAST. The results indicates that this strain belongs to the *Bacillus* genus.

[00327] *Average Nucleotide Identity Analysis*

[00328] In order to identify the species of CK2 strain, an Average Nucleotide Identity (ANI) analysis with members of *Bacillus* genus and CK2 genome was performed. The results indicates that this strain belongs to B. cereus group species (FIG. 17, FIG. 18).

[00329] *Multi Locus Sequence Typing and panC Gene Phylogenetic Analysis*

[00330] Members of *B. cereus* group includes several species with closely related phylogeny, so in order to correctly identify the specific clade that this strain belongs to, two sequence analyses were performed: an analysis using the Multi Locus Sequence Typing (MLST) from PubMLST and an analysis of the *panC* gene.

[00331] All genes of the MLST found in this strain have 100% identity with strains included in clonal complex ST-18 (*B. cereus sensu stricto*) of PubMLST typing schema. The phylogenetic analysis of *panC* gene sequence positions this strain in Group IV (*B. cereus sensu stricto*). Overall, these results indicates that this strain belongs to the species *B. cereus sensu stricto*.

Example 18: Expression of green fluorescent (GFP) in CK1

[00332] *Spontaneous mutant of CK1 resistant to rifampicin:* CK1 was cultured in LB liquid medium for 24 h at 30 ºC, and 250 rpm. After the incubation, the cell density was adjusted to an OD (600nm) = 1 and 100 µL of CK1 was cultured in agar plates (previously prepared with LB medium supplemented with 100 µg mL-1 of rifampicin). The plates were incubated for 24-48 h in the absence of light at 30 ºC until colonies appeared. Finally, CK1 was re-cultured in LB agar plates with a concentration of 50 µg mL-1 of rifampicin. The spontaneous mutants of CK1 resistant to rifampicin were stored at -70°C.

[00333] *Rifampicin preparation:* Rifampicin was weighed in laminar flow trying to maintain sterility, and then dissolved in pure methanol to obtain a final concentration of 50 µg/mL. Two drops of NaOH 10 M were also added to the complete dissolution of the antibiotic.

[00334] *Bacteria conjugations*

[00335] The conjugations performed were four-parent with the following bacteria:

[00336] - Helper E. coli 2013 is kanamycin resistant, and the bacteria has the conjugation gen in the plasmid.

[00337] - Transposase E. coli S17.1 pUX-BF1 is ampicillin resistant.

[00338] - Green fluorescent E. coli XL1-Blue pBK-miniTN7-gfp3 is kanamycin resistant.

[00339] - CK1 with the spontaneous mutant to rifampicin.

[00340] The bacteria were cultured in different LB agar plates with the addition of each resistant antibiotic in a final concentration of 50 µg/mL, and incubated overnight at 30 °C. After 24 h of incubation, the four bacteria were mixed for conjugation in LB agar plate (without antibiotics) for 24 h at 30 °C. Once the conjugation takes place and the bacteria were re-cultured in a 2ii solid medium with the addition of rifampicin and kanamycin to allow the growth of CK1 with the expression of GFP.

[00341] *Medium 2ii composition* g/L: 0.125 K2HPO4, 4 (NH4)2S04, 7.5 sodium citrate, 0.2 MgSO4, 15 agar. pH=8.

[00342] *Ampicillin and Kanamycin preparation*: The ampicillin and kanamycin were weighed in laminar flow trying to maintain sterility, and then dissolved in sterile distilled water to obtain a final concentration of 50 µg/mL.

[00343] *Production of Extremia mix-GFP*

[00344] *CK1-GFP bacterial growth*: The strain (previously cultured overnight in LB broth medium with kanamycin) was re-cultured in falcons (50 mL of capacity) containing 10 mL of LB medium with the addition of kanamycin at 30 °C, 230 rpm for 24 h. The morphology of the bacteria was controlled under the microscope and with Gram´s method, in order to check their purity over time.

[00345] *Xanthan gum preparation*: The Xanthan gum was added under constant stirring and in a rain form in order to avoid conglomerates to a physiological solution (0.8 w/v) in a final concentration of 2 %

(w/v). Then, an antifoam was added to the process in a proportion 1:1000. Finally, all the solution was sterilized at 121 °C, for 45 minutes.

[00346] *Extremia mix preparation*: In this step CK1 and the Xanthan gum were mixed in the following proportion: 75:25 (v/v) in order to obtain a final concentration of the gum 0.5 % (v/v).

[00347] *Inoculation of soybean seeds with Extremix-GFP*

[00348] 200 g of soybean seeds were weighed in polyethylene bags and inoculated with 1 mL Extremia-GFP (dose of 5 kg/mL). Then, the bags were homogenized carefully and let the seeds dry for 10 min. Next, plastic trays were filled with sterile sand (121 °C, 1 atm for 15 minutes) and the seeds were sowed (20 per tray). The seeds were irrigated with distilled sterile water and the trays were covered with plastic bags to keep them moist until the germination of seeds (2-3 days). The trays were incubated at 30°C for a week and irrigated every 48 h (once the seeds germinate, the plastic was removed, and the incubation continues).

[00349] After a week of incubation, the plants were carefully removed and prepared to be observed in the Confocal Laser Scanning Microscope (LCSM). For which, the roots, stems (corresponding to the 1st, 2nd and 3rd portion) and leaves were cut with a scalpel. The plant tissues were placed on a slide with drops of agarose (0.8 w/v) previously tempered. A coverslip was placed on top until they dry. Finally, the samples were placed in the refrigerator until they were observed in the LCSM.

[00350] *Results:*

[00351] After 7 days of growth, CK1-GFP was found in the simple leaves, in the three portions of the stems (FIG. 19, FIG. 20, FIG. 21).

Example 19: Purification and Structural Characterization of CK1 Exopolysaccharides (EPS)

[00352] *EPS Purification*

[00353] The EPS extract was resuspended in doubly distilled water (H2Odd), sonicated, and dialyzed for 16 h (3500 Mw cut-off) against H2Odd. Anion exchange chromatography was then performed on a DE52 column (Whatman, 4057200). The resin was regenerated according to the manufacturer's protocol and the procedure was performed in batch. The fractions were eluted with NaCl (0-0.5 M). The total carbohydrate content in the different fractions was evaluated using the phenol-sulfuric acid method. The presence of DNA and proteins in each fraction was determined by measuring absorbance at 260 and 280 nm, respectively. The fractions containing carbohydrates were collected, dialyzed, and lyophilized for further analysis.

[00354] *MRI Analysis*

[00355] The samples of EPS (≈ 50 mg) were dissolved in 500 µL of D2O and measured in a nuclear magnetic resonance (NMR) spectrometer advance III 600 MHz (Bruker, Germany). Unidimensional 1 H and two-dimensional spectra 1 H-13 C heteronuclear single quantum coherence (HSQC), 1 H-1 H total correlated spectroscopy (TOCSY), 1 H–13C heteronuclear multiple bond correlation (HMBC) and 1 H–1H nuclear overhauled effect spectroscopy (NOESY). To analyze the composition of monosaccharides samples were previously hydrolyzed with TFA 2 N for 2 h at 100 ° C (2). The hydrolysate was dried in a lyophilizer and finally resuspended in 500 mL of sodium phosphate buffer (100 mM dissolved in D 2 O,

pH: 7.4), supplemented with 3-trimethylsilyl- [2,2,3,3,-2H4]-propionate (TSP) (final concentration 0.33 mM), as a reference of chemical displacement, for NMR analysis.

[00356] *Determination of neutral and acidic sugars by HPAEC-PAD*

[00357] The samples were diluted in 200 µL of H2Odd. They were then hydrolyzed. The hydrolysate was dried in a lyophilizer and resuspended in 300 µL of H2Odd. A high-performance anion exchange chromatography (HPAEC-PAD) was then performed on a Bio LC DX-3000 (Dionex) device using an amperometric pulse detector using the Carbopac P20 column with P20 pre-column (Dionex). For the determination of neutral sugars and amino sugars, NaOH 200 mM was used as solvent A and H2Odd was used as solvent B. An isocratic program was performed in 8 % A and 92 % B. For the determination of acidic sugars NaOH 200 mM was used as solvent A, H2Odd was used as solvent B and 1M NaAcO was used as solvent C. An isocratic program was performed in 25 % A, 10 % C, 65% B at a flow of 0.4 mL/min.

[00358] D-glucosamine (Sigma), L-fucose (Sigma), D-mannose (Sigma), D-galactose (Sigma), D-galacturonic acid (Sigma), D-glucuronic acid (Sigma), sialic acid (Sigma), D-glucose (Merck), and an acid-containing alginate hydrolysate were used as standards. Alternatively, D-manuronic acid and D-guluronic acid were used as standards. The sugars were dried in a vacuum desiccator for 48 h. The dry cores were weighed to prepare solutions from which the necessary dilutions for analysis were made. The solutions were stored at –20 °C.

[00359] *Analysis by gas chromatography coupled to mass spectrometry (GC-MS)*

[00360] The polysaccharide was methylated by the NaOH/CH 3I method. The sample (≈ 5 mg) was dissolved in dimethyl sulfoxide (0.5 mL), fine NaOH powder (20 mg), and methyl iodide (0.1 mL). The mixture was stirred for 6 minutes in a closed tube at 25 °C. Then, H2Odd (1 mL) and chloroform (1 mL) were added. The chloroformic fas was isolated and washed with H2Odd (3 x 10 mL). It eventually evaporated to dryness. The methylated polysaccharide was hydrolyzed by the procedure described above. The resulting O-methylated monosaccharides were reduced to the corresponding alditols by dissolving them in 95% ethanol and adding aqueous NaBD4 (in 1 M NH4OH) for 2 h at room temperature. An acetic acid/methanol solution (1:9 v /v) was then added and evaporated at room temperature. Three washes and evaporations with acetic acid/methanol 1:9 (V/V) and two washes and evaporations with methanol were performed. The O- methylated alditols were O-acetylated with acetic anhydride for 3 h at 100 °C. Finally, O-methylated and O-acetylated alditols were extracted in methylene chloride and evaporated to dryness. The products were analyzed by GC-MS with a 30 m HP5 column in splitless mode (HP). The following temperature schedule was followed: two minutes at 60 °C, then an increase to 120 °C (10 °C/min) holding for 2 min at 120 °C, then an increase up to 280 °C (3 °C/min) and finally remained at 280 °C for 5 min. Mass spectra were recorded continuously by scanning from 40 to 1000 m/z. The operating parameters of the MS were: ionization voltage of 70 eV, electron multiplier energy of 1600 V, and ion source temperature of 200 °C.

[00361] *Results*

[00362] *EPS Purification*

[00363] As a result of anion exchange chromatography, the profile of Figure 22 was obtained. A peak of the majority carbohydrate concentration was observed at 200 mM NaCl (fractions 11 to 14). The purification was carried out in triplicate, obtaining in all cases similar results. Fractions 11 to 14 of the three trials were combined to continue further analysis (purified EPS).

[00364] *Determination of the composition of monosaccharides*

[00365] *MRI Analysis*

[00366] A ^{1}H NMR spectrum was performed on an aliquot portion of purified EPS (Fig. 23). As a result, eight resonances belonging to anomeric protons could be identified. (Fig. 23, signals A-H). This result indicates that the EPS is made up of at least eight residues of sugars different or in different conformations.

[00367] In order to determine the identity of the monosaccharides constituting EPS, a spectrum ^{1}H-13 C-HSQC was performed from a previously hydrolyzed sample (Fig. 24). From the spectrum obtained, and by comparison with public databases, the following monosaccharides were identified: D-Glucose, D-Mannose, D-Galactose, and D-Glucosamine. To confirm the assignment, ^{1}H-^{13}C-HSQC spectra were performed with the corresponding patterns (Fig. 24). The results confirmed the identity of the monosaccharides found. Table 47 shows the relationship of areas between the anomeric gates of each residue.

Table 47: Area Ratio between anomeric protons identified by ^{1}H NMR

Residue	Area Relationship
A	5
B	5
C	5
D	5
And	5
F	5
G	1
H	1

[00368] *Analysis by HPAEC-PAD*

[00369] *Neutral sugars and amino sugars*

[00370] In order to confirm the previous results, an analysis of the composition of monosaccharides by HPAEC-PAD was performed. An aliquot of the purified EPS was subjected to hydrolysis, as previously described, and diluted 1:5. The following were used as witnesses: D- Fucose (Fuc, 3.16 min); D-Glucosamine (GlcNH2, 6.21 min); D-Galactose (Gal, 7.60 min); D-Glucose (Glc, 8.25 min) and D-Mannose (Man, 9.25 min) (Fig. 25).

[00371] Additionally, the presence of acidic sugars was analyzed (Fig. 26). The results did not show the presence of any acidic monosaccharide. The following were used as witnesses: ac. sialic 3.35 min; GalA 11.50 min; GulA 12.60 min; GlcA 15.20 min; ManA 16.86 min.

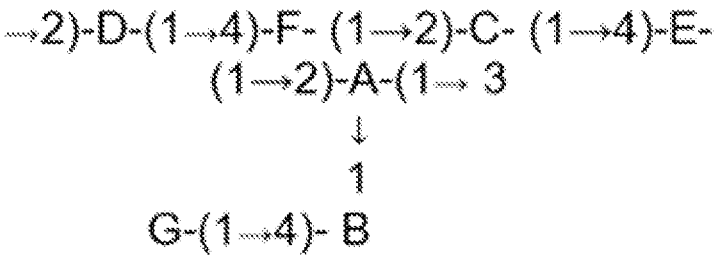
[00372] As a result of this analysis, it was confirmed that the EPS sample showed the presence of D-Glucosamine, D-Galactose, D-Glucose and D-Mannose in a ratio of 1:10:6:16, respectively. No acid sugars were identified among the components of EPS.

[00373] *Structural Analysis of EPS*

[00374] *MRI Analysis*

[00375] In order to characterize the structure of the EPS and determine the sequence, anomeric configurations and ramifications, the following NMR experiments were performed: ^{1}H-^{13}C-HSQC, ^{1}H-^{1}H-TOCSY, ^{1}H-^{13}C-HMBC, and ^{1}H–^{1}H-NOESY.

[00376] Figure 27 illustrates a region of spectro ^{1}H-^{13}C-HSQC of purified EPS where the resonances of ^{1}H and ^{13}C anomeric are appreciated. Figure 28 shows a region of spectrum ^{1}H-^{1}H-TOCSY (mixing time 200 ms), and Figure 29 shows the corresponding region of spectrum ^{1}H–^{1}H-NOESY (mixing time 300 ms). From these spectra it was possible to determine the sequence and branching of the EPS resulting in the following connectivity:



[00377] *Analysis by GC-MS*

[00378] In order to confirm the results obtained by NMR, an analysis by GC-MS of the monosaccharides derived from the purified EPS was performed. The results obtained are presented in Figure 30 and Table 48.

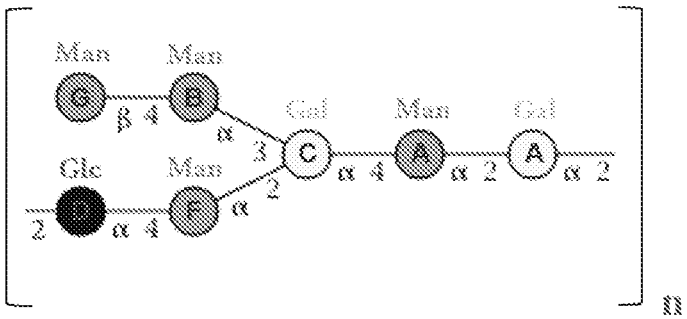
Table 48: GC-MS analysis of monosaccharides derived from purified EPS

	Methylated and Acetylated Derivative	Retention time (min)	Type of Union	Mass Fragments (m/Z)
1	1,2,5-Tri-O-acetyl-3,4,6-tri-O-methyl-D-glucose	22.16	→2)-Glcp-(1→	189, 161, 129, 87
2	1,5-Di-O-acetyl-2,3,4,6-tetra-O-methyl-D-manosa	22.77	Manp-(1→	205, 161, 145, 129, 101, 87
3	1,2,5-Tri-O-acetyl-4,3,6-tri-O-methyl-D-galactosa	25.48	→2)-Galp-(1→	189, 161, 145, 129, 101
4	1,4,5-Tri-O-acetyl-2,3,6-tri-O-methyl-D-manosa	25.54	→4)-Manp-(1→	233, 117, 101, 99
5	1,2,3,5-Tetra-O-acetyl-4,6-di-O-methyl-D-galactose	25.65	→2)-3)-Galp-(1→	261, 202, 161, 129, 101, 87

[00379] The mass spectra of the identified species confirmed the presence of monosaccharides previously assigned by NMR and HPAEC-PAD. Additionally, these results provided information on the connectivity between EPS residues which is consistent with NMR results.

