A metaproteomic approach dissecting major bacterial functions in the rhizosphere of plants living in serpentine soil

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A metaproteomic approach dissecting major bacterial functions in the rhizosphere of plants living in serpentine soil

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Dear Editor,

we carefully analysed the queries of the two referees and we answered to not clear points. In the revised version of the manuscript we incorporated the requested modifications and corrections. In the discussion section we also inserted a citation of a very recent work [Theriault G, Nkongolo KK. Evidence of prokaryote like protein associated with nickel resistance in higher plants: horizontal transfer of TonB-dependent receptor/protein in *Betula* genus or de novo mechanisms? *Heredity* (2016) 1-8], which can support the data obtained in our study.

We hope that this revised version of the manuscript could fulfil the requirements for publication in Analytical and Bioanalytical Chemistry.

Best Regards

Giovanna Visioli

Response to Referees' comments

Referee A

1. For example, there is no discussion of the different protein extraction methods in the results/discussion sections. How do the protein lists differ from each other? Is it really necessary to perform all 3 extractions, is one superior over the others? Any systematic effects?

Answer: We thank the Referee for the suggestion to improve the manuscript; thus, beyond the list of the identified proteins for each method and soil, already reported in Online Resource 2, the results obtained from the three different methods were also presented and discussed in more detail in the "Results" and "Discussion" sections, supporting them by the most recent literature. In particular, in the revised manuscript we pointed out that our results confirm what observed in other works [S.H. Hansen et al., *Proteomics* 14 (2014) 2535-2539; K.M. Keiblinger et al., *Soil Biology and Biochemistry* 54 (2012)14-24] regarding the high number of unique protein identification associated to different extraction methods (for this reason, in our opinion, it is not possible to consider a method superior than another). Actually, in our work the selection of extraction approaches, among published methods or commercial kit, was in this direction: i.e exploiting different chemical-physical principles for cell lysis and protein extraction/dissolution, to finally combine the information arising from the different procedures. As specified in the manuscript, we took advantage of the application of different extraction approaches in order to improve the amount of identified proteins, with the final aim to characterize, for the first time, the main bacterial functions associated to serpentine soil. In addition, we observed that the methods were not strongly biased toward particular protein classes and/or phyla, however, in accordance with literature [S.H. Hansen et al., *Proteomics* 14 (2014) 2535-2539], the strong cell lysis by beat beating (NoviPure^{TM} commercial kit) seems to favour the extraction of intracellular proteins.

2. Also, the results of the 16S rDNA profiling are only mentioned in the supplementary information; they should at least be shortly summarized in the main text.

Answer: We inserted a paragraph in the "Results" section about the identification of bacterial genera in the rhizosphere samples and in bulk soil based on DNA sequencing and a figure (new Figure 2) representing the distribution of the main Phyla. The results were also commented in the "Discussion" section.

3. Why is the number of identified proteins so low? How much protein was used for digestion? As the overlap of identified proteins between the different samples is rather larger, would it be possible to perform a semi-quantitative analysis of protein abundance (e.g. based on spectral counts) that might indicate the increased presence of a specific type of bacteria?

Answer: Metaproteomic studies, in particular soil metaproteomics, has still to overcome several issues like complexity and heterogeneity nature of matrix, which contain also some components that can interfere with the protein extraction and purification (in the case of soil samples they are mainly represented by humic substances and mineral particles), low protein extraction yields and also microbial protein sequence poorly covered by metagenomics data [K.M. Keiblinger et al., *Soil Biology and Biochemistry* 54 (2012)14-24; F. Bastida et al., *Journal of Proteomics* 101 (2014) 31-42; M.A. Williams et al., *Microbial Ecology* 59 (2010) 390-399]. A recent work of Bastida and coworkers [F. Bastida et al, *Journal of Proteomics* 101 (2014) 31-42], specifically focused on the evaluation and comparison of three different protein extraction methods for soil metaproteomic analysis from semiarid environment, showed that the amount of protein extracted from soil by any of the investigated method was very scarce, with usual yields below 3 %; in addition, it was observed that the extraction yield as well as the number of identified proteins depend not only on the exploited extraction approach but also on the soil type. In fact, in the same study [F. Bastida et al, *Journal of Proteomics* 101 (2014) 31-42], the Chourey method led to very different extraction yield and number of identified proteins for soils characterized by different chemical-physical properties: more precisely, the lowest number of identified protein (95±75) was obtained for a highly degraded soil with very low organic carbon content, not covered by vegetation. Also in our case, the investigated serpentine soil represents a very stressful environment [A. Lombini et al., *Journal of Geochemical Exploration* 64 (1998) 19-33; G. Visioli et al., *Chemosphere* 90 (2013) 1267-1273] not only for the high concentrations of metals, but also for the paucity of many essential macronutrients; in addition, it is generally stony with limited ability to retain moisture, thus being a very arid soil, rich of ultramafic rocks included within chaotic shales, limestones and flysch.

As reported in the original manuscript, after extraction we performed the quantification of protein content by commercial RC DC protein assay kit, in order to calculate the amount of trypsin to be added so that the enzyme-to-protein ratio was 1:100. All the available protein amount was digested. However, it has to be also considered that after digestion, purification and desalting steps were carried out in order to make the sample compatible with LC-ESI-MS analysis: this is due to the matrix complexity and the possible presence of interfering compounds from reagents used during cell lysis and protein extraction.

Taking into consideration that the overlap of identified proteins between the different samples is not large, we did not perform a semi-quantitative analysis of protein abundance. However, it can be pointed out that in case of semi-quantitative analysis, the information that could arise is not directly associated to the lower or higher presence of a specific type of bacteria, but it could be interpreted by its lower or higher metabolic activity in different edaphic conditions.

4. Line 282: "All common contaminants (e.g., trypsin, keratins) were removed from the protein lists prior to analyses." Why was this done? Does this not increase the risk of falsely assigning *contaminant peptides to bacterial proteins? A more common approach would be to pre-filter the dataset with a database only containing contaminants and then screen the remainder for targets.*

Answer: Actually, the sentence was not very clear in the text, thus it was rewritten in the revised text. In fact, the protein database used to search the samples included also all common contaminants (e.g., trypsin, keratins). After the database search, all the common contaminants were removed from the protein list used for further bioinformatics analysis (as taxonomy and GO assignment).

5. Line 246 "Protein quantification, reduction, alkylation and digestion reactions as well as SCX and C18 column purifications were carried out as described in the 2.4.1.1 paragraph." This sentence appears several times in the experimental section – yet, as far as I can tell, there is no section 2.4.1.1 and the mentioned information is actually missing from the manuscript.
We apologise for the inconvenience: the text was corrected.

6. Line 396 "Soil samples were collected in an area of 10 mq". Mq = square meters?
It is correct; for clarity, in the text "10 mq" was replaced by "10 m^2".

Referee B

1. Page 4, line 148: Better, "… ultra-purified water was …"

Answer: It was modified according to Referee's suggestion.

2. Experimental section: as IUPAC indicates, ml should be mL (litres in capital letter: L). Check it through the manuscript.

Answer: We thank the Referee for the suggestion. In the text, "µl" and "ml" were replaced by "µL" and "mL", respectively.

3. Page 6, lines 251-255:
3.1- Eksigent Technologies is the brand corresponding to the micro-LC system and they only commercialize micro-, nano-flow systems. Are the authors sure that the HALO LC reversed phase column is also distributed by Eksigent?

Answer: At present, Eksigent is a part of AB Sciex that distributes the *HALO* column, but the brand indicated on the column is Eksigent.

3.2- "… system with as stationary phase a HALO Fused C18 column (0.5 x 100 mm, 2.7 µm; …" This sentence should be modified, for instance "… system with a reversed phase HALO Fused C18 column (100 x 0.5 mm, 2.7 µm; …"

Answer: The sentence was modified as suggested by the Referee.

4. Page 7, lines 256-266:

4.1- Better, "… The micro-LC system was coupled to a 5600+ TripleTOF mass spectrometer (AB Sciex …"

Answer: The sentence was modified according to Referee's suggestion.

4.2- The sentence "… the mass spectrometer analysis was performed using a mass range of 100-150 Da …" should be modified, for instance "… the mass spectrometry data was acquired within the m/z range 100-150 …"

Answer: As requested by the Referee, the sentence was modified as "the mass spectrometry data was acquired within the 100-1500 *m/z* range".

4.3- Information about the mass resolution at which the mass spectrometer was operated should be included in the experimental section.

Answer: As requested, this information was added in the text.

5. Page 7, lines274-276: The instrument used was a q-TOF, why was the search performed using a mass tolerance of only 0.4Da? The selectivity would be better using a lower mass tolerance.

Answer: It is right. We apologise for the typing error about the tolerance on precursor ions. In fact, the tolerance of 0.4 Da is referred only to MS/MS fragments, whereas for the precursor ion a tolerance of 50 ppm was used for database search. The value was corrected in the revised manuscript.

A metaproteomic approach dissecting major bacterial functions in the rhizosphere of plants living in serpentine soil

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Abstract

A metaproteomic approach, based on liquid chromatography-high resolution mass spectrometry analysis, was followed to map the major bacterial metabolic functions associated with the rhizosphere of metal tolerant and metal hyperaccumulator plants, growing in a serpentine soil naturally contaminated by heavy metals such as Ni, Co, Cr. In particular, an “in-house” bacterial protein database was built based on the genera recognized by 16S rDNA profiling, then it was used for protein identification from LC-MS data. The combination of the information arising from three different extraction protocols, applied to each soil sample, permitted to identify almost 800 proteins, corresponding to functions assigned to proper Gene Ontology categories. Mainly proteins involved in response to stimulus or in transport of metals and nutrients revealed variability of bacteria responses to microenvironment conditions. As for taxonomy, *Phyllobacterium, Microbacterium oxidans*, *Pseudomonas oryzihabitans*, *Stenotrophomonas rhizophila* and *Bacillus methylotrophicus* bacterial species showed to be more represented in the rhizosphere samples of the metal tolerant *Biscutella laevigata* and of the Ni hyperaccumulator *Noccaea caerulescens* respect to bulk soil. Combining 16S rRNA gene—based sequencing and metaproteomic analysis we get insights into microbial community functions and their interaction with plants colonising the stressful environment of serpentine soils.

Keywords: *metaproteomics, serpentine soil, Ni tolerant plant, Ni hyperaccumulator, liquid chromatography-high resolution mass spectrometry*

Introduction

Serpentine rocks and the associated soils represent well known example of extreme environments, due to the high concentration of heavy metals (Co, Cr and particularly Ni) and to the anomalous ratio between Ca and Mg cations [1]. Plant communities inhabiting serpentine areas (metallophytes) have evolved two strategies to achieve metal tolerance: the first involving restriction of metal ion entry, while the second tolerating and accumulating heavy metal ions in the body of the plant (so-called "hyperaccumulators") [2]. In particular, attention toward hyperaccumulators is increasing due to the possibility to use them in biotechnological applications for decontamination of polluted sites (phytoremediation), for phytomining (commercially producing metals, metal products or catalysts) and for their emerging role in nanotechnology [3, 4]. In the below ground serpentine environments also soil microbial communities represent an important component, exerting specific roles. In fact, rhizosphere bacteria are known to enhance plant nutrient and water uptake as well as to protect plant against toxic conditions, thus greatly contributing to plant growth and fitness in harsh edaphic conditions. In fact, the role of bacteria in the plant metal hyperaccumulation process has been recently demonstrated by different authors [5-7]. Traditional culture-dependent methods have represented, so far, the main approach for the study of bacteria in the rhizosphere of hyperaccumulators [8, 9]. Metagenomics based on DNA extraction from soil and recent progresses in Next Generation Sequencing (NGS) can give important additional information on the bacterial community surrounding roots, considering the presence also of the huge proportion of unculturable bacteria in the root-soil environment. NGS technology, in particular, was recently applied to analyse bacterial community in heavy metals polluted soil and to elucidate the impact of heavy metal contamination on bacterial community composition [10, 11]. Even though these techniques have greatly improved the knowledge on the soil microbial diversity, DNA abundance correlates too weakly with protein abundance to obtain a real picture of soil microbial functions. At this purpose metaproteomics, namely the study of all proteins recovered directly from environmental samples [12-14], is very promising to study soil microbial activity and to obtain a deeper understanding of root-microbial interactions.

In the last years, technological improvements in high-resolution mass spectrometry (HRMS), combined with the separation power of liquid chromatography (LC), even in high throughput multidimensional configurations, paved the way to advanced bottom-up and gel-free shotgun soil metaproteomic studies [15-17]. For reliable metaproteomic investigation, great efforts must be placed also on computationally elaboration, in order to convert the raw spectral data into peptide sequence followed by protein inference. However, despite remarkable breakthroughs provided by progress of MS-based techniques and bioinformatics tools, the development of analytical strategies for soil metaproteomics is still a very challenging issue due to sample complexity, especially in terms of matrix components, high level of organismal diversity and wide range of protein abundance levels. A critical aspect for the success of soil metaproteomic studies is the sample treatment protocol [18, 19], in terms of protein extraction and extract clean-up, which can suffer from low efficiency due to high matrix complexity, and co-extraction of interfering humic compounds [17, 20, 21]. Recently, some methods have been proposed for direct extraction of microbial protein from soil [20, 22]; most of them involve mechano-physical cell lysis combined with the use of organic/inorganic compounds or buffers containing detergents, chaotropic agents and/or reducing reagents [17]. Soil heterogeneity prevents the possibility to develop an universal extraction protocol suited for all the different soil types; in addition, it is widely demonstrated that in metaproteomics current extraction methods suffer taxonomic and functional bias [19, 21, 23], each giving a high number of unique peptide identification [23]. For this reason, in order to achieve a significantly higher representation and coverage of the total protein content from a soil sample, it might be appropriate to combine the information arising from different extraction methods.

Soil metaproteomics was applied to characterise proteins extracted from contaminated soil and groundwater [24, 25] and to identify functions in crop rhizospheric environments [26, 30], but, to our knowledge, none of such studies were performed, so far, to get insight into the tolerant and hyperaccumulator-rhizobiome interactions in the soil.

To this aim, in the present work, a LC-HRMS-based metaproteomic approach was exploited for the study of the rhizosphere of two Brassicaeae species, the metal tolerant *Biscutella laevigata* and the Ni hyperaccumulator *Noccaea caerulescens* growing on a serpentine soil. We aimed to i) obtain a comprehensive proteome coverage of the major bacterial functions of the metal contaminated soil and of the rhizosphere of both plant species, utilising information deriving from 16S rRNA gene-based community profiling and ii) classify different bacterial soil protein functions in relation to root-bacteria processes.

Materials and methods

Chemicals and materials

Ammonium bicarbonate, dithiothreitol (DTT), iodoacetamide (IAA), trypsin, formic acid (FA), trichloroacetic acid (TCA), acetone HPLC grade and methanol HPLC grade were purchased from Sigma-Aldrich (Milan, Italy). Sodium dodecyl sulphate (SDS), tris(hydroxymethyl)aminomethane hydrochloride (Tris-HCl), sodium chloride, ethylenediaminetetraacetic acid (EDTA), magnesium chloride, potassium chloride phenol were purchased from Sigma Aldrich. Acetonitrile HPLC grade (ACN) was purchased from VWR International (Milan, Italy). ~~Deionized~~ Ultra-purified water was obtained from an in house Milli-Q water purification system Alpha Q-Water (Millipore, Billerica, MA, USA). NoviPure^{TM} Soil Protein Extraction Kit (MO BIO Laboratories, Inc.) was purchased from Cabru (Arcore, Milan, Italy). FastDNA® Spin Kit for Soil was purchased from MP Biomedicals (Santa Ana, CA). Strong cation exchange (SCX) spin columns were from ThermoFisher Scientific (Milan, Italy). Sep-Pak C18 columns were from Waters (Milan, Italy). RC DC Protein Assay Kit II was purchased from Bio-Rad Laboratories (Milan, Italy).

Sample collection

Soil samples were collected in April 2015 from a metal-contaminated site (44.64282°N–10.07951°E, 736 a.s.l.) on Mount Prinzera, a Natural Reserve in the Northern Apennines (Italy). Soil samples derived from the rhizosphere of two endemic *Brassicaceae* species, the Ni hyperaccumulator *Noccaea caerulescens* (NCS) and the Ni tolerant *Biscutella leavigata* L. subsp. montanina (BLS) were gently separated from roots, sieved at 2 mm, and immediately frozen in dry ice *in situ* until reaching the laboratory where they were left at -80 °C. A sample of bulk soil (BS) was also collected nearby. Three biological replicates were collected for each sample and were pooled to obtain the proper amount of soil requested for protein extraction by three different procedures and for DNA extraction.

16S rRNA gene-based community analysis

DNA was extracted from BS, BLS and NCS samples starting from 500 mg of soil with the FastDNA® Spin Kit for Soil and visualised by electrophoresis on 0.8% (w/v) agarose gels, to test for DNA integrity.

Partial 16S rRNA gene sequences were amplified from extracted DNA using primer pair Probio_Uni and /Probio_Rev, which target the V3 region of the 16S rRNA gene sequence [31]. 16S rRNA gene amplification and amplicon checks were carried out as previously described [31]. 16S rRNA gene sequencing was performed using a MiSeq (Illumina) at the DNA sequencing facility of GenProbio srl (www.genprobio.com) according to the protocol previously reported [31]. Following sequencing, the obtained individual sequence reads were filtered by the Illumina software to remove low quality and polyclonal sequences. All Illumina quality-approved, trimmed and filtered data were exported as .fastq files. The .fastq files were processed using a custom script based on the QIIME software suite [32]. Paired-end reads pairs were assembled to reconstruct the complete Probio_Uni / Probio_Rev amplicons. Quality control retained sequences with a length between 140 and 400 bp and mean sequence quality score >20 while sequences with homopolymers >7 bp and mismatched primers were omitted. In order to calculate downstream diversity measures (alpha and beta diversity indices, Unifrac analysis), 16S rRNA Operational Taxonomic Units (OTUs) were defined at ≥ 97 % sequence identity using uclust [33]. All reads were classified to the lowest possible taxonomic rank using QIIME and a reference dataset from the SILVA database [34]. Similarities between samples were calculated by unweighted uniFrac [35]. The range of similarities is calculated between the values 0 and 1.

Metaproteomic analysis

Sample preparation

For protein extraction, three different sample treatment methods were applied to homogenized aliquots of soil (5 g each): NoviPure$^{\text{TM}}$, Chourey and Phenol-SDS methods.