[00380] *Conclusions and Model*

[00381] From the results, the following model of the EPS structure was obtained:



[00382] This model satisfies the experimental data of NMR, GC-MS, HPAEC-PAD, and the relationships of the monosaccharide constituents of EPS. Although the data indicated the presence of glucosamine in the polysaccharide, it was not possible to obtain experimental information that demonstrates its connectivity with the rest of the molecule. This is mainly due to its low ratio in EPS (1:16 with respect to Mannose) and its low signal intensity in NMR experiments (e.g., FIG. 23 and Fig. 27).

[00383] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments described herein may be employed. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

CLAIMS

WHAT IS CLAIMED IS:

1. A composition comprising a microorganism and at least one seed formulation component, wherein the microorganism is selected from *Klebsiella sp.*, *Bacillus cereus*, *Exiguobacterium undeae,* or a combination thereof.

2. The composition of claim 1, wherein the seed formulation component is an adjuvant, an additive, or a stabilizer.

3. The composition of claim 1 or claim 2, wherein the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum.

4. The composition of any one of claims 1 to 3, further comprising one or more of peptone, tryptone, or meat extract.

5. The composition of any one of claims 1 to 4, wherein the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml.

6. The composition of any one of claims 1 to 4, wherein the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml.

7. The composition of any one of claims 1 to 6, wherein the microorganism is selected from *Klebsiella aerogenes, Bacillus cereus*, *Exiguobacterium undeae,* or a combination thereof.

8. The composition of claim 7, wherein the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof.

9. The composition of claim 8, wherein the strain CK1 has a DSMZ accession number DSM 34332.

10. The composition of any one of claims 7 to 9, wherein the *Bacillus cereus* is a strain CK2 or a derivative thereof.

11. The composition of claim 10, wherein the strain CK2 has a DSMZ accession number DSM 34322.

12. The composition of any one of claims 7 to 11, wherein the *Exiguobacterium undeae,* is a strain CK3 or a derivative thereof.

13. The composition of claim 12, wherein the strain CK3 has a DSMZ accession number DSM 34323.

14. The composition of any one of claims 1 to 13, wherein the composition has a shelf life of at least about 6 months.

15. The composition of any one of claims 1 to 14, wherein the composition is a liquid.

16. The composition of any one of claims 1 to 15, wherein the composition confers anti-fungal activity.

17. The composition of claim 16, wherein the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*.

18. The composition of any one of claims 1 to 17, wherein the composition confers plant growth regulatory activity.

19. The composition of any one of claims 1 to 18, wherein the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification.

20. The composition of claim 19, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25.

21. The composition of any one of claims 1 to 20, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29.

22. The composition of any one of claims 1 to 21, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35.

23. The composition of any one of claims 1 to 22, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa).

24. The composition of any one of claims 1 to 23, wherein the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification.

25. The composition of claim 24, wherein the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26.

26. The composition of any one of claims 1 to 25, wherein the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29.

27. The composition of any one of claims 1 to 26, wherein the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46.

28. The composition of any one of claims 1 to 27, comprising a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU).

29. The composition of any one of claims 1 to 28, wherein the composition is suitable to be applied to the seeds in combination with a second seed treatment optionally comprising a nutrient or a pesticide.

30. The composition of any one of claims 1 to 29, wherein the composition is suitable to be applied to the seeds with a liquid or solid carrier.

31. The composition of any one of claims 1 to 30, wherein the microorganism is present as a granule, a capsule, a dust, a powder, a slurry, a film, a liquid suspension, or a combination thereof.

32. A composition comprising a microorganism isolated from a plant growing in the high desert and at least one seed formulation component.

33. The composition of claim 32, wherein the microorganism is isolated from a plant growing in Puna de Atacama.

34. The composition of claim 32 or claim 33, wherein the microorganism is isolated from a soil, a sediment, or a rhizosphere of the plant.

35. The composition of any one of claims 32 to 34, wherein the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*.

36. The composition of any one of claims 32 to 35, wherein the bacterium is *Klebsiella aerogenes*, *Bacillus cereus*, or *Exiguobacterium undeae*.

37. The composition of claim 36, wherein the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof.

38. The composition of claim 37, wherein the strain CK1 has a DSMZ accession number DSM 34332.

39. The composition of any one of claims 36 to 38, wherein the *Bacillus cereus* is a strain CK2 or a derivative thereof.

40. The composition of claim 39, wherein the strain CK2 has a DSMZ accession number DSM 34322.

41. The composition of any one of claims 36 to 40, wherein the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof.

42. The composition of claim 41, wherein the strain CK3 has a DSMZ accession number DSM 34323.

43. The composition of any one of claims 32 to 40, wherein the seed formulation component is selected from one or more of polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum.

44. The composition of any one of claims 32 to 41, further comprising one or more of peptone, tryptone, or meat extract.

45. The composition of any one of claims 32 to 44, wherein the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml.

46. The composition of any one of claims 32 to 44, wherein the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml.

47. The composition of any one of claims 32 to 45, wherein the composition has a shelf life of at least about 6 months.

48. The composition of any one of claims 32 to 46, wherein the composition is a liquid.

49. The composition of any one of claims 32 to 48, wherein the composition confers anti-fungal activity.

50. The composition of claim 49, wherein the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*.

51. The composition of any one of claims 32 to 50, wherein the composition confers plant growth regulatory activity.

52. The composition of any one of claims 32 to 51, wherein the seed treatment comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification.

53. The composition of claim 52, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25.

54. The composition of any one of claims 32 to 53, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29.

55. The composition of any one of claims 32 to 54, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35.

56. The composition of any one of claims 32 to 55, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa).

57. The composition of any one of claims 32 to 56, wherein the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification.

58. The composition of claim 57, wherein the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26.

59. The composition of any one of claims 32 to 58, wherein the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29.

60. The composition of any one of claims 32 to 59, wherein the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46.

61. The composition of any one of claims 32 to 60, comprising a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU).

62. The composition of any one of claims 32 to 61, wherein the composition is suitable to be applied to the seeds in combination with a second seed treatment, optionally comprising a nutrient or a pesticide.

63. The composition of any one of claims 32 to 62, wherein the composition is suitable to be applied to the seeds with a liquid or a solid carrier.

64. The composition of any one of claims 32 to 63, wherein the microorganism is present as a granule, a capsule, a dust, a powder, a slurry, a film, a liquid suspension, or a combination thereof.

65. The composition of any one of claims 1 to 64, wherein the composition further comprises water.

66. A treated seed comprising a plant seed and the composition of any one of claims 1 to 65.

67. A plant grown from the treated seed of claim 66.

68. A method of controlling fungal growth, the method comprising contacting a plant seed to the composition of any one of claims 1 to 65; and germinating the plant seed under a condition capable of exposing the plant seed to a fungus, whereby the seed treatment reduces growth of the fungus on or around the plant seed.

69. A method of protecting plant health, the method comprising contacting a plant seed to the composition of any one of claims 1 to 65; whereby germination rate, quality of germinated seed, or a combination thereof is improved as compared to an untreated plant seed.

70. A method of increasing crop yield, the method comprising contacting a set of plant seeds to the composition of any one of claims 1 to 65; planting the set; growing plants from the planted set to harvest; and harvesting the plants or a portion thereof, wherein the crop yield is increased as compared to crop yield from an untreated set of plant seeds.

71. A method of promoting growth of a plant, the method comprising contacting seed of the plant to the composition of any one of claims 1 to 65; germinating the seed of the plant; and growing the resulting plant for a time period sufficient to develop leaves and roots, whereby biomass of the plant, root development of the plant, or a combination thereof is improved compared to a plant grown from an untreated seed.

72. The method of claim 71, wherein root development comprises length of the roots, number of lateral roots, or a combination thereof.

73. A method of increasing fertility of a soil, the method comprising contacting a plurality of seeds of a plant to the composition of any one of claims 1 to 65; planting the plurality of seeds in the soil; and growing a plurality of plants grown from the plurality of seeds in the soil, thereby increasing the fertility of the soil.

74. The method of any one of claims 68 to 73, wherein the composition is contacted to the seeds in a liquid or solid carrier.

75. The method of any one of claims 68 to 74, wherein the composition is contacted to the seeds in combination with a second seed treatment composition.

76. The method of claim 75, wherein the second seed treatment composition comprises a nutrient or a pesticide.

77. The method of any one of claims 68 to 76, wherein the seeds are monocotyledons.

78. The method of any one of claims 68 to 76, wherein the seeds are dicotyledons.

79. The method of any one of claims 68 to 78, wherein the seeds are soybean seeds, corn seeds, wheat seeds, or a combination thereof.

80. The method of any one of claims 68 to 79, wherein the composition is contacted to the seeds by a means selected from aerosol application, spray-dried application, liquid application, powder

application, mist application, atomized application, semi-solid application, gel application, coating application, lotion application, linked or linker material application, material application, in-furrow application, spray application, irrigation, injection, dusting, pelleting, coating of the plant, coating of the plant seed, or coating of the planting medium.

81. A method of preparing a seed treatment, the method comprising growing a microorganism selected from a genus of *Klebsiella, Bacillus*, *Exiguobacterium*, or a combination thereof to from about 1 x 10^4 CFU to about 1 x 10^{10} CFU/g in a liquid media; and preparing a composition comprising a liquid media, the microorganism, at least one formulation component selected from polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum.

82. The method of claim 81, wherein the microorganism is *Klebsiella aerogenes*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof.

83. The method of claim 82, wherein the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof.

84. The method of claim 83, wherein the strain CK1 has a DSMZ accession number DSM 34332.

85. The method of any one of claims 82 to 84, wherein the *Bacillus cereus* is a strain CK2 or a derivative thereof.

86. The method of claim 85, wherein the strain CK2 has a DSMZ accession number DSM 34322.

87. The method of any one of claims 82 to 86, wherein the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof.

88. The method of claim 87, wherein the strain CK3 has a DSMZ accession number DSM 34323.

89. The method of any one of claims 81 to 88, further comprising applying the seed treatment to a plant seed.

90. The method of any one of claims 81 to 89, wherein the liquid media comprises one or more of peptone, tryptone, or meat extract.

91. The method of any one of claims 81 to 90, wherein the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml.

92. The method of any one of claims 81 to 90, wherein the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml.

93. The method of any one of claims 81 to 92, wherein the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml for at least 6 months at 25 °C.

94. The method of any one of claims 81 to 92, wherein the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml for at least 6 months at a temperature from about 20 °C to about 35 °C.

95. The method of any one of claims 81 to 92, wherein the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml for at least 6 months at 25 °C.

96. The method of any one of claims 81 to 92, wherein the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml for at least 6 months at a temperature from about 20 °C to about 35 °C.

97. A composition comprising a microorganism and at least one soil or plant amendment component, wherein the microorganism is selected from *Klebsiella*, *Bacillus cereus*, *Exiguobacterium undeae,* or a combination thereof.

98. The composition of claim 97, wherein the soil or plant amendment comprises polyvinylpyrrolidone (PVP), gum Arabic, or Xanthan gum.

99. The composition of claim 97 or claim 98, further comprising one or more of peptone, tryptone, or meat extract.

100. The composition of any one of claims 97 to 99, wherein the microorganism is present at a concentration of greater than about 1 x 10^8 CFU/ml.

101. The composition of any one of claims 97 to 99, wherein the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml.

102. The composition of any one of claims 96 to 101, wherein the microorganism is selected from *Klebsiella aerogenes, Bacillus cereus*, *Exiguobacterium undeae,* or a combination thereof.

103. The composition of claim 102, wherein the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof.

104. The composition of claim 103, wherein the strain CK1 has a DSMZ accession number DSM 34332.

105. The composition of any one of claims 102 to 104, wherein the *Bacillus cereus* is a strain CK2 or a derivative thereof.

106. The composition of claim 105, wherein the strain CK2 has a DSMZ accession number DSM 34322.

107. The composition of any one of claims 102 to 106, wherein the *Exiguobacterium undeae,* is a strain CK3 or a derivative thereof.

108. The composition of claim 107, wherein the strain CK3 has a DSMZ accession number DSM 34323.

109. The composition of any one of claims 97 to 108, wherein the composition has a shelf life of at least about 6 months.

110. The composition of any one of claims 97 to 109, wherein the composition is a liquid.

111. The composition of any one of claims 97 to 110, wherein the composition confers anti-fungal activity.

112. The composition of claim 111, wherein the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae*, *Septoria sp.*, or *Sclerotinia sclerotiorum*.

113. The composition of any one of claims 97 to 112, wherein the composition confers plant growth regulatory activity.

114. The composition of any one of claims 97 to 113, wherein the composition comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification.

115. The composition of claim 114, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25.

116. The composition of any one of claims 97 to 115, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29.

117. The composition of any one of claims 97 to 116, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35.

118. The composition of any one of claims 97 to 117, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa).

119. The composition of any one of claims 97 to 118, wherein the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification.

120. The composition of claim 119, wherein the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26.

121. The composition of any one of claims 97 to 120, wherein the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29.

122. The composition of any one of claims 97 to 121, wherein the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46.

123. The composition of any one of claims 97 to 122, comprising a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU).

124. The composition of any one of claims 97 to 123, wherein the composition is suitable for application with a second treatment, optionally comprising a nutrient, a pesticide, or another seed treatment.

125. The composition of any one of claims 97 to 124, wherein the composition further comprises a liquid or a solid carrier.

126. The composition of any one of claims 97 to 125, wherein the microorganism is present as a granule, a capsule, a dust, a powder, a slurry, a film, a liquid suspension, or a combination thereof.

127. A composition comprising a microorganism isolated from a plant growing in the high desert and at least one soil or plant amendment component.

128. The composition of claim 127, wherein the microorganism is isolated from a plant growing in Puna de Atacama.

129. The composition of claim 127 or claim 128, wherein the microorganism is isolated from a soil, a sediment, or a rhizosphere of the plant.

130. The composition of any one of claims 127 to 129, wherein the bacterium is of the genus *Klebsiella*, *Bacillus*, or *Exiguobacterium*.

131. The composition of any one of claims 127 to 130, wherein the bacterium is *Klebsiella aerogenes*, *Bacillus cereus*, or *Exiguobacterium undeae*.

132. The composition of any one of claims 127 to 131, wherein the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof.

133. The composition of claim 132, wherein the strain CK1 has a DSMZ accession number DSM 34332.

134. The composition of any one of claims 127 to 133, wherein the *Bacillus cereus* is a strain CK2 or a derivative thereof.

135. The composition of claim 134, wherein the strain CK2 has a DSMZ accession number DSM 34322.

136. The composition of any one of claims 127 to 135, wherein the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof.

137. The composition of claim 136, wherein the strain CK3 has a DSMZ accession number DSM 34323.

138. The composition of any one of claims 127 to 137, wherein the soil or plant amendment component comprises polyvinylpyrrolidone (PVP), gum Arabic, or Xanthan gum.

139. The composition of any one of claims 127 to 138, further comprising one or more of peptone, tryptone, or meat extract.

140. The composition of any one of claims 127 to 139, wherein the microorganism is present at a concentration of greater than about 1×10^8 CFU/ml.

141. The composition of any one of claims 127 to 139, wherein the microorganism is present at a concentration of from about 1×10^4 CFU/ml to about 1×10^{10} CFU/ml.

142. The composition of any one of claims 127 to 141, wherein the composition has a shelf life of at least about 6 months.

143. The composition of any one of claims 127 to 142, wherein the composition is a liquid.

144. The composition of any one of claims 127 to 143, wherein the composition confers anti-fungal activity.

145. The composition of claim 144, wherein the anti-fungal activity is against one or more of *Macrophomina phaseolina*, *Fusarium sp.*, *Fusarium tucumaniae* *Septoria sp.*, or *Sclerotinia sclerotiorum*.

146. The composition of any one of claims 127 to 145, wherein the composition confers plant growth regulatory activity.

147. The composition of any one of claims 127 to 146, wherein the composition comprises *Klebsiella aerogenes* and wherein the *Klebsiella aerogenes* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification.

148. The composition of claim 147, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a nitrogen pathway signature gene set forth in Table 25.

149. The composition of any one of claims 127 to 148, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a phosphate solubilization signature gene set forth in Table 29.

150. The composition of any one of claims 127 to 149, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* comprises a plant growth regulatory signature gene set forth in Table 35.

151. The composition of any one of claims 127 to 150, wherein the composition comprises *Klebsiella aerogenes* and the *Klebsiella aerogenes* does not produce carbapenemase (KPC), metallo-beta-lactamases (MLB), or oxacillinase (Oxa).

152. The composition of any one of claims 127 to 151, wherein the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a nitrogen pathway signature comprises at least one of assimilatory nitrogen reduction; dissimilatory nitrate reduction; and the absence of all or a portion of nitrogen fixation, nitrification, and denitrification.

153. The composition of claim 152, wherein the *Bacillus cereus* comprises a nitrogen pathway signature gene set forth in Table 26.

154. The composition of any one of claims 127 to 153, wherein the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a phosphate solubilization signature gene set forth in Table 29.

155. The composition of any one of claims 127 to 154, wherein the composition comprises *Bacillus cereus* and the *Bacillus cereus* comprises a plant growth regulatory signature gene set forth in Table 46.

156. The composition of any one of claims 127 to 155, comprising a combination of *Klebsiella aerogenes* and *Bacillus cereus* in a 50:50 ratio (CFU/CFU).

157. The composition of any one of claims 127 to 156, wherein the composition is suitable for application with a second treatment, optionally comprising a nutrient, a pesticide, or another seed treatment.

158. The composition of any one of claims 127 to 157, wherein the composition further comprises a liquid or a solid carrier.

159. The composition of any one of claims 127 to 158, wherein the microorganism is present as a granule, a capsule, a dust, a powder, a slurry, a film, a liquid suspension, or a combination thereof.

160. The composition of any one of claims 97 to 159, wherein the composition further comprises water.

161. A plant grown with the composition of any one of claims 97 to 160.

162. A method of controlling fungal growth, the method comprising contacting a plant to the composition of any one of claims 96 to 160; and growing the plant under a condition capable of exposing the plant to a fungus, whereby the composition reduces growth of the fungus on or around the plant.

163. A method of protecting plant health, the method comprising contacting a plant to the composition of any one of claims 96 to 160; whereby plant growth is improved as compared to an untreated plant.

164. A method of increasing crop yield, the method comprising contacting a set of plants to the composition of any one of claims 96 to 160; growing plants from the set of plants to harvest; and harvesting the plants or a portion thereof, wherein the crop yield is increased as compared to crop yield from an untreated set of plants.

165. A method of promoting growth of a plant, the method comprising contacting the plant to the composition of any one of claims 96 to 160; growing the plant for a time period sufficient to develop leaves and roots, whereby biomass of the plant, root development of the plant, or a combination thereof is improved compared to an untreated plant.

166. The method of claim 165, wherein root development comprises length of the roots, number of lateral roots, or a combination thereof.

167. A method of increasing fertility of a soil, the method comprising contacting a plurality of plants to the composition of any one of claims 96 to 160; and growing a plurality of plants in the soil, thereby increasing the fertility of the soil.

168. The method of any one of claims 162 to 167, wherein the composition is contacted to the plants in a liquid or solid carrier.

169. The method of any one of claims 162 to 168, wherein the composition is contacted to the plants in combination with a second soil or plant amendment composition.

170. The method of claim 169, wherein the second soil or plant amendment composition comprises a nutrient or a pesticide.

171. The method of any one of claims 162 to 170, wherein the plants are monocotyledons.

172. The method of any one of claims 162 to 170, wherein the plants are dicotyledons.

173. The method of any one of claims 162 to 172, wherein the plants are soybean, corn, wheat, or a combination thereof.

174. The method of any one of claims 68 to 173, wherein the composition is contacted to the plants by a means selected from aerosol application, spray-dried application, liquid application, powder application, mist application, atomized application, semi-solid application, gel application, coating application, lotion application, linked or linker material application, material application, in-furrow application, spray application, irrigation, injection, dusting, pelleting, coating of the plant, coating of the plant seed, or coating of the planting medium.

175. A method of preparing a soil or plant amendment, the method comprising growing a microorganism selected from a genus of *Klebsiella, Bacillus*, *Exiguobacterium*, or a combination thereof

to at least 1 x 10^8 CFU/g in a liquid media; and preparing a composition comprising a liquid media, the microorganism, at least one formulation component selected from polyvinylpyrrolidone (PVP), gum Arabic, and Xanthan gum.

176. The method of claim 175, wherein the microorganism is *Klebsiella aerogenes*, *Bacillus cereus*, *Exiguobacterium undeae*, or a combination thereof.

177. The method of claim 176, wherein the *Klebsiella aerogenes* is a strain CK1 or a derivative thereof.

178. The method of claim 177, wherein the strain CK1 has a DSMZ accession number DSM 34332.

179. The method of any one of claims 175 to 178, wherein the *Bacillus cereus* is a strain CK2 or a derivative thereof.

180. The method of claim 179, wherein the strain CK2 has a DSMZ accession number DSM 34322.

181. The method of any one of claims 175 to 180, wherein the *Exiguobacterium undeae* is a strain CK3 or a derivative thereof.

182. The method of claim 181, wherein the strain CK3 has a DSMZ accession number DSM 34323.

183. The method of any one of claims 175 to 182, further comprising applying the seed treatment to a plant seed.

184. The method of any one of claims 175 to 183, wherein the liquid media comprises one or more of peptone, tryptone, or meat extract.

185. The method of any one of claims 175 to 184, wherein the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml.

186. The method of any one of claims 175 to 184, wherein the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml.

187. The method of any one of claims 175 to 186, wherein the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml for at least 6 months at 25 °C.

188. The method of any one of claims 175 to 186, wherein the microorganism is present at a concentration of greater than 1 x 10^8 CFU/ml for at least 6 months at a temperature from about 20 °C to about 35 °C.

189. The method of any one of claims 175 to 186, wherein the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml for at least 6 months at 25 °C.

190. The method of any one of claims 175 to 186, wherein the microorganism is present at a concentration of from about 1 x 10^4 CFU/ml to about 1 x 10^{10} CFU/ml for at least 6 months at a temperature from about 20 °C to about 35 °C.

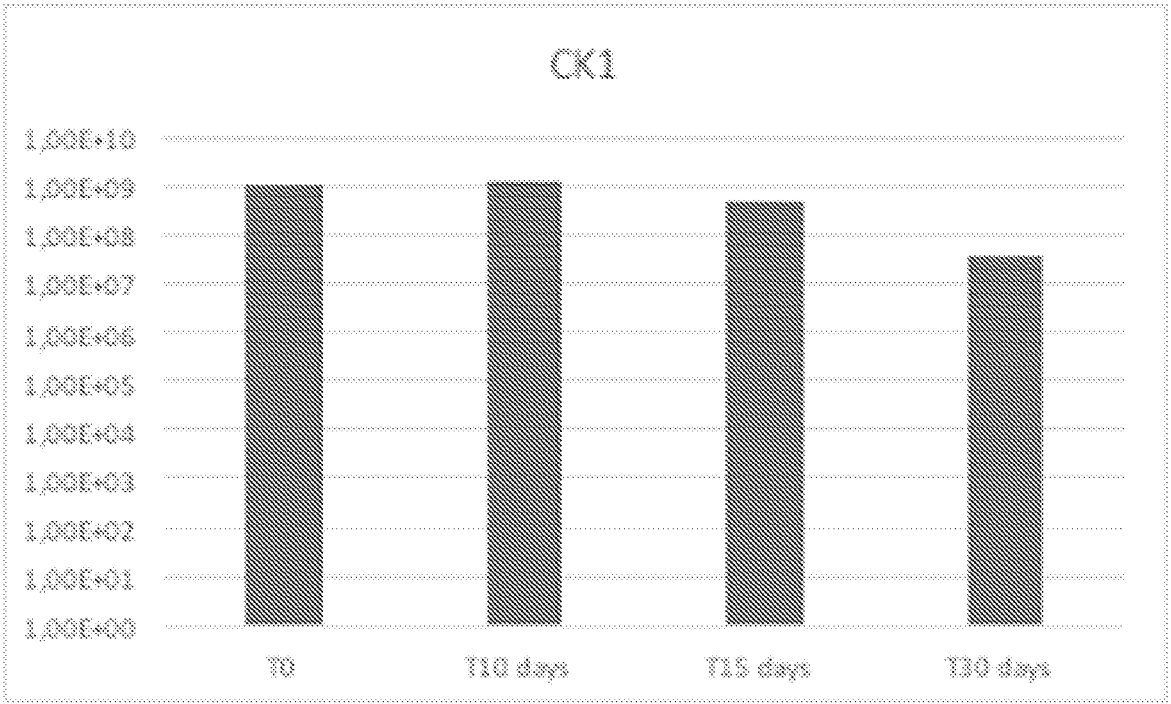


FIG. 1

DNS (dinitrosalicylic acid reaction)

M1 before being sterilized by autoclave 3,04g/L M1 after being sterilized by autoclave 2,51g/L	18%
M2 before being sterilized by autoclave 3,05g/L M2 after being sterilized by autoclave 2,97g/L	2,6%

FIG. 2

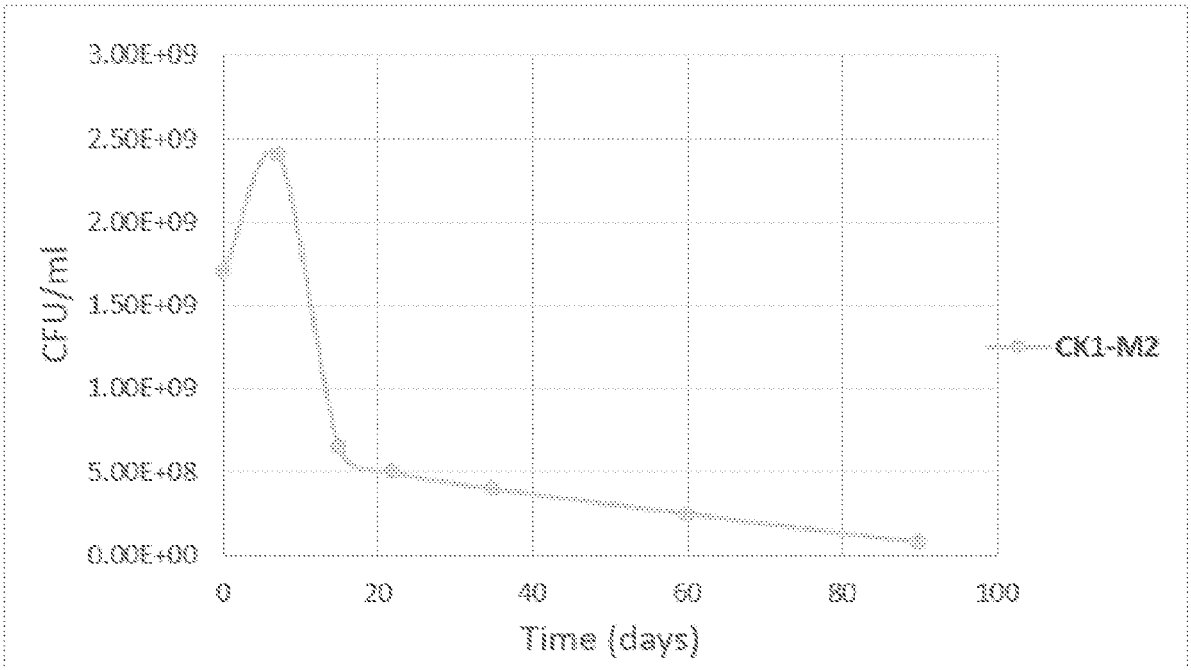

3.00E+09
2.50E+09
2.00E+09
1.50E+09
1.00E+09
5.00E+08
0.00E+00
CFU/ml
0
20
40
60
80
100
Time (days)
CK1-M2

FIG. 3

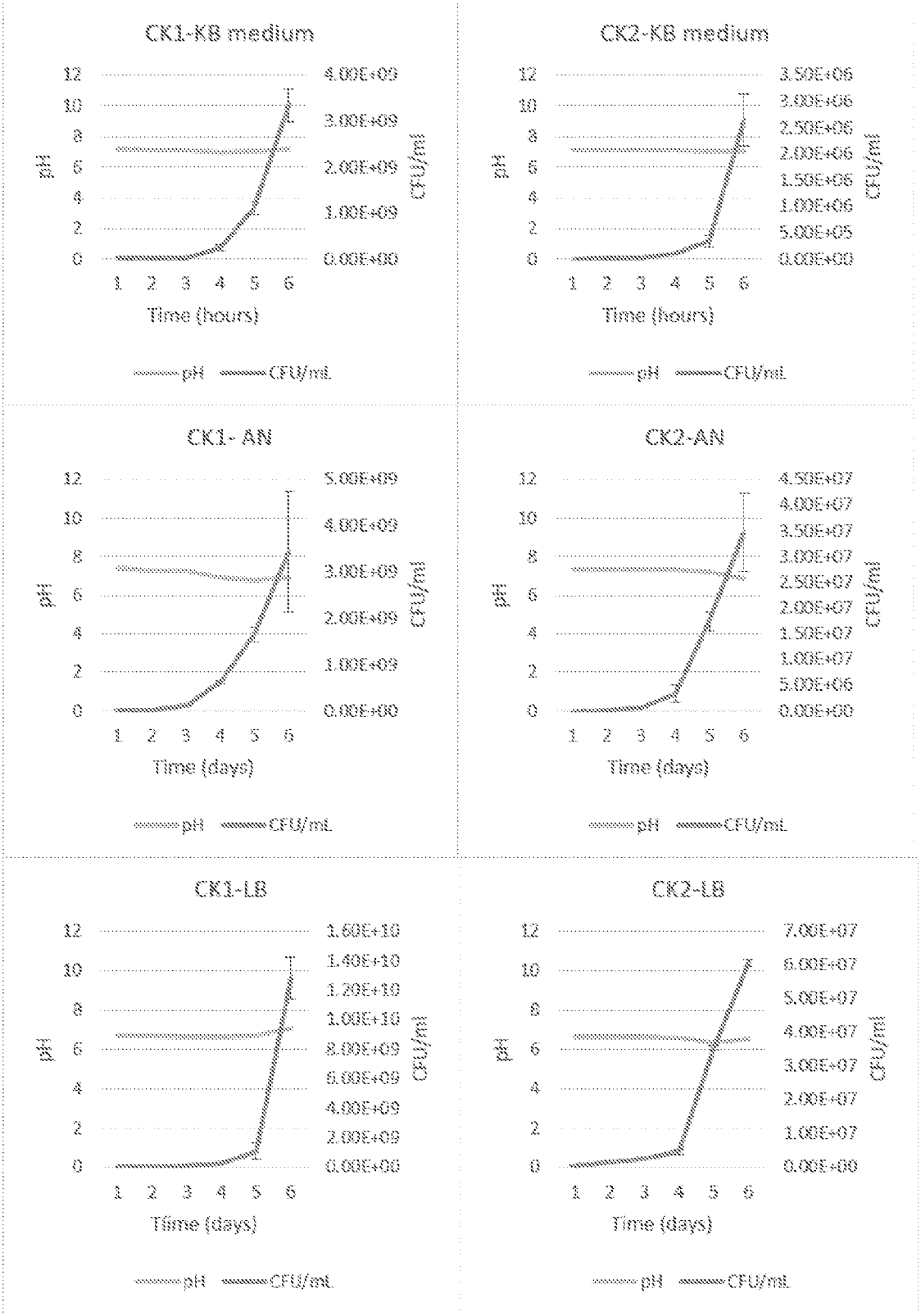

CK1-KB medium
pH
CFU/ml
Time (hours)
pH
CFU/mL
CK2-KB medium
pH
CFU/ml
Time (hours)
pH
CFU/mL
CK1- AN
pH
CFU/ml
Time (days)
pH
CFU/mL
CK2-AN
pH
CFU/ml
Time (days)
pH
CFU/mL
CK1-LB
pH
CFU/ml
Tfime (days)
pH
CFU/mL
CK2-LB
pH
CFU/ml
Time (days)
pH
CFU/mL