NoviPure$^{\text{TM}}$ soil protein extraction was performed according to Kit manufacturer's instructions, involving the extraction with two different buffers (undeclared composition), with the addition of 10 mM DTT, and bead beating with a provided bead mix. After protein extraction, precipitation with TCA and washing steps with acetone, protein pellets were air-dried until all acetone evaporated, then solubilized in 425 ~~µl~~ µL of 50 mM ammonium bicarbonate buffer at pH 8. A volume of 25 ~~µl~~ µL of extract was used to quantify protein content by RC DC protein assay kit, using bovine serum albumine as standard. The remaining 400 ~~µl~~ µL of extract underwent reduction reaction by incubation with 20 mM DTT for 40 min at 37 °C; then, for alkylation reaction 40 mM IAA was added, followed by incubation for 40 min at room temperature (RT) in the dark. The digestion was carried out by using trypsin (1:100 enzyme-to-protein ratio) and keeping at 37°C overnight. The digestion reaction was quenched by adding 100% FA to achieve 5% (v/v) FA as final concentration. After proteolytic digestion, samples were purified by SCX spin columns for lingering detergent removal, and desalted with C18 columns, following instructions reported in the NoviPure$^{\text{TM}}$ Soil Protein Extraction Kit. Briefly, SCX spin column was conditioned with 400 ~~µl~~ µL of 0.1% FA/5% ACN; then, the sample was loaded and washing was carried out twice with 400 ~~µl~~ µL of 0.1% FA/5% ACN. Elution involved increasing salt concentration: a fist elution with 400 ~~µl~~ µL 50:50 (0.1% FA/5% ACN):(0.1% FA/25% ACN/500mM KCl) and a second one with 400 ~~µl~~ µL 0.1% FA/25% ACN/500mM KCl. The two eluates were combined (final volume of about 800 ~~µl~~µL). Spin column centrifugation after each step was performed at 2000 ×g for 5 min. The Sep-

Pak C18 column was mounted on a 10 ~~ml~~ mL syringe; syringe and C18 column were previously conditioned with 10 ~~ml~~ mL of 100 % ACN and 10 ~~ml~~ mL of 0.1% FA/2% ACN, avoiding bubble formation. After sample loading, followed by the loading also of 1.6 ~~ml~~ mL of 0.1% FA/2% ACN, two washing steps were performed with 0.1% FA/2% ACN. Elution was carried out with 1.6 ~~ml~~ mL of 0.06% FA/40% ACN; then the sample was placed into a concentrator until dryness. Peptide pellet was stored at -20 °C before analysis.

The Chourey method was performed according to a published procedure [22]. Frozen soil was thawed partially and 5 g soil weighted in a 50 ~~ml~~ mL Pyrex glass bottle to which 10 ~~ml~~ mL of Alkaline-SDS buffer was added (5% SDS, 50 mM Tris-HCl, pH 8.5; 0.15 M NaCl; 0.1 mM EDTA; 1 mM MgCl$_2$; 50 mM DTT). After vigorous vortexing for 2-3 min, the sample was immersed in a boiling water bath for 10 min. The resulting slurry was cooled for 5 min and then transferred to a 50 ~~ml~~ mL conical tube followed by vigorous vortex mixing for 3 min. The solution was centrifuged at 2095 ×g for 10 min and the supernatant was transferred to fresh tubes. To each tube, chilled 100% (w/v) TCA was added to achieve about 25% TCA as final concentration. Tubes were kept in freezer overnight to precipitate proteins present in the solution. Samples were centrifuged at 20000× g for 20 min to obtain a concentrated protein pellet and the supernatant was discarded. Protein pellets were washed with 1 ~~ml~~ mL chilled acetone followed by centrifugation at 20 000×g for 10 min. After centrifugation, acetone was gently removed and discarded, and a fresh 1 ~~ml~~ mL of acetone was added. This acetone washing step was repeated three times. Protein pellets were air-dried until all acetone evaporated, then solubilized in 425 ~~µl~~ µL of 50 mM ammonium bicarbonate buffer at pH 8. Protein quantification, reduction, alkylation and digestion reactions as well as SCX and C18 column purifications were carried out as previously described for NoviPure^{TM} method. ~~in the 2.4.1.1 paragraph.~~

As for Phenol-SDS method, protein extraction was performed according to the procedure described by Keiblinger et al. [20]. In brief, 5 g soil of soil samples were suspended in 1:1 (v/v) SDS-phenol buffer (50 mM Tris, 1% SDS pH 7.5) and phenol (pH 8.0) and immediately vortexed for 5 min and put in a sonication bath for 10 min. The suspension was than shaken for 1 h and vortexing and sonication was repeated prior to centrifugation for 20 min and 4 °C at 3200 ×*g*. The lower phenol phase was carefully recovered and proteins were precipitated with 0.1 M ammonium acetate in methanol over-night.

Samples were then centrifuged at 20 000× g for 20 min to obtain a concentrated protein pellet and the supernatant was discarded. Protein pellets were washed with 1 ~~ml~~ mL chilled Methanol followed by centrifugation at 20000 ×g for 10 min. After centrifugation, methanol was gently removed and discarded, and a fresh 1 mL of acetone was added. This acetone washing step was repeated three times. Protein pellets were air-dried until all acetone evaporated, then solubilized in 425 ~~µl~~ µL of 50 mM ammonium bicarbonate buffer at pH 8. Protein quantification, reduction, alkylation and digestion reactions as well as SCX and C18 column purifications were carried out as described in detail for NoviPure^{TM} method~~in the 2.4.1.1 paragraph~~.

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LC-HRMS analysis

LC-MS/MS analyses were performed using a micro-LC Eksigent Technologies (Dublin, USA) system with a reversed phase ~~as stationary phase a~~ H~~alo~~ALO Fused C18 column (0.5 x 100 mm, 2.7 µm; Eksigent Technologies Dublin, USA). The injection volume was 4.0 ~~µl~~ µL and the oven temperature was set at 40 °C. The mobile phase was a mixture of 0.1% (v/v) formic acid in water

(A) and 0.1% (v/v) formic acid in acetonitrile (B), eluting at a flow-rate of 15.0 ~~µl~~µL/min at an increasing concentration of solvent B from 2% to 40 % in 30 minutes. The micro-LC system was ~~interfaced~~ coupled to ~~with~~ a 5600+ TripleTOF ~~system~~ mass spectrometer (AB Sciex, Concord, Canada) equipped with a DuoSpray Ion Source and CDS (Calibrant Delivery System). The samples were subjected to data-dependent acquisition (DDA): the mass spectrometry data was acquired within the ~~the mass spectrometer analysis was performed using a mass range of~~ 100-1500 *m/z* range ~~Da~~ (TOF scan with an accumulation time of 0.25 s), followed by a MS/MS product ion scan from 200 to 1250 Da (accumulation time of 5.0 ms) with the abundance threshold set at 30 cps (35 candidate ions can be monitored during every cycle). The ion source parameters in electrospray positive mode were set as follows: curtain gas (N_2) at 25 psig, nebulizer gas GAS1 at 25 psig, and GAS2 at 20 psig, ionspray floating voltage (ISFV) at 5000 V, source temperature at 450 °C and declustering potential at 25 V. The mass spectrometer operated at FWHM (full width at half maximum) resolution of about 30000. The MS data were acquired with Analyst TF 1.7 (AB SCIEX, Concord, Canada). Three replicates for each sample were subjected to the DDA analysis.

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In-house database building and protein database search

The taxonomy entries at genera level obtained by the 16S rRNA gene-based community analyses were utilised to pick out from the UniProtKB database all the protein sequences available both manually annotated and reviewed (Swiss-Prot) and automatically annotated and not reviewed (tr EMBL). Non redundant sequence proteins were collected and the fasta files were merged to obtain the database (308657 entries). The mass spectrometry files were searched using Mascot (Matrix Science Inc., Boston, USA). The Mascot search was performed on Mascot v. 2.4, the digestion enzyme selected was trypsin, with 4 missed cleavages, a search tolerance of ~~0.4 Da~~50 ppm was specified for the peptide mass tolerance, and 0.4 Da for the MS/MS tolerance. The charges of the peptides to search for were set to 2+, 3+ and 4+, and the search was set on monoisotopic mass. The instrument type was set to electrospray-quadrupole-time of flight (ESI-QUAD-TOF) and the following modifications were specified for the search: carbamidomethyl cysteins as fixed modification and oxidized methionine as variable modification. Dual filtering criteria for protein identification were used by combining a peptide confidence above 95% probability and a protein confidence above 90% with at least one peptide assigned to a respective protein [20, 21, 23]. ~~All common contaminants (e.g., trypsin, keratins) were removed from the protein lists prior to analyses.~~ All common contaminants (e.g., trypsin, keratins) identified in the samples were removed from the protein lists prior to the following bionformatics elaboration (GO and taxonomy annotation).

Functional annotation, GO term assignment and protein topology prediction

Protein hits obtained in the database searches were assigned to phylogenetic groups by using UniProtKB taxonomy database. BLAST2GO bioinformatics platform [36] was used to assign Gene ontology (GO) terms to proteins identified by MS/MS. To this purpose, BLASTP search was conducted against the RefSeq protein database at NCBI and the recovery of up to 20 hits (e-value $<10^{-3}$) was allowed. Interpro search and subsequent mapping and annotation (e-value hit filter: $<10^{-6}$) steps were conducted using default parameters. Protein distribution within GO terms was retrieved from GO level 3, with few exceptions (“response to stimulus”, “transport”, “metal ion binding” and “DNA binding”). The presence of putative signal secretion peptides or transmembrane domains was inferred using Phobius [37].

Results

Metaproteomic analysis workflow

The extreme complexity of the matrix, the low protein content as well as the high microbial biodiversity still make protein recovery from soil and protein identification a very challenging analytical issue for soil metaproteomic studies. Fig. 1 shows the workflow for the soil metaproteomic approach integrated with 16S rRNA gene-based community profiling followed in the present study. A tailored "in-house" database for protein identification was built on the basis of the result from 16S rDNA gene sequencing, that permitted to identify the bacteria soil community. The proteins deriving from 16S rDNA community data (Online Resource 1), present in UNiProtKB and tr EMBL databases, were collected and combined in order to query the resulting high-accuracy MS data, thus gaining in identification reliability for the investigated soil.

For each soil sample, the information arising from the application of three different extraction protocols for direct extraction were combined in order to reduce the risk of biased results [20]. In fact, they were based on different chemical-physical principles for cell lysis and protein extraction, thus improving their extraction complementarity. In particular, the method developed by Chourey and co-workers [22] was selected also because it was previously demonstrated particularly efficient for protein extraction from semiarid soils [21], such as serpentine one.

A total of ~~267~~260, ~~246~~ 238 and ~~299~~ 294 unique bacterial proteins were detected and identified by ~~by~~ combining the results from the three extraction methods for~~MS/MS analysis from~~ BS, BLS and NCS respectively (Online Resource 2). As expected [19, 23], each method had a high number of unique protein identification for the investigated soils; in particular, up to 1.5% proteins were identified in common, by more than one method, for a single soil. The obtained data suggests that the assignment between the methods are very similar, without strong bias towards specific classes of proteins or phyla [23]. Anyway, the method comparison in terms of membrane or intracellular proteins extraction pointed out a slight bias of Chourey method towards membrane proteins (corresponding to a percentage of about 60% of the total of proteins assigned to cellular component), whereas the NoviPure^{TM} seems to favour the extraction of intracellular proteins (corresponding to a percentage of about 60% of the total of proteins assigned to cellular component), probably thanks to the stronger cell lysis through beat beating [23]. Despite the hydrophobic nature of phenol, the Phenol-SDS method did not enrich for membrane proteins, as discussed by Leary et al. [19]; in fact we observed that, considering the proteins assigned to cellular component, Phenol-SDS method allowed to extract proteins equally distributed between intracellular and membrane cell parts.

In addition, as for protein concentration assessed by colorimetric assay, the method yielding the lowest values (in the 100-350 mg/L range) was the NoviPure^{TM} extraction; however, as recently discussed [23], this does not necessarily implicate a low number of identified proteins.

After extraction, a shotgun proteomic analysis based on microLC-HRMS technique was performed on tryptic digests, thus without previous protein pre-fractionation.

DNA-based bacterial composition in the rhizosphere samples and in bulk soil

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A total of 333694 raw pyrosequencing reads was obtained from the three soil samples (BS, BLS, NCS). After quality trimming a total of 257109 sequences were obtained including: 91953 reads for BS, 70707 reads for BLS, 94449 reads of NCS. Phylogenetic analysis of the BS and BLS and NCS revealed a microbial composition and complexity with at 12 phyla represented >1% at sequence level (Fig. 2). Among those the most represented ones were Actinobacteria (BS 43%, BLS 38%, NCS 48%), Proteobacteria (BS 16%, BLS 22%, NCS 31%) and Acidobacteria (BS 13% , BLS 12%, NCS 6%). Other phyla which were represented less than 10% of total were Chloroflexi, Cyanobacteria, Firmicutes, Gemmatimonadetes, Nitrospirae, Planctomycetes, Verrucomicrobia (Fig. 2). In addition, Bradyhizobium, unculturable Rhizobilaes and Solirubrobacter were found >4% in NCS and less abundant in BLS and BS (<1%) while Rubrobacter, uncultured Conexibacter sp., uncultured Chloroflexi sp., uncultured Acidithiobacillus sp. were found >4% in BS and BLS and less abundant in NCS (<1%). At genus level around 30% sequences belong to unculturable bacteria.

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Protein-based bacterial composition in the rhizosphere samples and in bulk soil

~~A total of 267, 246 and 299 unique bacterial proteins were detected and identified by MS/MS analysis from BS, BLS and NCS respectively (Online Resource 2).~~

At first, protein based phylogeny was assessed to analyse microbial functional community abundance. On the basis of the ratio between the number of proteins assigned to a certain phylum respect to the number of total identified protein, at phylum levels bacterial community was dominated by Proteobacteria in the three samples (Fig. 3~~2~~a). In BS and NCS Proteobacteria were about 70%, whereas in BLS were about 67%. The α-Proteobacteria class was dominated by Rhizobiales (BS 29.5%; BLS 26.4%; NCS 31.9 % of identified proteins), whereas the Sphingomonadales were only found in NCS 1% and BS 0.75% of total bacterial community (Fig. 3~~2~~b). The β-Proteobacteria were dominated by Burkholderiales with 5 % in BS and BLS samples and 3% in NCS respect to the total bacterial community. In the γ-Proteobacteria class most proteins were originated from Enterobacteriales (BS 12.5%; BLS 13.6%; NCS 9.1%), Pseudomonadales (BS 9.8%; BLS 9%; NCS 9.5%) and Xanthomonadales (BS 12.1%; BLS 12.3%; NCS 14.6%) (Fig. ~~2b~~3b).

Besides Proteobacteria, the Actinobacteria proteins represented up to 24% of those identified in the microbial community (Fig. 3~~2~~a). Corinebacteriales (BS 8%; BLS 10%; NCS 6.8%) and Micrococcales (BS 14.7%; BLS 13.6%; NCS 14.6%) were also present in all the three samples (Fig. 3~~2~~b). The specific class of Nocardioides was only present in BS and NCS at 0.4% and 0.6% of the total bacterial proteins respectively. Bacterioidetes were represented by Flavobacteriales at 0.7% 0.4% and 0.3% in BS, BLS and NC respectively, and Firmicutes phylum is also represented with *Bacillus methylotrophicus* (Bacteriales) and *Desulfitobacterium metallireducens* (Clostridiales) species (Fig. 4~~3~~). As far as the most representative species are concerned (>2%) *Methilobacterium mesophylicum* represents the 17.7 % of total proteins identified in BS, the 11.5% in BLS and the 13.5% in NCS sample, whereas *Phyllobacterium, Microbacterium oxidans*, *Pseudomonas oryzihabitans*, *Stenotrophomonas rhizophila* showed to be more represented in NCS (from 8.1 to 9.5% of total proteins) and in BLS (from 7 to 8.6% of total proteins) respect to BS (from 5.6 to 7.5 % of total proteins) sample. Finally, *Bacillus methylotrophicus* proteins were 2% in NCS and 0.8% both in BS and BLS (Fig. 4~~3~~).

Bacteria protein functions

According to Gene Ontology (GO) annotation (Fig. 5~~4~~) highly represented categories in all the three samples were associated with cellular and organic substances metabolic processes (45-50 %) in Biological Process (BP), organic and ion binding (35%-40%) in Molecular Function (MF) and intracellular localisation (27-32%) in Cellular Components (CC). Among the proteins not belonging to any of GO categories, which represented on average the 11% of total proteins, half showed a predicted signal peptide for protein secretion or transmembrane domain(s) while the remaining were considered as unclassified proteins. A selection of proteins belonging to GO terms "response to stimulus", "small molecule metabolic process", "oxidation-reduction process", "transport", "small molecule binding", "metal ion binding", "DNA binding", and "hydrolase activity" is indicated in Online Resource 3. Despite the few differences in abundance of GO categories, there are few common functions between samples (Online Resource 3). This heterogeneity is even more evident in Table 1, which shows the details on a selection of proteins focuses on the species showing a higher abundance of proteins in BLS and NCS respect to BS (*Phyllobacterium*, *Microbacterium oxidans*, *Pseudomonas oryzihabitans*, *Stenotrophomonas rhizophila*), and belonging to the GO terms "response to stimulus" and "transport". Among the proteins associated to "response to stimulus", there are protein functions only identified in rhizospheres and absent in BS: histidine kinase and putative sensor histidine kinase TcrY, a two-component signal transduction systems enabling bacteria to sense, respond, and adapt to a wide range of environments, stressors, and growth conditions; TonB-dependent receptor, a bacterial outer membrane protein that bind and transport ferric chelates called siderophores, nickel complexes, and carbohydrates; a signal recognition particle receptor TcrY, involved in targeting and insertion of nascent membrane proteins into the cytoplasmic membrane; a methyl accepting chemotaxis protein, a member bacterial receptors that mediate chemotaxis to diverse signals, responding to changes in the concentration of attractants and repellents in the environment by altering swimming behaviour. In addition, some proteins were only identified in NCS: a methytransferase which is known to function in modulating the action of chemotaxis proteins *vs* attractants; a protein-glutamate methylesterase which regulates bacterial chemotaxis and cellular movement directed in response to chemical gradients; an alkaline phosphatase synthesis sensor protein PhoR; a member of the two-component regulatory system PhoP/PhoR involved in the alkaline phosphatase genes regulation. PhoR functions as a membrane-associated protein kinase that phosphorylates PhoP in response to environmental signals.

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Differences between samples were also evident in the transport process. In particular, members of the protein family of ABC transporters from *Phyllobacterium* and *Pseudomonas oryzihabitans* species were present in both BLS and NCS and absent in the BS sample. In particular, an ABC-type metal ion transport system was identified in NCS along with ABC transporters, which have been identified also in BLS sample involved in uptake of sugar and aminoacids, together with porin subfamily and uracil-xanthine permease. Instead, multidrug efflux transporters were identified in BS soil and a glutathione-binding protein GsiB from *Microbacterium oxidans,* which is part of the ABC transporter complex GsiABCD involved in glutathione import. Cation:proton antiporters were found in all the samples.

Discussion

The bottlenecks of soil metaproteomics rely in the high complexity and heterogeneity of the soil matrix, the complexity of microbial community composition in the soil/rhizosphere samples together with the scarce bacteria soil genomic and protein databases and the high percentage of uncultivated genera, which largely affect protein identification as already evidenced by different authors [20, 28, 30]. The high number of unique identified proteins extracted by the three methods, supported the recommendation to combine different extraction approaches to gain better coverage and information amount from metaproteomic studies. In addition, ~~O~~our combined approach based on 16S rDNA profiling and metaproteomic analyses significantly improved protein identification in the soil samples collected from the heavy metal contaminated soil of Mount~~t.~~ Prinzera.

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At this purpose the Actinobacteria, which were more represented than Proteobacteria according to 16S rRNA gene-based community analysis were under-represented in the proteome fractions being the Proteobacteria the most represented phylum which was dominated by the α-Proteobacteria class (Rhizobiales order). This result can be explained with the *r*/*K* selection theory being Actinobateria *K-strategists*, with slow growth and low metabolic rates as compared to *r-strategists* like most Proteobacteria [38]. In addition, the Acidobacteria phylum which represents from 13 to 6% of the 16S rRNA gene-based community data was not detected in the metaproteomic analysis. This most likely resulted from insufficient genomic information of Acidobacteria, a recently devised phylum of Bacteria an *K-strategist* as well [39] not allowing protein identification.