FIG. 4

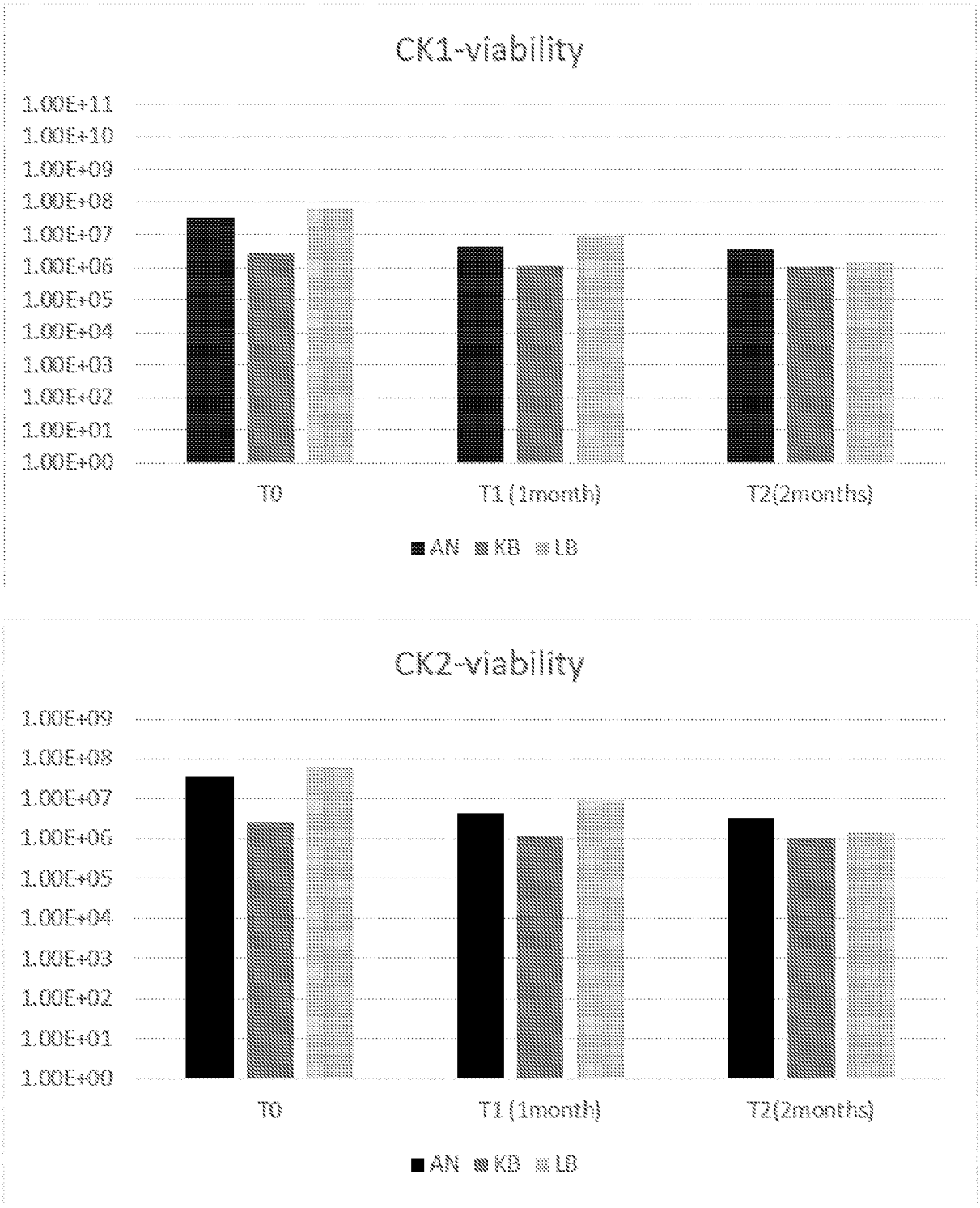

CK1-viability
1.00E+11
1.00E+10
1.00E+09
1.00E+08
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
1.00E+01
1.00E+00
T0
T1 (1month)
T2(2months)
AN
KB
LB
CK2-viability
1.00E+09
1.00E+08
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
1.00E+01
1.00E+00
T0
T1 (1month)
T2(2months)
AN
KB
LB

FIG. 5

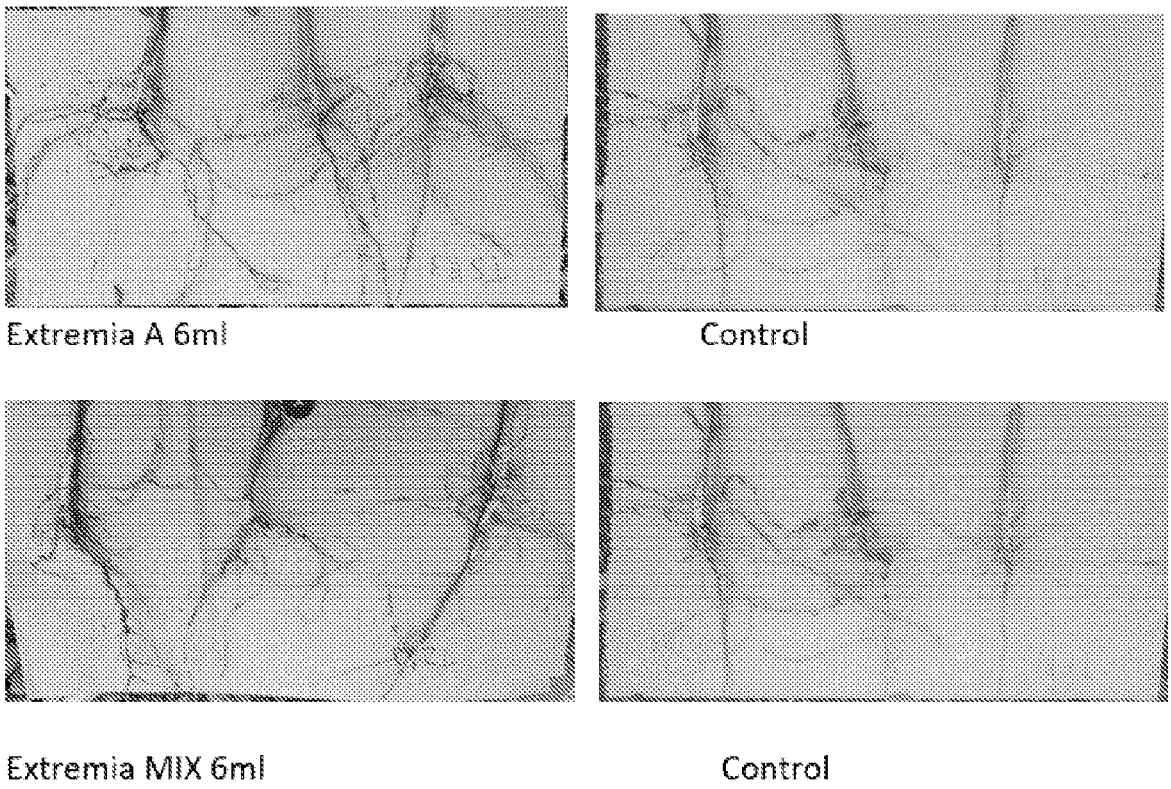
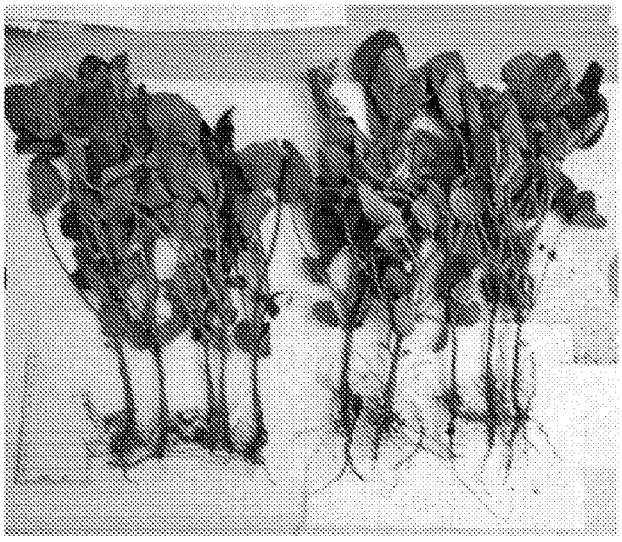


FIG. 6

Control vs Extremia MIX 6ml



Control vs Extremia A 6ML

Control vs Extremia MIX 5ml

FIG. 7

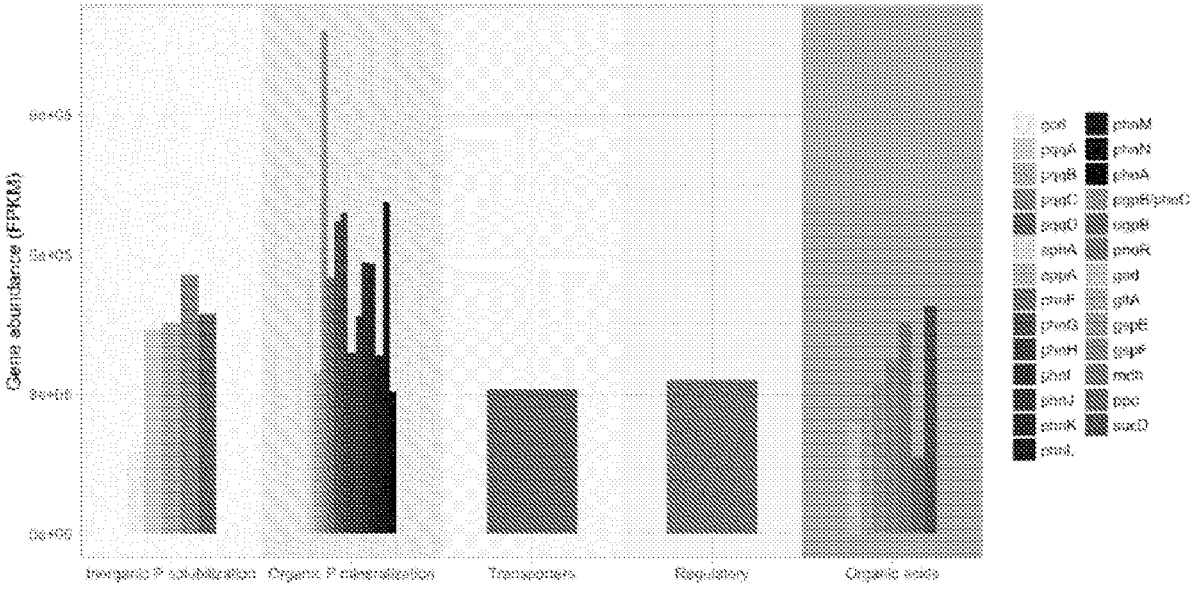

Gene abundance (FPKM)
Inorganic P solubilization
Organic P mineralization
Transporters
Regulatory
Organic acids
gcd
pqqA
pqqB
pqqC
pqqD
sqhA
sqhA
pstA
pstB
pstC
pstS
ugpB
ugpA
ugpE
ugpC
phoA
phoD
phoN
phyC
phoP
phoR
gltA
gspE
gspF
mdh
ppc
sucD

FIG. 8

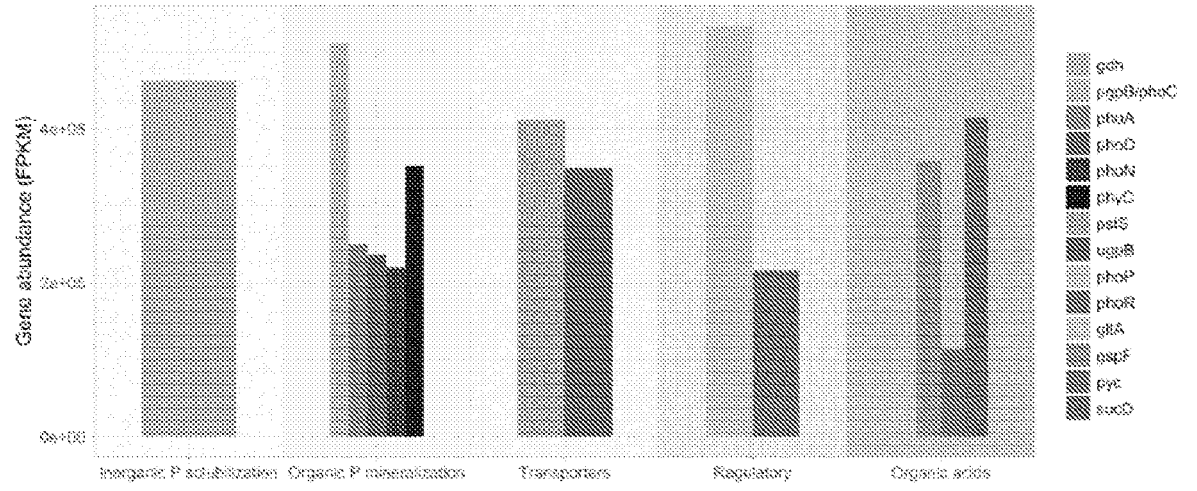

Gene abundance (FPKM)
Inorganic P solubilization
Organic P mineralization
Transporters
Regulatory
Organic acids
gcd
pqqB/phoC
phoA
phoD
phoN
phyC
pstS
ugpB
phoP
phoR
gltA
gspE
pyc
sucD

FIG. 9

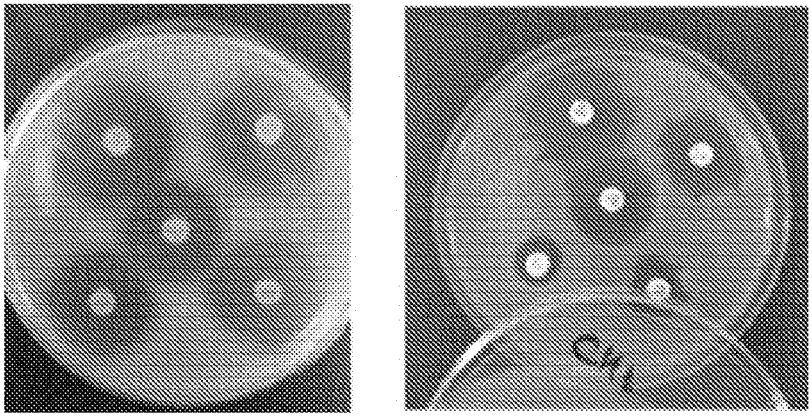


FIG. 10

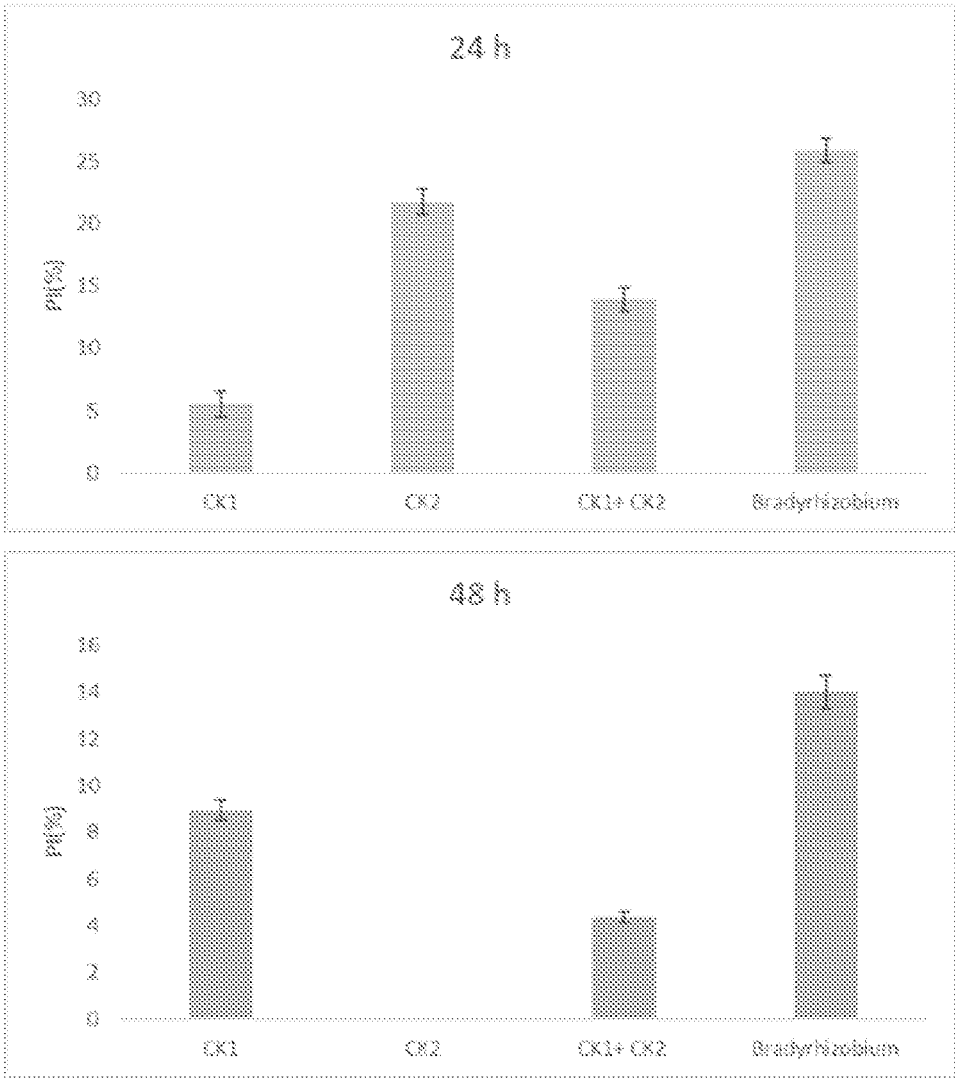

24 h
30
25
20
15
10
5
0
CK1
CK2
CK1+ CK2
48 h
16
14
12
10
8
6
4
2
0
CK1
CK2
CK1+ CK2

FIG. 11

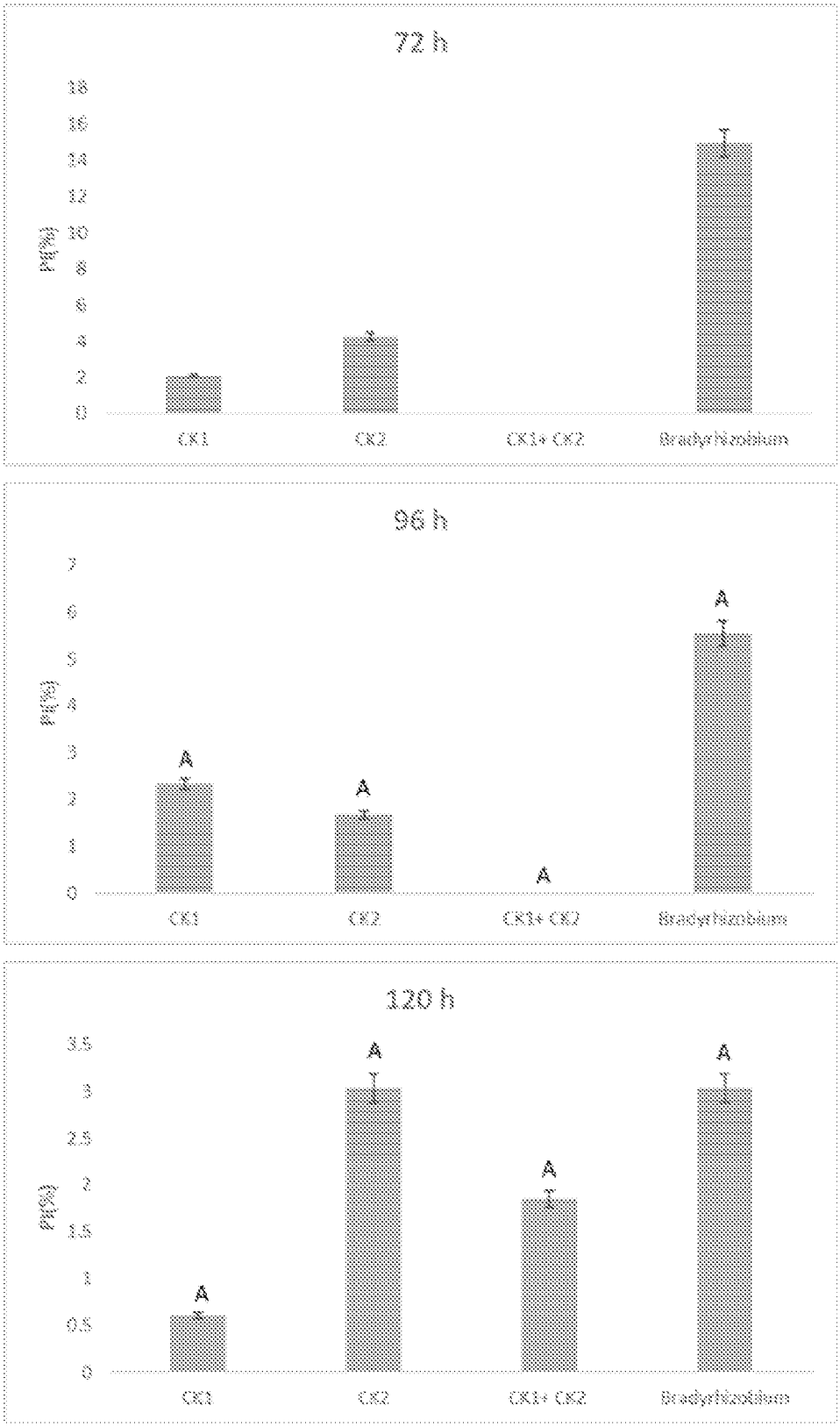


FIG. 11 (continued)

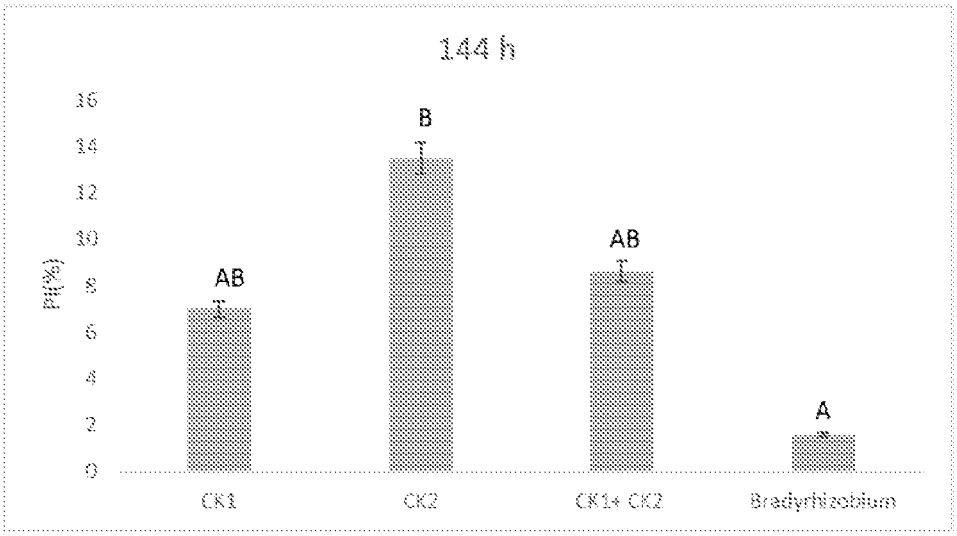


FIG. 11 (continued)