Both 16S rRNA gene-based community analysis and m~~M~~etaproteomic analysis did not reveal specific bacteria genera present in only one sample and no large differences in the percentage of different GO categories were evidenced between BS, BLS and NCS. Soil samples were collected in an area of 10 m^2 ~~mq~~ and the peculiar chemical-physical characteristics of serpentine soil [40] as well as its ancient age may have allowed for a selection of specific bacterial genera adapted to grow in this extreme environment rather than for specific plant species-rhizosphere environment. Only slight differences in the percentage of single genera were observed in the NCS and BLS respect to BS. This microbial diversity would be consistent with the rhizosphere effect of the plant species [41]. Root exudates influence their associated microbial community by selecting specific group at the taxonomic level but most importantly at the functional level. Exudation provides a valuable source of carbon, while microorganisms that colonise the rhizosphere help plants to acquire not only phosphorous and potassium, but also Ni [42]. In addition, the results of the metaproteomic analysis revealed different functions of the most represented bacterial species present in the three samples, thus revealing a modulation of the bacterial functions according to the specific micro-environment (rhizosphere of *vs* bulk soil and rhizosphere of the two species).

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Most of the identified proteins were from bacterial strains which are known to be present in heavy metal polluted soils as *Methylobacterium mesophilicum* [43], *Rahnella* [44], *Tsukamurella paurometabola* [45]. Other bacteria with a high percentage of identified proteins, and more represented in the BLS and NCS samples, were also previously isolated from the rhizosphere of plant species growing on contaminated soil by cultivation dependent approaches most of them showing plant growth promoting traits [7]. In particular, *Bacillus methilotrophycus* and *Microbacterium oxidans* have already been isolated in other Ni-hyperaccumulator species such as *Alyssum bertolonii* [46], *Alyssum murale* [47], *Thlaspi goesingense* [43] and *N. caerulescens* [7]. *Pseudomonas oryzinabitans* is known to be a root colonising bacteria from the rhizoplane of pea (*Pisum sativum* L.) and Indian mustard (*Brassica juncea* L.) in polluted soils [48], while *Stenothophomonas rhizophila* was found to promote Zn uptake and biomass production in the hyperaccumulator *Sedum alfredii* [49]. *Phyllobacterium sp.* are known to colonise roots of different species and are metal mobilising plant growth beneficial bacteria that can have an active role in metal phytoextraction from soil [50].

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As far as protein functions are concerned, the results of our study show few proteins in commons between samples which could suggest a variability of responses of the same microorganism to microenvironment conditions. Differences in the types of proteins of the major components of soil microbial community are probably mediated by the presence of root exudates and can help to discriminate bacterial rhizospheric functions from bulk soil ones. This was evident as an example for the GO categories “response to stimulus” and “transport”.

The two component system (histidine kinase and a response regulator histidine kinase TcrY), identified in the rhizosphere samples BLS and NCS, is known to respond to a variety of environmental stimulus and it is postulated to play an important role in bacteria root colonisation [51]. In addition, in the rhizosphere soils the presence of TonB-dependent receptor indicates a cross-talk between bacteria and root environment since they are involved in the transport of ferric chelates called siderophores, as well as vitamin B12, nickel complexes, and carbohydrates [52]. Their action is mediated by TonB energy transducer which drive the active transport of ferric siderophores, and other ligands across the outer membrane [53]. Interestingly, very recently, a Ton-B receptor gene was identified also in the genus *Betula*, and high levels of Ton-B receptor transcript were found to be associated with Ni-resistant genotypes, suggesting the intriguing possibility of an event of horizontal gene transfer from bacteria to plants during the evolution of the genus *Betula* as a result of plant Ni tolerance [54].

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In the transport category a number of ABC transporters have been found mainly in the rhizosphere soil samples BLS and NCS. These complexes are multicomponent systems, which include one or two integral membrane proteins that constitute the channel across the membrane, and ATP binding protein that hydrolyses ATP and drives the transport, and in most cases an extracellular solute binding protein. Sugar ABC transporters facilitate the transport of a variety of sugars [~~54~~55]. Some microorganisms utilise highly efficient sugar ABC transporters to survive when substrate concentrations are extremely low.

The presence of the proteins involved in membrane transport and signal transduction might be related to the utilisation of rhizodeposition by root-associated bacteria as in our case *Phyllobacterium* and *Pseudomonas oryzihabitans Stenotrophomonas rhizophyla*, *Pseudomonas oryzihabitans*, and *Microbacterium oxidans*. This probably facilitates root colonisation by these bacteria [29].

Conclusions

In the present study, soil metaproteomics combined with 16S rDNA gene-based community analysis permitted to map the specific functions associated with microbial community colonising the heavy metal contaminated soil of Mount~~t~~. Prinzera Natural Reserve (Italy) and the rhizosphere of metal tolerant and hyperaccumulator plant species. Our metaproteomic results provide a solid foundation to understand the microbial community functions in a metal rich soil and the possible interactions with plants colonising that stressful environment. Studies dealing with environmental proteomics for structural and functional characterization of microbial communities in their natural habitat require high performance MS instruments, availability of suited databases for reliable protein search and identification as well as efforts for the development and/or evaluation of protocols for efficient soil protein extraction and extract clean-up.

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References

1. Baker AJM, Ernst WHO, van der Ent A, Malaisse F, Ginocchio R. Metallophytes: the unique biological resource, its ecology and conservational status in Europe, central Africa and Latin America. In Batty LC, Hallberg K B, editors. Ecology of industrial pollution. Cambridge University Press, Cambridge; 2010, pp.7-40.

2. Baker AJM, McGrath SP, Reeves RD, Smith JAC. Metal hyper accumulator plants: a review of the ecology and physiology of a biological resource for phytoremediation of metal-polluted soils. In Terryand N, Bañuelos G, editors. Phytoremediation of Contaminated Soil and Water. Boca Raton, FL:CRC Press; 2000, pp.85-107.

3. Chaney RL, Angle JS, Broadhurst CL, Peters CA, Tappero RV, Sparks DL. Improved understanding of hyperaccumulation yields commercial phytoextraction and phytomining technologies. J Environ Qual. 2007;36:1429-43.

4. Krzciuk K, Gałuszka A. Prospecting for hyperaccumulators of trace elements: a review. Crit Rev Biotechnol. 2015;35:522-32.

5. Alford EM, Pilon-Smits EAH, Paschke MW. Metallophytes-a view from the rhizosphere. Plant Soil. 2010;337:33-50.

6. Ma Y, Prasad MNV, Rajkumar M, Freitas H. Plant growth promoting rhizobacteria and endophytes accelerate phytoremediation of metalliferous soils. Biotechnol Adv. 2011;29:248-58.

7. Visioli G, D'Egidio S, Vamerali T, Mattarozzi M, Sanangelantoni AM. Culturable endophytic bacteria enhance Ni translocation in the hyperaccumulator *Noccaea caerulescens*. Chemosphere. 2014;117:538-44.

8. Sessitsch A, Kuffner M, Kidd P, Vangronsveld J, Wenzel WW, Fallman K, Puschenreiter M. The role of plant-associated bacteria in the mobilization and phytoextraction of trace elements in contaminated soils. Soil Biol Biochem. 2013;60:182-94.

9. Visioli G, Vamerali T, Mattarozzi M, Dramis L, Sanangelantoni AM. Combined endophytes inoculants enhance nickel phytoextraction from serpentine soil in the hyperaccumulator *Noccaea caerulescens*. Front Plant Sci. 2015;6:article 638.

10. Berg J, Brandt KK, Al-Soud WA, Holm PE, Hansen LH, Sørensen SJ, Nybroe O. Selection for Cu-tolerant bacterial communities with altered composition, but unaltered richness, via long-term Cu exposure. Appl Environ Microbiol. 2012;78:7438-46.

11. Gołębiewski M, Deja-Sikora E, Cichosz M, Tretyn A, Wróbel B. 16S rDNA pyrosequencing analysis of bacterial community in heavy metals polluted soils. Microb Ecol. 2014;67:635-47.

12. Hettich RL, Sharma R, Chourey K, Giannone RJ. Microbial metaproteomics: identifying the repertoire of proteins that microorganism use to compete and cooperate in complex environmental communities. Curr Opin Microbiol. 2012;15:373-80.

13. Wilmes P, Heintz-Buschart A, Bond PL. A decade of metaproteomics: where we stand and what the future holds. Proteomics. 2015,15:3409-17.

14. Arsène-Ploetze F, Bertin PN, Carapito C. Proteomic tools to decipher microbial community structure and functioning. Environ Sci Pollut Res. 2015;22:13599-612.

15. Bastida F, Moreno JL, Nicolás C, Hernández T, García C. Soil metaproteomics: a review of an emerging environmental science. Significance, methodology and perspectives. Eur J Soil Sci. 2009;60:845-59.

16. Hettich RL, Pan C, Chourey K, Giannone RJ. Metaproteomics: Harnessing the Power of High Performance Mass Spectrometry to Identify the Suite of Proteins That Control Metabolic Activities in Microbial Communities. Anal Chem. 2013;85:4203-14.

17. Becher D, Bernhardt J, Fuchs S, Riedel K. Metaproteomics to unravel major microbial players in leaf litter and soil environments: Challenges and perspectives. Proteomics. 2013;13:2895-909.

18. Giagnoni L, Magherini F, Landi L, Taghavi S, Modesti A, Bini L, Nannipieri P, Van der leliec D, Renella G. Extraction of microbial proteome from soil: potential and limitations assessed through a model study. Eur J Soil Sci. 2011;62:74-81.

19. Leary DH, Hervey WJ, Deschamps JR, Kusterbeck AW, Vora GJ. Reprint of "Which metaproteome? The impact of protein extraction bias on metaproteomic analyses. Mol Cell Probes. 2014,28:51-7.

20. Keiblinger KM, Wilhartitz IC, Schneider T, Roschitzki B, Schmid E, Eberl L, Riedel K, Zechmeister-Boltenstern S. Soil metaproteomics - Comparative evaluation of protein extraction protocols. Soil Biol Biochem. 2012;54:14-24.

21. Bastida F, Hernández T, García C. Metaproteomics of soils from semiarid environment: Functional and phylogenetic information obtained with different protein extraction methods. J Proteomics. 2014;101:31-42.

22. Chourey, K.; Jansson, J.; VerBerkmoes, N.; Shah, M.; Chavarria, K. L.; Tom, L. M.; Brodie, E. L.; Hettich, R. L. Direct Cellular Lysis/Protein Extraction Protocol for Soil Metaproteomics. J Proteome Res. 2010,9:6615-22.

23. Hansen SH, Stensballe A, Nielsen PH, Herbst F-A. Metaproteomics: Evaluation of protein extraction from activated sludge. Proteomics. 2014;14:2535-9.

24. Benndorf D, Balcke GU, Harms H, von Bergen M. Functional metaproteome analysis of protein extracts from contaminated soil and groundwater. ISME J. 2007;1:224-34.

25. Bastida F, Jehmlich N, Lima K, Morris BEL, Richnow HH, Hernández T, von Bergen M, García C. The ecological and physiological responses of the microbial community from a semiarid soil to hydrocarbon contamination and its bioremediation using compost amendment. J Proteomics. 2016;135:162-9.

26. Wu L, Wang H, Zhang Z, Lin R, Zhang Z, Lin W. Comparative Metaproteomic Analysis on Consecutively *Rehmannia glutinosa*-Monocultured Rhizosphere Soil. PLoS One. 2011;6:e20611.

27. Wang H-B, Zhang Z-X, Li H; He H-B, Fang C-X, Zhang A-J, Li Q-S, Chen R-S, Guo X-K, Lin H-F, Wu L-K, Lin S, Chen T, Lin R-Y, Peng X-X, Lin W-X. Characterization of Metaproteomics in Crop Rhizospheric Soil. J Proteome Res. 2011;10:932-40.

28. Knief C, Delmotte N, Chaffron S, Stark M, Innerebner G, Wassmann R, von Mering C, Volholt JA. Metaproteogenomic analysis of microbial communities in the phyllosphere and rhizosphere of rice. ISME J. 2012;6:1378-90.

29. Lin W, Wu L, Lin S, Zhang A, Zhou M, Lin R, Wang H, Chen J, Zhang Z, Lin R. Metaproteomic analysis of ratoon sugarcane rhizospheric soil. BMC Microbiol. 2013;13:article135.

30. Bao Z, Okubo T, Kubota K, Kasahara Y, Tsurumaru H, Anda M, Ikeda S, Minamisawa K. Metaproteomic identification of diazotrophic methanotrophs and their localization in root tissues of field-grown rice plants. Appl Environ Microbiol. 2014;80:5043-52.

31. Milani C, Hevia A, Foroni E. Duranti S, Turroni F, Lugli GA, Sanchez B, Martín R, Gueimonde M, van Sinderen D, Margolles A, Ventura M. Assessing the fecal microbiota: an optimized ion torrent 16S rRNA gene-based analysis protocol. PLoS One. 2013;8:e68739.

32. Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK, Fierer N, Gonzalez Peña A, Goodrich JK, Gordon JI, Huttley GA, Kelley ST, Knights D, Koenig JE, Ley RE, Lozupone CA, McDonald D, Muegge BD, Pirrung M, Reeder J, Sevinsky JR, Turnbaugh PJ, Walters WA, Widmann J, Yatsunenko T, Zaneveld J, Knight R. QIIME allows analysis of high-throughput community sequencing data. Nat Methods. 2010;7:335-6.

33. Edgar RC. Search and clustering orders of magnitude faster than BLAST. Bioinformatics. 2010;26:2460-1.

34. Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P, Peplies J, Glöckner FO. The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. Nucl. Acids Res. 2013;41:D590-6.

35. Lozupone C, Knight R. UniFrac: a new phylogenetic method for comparing microbial communities. Appl Environ Microbiol. 2005,71:8228-35.

36. Conesa A, Götz S, García-Gómez JM, Terol J, Talón M, Robles M. Blast2GO: a universal tool for annotation, visualization and analysis in functional genomics research. Bioinformatics. 2005;21:3674-6.

37. Kall L, Krogh A, Sonnhammer EL. A combined transmembrane topology and signal peptide prediction method. J Mol Biol. 2004;338:1027-36.

38. Freilich S, Kreimer A, Meilijson I, Gophna U, Sharan R, Ruppin E. The large-scale organization of the bacterial network of ecological co-occurrence interactions. Nucleic Acids Res. 2010;38:3857-68.

39. Naether A, Foesel BU, Naegele V, Wüst PK, Weinert J, Bonkowski M, Alt F, Oelmann Y, Polle A, Lohaus G, Gockel S, Hemp A, Kalko EKV, Linsenmair KE, Pfeiffer S, Renner S, Schöning I, Weisser WW, Wells K, Fischer M, Overmann J, Friedrich MW. Environmental Factors Affect Acidobacterial Communities below the Subgroup Level in Grassland and Forest Soils. Appl Environ Microbiol. 2012;78:7398-406.

40. Visioli G, Vincenzi S, Marmiroli M, Marmiroli N. Correlation between phenotype and proteome in the Ni hyperaccumulator *Noccaea caerulescens* subsp.caerulescens. Environ Exp Bot. 2012;77:156-64.

41. Reinhold-Hurek B, Bünger W, Burbano CS, Sabale M, Hurek T. Roots shaping their microbiome: global hotspots for microbial activity. Annu Rev Phytopathol. 2015;53:403-24.

42. Ma Y, Rajkumar M, Freitas H. Isolation and characterization of Ni mobilizing PGPB from serpentine soils and their potential in promoting plant growth and Ni accumulation by Brassica spp. Chemosphere. 2009;75:719-25.

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43. Idris R, Trifonova R, Puschenreiter M, Wenzel WW, Sessitsch A. Bacteria communities associated with flowering plants of the Nihyperaccumulator *Thlaspi goesingense*. Appl Environ Microbiol. 2004;70:2667-77.

44. He H, Ye Z, Yang D, Yan J, Xiao L, Zhong T, Yuan M, Cai X, Fang Z, Jing Y. Characterization of endophytic Rahnella sp. JN6from Polygonum pubescens and its potential in promoting growth and Cd, Pb, Zn uptake by Brassica napus. Chemosphere. 2013;90:1960-5.

45. Farinati S, DalCorso G, Panigati M, Furini, A. Interaction between selected bacterial strains and *Arabidopsis halleri* modulates shoot proteome and cadmium and zinc accumulation. J Exp Bot. 2011,62:3433-47.

46. Barzanti R, Ozino F, Bazzicalupo M, Gabrielli R, Galardi F, Gonnelli C, Mengoni A. Isolation and characterization of endophytic bacteria from the nickel hyperaccumulator plant *Alyssumbertolonii*. Microb Ecol. 2007;53:306-16.

47. Abou-Shanab RA, Angle JS, Chaney RL. Bacterial inoculants affecting nickel uptake by Alyssum murale from low, moderate and high Ni soils. Soil Biol Biochem. 2006;38:2882-9.

48. Belimov AA, Safronova VI, Sergeyeva TA, Egorova TN, Matveyeva VA, Tsyganov VE, Borisov AY, Tikhonovich IA, Kluge C, Preisfeld A, Dietz K.-J, Stepanok VV. Characterization of plant growth promoting rhizobacteria isolated from polluted soils and containing 1-aminocyclopropane-1-carboxylate deaminase. Can J Microbiol. 2001;47:642-52.

49. Long X-X, Chen X-M, Wong JW-C, Wei Z-B, Wu Q-T. Feasibility of enhanced phytoextraction of Zn contaminated soil with Zn mobilizing and plant growth promoting endophytic bacteria. Trans. Nonferrous Met Soc China. 2013;23:2389-96.

50. Rajkumar M, Ae N, Freitas H. Endophytic bacteria and their potential to enhance heavy metal phytoextraction. Chemosphere. 2009;77:153-60.

51. Dekkers LC, Bloemendal CJP, de Weger LA, Wijffelman CA, Spaink HP, Lugtenberg BJ. A two-component system plays an important role in the root-colonising ability of Pseudomonas fluorescens strain WCS365. Mol Plant Microbe Interact. 1998;11:45-56.

52. Nojnai N, Guillier M, Barnard TJ, Buchanan SK. TonB-dependent transporters: regulation, structure, and function. Annu Rev Microbiol. 2010;64:43-60.

53. Binkman KK, Larsen RA. Interactions of the Energy Transducer TonB with Noncognate Energy-Harvesting Complexes. J Bacteriol. 2008;190:421-7.

54. Theriault G, Nkongolo KK. Evidence of prokaryote like protein associated with nickel resistance in higher plants: horizontal transfer of TonB-dependent receptor/protein in *Betula* genus or de novo mechanisms? Heredity 2016; 1-8.

545. Elferink MG, Albers SV, Konings WN, Driessen AJ. Sugar transport in Sulfolobus solfataricus is mediated by two families of binding protein-dependent ABC transporters. Mol Microbiol. 2001;39:1494-5.

Fig. 1 Schematic workflow for the integrated 16Sr DNA and metaproteomic approach followed in the present study

Fig.2 Taxonomic distribution of phyla based on 16S rDNA reads across the three soil samples (BS, BLS and NCS).