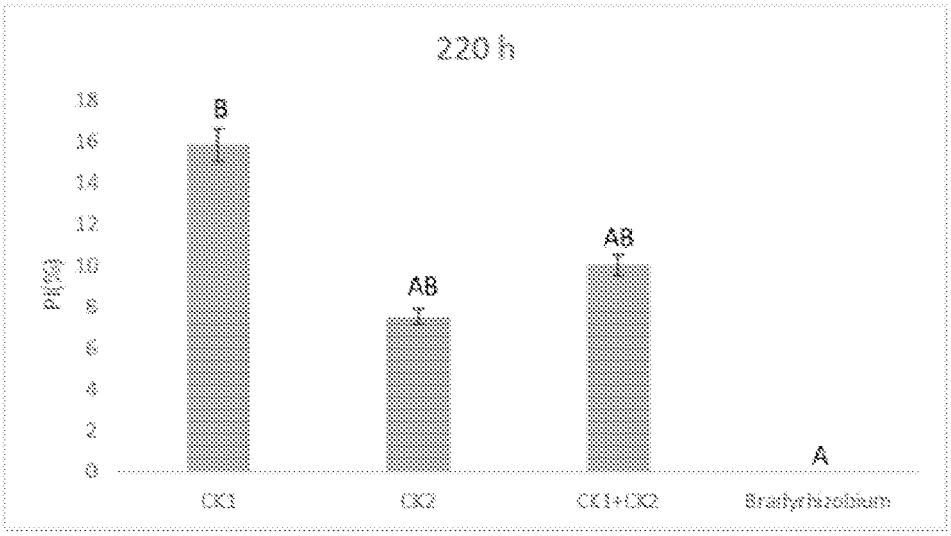


FIG. 12

FIG. 13

FIG. 14

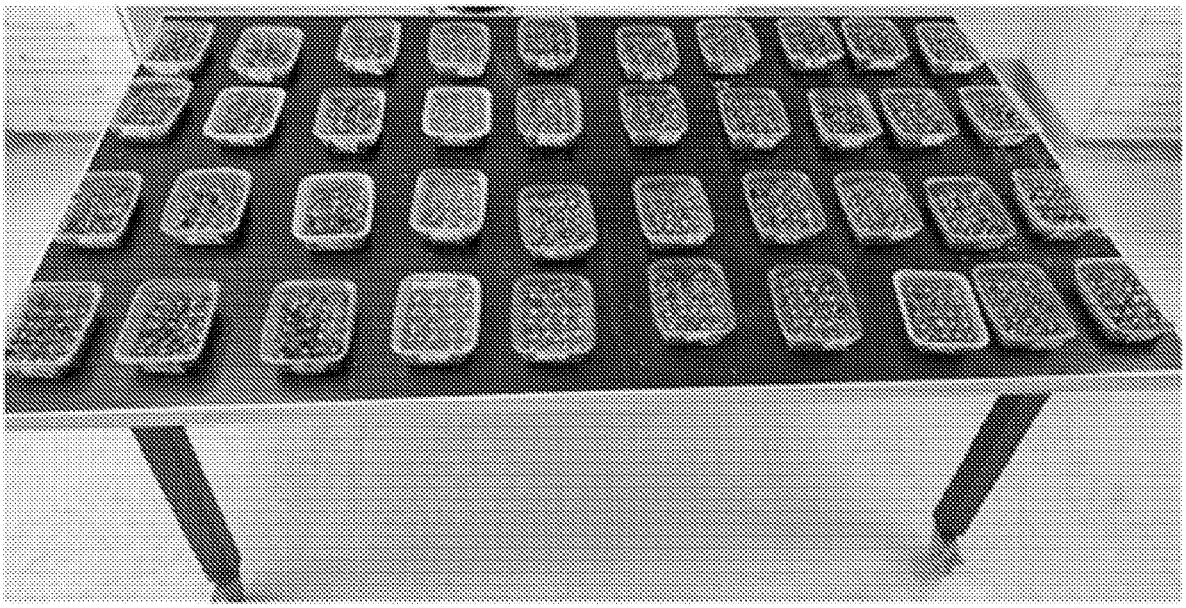


FIG. 15

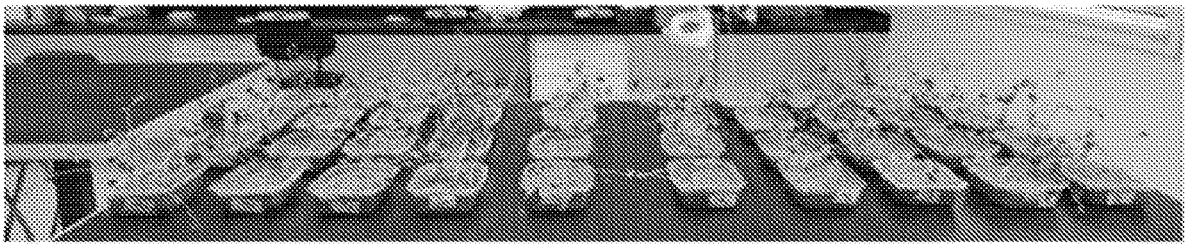


FIG. 16

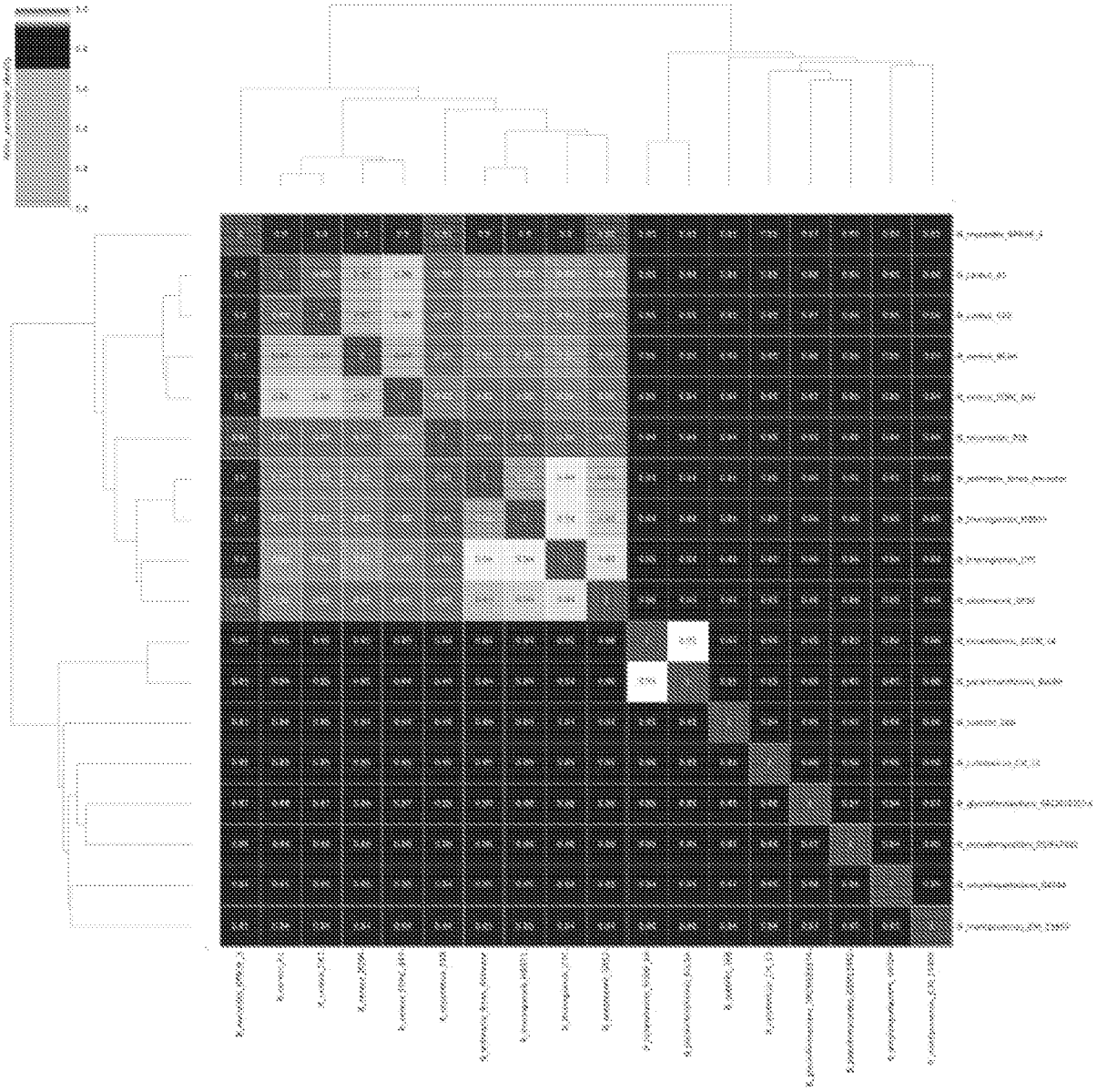


FIG. 17

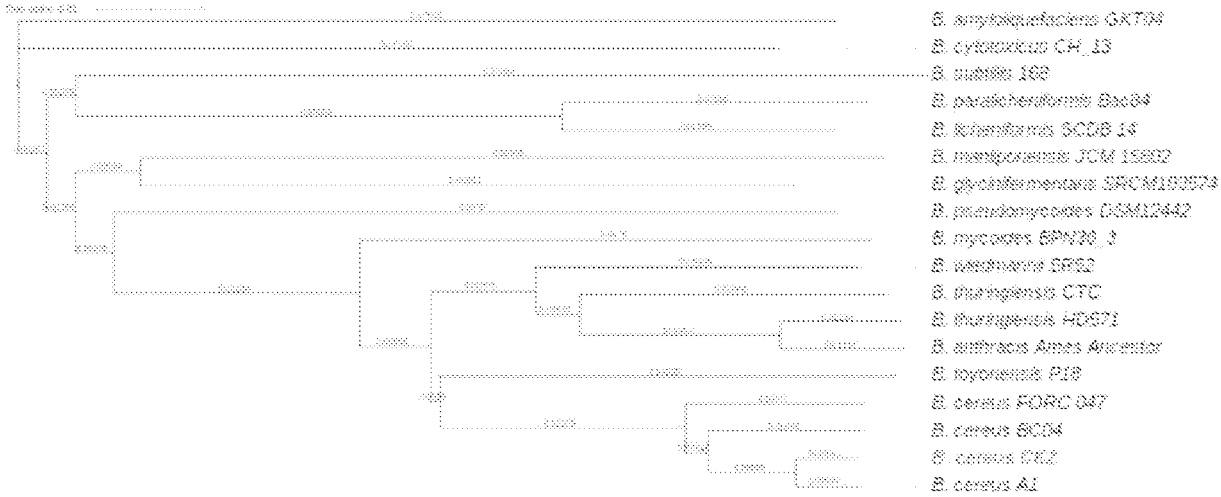

B. amyloliquefaciens GKT34
B. cytotoxicus CH_13
B. subtilis 168
B. paralicheniformis Bac84
B. licheniformis SCDB 14
B. mesoterricus JCM 15802
B. glycinifermentans SRCM103574
B. pseudomycoides DSM12442
B. mycoides BPV28_3
B. wiedmannii SRS2
B. thuringiensis CTC
B. thuringiensis HD671
B. anthracis Ames Ancestor
B. toyonensis P18
B. cereus FORC 047
B. cereus BC04
B. cereus CK2
B. cereus A1

FIG. 18

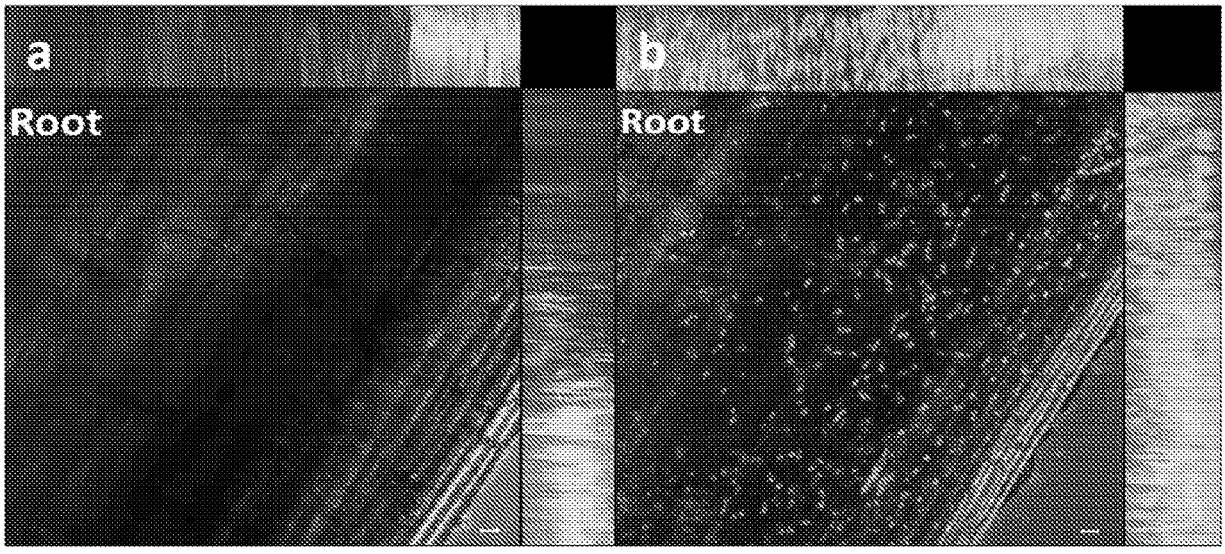

a
Root
b
Root

FIG. 19

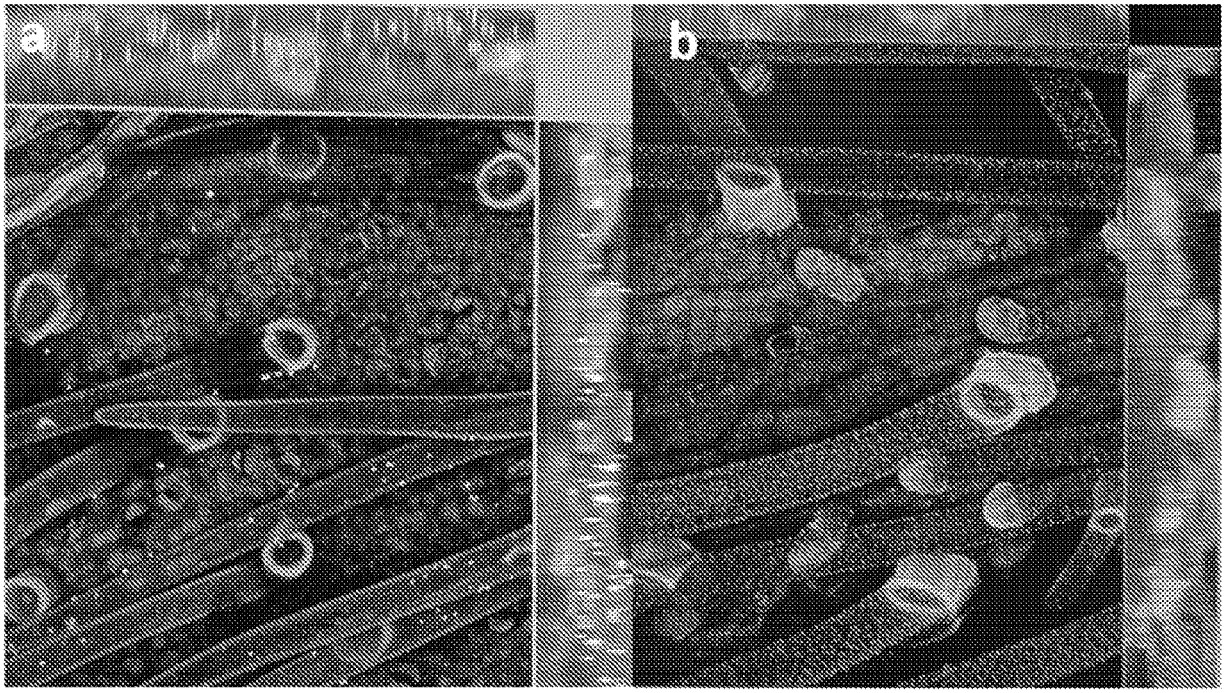


FIG. 20

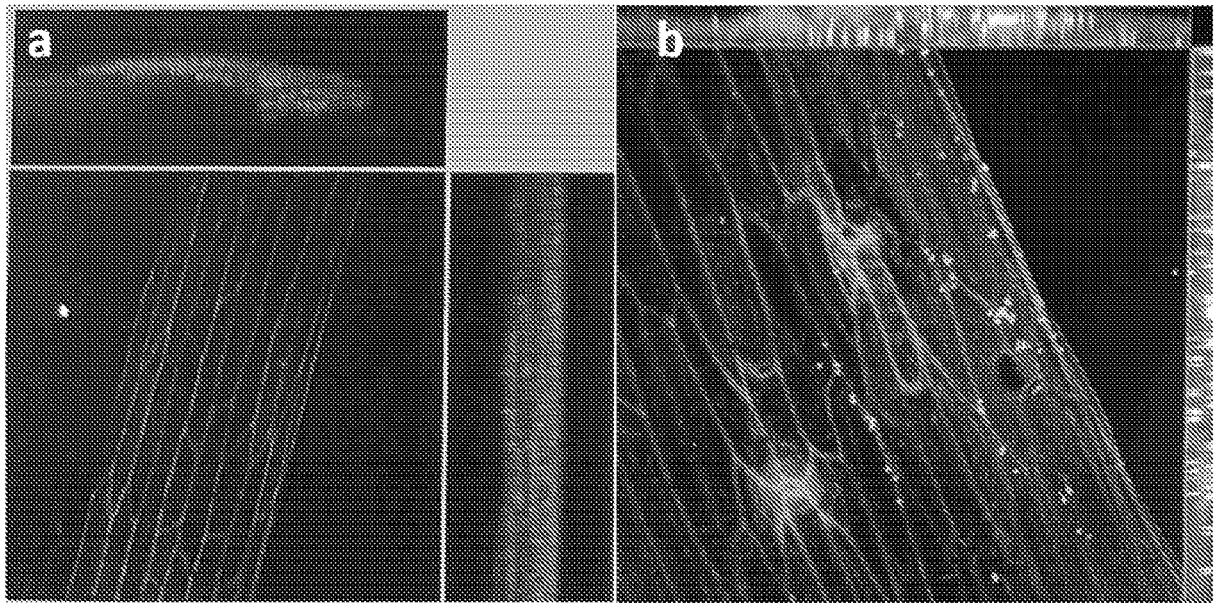


FIG. 21

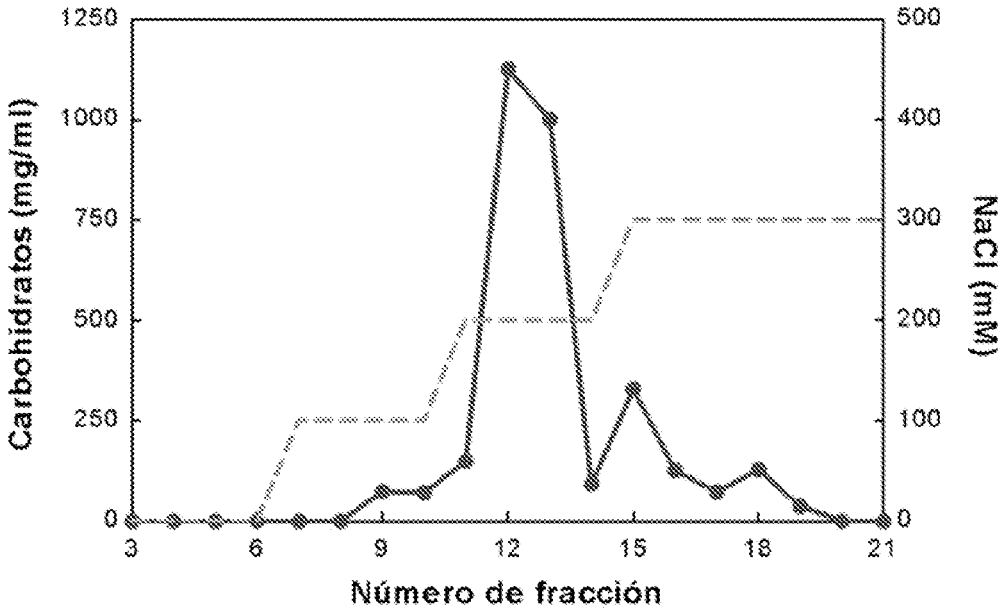

Carbohidratos (mg/ml)
1250
1000
750
500
250
0
NaCl (mM)
500
400
300
200
100
0
3
6
9
12
15
18
21
Número de fracción

FIG. 22

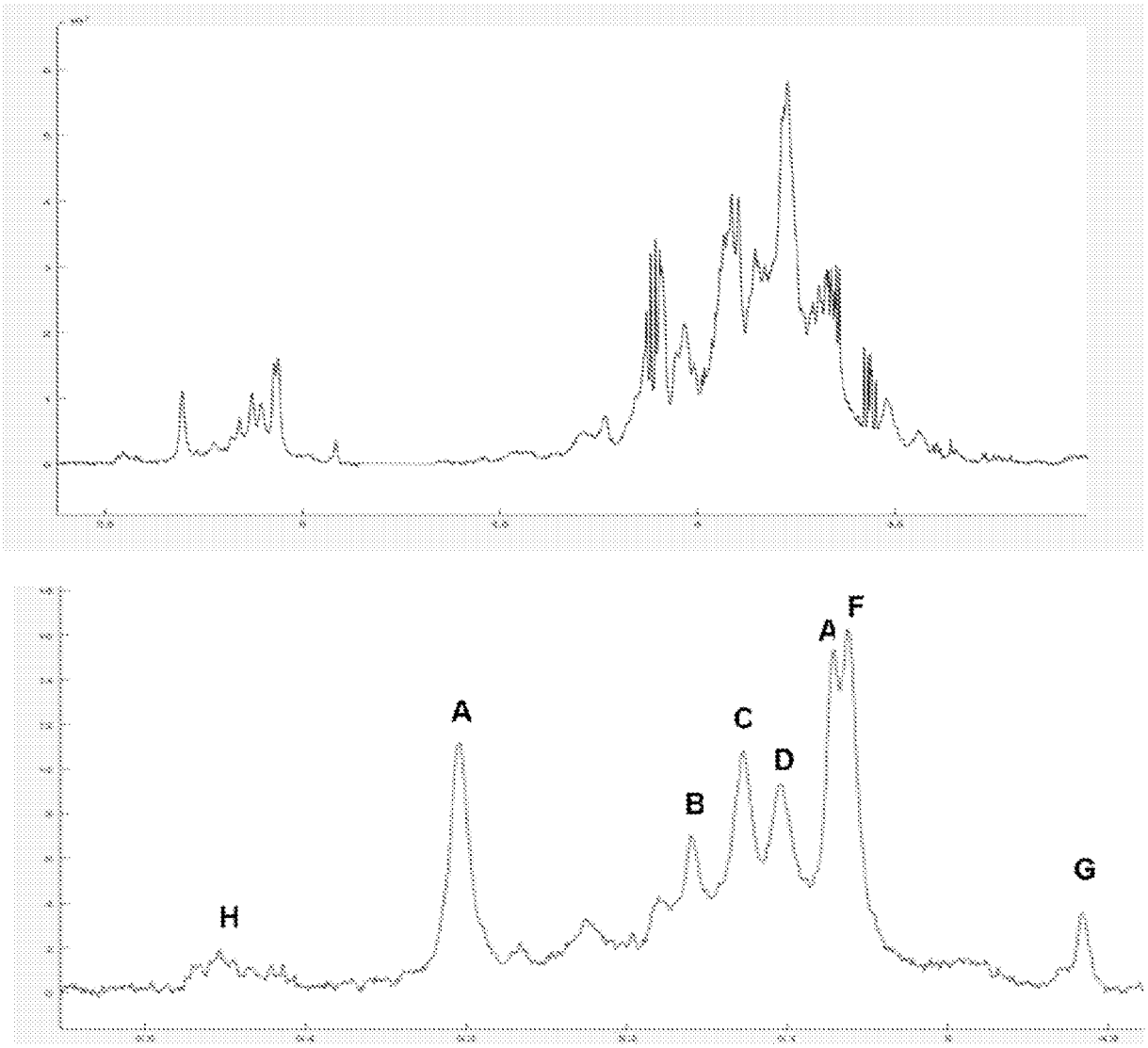


FIG. 23

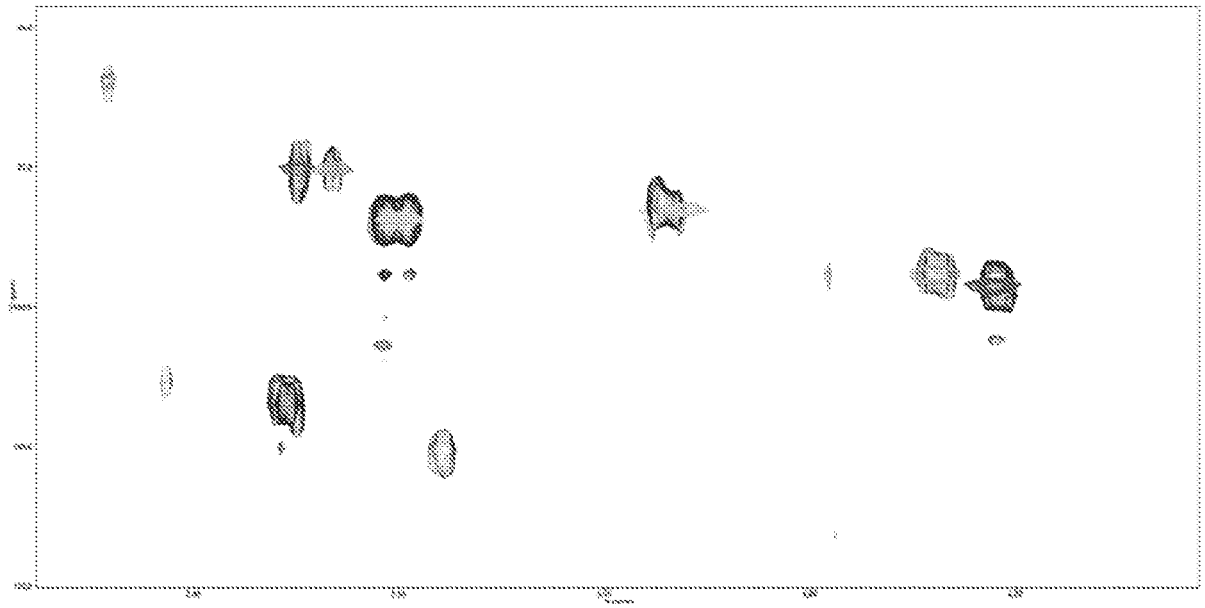


FIG. 24

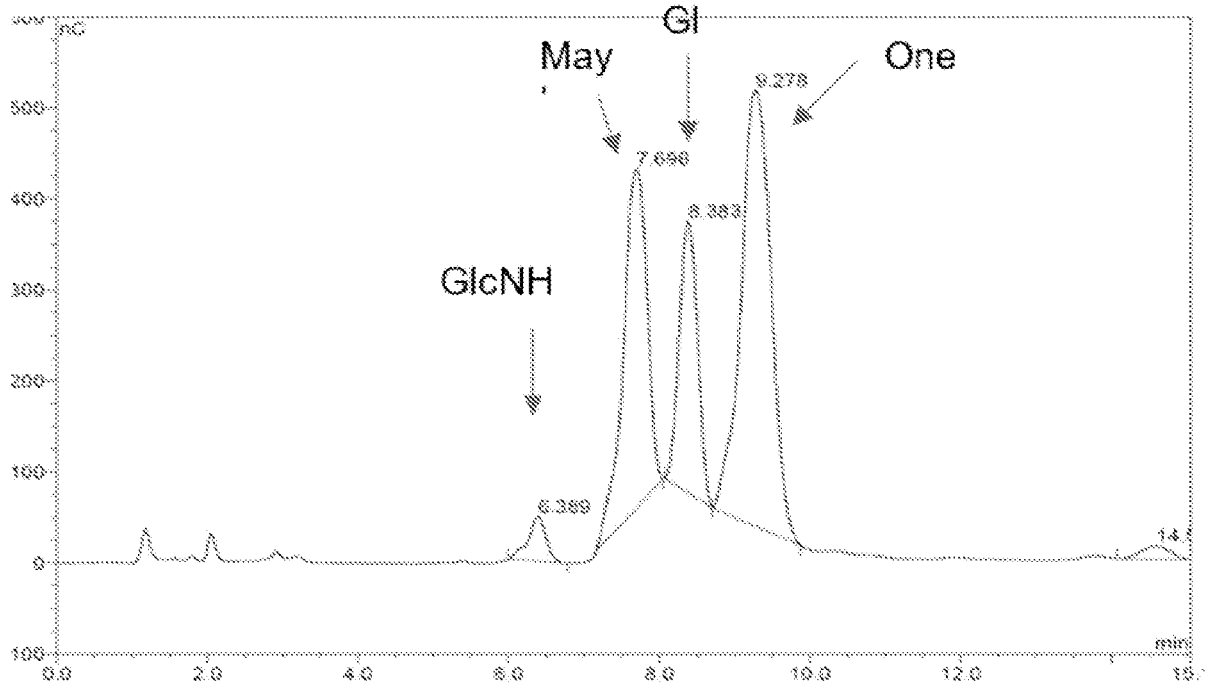

mAU
500
400
300
200
100
0
-100
May
Gl
One
GlcNH
7.690
8.383
9.278
6.369
14.
min
0.0
2.0
4.0
6.0
8.0
10.0
12.0

FIG. 25

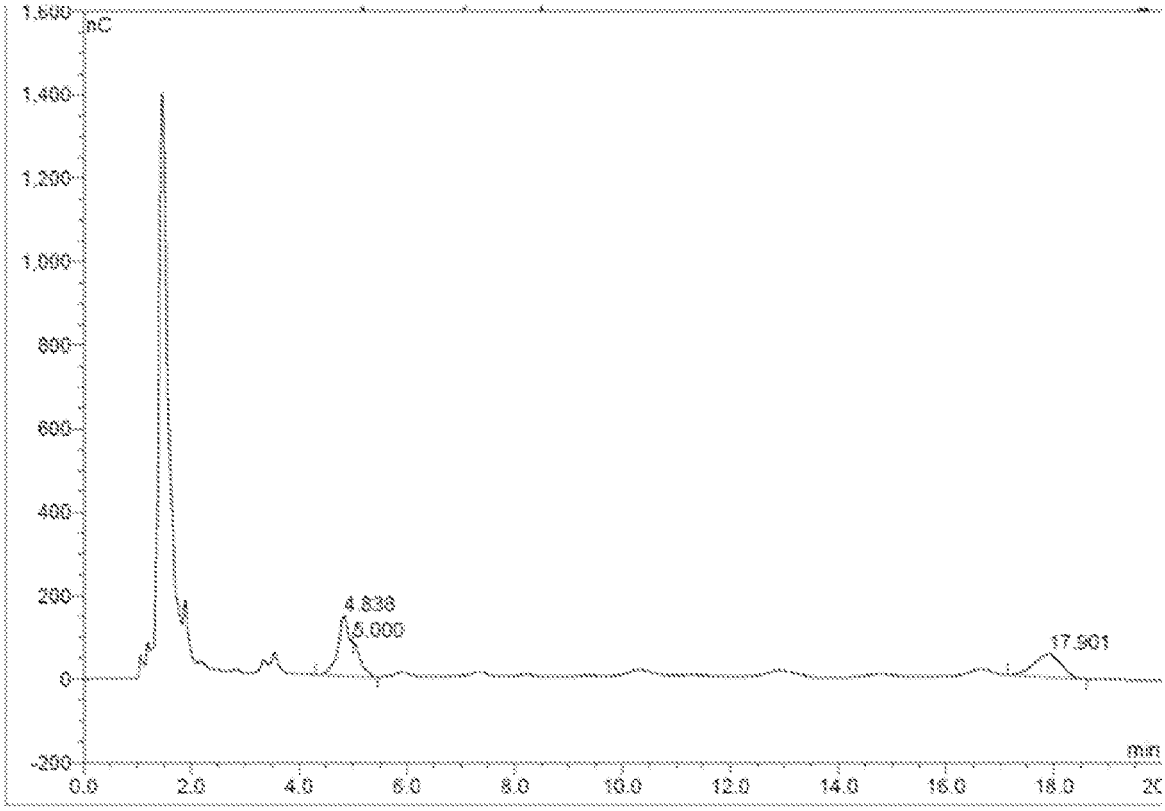

nC
1,600
1,400
1,200
1,000
800
600
400
200
0
-200
4.838
5.000
17.901
min
0.0
2.0
4.0
6.0
8.0
10.0
12.0
14.0
16.0
18.0