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Fig. ~~3 ~~-3 Taxonomic distribution of phyla based on LC-MS/MS protein data a) at phylum level and b) at order level across the three soil samples: bulk soil (BS), *Biscutella laevigata* rhizosphere (BLS) and *Noccaea caerulescens* rhizosphere (NCS)

Fig. 44 Most represented species (y-axis) in the three soil samples, bulk soil (BS), *Biscutella laevigata* rhizosphere (BLS) and *Noccaea caerulescens* rhizosphere (NCS) according to percentage of protein functions considered >2% at least in one sample (x-axis)

Fig.~~ 5~~5 Gene Ontology (GO) for the identified soil proteins. In the x-axis are represented the different GO classes respect to Molecular functions, Biological Processes and Cellular compartment. The y-axis represents the proportion of proteins for every GO annotation

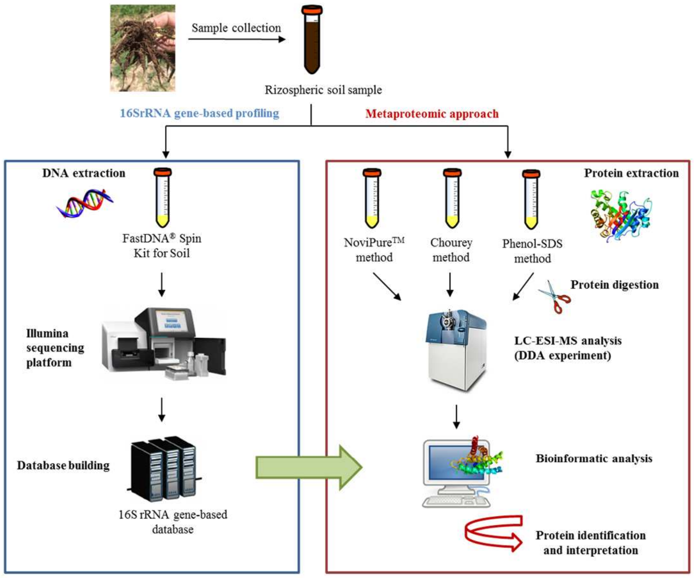

Fig.1 Schematic workflow for the integrated 16Sr DNA and metaproteomic approach followed in the present study

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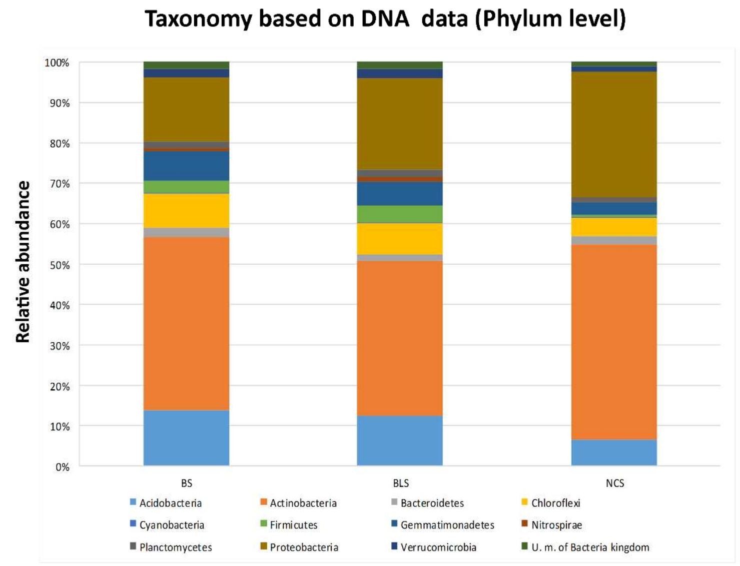

Fig.2 Taxonomic distribution of phyla based on 16S rDNA reads across the three soil samples (BS, BLS and NCS).

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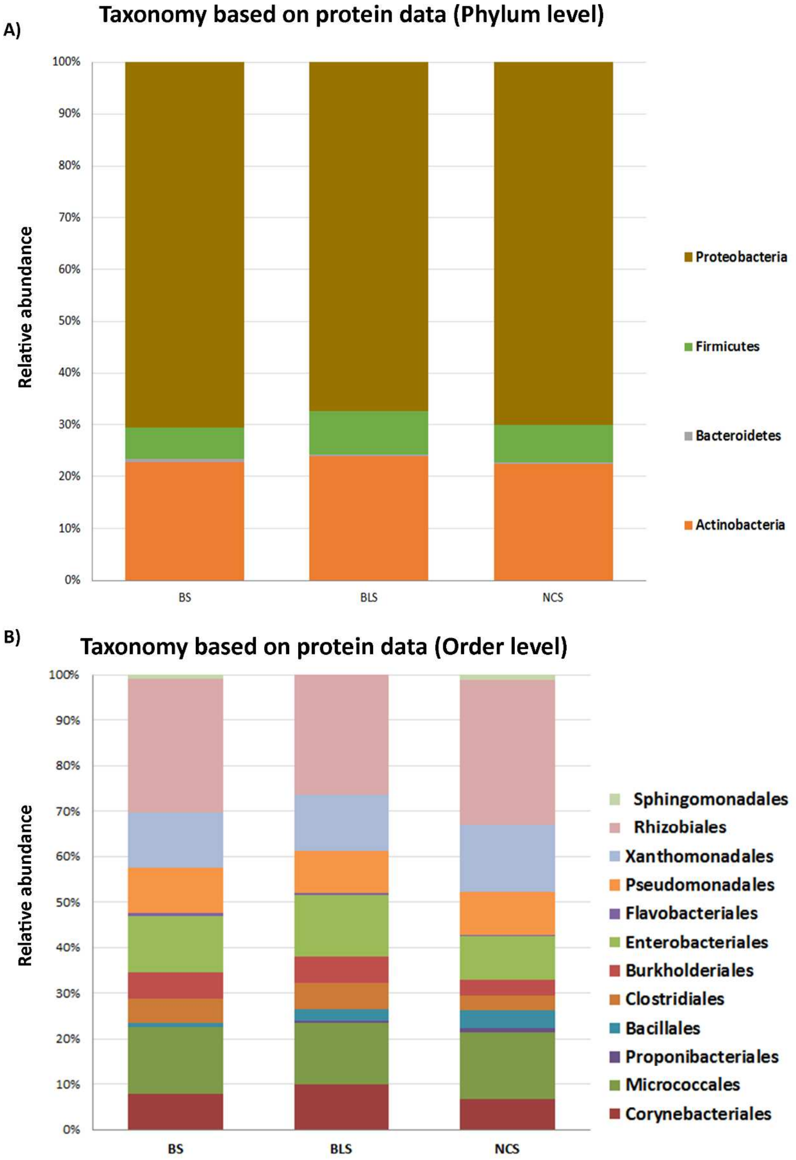

Fig.3 Taxonomic distribution of phyla based on LC-MS/MS protein data a) at phylum level and b) at order level across the three soil samples: bulk soil (BS), Biscutella laevigata rhizosphere (BLS) and Noccaea caerulescens rhizosphere (NCS)

209x297mm (300 x 300 DPI)

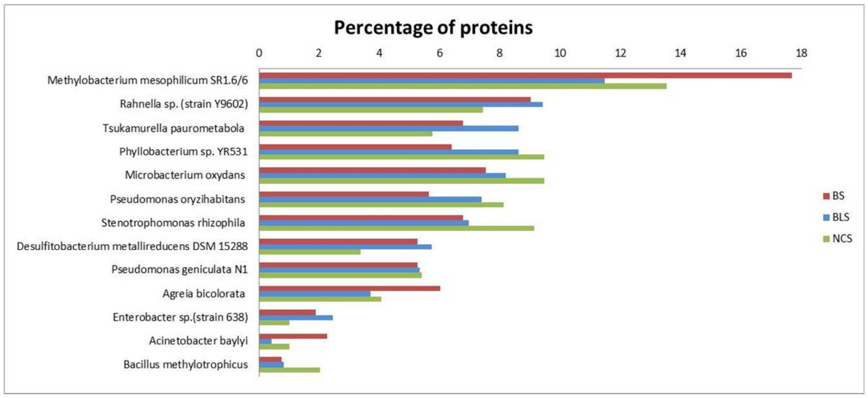

Fig.4 Most represented species (y-axis) in the three soil samples, bulk soil (BS), Biscutella laevigata rhizosphere (BLS) and Noccaea caerulescens rhizosphere (NCS) according to percentage of protein functions considered >2% at least in one sample (x-axis)

297x209mm (300 x 300 DPI)

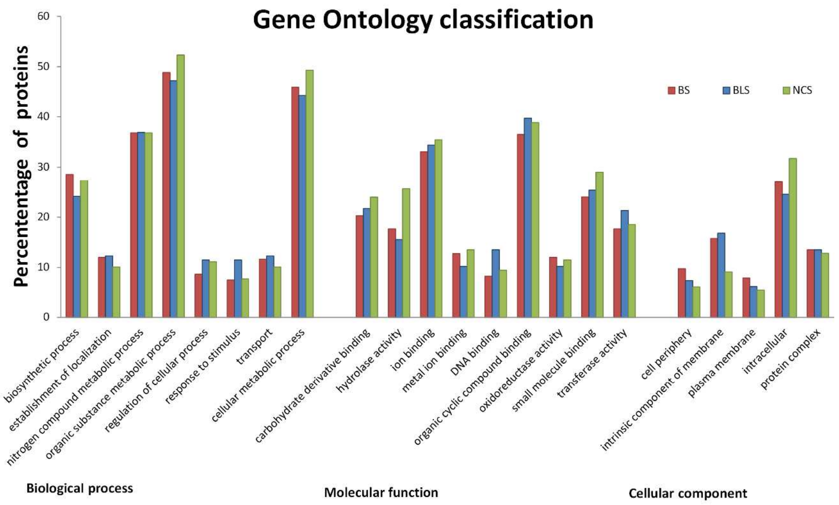

Fig. 5 Gene Ontology (GO) for the identified soil proteins. In the x-axis are represented the different GO classes respect to Molecular functions, Biological Processes and Cellular compartment. The y-axis represents the proportion of proteins for every GO annotation

297x209mm (300 x 300 DPI)

Table 1 List of proteins belonging to GO terms "response to stimulus" and "transport" in the three soil samples, focusing on the most represented species in *Biscutella laevigata* rhizosphere (BLS) and *Noccaea caerulescens* rhizosphere (NCS) respect to bulk soil (BS)

	Species	Accession number	Protein
		BS	
Response to stimulus	*Phyllobacterium*	J3HQ21	Diguanylate cyclase (GGDEF) domain-containing protein
	Pseudomonas oryzihabitans	A0A0D7FJ11 A0A0D7FLL5	Flagellar rod assembly protein FlgJ Chemotaxis protein
	Stenotrophomonas rhizophila	A0A023Y6Q8 A0A023Y1S1	Histidine kinase DeoR family transcriptional regulator
Transport	*Microbacterium oxydans*	A0A0F0KHN1 A0A0F0L8E2	Glutathione-binding protein GsiB Na(+)/H(+) antiporter NhaA
	Stenotrophomonas rhizophila	A0A023XZA6 A0A023XZI7 A0A023Y8Q3	Multidrug transporter MatE Multidrug transporter Membrane protein
		BLS	
Response to stimulus	*Microbacterium oxydans*	A0A0F0LD64 A0A0F0KXV3	Putative 3-methyladenine DNA glycosylase Putative sensor histidine kinase TcrY
	Pseudomonas oryzihabitans	A0A0D7FMB2	Cold-shock protein
	Stenotrophomonas rhizophila	A0A023Y216	TonB-dependent receptor
Transport	*Microbacterium oxydans*	A0A0F0LBN3 A0A0F0L713	ATP-binding/permease protein CydD Oligopeptide-binding protein OppA
	Phyllobacterium	J2VEM8 J2V3B6 J2VYX2 J3C6R8 J3HM91	ATPase component of various ABC-type transport systems with duplicated ATPase domain RND family efflux transporter, MFP subunit Putrescine-binding periplasmic protein ABC-type sugar transport system, periplasmic component ATPase component of uncharacterized ABC-type transporter
	Pseudomonas oryzihabitans	A0A0D7F6W1 A0A0D7F8R6 A0A0D7FAY5	Amino acid ABC transporter substrate-binding protein MFS transporter Protein-export protein SecB
	Stenotrophomonas rhizophila	A0A023Y0X6	Membrane protein TolA
		NCS	

Response to stimulus	*Microbacterium oxydans*	A0A0F0L9I6	Alkaline phosphatase synthesis sensor protein PhoR
		A0A0F0L7R0	Putative sensor histidine kinase TcrY
		A0A0F0L4I6	Signal recognition particle receptor FtsY
	Pseudomonas oryzihabitans	A0A0D7FBB2	Histidine kinase
		A0A0D7FBT3	Protein-glutamate methylesterase
		A0A0D7FCL7	Energy transducer TonB
	Stenotrophomonas rhizophila	A0A023Y6D3	TonB-dependent receptor
		A0A023Y3L3	Chemotaxis protein
		A0A023Y190	Uncharacterized protein
		A0A023Y3A7	Histidine kinase
		A0A023Y788	Methyltransferase
Transport	*Phyllobacterium*	J3HSJ8	ABC-type metal ion transport system, periplasmic component/surface adhesin
		J3CBG2	ABC-type polar amino acid transport system, ATPase component
		J3C5F3	Porin subfamily
		J3HPJ5	Uracil-xanthine permease
	Pseudomonas oryzihabitans	A0A0D7F835	Sugar ABC transporter ATPase
		A0A0D7FBB1	Glutamine ABC transporter ATP-binding protein
	Stenotrophomonas rhizophila	A0A023XZ46	Cation:proton antiporter

On-line resource 1. List of bacterial genera and species identified by 16S rRNA profiling and utilised to build an "in-house" bacterial protein database.

Taxon

U. m. of Actinobacteria class
U. m. of Alphaproteobacteria class
U. m. of Bradyrhizobium genera
U. m. of Thermoleophilia class
U. m. of Sphingomonas genera
U. m. of Pseudonocardia genera
U. m. of Rubrobacter genera
U. m. of Actinobacteria phylum
U. m. of RB41 family
U. m. of Acetobacteraceae family
U. m. of Solirubrobacter genera
U. m. of Actinoplanes genera
U. m. of Geodermatophilaceae family
U. m. of Gemmatimonadaceae family
U. m. of Acidobacteria class
U. m. of 480-2 family
U. m. of Bacteria kingdom
U. m. of Acidimicrobiia class
U. m. of Xanthobacteraceae family
U. m. of Micromonosporaceae family
U. m. of Streptomyces genera
U. m. of Patulibacter genera
U. m. of KD4-96 class
U. m. of Gemmatimonas genera
U. m. of Mycobacterium genera
U. m. of DA111 family
U. m. of Nocardioides genera
U. m. of Crossiella genera
U. m. of DA101 soil group family
U. m. of Candidatus Alysiosphaera genera
U. m. of Blastocatella genera
Bradyrhizobium japonicum
U. m. of Roseiflexus genera
U. m. of TK10 class
U. m. of Chitinophagaceae family
U. m. of Nocardioidaceae family
Methylobacterium populi
U. m. of Streptosporangiaceae family
U. m. of Modestobacter genera
U. m. of Phycisphaerae class
U. m. of Reyranella genera
U. m. of Phenylobacterium genera
U. m. of 288-2 family

U. m. of Kineosporiaceae family
U. m. of Microlunatus genera
U. m. of Methylobacterium genera
U. m. of Holophagae class
U. m. of Thermomicrobia class
U. m. of 0319-6M6 family
U. m. of Rhodoplanes genera
U. m. of Rhizomicrobium genera
U. m. of Bradyrhizobiaceae family
U. m. of Sphingomonadaceae family
U. m. of Pseudonocardiaceae family
U. m. of Bryobacter genera
U. m. of Anaerolineaceae family
U. m. of Comamonadaceae family
U. m. of Rhodovastum genera
U. m. of Haliangium genera
U. m. of Devosia genera
U. m. of Nitrosomonadaceae family
U. m. of Deltaproteobacteria class
Kribbella catacumbae
Amycolatopsis orientalis
U. m. of Chloroplast class
U. m. of Betaproteobacteria class
U. m. of Actinomycetospora genera
U. m. of Candidatus Solibacter genera
U. m. of Geodermatophilus genera
U. m. of Phyllobacteriaceae family
U. m. of Marmoricola genera
U. m. of JG34-KF-361 family
U. m. of Craurococcus genera
U. m. of 11-24 family
U. m. of Microvirga genera
U. m. of ABS-19 family
U. m. of Gammaproteobacteria class
U. m. of Caulobacteraceae family
Rhizobium etli
U. m. of Dactylosporangium genera
U. m. of Brevundimonas genera
U. m. of Krasilnikovia genera
U. m. of Rhodospirillaceae family
U. m. of Chthoniobacter genera
U. m. of Nitrospira genera
U. m. of Pedomicrobium genera
U. m. of Planosporangium genera
U. m. of Gemmatimonadetes class
U. m. of Chloroflexia class
U. m. of 1174-901-12 family

U. m. of Lysinimonas genera
Rhodococcus erythropolis
U. m. of Chloroflexi phylum
U. m. of Ferruginibacter genera
U. m. of Cytophagaceae family
U. m. of Caldilineaceae family
U. m. of OPB35 soil group class
U. m. of Flavitalea genera
U. m. of Pseudolabrys genera
U. m. of Acidobacteriaceae (Subgroup 1) family
U. m. of Propionibacteriaceae family
U. m. of Massilia genera
U. m. of Gaiella genera
U. m. of Hirschia genera
U. m. of Elev-16S-1332 family
U. m. of Opitutus genera
U. m. of Paenibacillus genera
U. m. of Spartobacteria class
Bacillus nealsonii
U. m. of Iamia genera
U. m. of Chryseolinea genera
U. m. of Flavobacterium genera
U. m. of Microbacteriaceae family
U. m. of Flavisolibacter genera
U. m. of Byssovorax genera
U. m. of Sorangium genera
U. m. of CL500-29 marine group genera
Nocardioides hankookensis
U. m. of Phaselicystis genera
U. m. of MB-A2-108 class
U. m. of Beijerinckiaceae family
U. m. of Proteobacteriaphylum
U. m. of Planctomycetaceae family
U. m. of KF-JG30-B3 family
Planctomycetales bacterium Ellin7224
U. m. of Hyphomicrobiaceae family
U. m. of Candidate division TM7 phylum
U. m. of S085 class
U. m. of Desulfurellaceae family
U. m. of Polyangiaceae family
U. m. of Verrucomicrobiaceae family
U. m. of Friedmanniella genera
U. m. of Chitinophaga genera
U. m. of MNG7 family
U. m. of Sandaracinaceae family
U. m. of Bacillus genera
U. m. of Leptothrix genera

U. m. of YNPFFP1 family
U. m. of WCHB1-60 phylum
U. m. of Tardiphaga genera
U. m. of Acidimicrobiaceae family
U. m. of Woodsholea genera
U. m. of env.OPS 17 family
U. m. of Ktedonobacteria class
U. m. of A0839 family
Cohnella soli
U. m. of Gemmata genera
U. m. of DUNssu371 family
U. m. of Hyphomicrobium genera
U. m. of Rhodobium genera
U. m. of P2-11E class
U. m. of Nakamurella genera
U. m. of Variovorax genera
U. m. of OM27 clade genera
U. m. of AKYH767 family
U. m. of Siphonobacter genera
U. m. of Segetibacter genera
U. m. of Saprospiraceae family
U. m. of BD1-5 phylum
Methylobacterium hispanicum
U. m. of Steroidobacter genera
U. m. of Candidatus Microthrix genera
U. m. of Bacteroidetesphylum
U. m. of Oxalobacteraceae family
U. m. of Anaeromyxobacter genera
Pseudonocardia halophobica
U. m. of Niastella genera
U. m. of Sediminibacterium genera
U. m. of Nocardia genera
U. m. of Kibdelosporangium genera
uncultivated soil bacterium clone C112
U. m. of ML635J-21 class
U. m. of Rhizobium genera
U. m. of Bdellovibrio genera
U. m. of Caenimonas genera
U. m. of Nordella genera
U. m. of Actinoallomurus genera
Conexibacter woesei Iso977N
Chitinophaga sp. SKC's SSSS
U. m. of I-10 family
U. m. of Dongia genera
U. m. of FFCH12655 family
U. m. of Fibrobacteraceae family
U. m. of Q3-6C1 family

uncultured bacterium CSL142
U. m. of SHA-109 phylum
U. m. of Armatimonadetesphylum
U. m. of FFCH7168 family
U. m. of Rhodomicrobium genera
U. m. of Arenimonas genera
U. m. of DS-100 family
Azospirillum brasilense
U. m. of Elstera genera
U. m. of Bacteroides genera
U. m. of Janthinobacterium genera
U. m. of Xanthomonadaceae family
U. m. of Geminicoccus genera
U. m. of Pir4 lineage genera
U. m. of Terrimonas genera
U. m. of JG30-KF-CM66 class
Paenibacillus alginolyticus
Gemmatimonadetes bacterium LX87
U. m. of Defluviicoccus genera
U. m. of Conexibacter genera
U. m. of Pirellula genera
uncultured bacterium 17F9 (Acidobacteria class)
U. m. of Nitrospinaceae family
Nocardioides albus
Nocardioides sp. MSL 24
U. m. of Sphingobacteriia class
U. m. of Methylocystis genera
U. m. of Amaricoccus genera
U. m. of Ramlibacter genera
delta proteobacterium LX33
Pseudomonas fulva
U. m. of Opitutae class
U. m. of NS9 marine group family
U. m. of SJA-149 family
U. m. of Microbacterium genera
U. m. of Flavihumibacter genera
uncultured sludge bacterium S41
Paenibacillus glycanilyticus
U. m. of Bacilli class
U. m. of Roseococcus genera
U. m. of Gitt-GS-136 class
U. m. of Cystobacteraceae family
U. m. of Candidatus Xiphinematobacter genera
U. m. of MSB-1E8 family
U. m. of Candidatus Entotheonella genera
uncultured bacterium 66 (Acidobacteria class)
Microbacterium flavescens

Actinomadura madurae
U. m. of KD3-93 family
uncultured bacterium #0319-6E22 (OPB56 famiily)
U. m. of Chloroflexus genera
Lysinibacillus fusiformis
U. m. of Lysinibacillus genera
U. m. of Nitrospiraceae family
Acidobacteria bacterium IGE-001
U. m. of Agromyces genera
U. m. of Aeromicrobium genera
Bacillus flexus
Bacillus mycoides
U. m. of 0319-6A21 family
U. m. of mitochondria family
U. m. of Rubellimicrobium genera
U. m. of Elusimicrobia class
U. m. of OM1 clade family
U. m. of Pla4 lineage class
U. m. of Rhodobiaceae family
U. m. of Candidatus Koribacter genera
U. m. of Ilumatobacter genera
bacterium Ellin6530
Chorispora bungeana
U. m. of Chungangia genera
Psychrobacillus psychrodurans
U. m. of Alcaligenaceae family
U. m. of Rhizobacter genera
U. m. of Chromatiaceae family
Pseudomonas brassicacearum
unidentified eubacterium EA25
U. m. of Candidate division WS3 phylum
U. m. of Soil Crenarchaeotic Group(SCG) class
Acidobacteria bacterium IGE-003
Acidobacteria bacterium IGE-011
uncultured bacterium 293 (Acidobacteria class)
D_uncultured bacterium 98 (Acidobacteria class)
U. m. of Acidobacteria phylum
U. m. of TakashiAC-B11 class
U. m. of Hymenobacter genera
U. m. of Ohtaekwangia genera
U. m. of Cytophagia class
Flavobacterium resistens
U. m. of NS11-12 marine group family
U. m. of 08D2Z23 family
U. m. of OPB56 family
U. m. of SJA-28 family
uncultured sludge bacterium S14

U. m. of Ardenticatenia class
U. m. of Crinalium genera
U. m. of Microcoleus genera
U. m. of Cyanobacteria class
U. m. of Melainabacteria class
Bacillus niacini
U. m. of Oceanobacillus genera
U. m. of Paenibacillaceae family
U. m. of Planococcaceae family
U. m. of Methylobacteriaceae family
U. m. of Lautropia genera
U. m. of Paucibacter genera
U. m. of Elev-16S-1158 family
U. m. of Enhygromyxa genera
U. m. of Nitrosococcus genera
U. m. of Spirochaeta genera

Bulk soil (BS)

Chourey method (MS/MS spectra: 9152)

	Accession Name	**Protein Name**	**Protein Mass**	**Length**	**Peptides**
1	ATPB_SPHAL	ATP synthase subunit beta OS=Sphingopyxis alaskensis	53945	513	MATAPATEK FTQAGSEVSALLGR
2	CH602_BURTA	60 kDa chaperonin 2 OS=Burkholderia thailandensis	57054	546	ALEEPLR AAVEEGIVPGGGVALIR
3	M7Y9R2_9RHIZ	RND family efflux transporter MFP subunit OS=Methylobacterium mesophilicum	54574	516	LSGTSGHDMFK EGDGGTTVTISPGK
4	A0A0D7FD14_9PSED	Thioredoxin OS=Pseudomonas oryzihabitans	11537	108	SGGLVQR
5	A0A0D7QNJ0_9MICO	Lipoprotein OS=Agreia bicolorata	48633	443	VTAAITR QSVTVPSYER
6	A0A0D7QMN7_9MICO	Ribonuclease 3 OS=Agreia bicolorata	25395	243	QAEASAAR
7	PCKG_ACIAD	Phosphoenolpyruvate carboxykinase [GTP] OS=Acinetobacter baylyi	67776	609	IASAMGR KMARMGK
8	M7YFV6_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	49208	472	ASRAIPR
9	D5UXT1_TSUPD	Diguanylate cyclase with PAS/PAC sensor OS=Tsukamurella paurometabola	47682	443	SAEEGAR
10	W0EDN5_9FIRM	Pseudouridine synthase OS=Desulfitobacterium metallireducens	28715	257	EVPQRVYPIGR
11	M7YUW6_9RHIZ	Peptidyl-prolyl cis-trans isomerase OS=Methylobacterium mesophilicum	19287	182	IVSMTLAEK
12	A0A0D7FDJ7_9PSED	Uncharacterized protein OS=Pseudomonas oryzihabitans	139381	1290	SALTGGNR
13	A0A0H3F3S2_RAHSY	Uncharacterized protein OS=Rahnella sp.	11570	101	IDALMQQSKDAIR
14	ACCD_ACIAD	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta OS=Acinetobacter baylyi	33274	298	MREAQSK
15	A0A0F0KI13_9MICO	Tryptophan 2,3-dioxygenase OS=Microbacterium oxydans	32641	283	QLLHELSSAR
16	M7XSW0_9RHIZ	Beta-lactamase domain-containing protein OS=Methylobacterium mesophilicum	60699	557	TLSGMSRGKLK
17	D5UU52_TSUPD	MMPL domain protein OS=Tsukamurella paurometabola	106516	1011	GFYLPEQGLTDPR

18	RNPA_PSYWF	Ribonuclease P protein component OS=Psychrobacter sp.	15120	130	KKIPTAVAR ATAADVKHKDK
19	M7XW44_9RHIZ	ABC transporter-like protein OS=Methylobacterium mesophilicum	57159	550	ALLGAVR
20	W0E9X5_9FIRM	NADH-quinone oxidoreductase subunit C OS=Desulfitobacterium metallireducens	18715	163	VKAILDHENPVIDSVTR
21	MURC_RHIL3	UDP-N-acetylmuramate--L-alanine ligase OS=Rhizobium leguminosarum bv. Viciae	50987	471	AEMLAELMR KSNPELIAAREKLLPVVRR
22	M7Y5N4_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	65204	593	RLCEVQPR EFVLPYIAIRNRKR
23	D5UN63_TSUPD	Amino acid adenylation domain protein OS=Tsukamurella paurometabola	402521	3786	SEEPFSALVDR VGAPLVIVPPAITGGR
24	A0ZNI0_9ACTN	DNA gyrase subunit B (Fragment) OS=Tsukamurella inchonensis	47290	428	TALTGVVK
25	A0A0H3FFF8_RAHSY	Potassium-transporting ATPase ATP-binding subunit OS=Rahnella sp.	73222	688	AMSAAALLR
26	A0A0H3FD69_RAHSY	Pyridoxal phosphate-dependent enzyme, D-cysteine desulfhydrase family OS=Rahnella sp.	35843	336	PAKISLLKTRLEAFDR
27	A0A0H3FE64_RAHSY	Ribose ABC transporter, periplasmic binding protein OS=Rahnella sp.	35696	328	VIEDLIAKK
28	ILVD_BURVG	Dihydroxy-acid dehydratase OS=Burkholderia vietnamiensis	67263	619	SLWRATGMK LHTDVPTVHAPTLK
29	A0A0D7FEA9_9PSED	Peptidase S24 OS=Pseudomonas oryzihabitans	15801	143	VGDIVVAVR
30	D5USV2_TSUPD	Transcriptional regulator, CarD family OS=Tsukamurella paurometabola	17745	162	LASGDVNK
31	A0A023Y885_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	78826	733	GDADAVR
32	A0A0D7FLK4_9PSED	Uncharacterized protein OS=Pseudomonas oryzihabitans	33933	307	QLPLSATPLAR
33	A0A0D7QLP3_9MICO	Polyphosphate kinase OS=Agreia bicolorata	35090	303	ESSQWYFQR LQNWIKASDRR
34	A0A0D7QSY9_9MICO	Glycoside hydrolase OS=Agreia bicolorata	52397	480	VQPGGSGR
35	NQRA_SERP5	Na(+)-translocating NADH-quinone reductase subunit A OS=Serratia proteamaculans	48492	449	TPAPGSTPR
36	A0A0L8A557_9GAMM	Uncharacterized protein OS=[Pseudomonas] geniculata	34371	321	QGAGKMK
37	J2VDV4_9RHIZ	Zinc metalloprotease OS=Phyllobacterium sp.	40663	378	VVTFADVQR
38	GLMM_BURPP	Phosphoglucosamine mutase OS=Burkholderia phytofirmans	47924	452	HSTGDGIVSALLVLAAMK

39	M7Y0T5_9RHIZ	Uracil-DNA glycosylase superfamily protein OS=Methylobacterium mesophilicum\	19377	171	MEGGLTGTVR
40	A0A0H3FF00_RAHSY	ABC transporter related protein OS=Rahnella sp.	59095	539	VLIDGEDITR
41	A0A0H3FEA3_RAHSY	Carbamoyl-phosphate synthase small chain OS=Rahnella sp.	41841	383	AKAFPGLK
42	J3HN07_9RHIZ	DNA mismatch repair protein MutS OS=Phyllobacterium sp.	99181	907	QSLADLMQSALK
43	M7XZV6_9RHIZ	General substrate transporter OS=Methylobacterium mesophilicum	60203	560	GITSTANPK
44	MRAY_ARTS2	Phospho-N-acetylmuramoyl-pentapeptide-transferase OS=Arthrobacter sp.	39291	369	QRSLGLDAKAK
45	ADE_BURPP	Adenine deaminase OS=Burkholderia phytofirmans	38975	350	LCVFDDLTK
46	W0EEE6_9FIRM	Uncharacterized protein OS=Desulfitobacterium metallireducens	4681	43	NKAMSLMRKGMRK
47	W0E8J4_9FIRM	Uncharacterized protein OS=Desulfitobacterium metallireducens	6158	52	KSAEQGMPQNHVKK
48	UBID_BURTA	3-octaprenyl-4-hydroxybenzoate carboxy-lyase OS=Burkholderia thailandensis	57654	519	DFIHSLEQRGELR
49	A0A0D7FIL9_9PSED	Phosphoglycerate mutase OS=Pseudomonas oryzihabitans	22297	203	AQAEAVGLALRER
50	A0A023Y8H8_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	63855	597	LLPGLPPSTRVR
51	A0A0H3FCR4_RAHSY	Protein HflC OS=Rahnella sp.	37628	346	SSAERDARVMK
52	A0A0H3FCY4_RAHSY	D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding protein OS=Rahnella sp.	44680	412	GIPEANAK MAKVSLEKDK
53	M7YFX3_9RHIZ	Drug resistance transporter, EmrB/QacA subfamily OS=Methylobacterium mesophilicum	56002	527	MSAVPAVGMPVPDAK
54	A0A0F0KZY1_9MICO	L-2-keto-3-deoxyarabonate dehydratase OS=Microbacterium oxydans	31952	305	VEAPPTAPK RMLPLVLIGLQGGIAWAVHK
55	A0A0D7QNY7_9MICO	Uncharacterized protein OS=Agreia bicolorata	46963	435	QALIWGRPEPAAGK
56	RL20_BRASO	50S ribosomal protein L20 OS=Bradyrhizobium sp.	13355	119	KVLSDLAINEPAAFEAIVVKAK
57	ACPH_ENT38	Acyl carrier protein phosphodiesterase OS=Enterobacter sp.	23009	193	FWQFYPRMMVQAK
58	M7YAP3_9RHIZ	ErfK/YbiS/YcfS/YnhG family protein OS=Methylobacterium mesophilicum	28841	268	QVVDYPTR
59	SECA_RHOJR	Protein translocase subunit SecA OS=Rhodococcus jostii	105723	955	HFHVQIMGGAALHFGNIAEMK
60	A0A023Y171_9GAMM	Phosphonoacetate hydrolase OS=Stenotrophomonas rhizophila	11949	111	QGTVIRNIR IKGLVLKTCFLKK
61	A0A0F0L6L9_9MICO	Calcineurin-like phosphoesterase superfamily domain protein OS=Microbacterium oxydans	29451	269	DYESATDIALR
62	M7Y6G0_9RHIZ	Cytochrome c-type biogenesis protein CcmE OS=Methylobacterium mesophilicum	18060	170	SPTDIAK WQEGGPSK

63	A0A0D7FMA6_9PSED	Holliday junction ATP-dependent DNA helicase RuvB OS=Pseudomonas oryzihabitans	38412	350	LLLTMIDK
64	A0A0H3FDF9_RAHSY	Phosphoglycerate kinase OS=Rahnella sp.	41241	387	DDEALSK ALPAVVMLEER
65	M7Y3Q1_9RHIZ	Malate/L-lactate dehydrogenase OS=Methylobacterium mesophilicum	33315	329	VVGDAAPR
66	J2V752_9RHIZ	L-threonine dehydratase OS=Phyllobacterium sp.	46889	419	RSLESGKRVK
67	A0A0H3FBR5_RAHSY	Luciferase-like, subgroup OS=Rahnella sp.	38267	353	GEPLAGTDNR
68	M7XT82_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	44446	418	SGGQSGAQTTGAGRN
69	IOLG_RHOE4	Inositol 2-dehydrogenase OS=Rhodococcus erythropolis	36983	346	VTVVNDYSLAR
70	A0A0D7QRG6_9MICO	50S ribosomal protein L18 OS=Agreia bicolorata	13130	123	SKGAARSRR
71	RL2_FLAJ1	50S ribosomal protein L2 OS=Flavobacterium johnsoniae	29960	274	RTKDGIPATVK
72	M7Y916_9RHIZ	Cytochrome o ubiquinol oxidase subunit III OS=Methylobacterium mesophilicum	22598	208	DGATPDR
73	A0A0F0KHK8_9MICO	3-oxoadipyl-CoA/3-oxo-5,6-dehydrosuberyl-CoA thiolase OS=Microbacterium oxydans	40682	383	ARIHQMTVR
74	M7Y2J1_9RHIZ	Dihydrolipoyl dehydrogenase OS=Methylobacterium mesophilicum	51032	479	EQGFAVKVGR
75	M7Y4N4_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	52675	478	QITESHK DGVGGLAAAGLALGVEVFNPVEKLKMLELGTK
76	D5UWB1_TSUPD	ABC transporter related protein OS=Tsukamurella paurometabola	47450	440	ELSGGMR IALPRPR
77	A0A0F0L233_9MICO	Uncharacterized protein OS=Microbacterium oxydans	141172	1316	ISGANPGLAGDVIAQATGTAGDR
78	J2VH97_9RHIZ	Pseudouridine synthase OS=Phyllobacterium sp.	38715	350	FEAPLPEDMFK GAVGLCNEGTRFLK
79	A0A0F0LAD1_9MICO	Bacterial alpha-L-rhamnosidase OS=Microbacterium oxydans	94690	868	EPIGIGEPAPR
80	A0A0H3FGJ4_RAHSY	GDP-mannose 4,6-dehydratase OS=Rahnella sp.	40893	362	VLVNPTK
81	M7Y045_9RHIZ	Precorrin 6A synthase OS=Methylobacterium mesophilicum	28234	262	DPAATDRAGAAG
82	UBIE_AGRFC	Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE OS=Agrobacterium fabrum	28844	259	VLKRGGR DAMVSALSPRK
83	A0A0D7FCW5_9PSED	tRNA-dihydrouridine synthase OS=Pseudomonas oryzihabitans	35743	330	ARRVLEHTGCDGLLIGR
84	A0A0H3FGG7_RAHSY	Guanylate kinase OS=Rahnella sp.	23532	207	KKMPQAR
85	M7YB40_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	6632	59	MDAFEHGESLR
86	M7Y951_9RHIZ	Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE OS=Methylobacterium mesophilicum	28571	261	MKAGDGASER

87	A0A0D7FGT2_9PSED	AraC family transcriptional regulator OS=Pseudomonas oryzihabitans	29269	263	KLPLHDAQGR
88	D5UZ40_TSUPD	Amino acid adenylation domain protein OS=Tsukamurella paurometabola	120716	1163	SVALGYR
89	M7YWH3_9RHIZ	Heat shock protein DnaJ domain-containing protein OS=Methylobacterium mesophilicum	27242	250	MALFAGLLACLTLWWLSK
90	A0A0H3FIM7_RAHSY	N-acetylglucosamine-6-phosphate deacetylase OS=Rahnella sp.	40980	379	GTHNPAFIR
91	D5UXJ5_TSUPD	Trigger factor OS=Tsukamurella paurometabola	50450	461	KGKAPAK
92	A0A023Y3M0_9GAMM	Membrane protein OS=Stenotrophomonas rhizophila	32392	301	PAPTPLR
93	A0A0F0KVB6_9MICO	2,5-diketo-D-gluconic acid reductase A OS=Microbacterium oxydans	30324	278	GIIVFPKSVR
94	GATA_BRASB	Glutamyl-tRNA(Gln) amidotransferase subunit A OS=Bradyrhizobium sp.	52572	491	AEGFGPEVR