FIG. 26

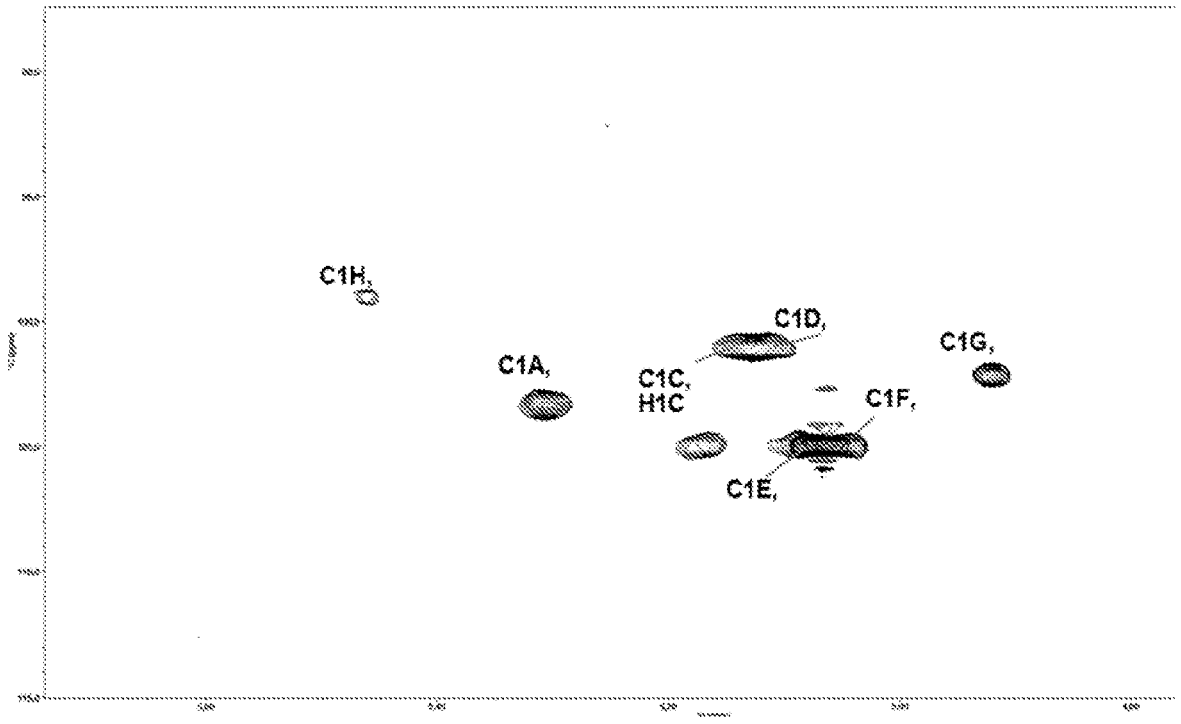

C1H,
C1D,
C1G,
C1A,
C1C,
H1C
C1F,
C1E,

FIG. 27

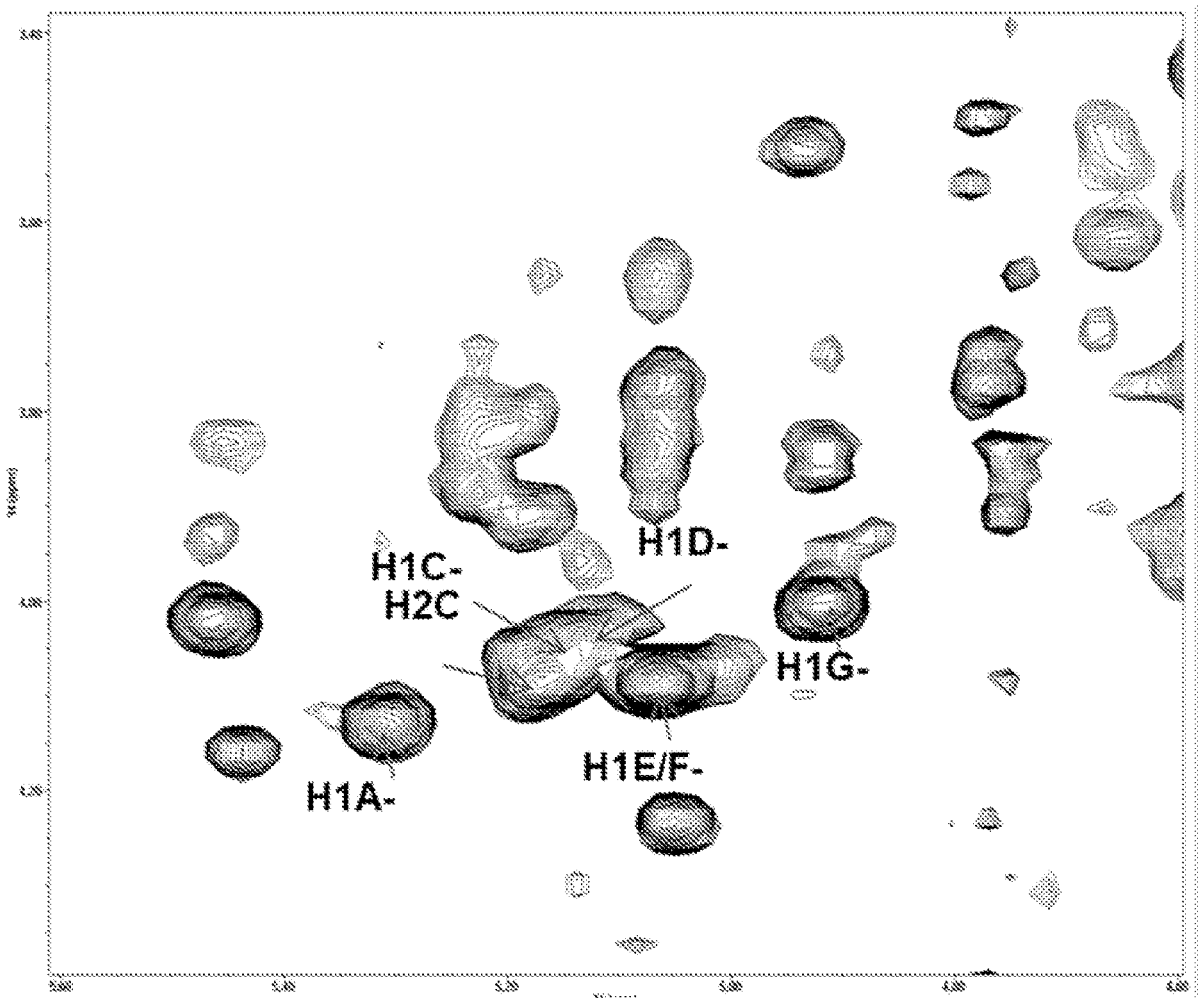


FIG. 28

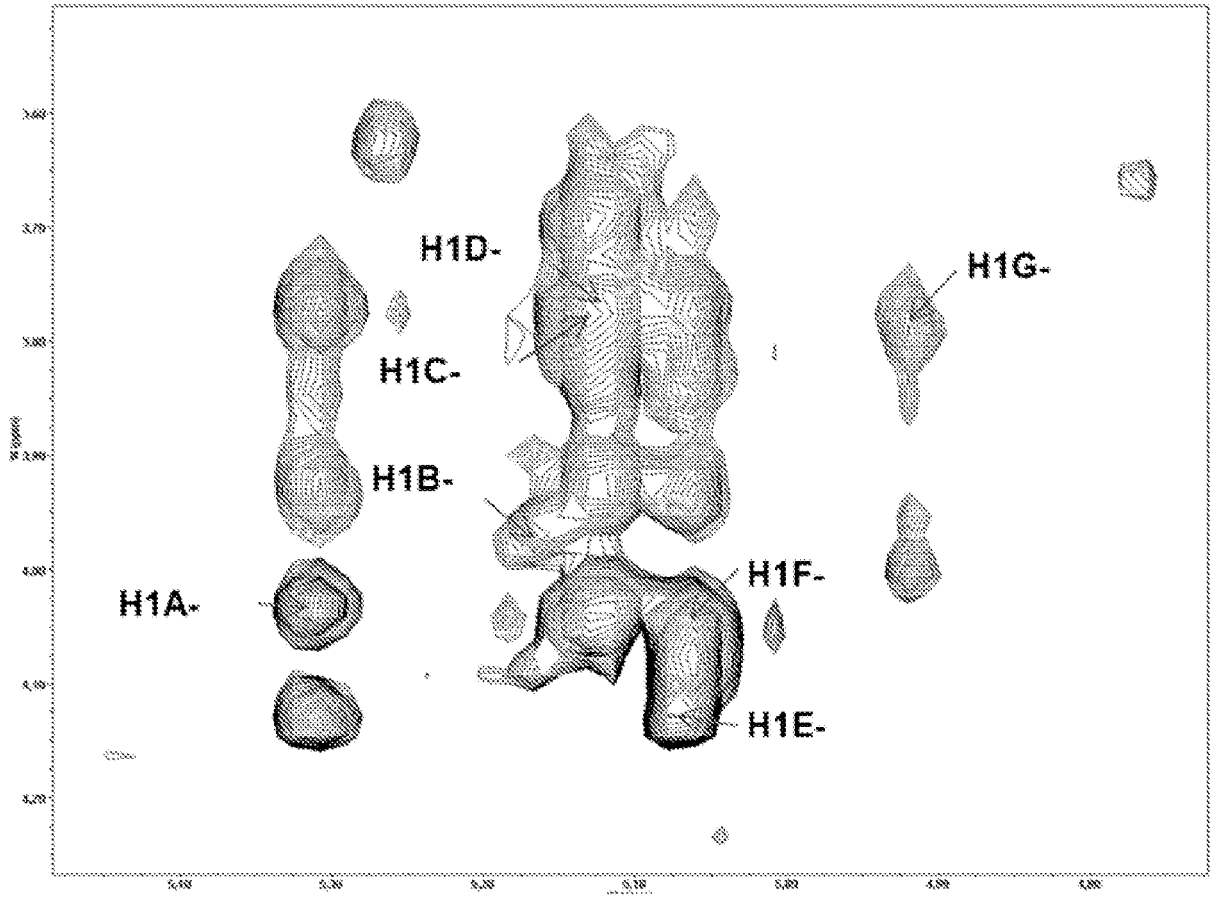

H1D-
H1G-
H1C-
H1B-
H1F-
H1A-
H1E-

FIG. 29

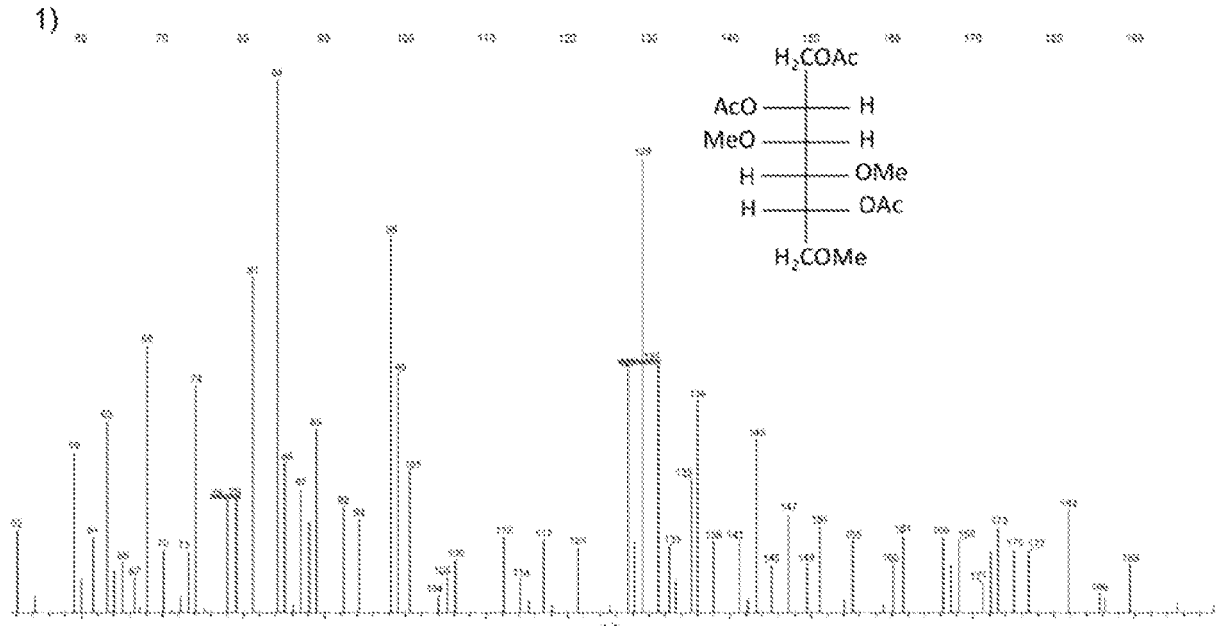
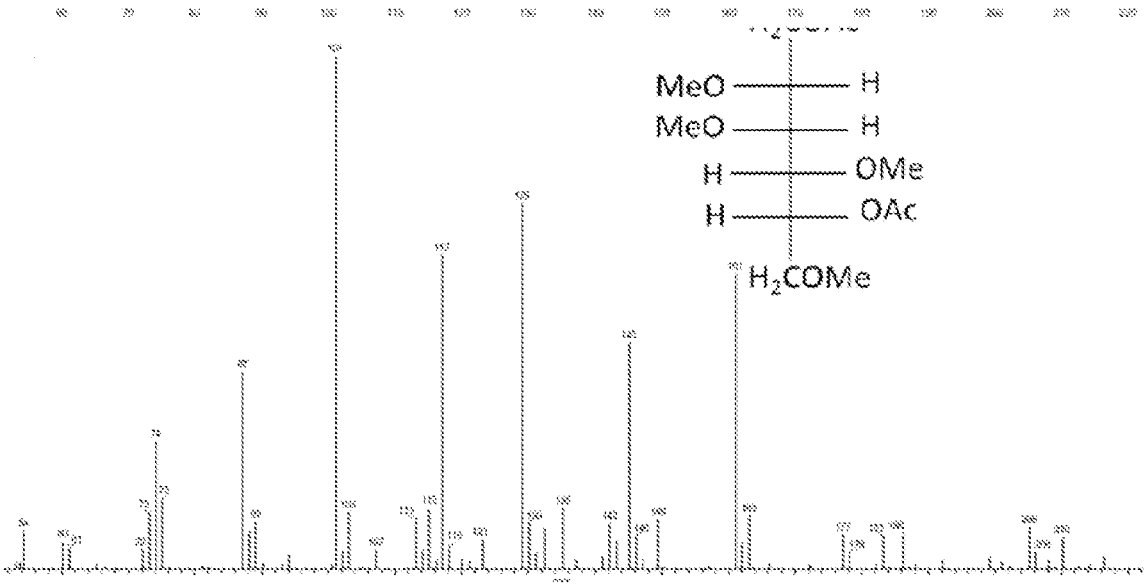

1)
H2COAc
AcO
H
MeO
H
H
OMe
H
OAc
H2COMe

FIG. 30

2)



3)

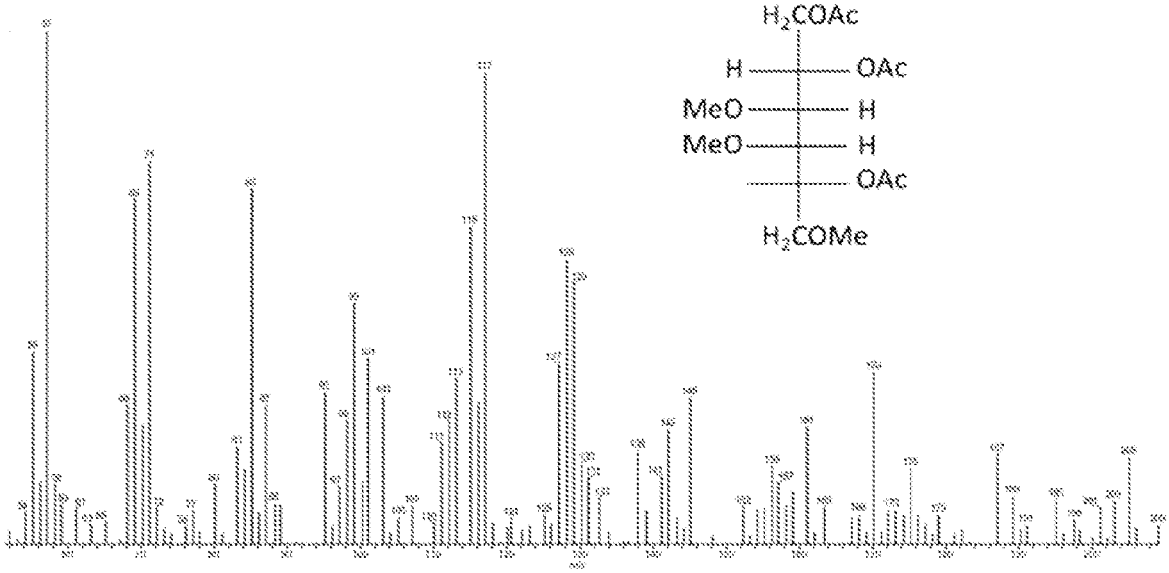
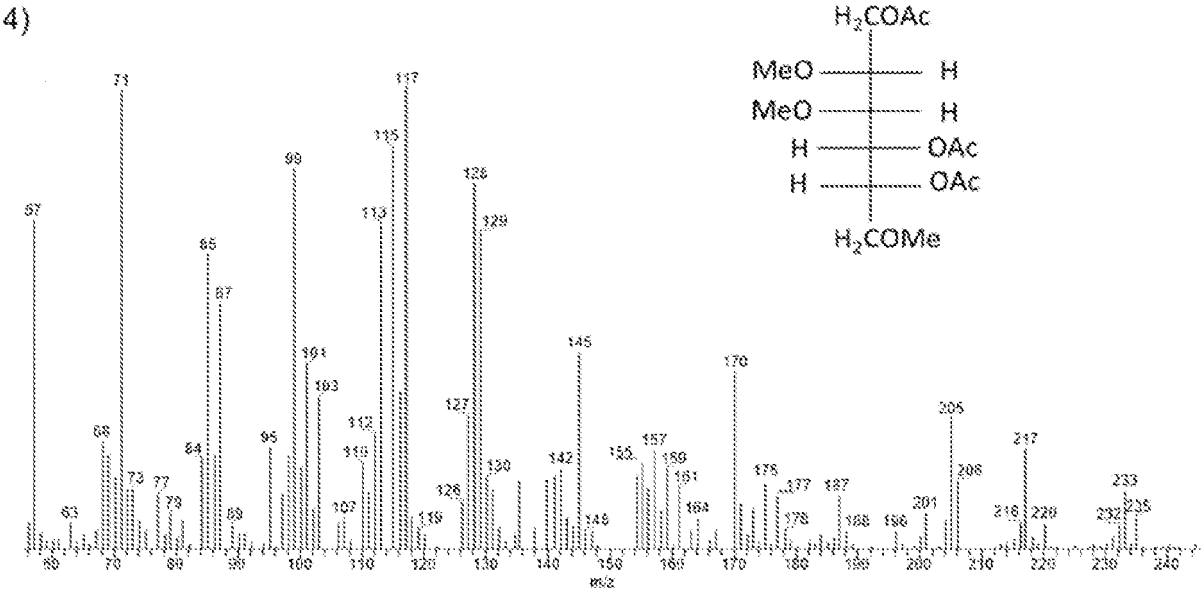


FIG. 30 (continued)

4)



5)

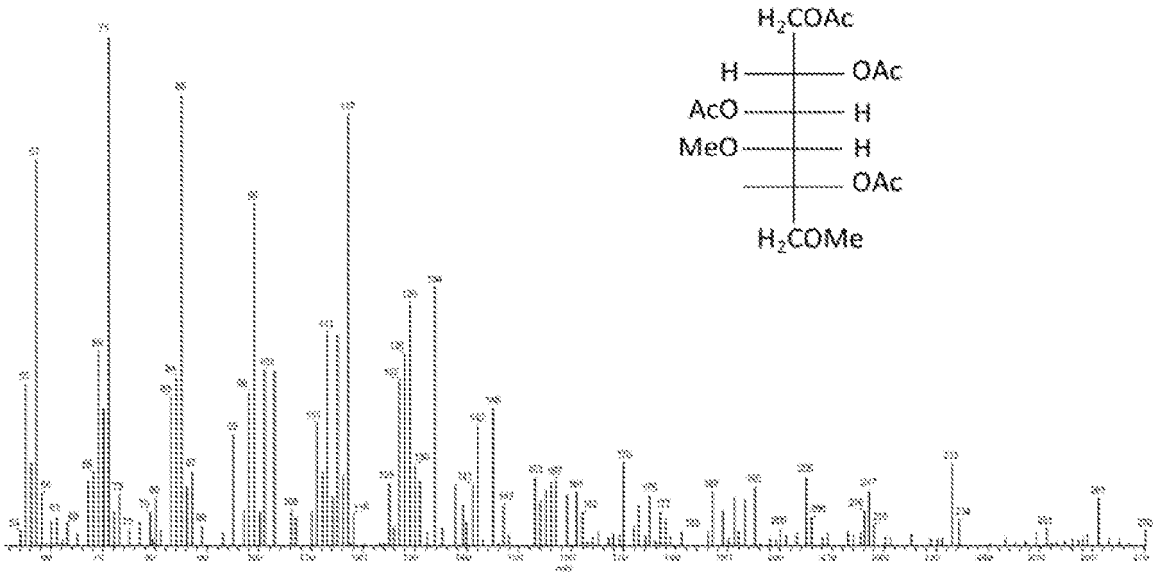


FIG. 30 (continued)