Phenol-SDS method (MS/MS spectra: 12563)

	Accession Name	Protein Name	Protein Mass	Length	Peptides
1	CH606_BRADU	60 kDa chaperonin 6 OS=Bradyrhizobium diazoefficiens	57716	546	APGFGDR AAVEEGIVPGGGVALLR
2	M7Z4T8_9RHIZ	Ribonucleotide-diphosphate reductase subunit alpha OS=Methylobacterium mesophilicum	135848	1243	LGEIFIDMHK KVEENAVPSFLWR
3	A0A0D7QR84_9MICO	ATPase OS=Agreia bicolorata	66245	642	VIAVGGPR LVTDAQNSSSR
4	RF3_ACIAD	Peptide chain release factor 3 OS=Acinetobacter baylyi	60622	529	ELFLQGK HRDRIAFMR
5	A0A0F0KS62_9MICO	Uncharacterized protein OS=Microbacterium oxydans	34661	304	IAKLAEK
6	M7Z2E7_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	41465	385	IGGRGSGK YAGTRLGR
7	J2V762_9RHIZ	Uncharacterized protein OS=Phyllobacterium sp.	18103	163	EKTLGPAAR
8	M7XZQ0_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	88955	778	ITHPALR
9	RL29_AZOVD	50S ribosomal protein L29 OS=Azotobacter vinelandii	7170	63	MKASELR
10	A0A0F0KLU4_9MICO	UDP-glucose:undecaprenyl-phosphate glucose-1-phosphate transferase OS=Microbacterium oxydans GN=wcaJ	56032	508	ASATEYR
11	M7XW44_9RHIZ	ABC transporter-like protein OS=Methylobacterium mesophilicum	57159	550	ALLGAVR AGAETTPALGR

12	ALGE4_AZOVI	Poly (beta-D-mannuronate) C5 epimerase 4 OS=Azotobacter vinelandii	57731	553	ITGMVRSAYGEETSNFGMR
13	A0A023XZA6_9GAMM	Multidrug transporter MatE OS=Stenotrophomonas rhizophila	48186	456	MSIASPTPR
14	W0EI07_9FIRM	Uncharacterized protein OS=Desulfitobacterium metallireducens	130211	1135	VDIEQSQSK MNKWINQLK
15	RS16_METC4	30S ribosomal protein S16 OS=Methylobacterium extorquens	13200	120	IVIADAR
16	A0A0F0KBR3_9MICO	Uncharacterized protein OS=Microbacterium oxydans GN=RN51	30289	276	IADAVARGPHGR
17	A0A0D7F6P7_9PSED	Methylmalonate-semialdehyde dehydrogenase OS=Pseudomonas oryzihabitans	53684	499	GVEEGAR NGVEADADMGPLVTGQHKAK
18	M7XY77_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	20475	204	AAMTLKR
19	A0A0D7QPE3_9MICO	NTP pyrophosphohydrolase OS=Agreia bicolorata	14888	138	ETLARLAALDLID
20	A0A023Y2N2_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	50491	469	YPEITFPK
21	M7Y842_9RHIZ	Porin OS=Methylobacterium mesophilicum	58310	550	TQTAYGTLR
22	A0A0L8AEX7_9GAMM	3-methylcrotonyl-CoA carboxylase OS=[Pseudomonas] geniculata	70962	660	LYAEDADR
23	XYLG_BURCH	Xylose import ATP-binding protein XylG OS=Burkholderia cenocepacia	56162	519	HAKLLILDEPSSSLSASETR
24	W0EFY0_9FIRM	GntR family transcriptional regulator OS=Desulfitobacterium metallireducens	27508	241	MDIKPIKSK
25	J3HQY6_9RHIZ	10 kDa chaperonin OS=Phyllobacterium sp.	10490	98	TAGGIIIPDTAK
26	A0A0L8AFR8_9GAMM	Uncharacterized protein OS=[Pseudomonas] geniculata	26771	235	GRREMTGSR
27	J3HS64_9RHIZ	Uncharacterized protein OS=Phyllobacterium sp.	14904	136	KAIKALTDQR
28	PABA_SALTY	Aminodeoxychorismate synthase component 2 OS=Salmonella typhimurium	21016	187	AAKVMHGK
29	D5UNL0_TSUPD	Transglutaminase domain protein OS=Tsukamurella paurometabola	33759	304	VATVMER
30	A0A0H3FG52_RAHSY	Oligogalacturonate-specific porin OS=Rahnella sp.	26630	226	YTKENTEDRKTNR
31	A0A0H3F951_RAHSY	Flagellar biosynthetic protein FlhB OS=Rahnella sp.	42546	384	MSAPKVLAK
32	W0EE80_9FIRM	Uncharacterized protein OS=Desulfitobacterium metallireducens	10077	88	AAVKGHR
33	D5UUI5_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	24422	241	VQGYAGPGGQPGRGR
34	MOCOS_EMENI	Molybdenum cofactor sulfurase OS=Emericella nidulans	93494	839	MALIRPTLDLER
35	A0A0L8AAE1_9GAMM	Transcriptional regulator OS=[Pseudomonas] geniculata	13015	120	IAAHPLK
36	M7YRY0_9RHIZ	Oxidoreductase domain-containing protein OS=Methylobacterium mesophilicum	46675	431	LAAVMSGSPDKAK
37	FOLD_BACMF	Bifunctional protein FolD OS=Bacillus methylotrophicus	30772	283	KKAAETMGMK
38	A0A023Y1S1_9GAMM	DeoR faimly transcriptional regulator OS=Stenotrophomonas rhizophila	77804	708	TRDRRMVGVEVLLR

39	J3HQ21_9RHIZ	Diguanylate cyclase (GGDEF) domain-containing protein OS=Phyllobacterium sp.	38821	361	KIPIGIGR
40	W0EC19_9FIRM	Peptide ABC transporter ATP-binding protein OS=Desulfitobacterium metallireducens	37537	340	LKQYPHEFSGGMRQR
41	W0E620_9FIRM	Sensory histidine kinase OS=Desulfitobacterium metallireducens	58699	534	GIRKSHPDITK
42	W0E604_9FIRM	Cell wall-binding protein OS=Desulfitobacterium metallireducens	56302	522	IGFTISN
43	J3CEW5_9RHIZ	Transcriptional regulator OS=Phyllobacterium sp.	21676	198	KMPKAQR MGLAGAKKMPK
44	A0A0H3FFW9_RAHSY	Glycyl-radical enzyme activating protein family OS=Rahnella sp.	33298	295	YGYTVTLGG MTLSVAPRTSSDLR
45	A0A0L8A5F9_9GAMM	10 kDa chaperonin OS=[Pseudomonas] geniculata N1	10000	95	SEGVEYK
46	A0A0D7FLL5_9PSED	Chemotaxis protein OS=Pseudomonas oryzihabitans	65176	601	LAALSEK EQALMHR
47	M7XVS3_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	12478	116	QTRKAFEPAVLPVLRRGR
48	RS14_RHIL3	30S ribosomal protein S14 OS=Rhizobium leguminosarum bv. viciae	11442	101	ASIKLASLPR
49	M7YS07_9RHIZ	UvrABC system protein B OS=Methylobacterium mesophilicum	101968	924	RDTPAGGSSK
50	J2VH78_9RHIZ	Putative peptidoglycan binding protein,Sel1 repeat protein OS=Phyllobacterium sp.	113574	1047	QNLEESYKWFAIAAEAGDKDAASKR
51	D5UT34_TSUPD	Carboxylic ester hydrolase OS=Tsukamurella paurometabola	54667	506	YTLVGFR
52	A0A0F0KYM4_9MICO	Uncharacterized protein OS=Microbacterium oxydans	40032	376	LLLEAVDDR
53	A0A0L8A5U4_9GAMM	Alpha,alpha-trehalose-phosphate synthase (UDP-forming) OS=[Pseudomonas] geniculata	50840	454	QAGTAATK RKERWHAMMDHLR
54	KDSB_RHIEC	3-deoxy-manno-octulosonate cytidylyltransferase OS=Rhizobium etli	27491	251	RILSARQN GLYFTRATAPYGK
55	A0A023XZI7_9GAMM	Multidrug transporter OS=Stenotrophomonas rhizophila	41844	391	EGLKAGER
56	A0A0D7F821_9PSED	Formate dehydrogenase OS=Pseudomonas oryzihabitans	91273	813	VMRGLSKLK
57	IPT1_ARATH	Adenylate isopentenyltransferase 1, chloroplastic OS=Arabidopsis thaliana	40910	357	DKVVVILGATGAGKSR
58	A0A0L8AFP7_9GAMM	Uncharacterized protein OS=[Pseudomonas] geniculata N1	40321	367	GRSMLLDVR
59	A0A0H3F4D0_RAHSY	S-adenosylhomocysteine deaminase OS=Rahnella sp.	49965	452	QALYLQRLK
60	J2V021_9RHIZ	Transcriptional regulator OS=Phyllobacterium sp.	21913	195	LVDIAMRSWPGSN
61	M7YCR5_9RHIZ	Hopanoid-associated sugar epimerase OS=Methylobacterium mesophilicum	37218	343	DGTRLMMR
62	FADB_ACIAD	Fatty acid oxidation complex subunit alpha OS=Acinetobacter baylyi	78334	717	LIGIDNAVEWIAMAAPK
63	A0A0L8A9H4_9GAMM	Pyridoxal phosphate biosynthesis protein OS=[Pseudomonas] geniculata N1	24211	225	GLMAIPAPWPEAERRR

64	A0A0F0L9G8_9MICO	50S ribosomal protein L14 OS=Microbacterium oxydans	13338	122	ETRRPDGSYIK
65	M7Y1B5_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	52920	489	RGLPVPKPR
66	J3HTC6_9RHIZ	Pyridoxamine 5~-phosphate oxidase-related, FMN binding protein OS=Phyllobacterium sp.	35376	319	TMELLDDPK
67	A0A0F0KHJ5_9MICO	Glycerol-3-phosphate dehydrogenase OS=Microbacterium oxydans	49736	466	RTRIGLVDADRTR
68	M7YWM3_9RHIZ	Protein TolR OS=Methylobacterium mesophilicum	16070	148	MGMAAGASQGGK
69	A0A0F0KH25_9MICO	50S ribosomal protein L19 OS=Microbacterium oxydans	13152	115	AKIKEKRDR LYYLRQLRGK
70	A0A0D7FJ11_9PSED	Flagellar rod assembly protein FlgJ OS=Pseudomonas oryzihabitans	43270	405	YLVAQAALETGWGKHMVK
71	A0A0D7FLN2_9PSED	(P)ppGpp synthetase OS=Pseudomonas oryzihabitans	83962	746	KPTNKPGK
72	M7XTI1_9RHIZ	Protein translocase subunit SecA OS=Methylobacterium mesophilicum	107918	963	MLGSFAK DPLNEYK
73	M7Y4H6_9RHIZ	Chaperone protein DnaK OS=Methylobacterium mesophilicum	68748	638	TYDDPMTQKDK
74	LPXK_AZOVD	Tetraacyldisaccharide 4~-kinase OS=Azotobacter vinelandii	36727	333	FSPALPLVMTEKDAVKCR
75	A0A0L8ADK3_9GAMM	DeoR faimly transcriptional regulator OS=[Pseudomonas] geniculata	35576	322	LIALLQAR
76	GLMU_BRASO	Bifunctional protein GlmU OS=Bradyrhizobium sp.	46656	448	LRPGTSLGDGAKIGNFVEAK
77	M7XZV6_9RHIZ	General substrate transporter OS=Methylobacterium mesophilicum	60203	560	IGDLVGR ADGAARPMSSAEK
78	J3HU94_9RHIZ	Uncharacterized protein OS=Phyllobacterium sp.	30295	284	ACKEAAALKK
79	M7YUB3_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	124782	1141	AIDDEDTPR
80	M7XXH1_9RHIZ	RND family efflux transporter MFP subunit OS=Methylobacterium mesophilicum	46185	446	RIMLPVR DAAPPPSPVVR
81	M7Z6B1_9RHIZ	Bifunctional protein PutA OS=Methylobacterium mesophilicum	129812	1224	EMAIGDPR
82	A0A023Y141_9GAMM	RNA polymerase sigma factor RpoE OS=Stenotrophomonas rhizophila	23613	206	AYRAIGSFR
83	A0A0H3FFX2_RAHSY	ABC transporter related protein OS=Rahnella sp.	66622	599	MAEPKKIK
84	M7Z5B6_9RHIZ	Major facilitator superfamily	51113	481	TLAPKILR
85	A0A0D7QNE7_9MICO	Uncharacterized protein OS=Agreia bicolorata	98513	897	GAVGHDR YDDALLVER
86	A0A023Y9M0_9GAMM	NADPH:quinone reductase OS=Stenotrophomonas rhizophila	35885	335	ARGKLVLEGF
87	A0A0H3FLE2_RAHSY	Dihydroxy-acid dehydratase OS=Rahnella sp.	66444	616	ERVVSLALRAYALLATSADK
88	A0A023Y4E1_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	67093	605	HVHGRTR LTREGRADPTVLQNRAEATR

89	D5UP01_TSUPD	Carboxylic ester hydrolase OS=Tsukamurella paurometabola	52131	496	FDEPSTALDGR
90	A0A0D7QQ75_9MICO	ATPase AAA OS=Agreia bicolorata	118739	1078	AWGLVAARLGNK
91	A0A023Y6Q8_9GAMM	Histidine kinase OS=Stenotrophomonas rhizophila	47312	423	HSLVSSALK
92	A0A0D7QQZ5_9MICO	Fis family transcriptional regulator OS=Agreia bicolorata	51618	474	KLAQYGISLPKIHA
93	A0A0F0L8E2_9MICO	Na(+)/H(+) antiporter NhaA OS=Microbacterium oxydans	40157	391	WYRRLAAAAS
94	A0A023Y8Q3_9GAMM	Membrane protein OS=Stenotrophomonas rhizophila	32878	302	VADNQPVTR
95	J3CGI5_9RHIZ	Uncharacterized protein OS=Phyllobacterium sp. YR531	23518	214	SSSNSIR MSSSNSIR
96	A0A0H3F6R1_RAHSY	NADH-quinone oxidoreductase subunit I OS=Rahnella sp.	20859	180	MAGMAIDGK
97	M7XYF7_9RHIZ	Formate dehydrogenase, alpha subunit OS=Methylobacterium mesophilicum	109163	990	VLEHWHTGSMTRR
98	D5USZ9_TSUPD	S-adenosyl-L-methionine-dependent methyltransferase OS=Tsukamurella paurometabola	30667	283	TDIEIQAVDDTAR
99	A0A0L8A7S1_9GAMM	Aconitate hydratase OS=[Pseudomonas] geniculata N1	98884	917	WNPAAEPDTEIAFMPAR
100	A0A023Y0Y1_9GAMM	Histidine kinase OS=Stenotrophomonas rhizophila	15641	143	KIVLHER
101	ILVC_BURXL	Ketol-acid reductoisomerase OS=Burkholderia xenovorans	36384	338	AMMPWIAKNKLVDQSKN
102	AROA_BURP8	3-phosphoshikimate 1-carboxyvinyltransferase OS=Burkholderia phymatum	46773	434	VMLDALEK
103	LPTD_BURCM	LPS-assembly protein LptD OS=Burkholderia ambifaria	86999	786	HSDLIVGAALK
104	D5UMP4_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	7405	68	RENLTGLRGR
105	SYP_ARTS2	Proline--tRNA ligase OS=Arthrobacter sp.	64945	603	DENDGGAWTAADTLK
106	ARGB_BURCH	Acetylglutamate kinase OS=Burkholderia cenocepacia	32090	299	AGTFIQGMR

NoviPureTM method (MS/MS spectra: 10374)

	Accession Name	Protein Name	Protein Mass	Length	Peptides
1	M7YWC4_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	10508	102	SPSLAGVR GGASGRMRAAAMAALSDGR

2	TILS_SERP5	tRNA(Ile)-lysidine synthase OS=Serratia proteamaculans	49669	436	WPHFAAATAR
3	A0A0D7FEZ2_9PSED	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B OS=Pseudomonas oryzihabitans	52845	482	AEIKNVNSFR
4	A0A023Y5I0_9GAMM	Cyclomaltodextrin glucanotransferase OS=Stenotrophomonas rhizophila	62868	571	GALSSVFGK QPQFGQIFDK
5	M7XP10_9RHIZ	Type II secretion system protein E OS=Methylobacterium mesophilicum	53191	480	LTLEQLVR
6	RL11_RHIL3	50S ribosomal protein L11 OS=Rhizobium leguminosarum bv. viciae	15138	143	AQIKSIAEAKMK
7	BIOB_FLAPJ	Biotin synthase OS=Flavobacterium psychrophilum	40687	362	YESLGEKPK NLELSGKGKN
8	M7YXS4_9RHIZ	Ferredoxin OS=Methylobacterium mesophilicum	11451	106	TVEGSVGATVMETALR
9	A0A0H3FHW2_RAHSY	Copper resistance D domain-containing protein OS=Rahnella sp.	32898	294	LVPLMGK
10	A0A0D7QSV4_9MICO	GntR family transcriptional regulator	13067	125	ARVLEQVTSGELPAGFR
11	A0A0D7QPF6_9MICO	Long-chain fatty acid--CoA ligase OS=Agreia bicolorata	65236	608	KEIIVTAAGK VFEKVYNSSEQK
12	MNMG_AGRFC	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG OS=Agrobacterium fabrum	69008	627	TALVTHK LTPVAQKAGILGR
13	SYA_SPHWW	Alanine--tRNA ligase OS=Sphingomonas wittichii	95086	887	AQPLIEETLK
14	A0A0D7QRP4_9MICO	Glucarate dehydratase OS=Agreia bicolorata	44879	415	DDTGYMRR
15	A0A0L8ABL4_9GAMM	Outer membrane protein assembly factor BamB OS=[Pseudomonas] geniculata N1	42028	402	VATVLLMGMALSGCSTVK
16	ATPG_ENT38	ATP synthase gamma chain OS=Enterobacter sp.	31631	287	LLADMKVWSDK
17	D5UW99_TSUPD	Conserved putative secreted protein OS=Tsukamurella paurometabola	13141	126	TSYWGNVGDTLGVAQNR
18	VIRC1_RHIRD	Protein virC1 OS=Rhizobium radiobacter	25852	231	DAFSAMK
19	W0EF77_9FIRM	Laccase domain protein OS=Desulfitobacterium metallireducens	30683	268	MAGWIRRKD
20	A0A023Y8A7_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	54222	502	ALPAQLPR
21	A0A0F0LDL0_9MICO	Uncharacterized protein OS=Microbacterium oxydans	11861	107	AQEIVIAGSIQAVGTALAAVISTYR
22	A0A0H3F723_RAHSY	Acetyltransferase Rahaq_1091 OS=Rahnella sp.	16334	141	AENDAVVSMYEK
23	A0A0F0KBR3_9MICO	Uncharacterized protein OS=Microbacterium oxydans	30289	276	VEELIDFVTAPPA
24	A0A0L8A5A2_9GAMM	DNA methylase OS=[Pseudomonas] geniculata N1	22285	195	RRDDPARK
25	A0A0F0KPU6_9MICO	Uncharacterized protein OS=Microbacterium oxydans	39658	372	VLGISTPEMMR

26	LIPB_RHIL3	Octanoyltransferase OS=Rhizobium leguminosarum bv. viciae	26740	239	TLDMMNVR TLDMMNVRGER
27	D5UYF4_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	47100	422	LWMTEVAMRGMHVAHEAVGGR
28	M7YAT8_9RHIZ	Elongation factor 4 OS=Methylobacterium mesophilicum	66895	600	RQTTEMLPGFK
29	W0E7Z6_9FIRM	Carbon monoxide dehydrogenase OS=Desulfitobacterium metallireducens	73447	672	VKTEEGPGSK
30	A0A023Y227_9GAMM	Fumarate hydratase OS=Stenotrophomonas rhizophila	54357	505	DAAHKRIVEMLDK
31	ARGB_ENT38	Acetylglutamate kinase OS=Enterobacter sp. (strain 638)	26991	257	IAEMTAAK
32	A0A0D7QMJ7_9MICO	Uncharacterized protein OS=Agreia bicolorata	8475	79	LDVLPPFAGG
33	A0A0H3FEK4_RAHSY	Transcription termination/antitermination protein NusG OS=Rahnella sp.	20484	181	VAQSLREHIK
34	A0A0F0KS62_9MICO	Uncharacterized protein OS=Microbacterium oxydans	34661	304	FDSLMKHAERR
35	MIAA_ACIAD	tRNA dimethylallyltransferase OS=Acinetobacter baylyi	36158	314	RIEQRLFK
36	A0A0L8AF72_9GAMM	Replicative DNA helicase OS=[Pseudomonas] geniculata N1	53082	476	VTSAIKMLK GVAVFSMEMSASQLAMR
37	A0A0F0KHN1_9MICO	Glutathione-binding protein GsiB OS=Microbacterium oxydans	59513	559	ALLLAMDR
38	M7Y5E4_9RHIZ	Peptidoglycan binding domain-containing protein OS=Methylobacterium mesophilicum	61045	581	VPVQSRR QRQLSASAAR
39	UVRC_BURMS	UvrABC system protein C OS=Burkholderia mallei	81185	747	MHAFAAELK
40	LPXK_ENT38	Tetraacyldisaccharide 4~-kinase OS=Enterobacter sp.	35660	325	MIARIWSGK
41	M7YA99_9RHIZ	AMP nucleosidase OS=Methylobacterium mesophilicum	69551	635	RRINQSR FGGLVGQAPGARKPTWHAQQACISLPGGRR
42	J2VIU6_9RHIZ	DNA-binding domain-containing protein, AraC-type OS=Phyllobacterium sp.	25254	227	FGHVDLRALRIGTAMAK
43	J3HM74_9RHIZ	Shikimate dehydrogenase (NADP(+)) OS=Phyllobacterium sp.	30218	278	HSRSPLIHGHWLK
44	A0A023Y2G8_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	17538	162	VPKVPKAPKAPK
45	A0A0F0KUH3_9MICO	23S rRNA (Uridine(2479)-2~-O)-methyltransferase OS=Microbacterium oxydans	29246	272	RAHAAGLRILAADVK
46	A0A0H3FGP5_RAHSY	50S ribosomal protein L34 OS=Rahnella sp.	5365	46	SHGFRARMATK
47	PYRC_ACIAD	Dihydroorotase OS=Acinetobacter baylyi	39128	344	KIKDSAHVNAIK
48	SYFA_AZOVD	Phenylalanine--tRNA ligase alpha subunit OS=Azotobacter vinelandii	38113	338	TMESSQPPIR
49	A0A0F0KSL8_9MICO	Chaperone protein ClpB OS=Microbacterium oxydans	81796	740	AREGKLDPVIGR
50	D5USC7_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	36909	345	ALLGVDAKIAQYVR

51	TATA_BURXL	Sec-independent protein translocase protein TatA OS=Burkholderia xenovorans	8588	79	ELPRNGAVDVDAK
52	RSMG_BURCM	Ribosomal RNA small subunit methyltransferase G OS=Burkholderia ambifaria	25074	228	HLIEVIVDEAN
53	M7XXR7_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	30824	282	TLAELGYLAYEPR
54	M7Z301_9RHIZ	Endonuclease III OS=Methylobacterium mesophilicum	28237	263	TIGLFNTK
55	RF1_BURM1	Peptide chain release factor 1 OS=Burkholderia multivorans	40730	360	IAGQGAYSRLK
56	A0A0D7FFC1_9PSED	Branched-chain alpha-keto acid dehydrogenase subunit E2 (Fragment) OS=Pseudomonas oryzihabitans	34112	315	KIAEKMQAAK
57	M7YCG0_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	16623	151	GENEIIARN
58	A0A0D7QWD8_9MICO	2-isopropylmalate synthase OS=Agreia bicolorata	65159	588	KNNQTASAMPIHK
59	ABDH_SERP5	Gamma-aminobutyraldehyde dehydrogenase OS=Serratia proteamaculans	51351	474	FFAGASR
60	D5URD5_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	27477	256	YKLDSDGAFR
61	D5USK0_TSUPD	AMP-dependent synthetase and ligase OS=Tsukamurella paurometabola	66011	624	MGTYADEYHR
62	A0A0L8AD80_9GAMM	Uncharacterized protein OS=[Pseudomonas] geniculata N1	32059	297	FLVDTGASAMAVAR
63	W0E537_9FIRM	Sulfide reductase OS=Desulfitobacterium metallireducens	17931	158	LSVEVMGFK
64	DEOC_ENT38	Deoxyribose-phosphate aldolase OS=Enterobacter sp.	27782	259	DMGVSKTVGFKPAGGVR

Biscutella laevigata rhizosphere (BLS)

Chourey method (MS/MS spectra: 8058)

	Accession Name	**Protein Name**	**Protein Mass**	**Length**	**Peptides**
1	CH603_BURCH	60 kDa chaperonin 3 OS=Burkholderia cenocepacia	56775	540	IEARVKSIR AAVEEGIVPGGGVALLR
2	A0A0F0KK12_9MICO	Uncharacterized protein OS=Microbacterium oxydans	54024	530	SGGLLDR
3	A0A0D7F8T1_9PSED	DNA topoisomerase 4 subunit A OS=Pseudomonas oryzihabitans	83053	750	QLARLEEMK
4	A0A0D7FD14_9PSED	Thioredoxin OS=Pseudomonas oryzihabitans	11537	108	SGGLVQR

5	A0A0F0L0N7_9MICO	Uncharacterized protein OS=Microbacterium oxydans	49865	461	MKINDAEVIRVSASTR
6	A0A023Y817_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	54679	517	AALAVGMSGSR
7	M7YUW6_9RHIZ	Peptidyl-prolyl cis-trans isomerase OS=Methylobacterium mesophilicum	19287	182	IVSMTLAEK
8	A0A0H3FLD3_RAHSY	TDP-4-keto-6-deoxy-D-glucose transaminase OS=Rahnella sp.	42523	376	GTNRSQFFRGQVDKYTWR
9	A0A0D7FLK4_9PSED	Uncharacterized protein OS=Pseudomonas oryzihabitans	33933	307	QLPLSATPLAR
10	A0A0F0KI13_9MICO	Tryptophan 2,3-dioxygenase OS=Microbacterium oxydans	32641	283	QLLHELSSAR
11	D5UT97_TSUPD	Peptidyl-dipeptidase Dcp OS=Tsukamurella paurometabola	73561	676	AGMELGR
12	A0A0D7QLS6_9MICO	Uncharacterized protein OS=Agreia bicolorata	24369	245	GVATAER
13	A0A0H3F7C7_RAHSY	Phage tail tape measure protein, TP901 family OS=Rahnella sp.	91525	863	GLGYIGMALK
14	M7Y0L2_9RHIZ	Integral membrane sensor signal transduction histidine kinase OS=Methylobacterium mesophilicum	46390	440	LGLAPLRRLR
15	A0A0L8ACA8_9GAMM	Nitrate reductase OS=[Pseudomonas] geniculata	59391	514	AGKLVPR
16	A0A0H3FDZ4_RAHSY	Aminotransferase class I and II OS=Rahnella sp.	43986	401	PDIADRLKNVSVSASVAMTQK
17	ATPG_BURCM	ATP synthase gamma chain OS=Burkholderia ambifaria	31853	291	TQLDLYSEGK
18	DCTA_RHIGA	C4-dicarboxylate transport protein OS=Rhizobium galegae	48738	461	FLDALTEPMFK
19	A0A0F0L446_9MICO	DNA-directed RNA polymerase subunit omega OS=Microbacterium oxydans	9717	85	MAGHHNK
20	J2VYX2_9RHIZ	Putrescine-binding periplasmic protein OS=Phyllobacterium sp.	39818	362	NPDDLAK
21	A0A0F0L9P0_9MICO	Formyl-coenzyme A transferase OS=Microbacterium oxydans	40308	381	VERPGSGDDTR
22	J3HM91_9RHIZ	ATPase component of uncharacterized ABC-type transporter OS=Phyllobacterium sp.	55449	510	VEILKALYR
23	PIMT_BURCH	Protein-L-isoaspartate O-methyltransferase OS=Burkholderia cenocepacia	33006	310	APRKSEGRPGER
24	A0A0L8A899_9GAMM	HupB OS=[Pseudomonas] geniculata N1	17198	164	QDGGGKRSGSAR
25	J3CHX8_9RHIZ	Urease accessory protein UreD OS=Phyllobacterium sp.	30417	277	DILDYPLVVQGR
26	UGPE_AGRFC	sn-glycerol-3-phosphate transport system permease protein UgpE OS=Agrobacterium fabrum	31749	282	LLFNSFVVALAIAIGK
27	M7XQN5_9RHIZ	Mammalian cell entry related domain protein OS=Methylobacterium mesophilicum	37667	360	LSGTGRREVEALSGDGQR
28	A0A0F0LDQ4_9MICO	Uncharacterized protein OS=Microbacterium oxydans	30434	289	ADIAGWSSDR
29	A0A0D7FEH8_9PSED	Glucosyltransferase I RfaG OS=Pseudomonas oryzihabitans	41998	372	APANAAEIR

30	A0A0H3F867_RAHSY	Cell division protein FtsK/SpoIIIE OS=Rahnella sp.	124097	1148	MSQEYTEDK
31	W0EFJ2_9FIRM	Glycolate oxidase iron-sulfur subunit OS=Desulfitobacterium metallireducens	47228	417	GLHITEQPRQMLK
32	A0A023Y5N6_9GAMM	Sugar phosphotransferase OS=Stenotrophomonas rhizophila	34170	310	DYAQQHRALPAR
33	A0A0F0LD33_9MICO	Ribose operon repressor OS=Microbacterium oxydans	36535	341	RPTLADVATLSGMSK
34	M7XXR7_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	30824	282	RDCAERGFCVSR

Phenol-SDS method (MS/MS spectra: 12786)

	Accession Name	**Protein Name**	**Protein Mass**	**Length**	**Peptides**
1	CH602_BURTA	60 kDa chaperonin 2 OS=Burkholderia thailandensis	57054	546	ALEEPLR ATLQELGRAK AAVEEGIVPGGGVALIR
2	A0A0D7QR84_9MICO	ATPase OS=Agreia bicolorata	66245	642	VIAVGGPR
3	CH103_BRADU	10 kDa chaperonin 3 OS=Bradyrhizobium diazoefficiens	11233	104	IDGQDLLIMK TAGGIIIPDTAK
4	M7YE77_9RHIZ	Porin OS=Methylobacterium mesophilicum	58654	553	TQTAYGTLR QFNQGGDSAGYPTR
5	A0A0F0KY75_9MICO	Oligo-1,6-glucosidase OS=Microbacterium oxydans	61616	556	AAPGSPERAR
6	A0A0D7QT09_9MICO	RNA polymerase sigma factor SigA OS=Agreia bicolorata	47625	441	LVVSLAK MRFGLGDGMPK
7	W0E4Z6_9FIRM	Chromosome segregation protein SMC OS=Desulfitobacterium metallireducens	98336	840	EHIINYLEGGK
8	D5US76_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	25184	230	VVTSGGPR
9	J2VG30_9RHIZ	FMN-dependent oxidoreductase, nitrilotriacetate monooxygenase family OS=Phyllobacterium sp.	48158	441	SRMVAFGR
10	M7YBF6_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	25306	236	LTGDPDR
11	A0A0F0KNH0_9MICO	Uncharacterized protein OS=Microbacterium oxydans	11731	102	MPPPTGR
12	D5UQ45_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	23185	198	GDTFTGR DITDIYMK
13	D5UXG7_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	7695	70	EETQSGR IIDAASAVK

14	M7YVR1_9RHIZ	Light-independent protochlorophyllide reductase iron-sulfur ATP-binding protein OS=Methylobacterium mesophilicum	32523	297	NPVVARK
15	M7YUW6_9RHIZ	Peptidyl-prolyl cis-trans isomerase OS=Methylobacterium mesophilicum	19287	182	IVSMTLAEK IVSMTLAEKGK
16	CH60_VARPS	60 kDa chaperonin OS=Variovorax paradoxus	57385	550	SFGAPTVTK AMLEDIAILTGGK
17	A0A0F0L7Y3_9MICO	UDP-N-acetyl-alpha-D-glucosamine C6 dehydratase OS=Microbacterium oxydans	66452	615	MIAMSGKK
18	A0A0F0L547_9MICO	Uncharacterized protein OS=Microbacterium oxydans	32150	290	SEASLGR
19	M7Z0G6_9RHIZ	ApbE family lipoprotein OS=Methylobacterium mesophilicum	33571	325	LGLADPR
20	J3HVE7_9RHIZ	Site-specific recombinase XerC OS=Phyllobacterium sp.	41715	384	SALRLAVR
21	W0EA79_9FIRM	Molybdenum ABC transporter substrate-binding protein OS=Desulfitobacterium metallireducens	28740	268	YGFSILK
22	A0A0F0KXV3_9MICO	Putative sensor histidine kinase TcrY OS=Microbacterium oxydans	46116	438	DAGGSGLGLAIAR
23	A0A023Y3S8_9GAMM	Glycosyl transferase OS=Stenotrophomonas rhizophila	25502	240	IIVALDR
24	RUTA_AGRVS	Pyrimidine monooxygenase RutA OS=Agrobacterium vitis	40445	367	SRNPNLKRNLDAA
25	A0A0D7FMB2_9PSED	Cold-shock protein OS=Pseudomonas oryzihabitans	21563	205	DTGDDIFVHFR
26	A0A0F0LCN3_9MICO	Uncharacterized protein OS=Microbacterium oxydans	39530	362	DVTSTSLMGRGR
27	D5UWH8_TSUPD	Transcriptional regulator, MerR family OS=Tsukamurella paurometabola	28764	254	LTGVSVR
28	M7Y5Y9_9RHIZ	ATP synthase gamma chain OS=Methylobacterium mesophilicum	32208	296	NAGEMIK
29	DUT_BRASO	Deoxyuridine 5~-triphosphate nucleotidohydrolase OS=Bradyrhizobium sp.	15687	152	IAQMVIASVVR
30	A0A023Y3G2_9GAMM	Histidine kinase OS=Stenotrophomonas rhizophila	104731	930	TGGTRIAPR
31	MNMG_PSYWF	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG OS=Psychrobacter sp.	70304	642	AGDQPSIKLAERLR
32	A0A0D7QSD5_9MICO	NAD-dependent dehydratase OS=Agreia bicolorata	54783	503	EQQAAGNVAR
33	J3HRP2_9RHIZ	Ribbon-helix-helix protein, copG family OS=Phyllobacterium sp.	16038	144	MANQSKKQR
34	GLNE_BRADU	Glutamate-ammonia-ligase adenylyltransferase OS=Bradyrhizobium diazoefficiens	110336	995	GGRLITLLGQNR TNYGVLYEIDMR
35	NUOH_NOCSJ	NADH-quinone oxidoreductase subunit H OS=Nocardioides sp.	48507	449	EGIIPKAADK
36	W0EFG4_9FIRM	Flagellin OS=Desulfitobacterium metallireducens	41877	403	EMSTFSK
37	A0A0F0KNY4_9MICO	Chaperone protein DnaK OS=Microbacterium oxydans	66528	621	REAAEVR LITENDDKLPEDVKTEVK

38	D5UT46_TSUPD	Transcriptional regulator, MarR family OS=Tsukamurella paurometabola	15914	143	LITLTAK
39	A0A0D7FFL0_9PSED	Fis family transcriptional regulator OS=Pseudomonas oryzihabitans	40165	361	QGDILPLAR
40	GATA_RHIEC	Glutamyl-tRNA(Gln) amidotransferase subunit A OS=Rhizobium etli	53031	493	AAGFGKEVKR DVRDAAILLK
41	A0A0F0L829_9MICO	PhoH-like protein OS=Microbacterium oxydans	41702	379	TYLAMAK GGAPRPGPRDRMPK
42	A0A023Y3E1_9GAMM	Polyketide cyclase OS=Stenotrophomonas rhizophila	11994	109	IASLEIAP
43	A0A0D7QLS5_9MICO	Aldo/keto reductase OS=Agreia bicolorata	36658	334	VLGKALK
44	A0A0L8ADW8_9GAMM	UvrABC system protein B OS=[Pseudomonas] geniculata N1	75983	674	VLAAIETIK
45	A0A0D7QSK7_9MICO	MarR family transcriptional regulator OS=Agreia bicolorata	39483	381	MLGVKITGER
46	TMP_BPSPB	Probable tape measure protein OS=Bacillus phage SPbeta	252157	2285	YTSDQKK
47	M7Y3Y6_9RHIZ	Acid phosphatase OS=Methylobacterium mesophilicum	30489	287	VPAVINLLER
48	J3HVI2_9RHIZ	Uncharacterized protein OS=Phyllobacterium sp. YR531	23638	200	LLDALTDAEIAAK
49	A0A0H3FDP1_RAHSY	Transcriptional regulator, XRE family OS=Rahnella sp.	48616	419	RSFMNISGR
50	M7YCV6_9RHIZ	NAD-binding 3-hydroxyacyl-CoA dehydrogenase OS=Methylobacterium mesophilicum	79061	733	GGTFYGQAEK
51	UGPC1_RHIL3	sn-glycerol-3-phosphate import ATP-binding protein UgpC 1 OS=Rhizobium leguminosarum bv. viciae	40048	369	RVVLGMRAEAAR
52	D5UW42_TSUPD	SMC domain protein OS=Tsukamurella paurometabola	93872	877	FSALAATLR
53	D5UTL8_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	33441	305	LAAAFAR
54	PAND_BACP2	Aspartate 1-decarboxylase OS=Bacillus pumilus	13968	127	TFMTSKLHK
55	SYI_AGRFC	Isoleucine--tRNA ligase OS=Agrobacterium fabrum	108928	967	VQSEEFK ESGADILRLWVMTTDYWEDQR
56	A0A0H3F7C7_RAHSY	Phage tail tape measure protein, TP901 family OS=Rahnella sp.	91525	863	DTAALMR
57	J3CEB9_9RHIZ	Putative cobalamin binding protein OS=Phyllobacterium sp.	25372	232	HNQMSGA
58	D5UWN2_TSUPD	AMP-dependent synthetase and ligase OS=Tsukamurella paurometabola	49209	472	VQKKLLL NPMGKVQK
59	W0E615_9FIRM	Transposase IS116 OS=Desulfitobacterium metallireducens DSM 15288	45617	404	SVLDLVFPK
60	M7Y663_9RHIZ	Integral membrane sensor signal transduction histidine kinase OS=Methylobacterium mesophilicum	50055	461	IGAMEEGRR
61	A0A0H3FAE9_RAHSY	Invasion gene expression up-regulator SirB OS=Rahnella sp.	14883	129	LALTKIPLLMG

62	W0EGI9_9FIRM	Glutamine--tRNA ligase OS=Desulfitobacterium metallireducens	64853	553	EDLKLKAPR IVSMKSSFKIN
63	D5UWS2_TSUPD	MaoC domain protein dehydratase OS=Tsukamurella paurometabola	327589	3102	AMIAIWTK
64	F1B2N8_9CAUD	Uncharacterized protein OS=Tsukamurella phage	66687	610	ASSPMAR
65	A0A0D7FIP2_9PSED	Membrane protein OS=Pseudomonas oryzihabitans	73271	660	LSGLSVR
66	ACEK_ENT38	Isocitrate dehydrogenase kinase/phosphatase OS=Enterobacter sp.	67148	573	FRAIPRPLAK
67	D5UTX5_TSUPD	Major facilitator superfamily MFS_1 OS=Tsukamurella paurometabola	42477	403	MPSVFVSLRTRNYR
68	A0A0D7FCR0_9PSED	ATP-dependent protease ATPase subunit HslU OS=Pseudomonas oryzihabitans	50226	449	GNTSGADVSR
69	PSD_BRASO	Phosphatidylserine decarboxylase proenzyme OS=Bradyrhizobium sp.	25237	232	EGQTVGAGER
70	W0EA67_9FIRM	Uncharacterized protein OS=Desulfitobacterium metallireducens	52854	453	LLKNFRGRVR
71	A0A0D7FDR6_9PSED	Penicillin-binding protein 1B OS=Pseudomonas oryzihabitans	85406	780	GTDPSCPNAVQMPYIR
72	IOLJ_BACMF	6-phospho-5-dehydro-2-deoxy-D-gluconate aldolase OS=Bacillus methylotrophicus	31508	290	AITLGHAK RMFQKNGDLYEPR
73	A0A0H3F982_RAHSY	Polysaccharide deacetylase OS=Rahnella sp.	33684	300	HTLGNMK
74	A0A023XZP1_9GAMM	RNA polymerase subunit sigma-24 OS=Stenotrophomonas rhizophila	33222	295	MAANQPLALR
75	J3HLY2_9RHIZ	Putative dehydrogenase OS=Phyllobacterium sp.	34929	333	NAATHTAMR
76	A0A0H3F5H0_RAHSY	Fumarate reductase flavoprotein subunit OS=Rahnella sp.	66735	599	TTELMQKTIDK
77	M7Y7Y5_9RHIZ	Phage integrase family OS=Methylobacterium mesophilicum	43669	387	GGVVQSSRVAELR
78	COXX_RHOJR	Protoheme IX farnesyltransferase OS=Rhodococcus jostii	32918	301	VMKRTAR
79	D5UNI3_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	9851	86	NAEIFETLSDELSSR
80	J2VD92_9RHIZ	3-oxoacyl-(Acyl-carrier-protein) synthase OS=Phyllobacterium sp.	44713	425	ISSLPVSSNK
81	A0A0D7QNM3_9MICO	Uncharacterized protein OS=Agreia bicolorata	29659	272	AGVTKSELNR
82	A0A0F0LC60_9MICO	Nuclease SbcCD subunit C OS=Microbacterium oxydans	106792	1000	DAATAAHAESIAAAEQQR
83	J3HPM1_9RHIZ	Trehalose-6-phosphate synthase OS=Phyllobacterium sp.	54126	474	KNGCENK
84	A0A0D7FDV1_9PSED	ATP-dependent protease OS=Pseudomonas oryzihabitans	90289	814	DANNVAFTPMKEGK
85	LPXB_BRADU	Lipid-A-disaccharide synthase OS=Bradyrhizobium diazoefficiens	43349	392	LAPALSEVLTDSDMRR
86	FMT_BURCH	Methionyl-tRNA formyltransferase OS=Burkholderia cenocepacia	34535	330	LQASAVK GAAPIHR
87	A0A0D7QQR1_9MICO	MFS transporter OS=Agreia bicolorata	42936	426	MTSTATTR
88	A0A0L8AD43_9GAMM	Uncharacterized protein OS=[Pseudomonas] geniculata N1	7628	70	VALDGEGGGTINR

89	A0A0H3FE41_RAHSY	Mammalian cell entry related domain protein OS=Rahnella sp.	19792	188	VEMDIDQK
90	A0A0L8AC50_9GAMM	Type VI secretion protein OS=[Pseudomonas] geniculata N1	40361	381	EMHGFLINDVK
91	M7Y4S4_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	18292	170	AGISNGPR
92	NUSB_BRASO	N utilization substance protein B homolog OS=Bradyrhizobium sp.	18766	168	MAENKPFRGPIR
93	A0A0H3F9X6_RAHSY	D-amino acid dehydrogenase OS=Rahnella sp.	47549	433	TAQQFESAAK
94	A0A0F0L713_9MICO	Oligopeptide-binding protein OppA OS=Microbacterium oxydans	58728	549	TIQTANR
95	A0A0D7FI45_9PSED	ATPase OS=Pseudomonas oryzihabitans	240495	2189	LVDGQPVILK
96	RL6_RHOE4	50S ribosomal protein L6 OS=Rhodococcus erythropolis	19348	179	VGQISANIR
97	D5UX33_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	11709	103	QAAAYAQK
98	M7XVD9_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	18115	169	DMISSYRRNR
99	A0A0H3F8M6_RAHSY	Putative prophage tail protein OS=Rahnella sp.	40169	366	IFPDEETAKR
100	J2VL81_9RHIZ	ABC-type Fe3+-hydroxamate transport system, periplasmic component OS=Phyllobacterium	33243	305	KLASGQVSAR
101	W0E6B0_9FIRM	DNA mismatch repair protein OS=Desulfitobacterium metallireducens DSM	69784	603	KVTNDFEMK
102	A0A0H3F463_RAHSY	BFD domain protein (2Fe-2S)-binding domain protein OS=Rahnella sp.	7646	64	MYVCLCNSVSDK
103	CYCY_RHILV	Thiol:disulfide interchange protein CycY OS=Rhizobium leguminosarum bv. viciae	19937	186	EGLVPAMEK
104	D5UPW3_TSUPD	Glycoside hydrolase family 5 OS=Tsukamurella paurometabola	44537	400	AIKAEIGK
105	A0A0D7F9A6_9PSED	UDP-galactopyranose mutase OS=Pseudomonas oryzihabitans	44865	392	SLTFKHETR
106	DNAK_VARPS	Chaperone protein DnaK OS=Variovorax paradoxus	69085	645	EIASGNK

NoviPureTM method (MS/MS spectra: 11832)

	Accession Name	**Protein Name**	**Protein Mass**	**Length**	**Peptides**
1	M7YRS7_9RHIZ	Porin	64559	614	VFVHGGIAK TQTAYGTLR AFIQFAGLTAGR
2	A0A023Y7V6_9GAMM	EtfB protein	26708	248	LDIADGK EQPDLVILGK
3	W0E7Y1_9FIRM	Aldehyde ferredoxin oxidoreductase	61861	574	EGTPLGR EKFKNAAQIFNK

4	EFTS_ENT38	Elongation factor Ts (EF-Ts)	30371	283	SVAQLLK
5	A0A0D7FKT3_9PSED	Bifunctional protein PutA	143009	1322	DGKLARPCR
6	PCAB_ACIAD	3-carboxy-cis,cis-muconate cycloisomerase (EC 5.5.1.2) (3-carboxymuconate lactonizing enzyme) (CMLE)	49316	451	INAIKAR
7	M7YXS4_9RHIZ	Ferredoxin	11174	106	TVEGSVGATVMETALR
8	SYV_BURMA	Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase) (ValRS)	106744	955	TTGLMNPR VQIQNGTSEQQR
9	A0A0F0LBN3_9MICO	ATP-binding/permease protein CydD	59231	565	AGVHNSAR
10	D3GN19_9ENTR	Uncharacterized protein	51833	455	SIAGNIK FSLLDDLAK
11	A0A0H3FD98_RAHSY	Aminotransferase class I and II	42635	380	APILERVMER
12	A0A0H3FEH7_RAHSY	Extracellular solute-binding protein family 3	29676	272	SAADLSNK IKSAADLSNK
13	A0A0L8AFK9_9GAMM	Adenylate cyclase OS=[Pseudomonas] geniculata	91654	829	SDQMVFAVDDVVGRLR
14	J2VSM6_9RHIZ	DNA mismatch repair protein MutL	69871	649	LGGAEPR
15	RSMA_RHIL3	Ribosomal RNA small subunit methyltransferase A	30120	275	AGIDPAR
16	LEU12_BACP2	2-isopropylmalate synthase 2	63211	553	QMAMDGAILVK
17	A0A023Y681_9GAMM	Phosphoribosylglycinamide formyltransferase 2	42412	394	EVAIELQR
18	A0A0H3FEL3_RAHSY	ABC transporter related protein	34272	307	NERSRMLSGGMK LEELFVTLVNGSEEKK
19	U5P045_9MICC	Uncharacterized protein	13941	136	RGGPPPPVWAVGGALR
20	A0A0L8ACP5_9GAMM	Membrane protein OS=[Pseudomonas] geniculata	49774	450	QYTVGSEKNK
21	A0A0H3FET4_RAHSY	Fusaric acid resistance protein conserved region	74600	675	TALILPR
22	M7Y8D7_9RHIZ	Major facilitator superfamily MFS_1	43119	408	SGTPVFR
23	D5UUW6_TSUPD	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	16294	152	LAGMPTK IGISRDAVAK
24	A0A023Y292_9GAMM	Fe/S biogenesis protein NfuA	20961	199	FGGGCQGCGMADVTLK
25	SMC_BURP1	Chromosome partition protein Smc	129041	1170	VAASLEDAR TQFLFISHNK
26	A0A0D7FD14_9PSED	Thioredoxin	11430	108	SGGLVQR
27	IOLG_SERP5	Inositol 2-dehydrogenase	36704	337	TLNIGVIGTGAIGRDHIRRCSK
28	A0A0D7FHJ6_9PSED	ATP-dependent DNA helicase	156963	1448	LVGLLLR

29	W0EA48_9FIRM	Formate acetyltransferase	85455	751	MAKQSCEAYGVHMDK
30	A0A0F0LD64_9MICO	Putative 3-methyladenine DNA glycosylase	25449	242	TIVAGSEVR
31	SYA_KOCRD	Alanine--tRNA ligase	96879	895	TYHGAEKAGEQGYDDDVRMR
32	A0A023Y216_9GAMM	TonB-dependent receptor	71635	645	MLTLGTVQAR APMYDYGLIK
33	W0E615_9FIRM	Transposase IS116	45475	404	TDPIDANR
34	A0A0F0LAH9_9MICO	Phosphoglucosamine mutase	47262	452	LTAVVAR KSGTEPLVRVMVEAADAESVQTYAER
35	A0A023Y6I8_9GAMM	DNA-directed RNA polymerase subunit beta	154297	1384	QRGMSYGAPLR
36	M7YIM5_9RHIZ	Uncharacterized protein	44036	405	RMFPVRATQALQR
37	A0A0L8A781_9GAMM	Histidine kinase	51123	467	TPLAVVR
38	A0A0H3FKN2_RAHSY	Pyridoxal phosphate-dependent enzyme	40203	375	MTALGVSTPR
39	TRUD_ENT38	tRNA pseudouridine synthase D	38648	349	KLRLGALQGNAFTLILRDVTDR
40	RF3_PSYWF	Peptide chain release factor 3	59809	531	YEKGMKMK
41	A0A069AW52_9MICC	Putative short-chain type dehydrogenase/reductase VdlC	6629	58	LNNLPGHHN
42	A0A0H3FK24_RAHSY	Uncharacterized protein	124296	1133	TLQPVNYSDK
43	Y965_SERP5	UPF0255 protein Spro_0965	47130	415	MGMANASDHVLK
44	A0A0L8AEE7_9GAMM	Pseudouridine synthase OS=[Pseudomonas] geniculata	27104	467	EADRLIAAR
45	RECA_BURCE	Protein RecA (Recombinase A)	37258	347	SKALAAALAQIEKQFGKGSIMR
46	A0A0D7F6W1_9PSED	Amino acid ABC transporter substrate-binding protein	29959	279	WYGTDLTLIQ
47	W0EA38_9FIRM	ABC transporter ATP-binding protein	54222	483	ESSFPQNISKDPILNASRPK
48	G6PI_RHIL3	Glucose-6-phosphate isomerase	58599	541	TFAEAKK
49	A0A023Y6K4_9GAMM	Nucleotide-binding protein DX03_15145	33131	296	RKVVTEFALNHGSK
50	D5US39_TSUPD	Uncharacterized protein	118163	1131	TLSTAGESK
51	J2VEM8_9RHIZ	ATPase component of various ABC-type transport systems with duplicated ATPase domain	30621	277	DKVTTEMRRK
52	D5USR1_TSUPD	Adenylate/guanylate cyclase	29718	275	TVAGIVRVAR
53	M7Z8Z9_9RHIZ	Group 1 glycosyl transferase	107420	985	ETLAVIQTSAGR
54	A0A0D7QTJ5_9MICO	Sucrose synthase	76722	730	VVETLGLVSGR
55	ENO_BACP2	Enolase	46526	430	LLTERLGSK

56	J3CIY2_9RHIZ	4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate decarboxylase	23682	223	EKGLIYE
57	J2V3B6_9RHIZ	RND family efflux transporter, MFP subunit	40837	389	RGGGQGTPLVVVK TLHVQARITNPK
58	A0A023Y0X6_9GAMM	Membrane protein TolA	38409	352	KKLADQQQKANDTK
59	SYA_BURMS	Alanine--tRNA	94695	874	FLKFFESK DKLKSAAIVLAAVDGGK
60	M7YKT6_9RHIZ	Acyl-CoA dehydrogenase type 2	40117	380	LGGSGSGLLR
61	A0A023XZW6_9GAMM	LysR family transcriptional regulator	33383	302	MNLSAPAMSR
62	A0A0D7FED5_9PSED	DNA-directed DNA polymerase	130690	1173	MTLLVMNAK
63	A0A069B2X4_9MICC	Type III restriction-modification system EcoPI enzyme Mod	23875	221	CTVATGK EAWGSGAR
64	A0A0H3FIK4_RAHSY	ImpA domain-containing protein	41009	349	EMPLNAR TGWTLIRR
65	J3HND7_9RHIZ	Putative hemolysin	32893	296	YVSHYAAEAKR
66	J3CEZ8_9RHIZ	Formate--tetrahydrofolate ligase	59539	559	LSAEFIR AMKMHGGVAK
67	W0EH24_9FIRM	Uncharacterized protein	13008	117	YGYELDDLHK
68	ACEK_BURCH	Isocitrate dehydrogenase kinase/phosphatase	69950	605	VRSVFMK HVRPGVLALDTVLLR
69	W0E8G7_9FIRM	Phosphoribosylformylglycinamidine synthase	139771	1268	TTPAEGMVAK
70	A0A023Y1Q7_9GAMM	Peptidase	76364	704	NPSGIEK DSYLGNVR
71	A0A0H3FCC4_RAHSY	Cys/Met metabolism pyridoxal-phosphate-dependent protein	42976	392	NAIESACS
72	M7XP91_9RHIZ	MCP methyltransferase/methylesterase	127269	1158	AIEPLLR EIGVFASDMRDR
73	J2VDT6_9RHIZ	UDP-N-acetylmuramoylalanine--D-glutamate ligase	49064	472	IPAHSMK IYWIAGGLPK
74	PLSB_ENT38	Glycerol-3-phosphate acyltransferase	91643	806	LAAVGPRLPAR
75	ILVC_BURL3	Ketol-acid reductoisomerase	36284	338	IVTEETKKAMK
76	M7XSC1_9RHIZ	Peptidase M16 domain-containing protein	45812	431	RAAARTFADGR
77	DUSC_AZOVI	tRNA-dihydrouridine(16) synthase	33181	309	LAPELRHGWR

78	M7YUU7_9RHIZ	Uncharacterized protein	15807	148	KAVASAEPPIDK
79	A0A0L8AA89_9GAMM	Pilus assembly protein	25103	232	GPEGIER LTRDGYR
80	PDXS_BACP2	Pyridoxal 5'-phosphate synthase subunit PdxS	31590	294	AAGGVARMADPR
81	A0A0L8A5X5_9GAMM	Rod shape-determining protein RodA OS=[Pseudomonas] geniculata	39226	367	GHRPVHGG
82	W0EED3_9FIRM	NADH-quinone oxidoreductase subunit A	13411	118	LVAPNKPHAEK
83	HLYA_SERMA	Hemolysin	165079	1608	NVSTQGAK VDDASSNKNGGDNYQNYR
84	DNLJ_RHOE4	DNA ligase	76277	700	APFANPR EGDVDVR
85	D5UU14_TSUPD	Glycoside hydrolase family 57	56615	512	VLRALPEAGVRVGTLR
86	ACCA_ENT38	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	35324	319	APLAAEAMGITAPR
87	A0A0D7F8R6_9PSED	MFS transporter	45318	428	VTLGTLAMASRRR
88	A0A0L8A591_9GAMM	Uncharacterized protein OS=[Pseudomonas] geniculata N1	64735	583	FYERLSSPIK
89	A0A0L8AD51_9GAMM	Fis family transcriptional regulator OS=[Pseudomonas] geniculata N1	49881	451	AAIMAEGELISER
90	A0A0H3F4P1_RAHSY	Tex-like protein	85581	776	NAHLTSR
91	A0A0D7FAY5_9PSED	Protein-export protein SecB	17051	154	MQTAGEA
92	M7Z301_9RHIZ	Endonuclease III	28026	263	TIGLFNTK
93	M7YWF3_9RHIZ	DNA repair protein RecN	58725	557	GDGRLVR
94	RLMD_ENT38	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	47927	431	SKYSRGQVKR
95	J3HRB5_9RHIZ	Glutathione S-transferase	24408	218	VRIALGEK
96	A0A0H3FHY0_RAHSY	Uncharacterized protein	11218	96	MTRNTTKDRKTFASR
97	D5UPV9_TSUPD	Uncharacterized protein	25113	241	AADVDTLK
98	RF1_FLAJ1	Peptide chain release factor 1	40492	358	KRSSQVSSGDRSAKIR
99	HOA3_BURXL	4-hydroxy-2-oxovalerate aldolase 3	36450	338	HSEVAAKK
100	J3C6R8_9RHIZ	ABC-type sugar transport system, periplasmic component	45970	420	LKRDVKAN
101	A0A023Y2K2_9GAMM	Protein SlyX homolog	8860	79	IEGSRNADLTR
102	A0A023Y3L9_9GAMM	Uncharacterized protein	152377	1523	VGMRWNW

Noccaea caerulescens rhizosphere (NCS)

Chourey method (MS/MS spectra:9261)

	Accession Name	**Protein Name**	**Protein Mass**	**Length**	**Peptides**
1	CH603_BURCM	60 kDa chaperonin 3 OS=Burkholderia ambifaria	57040	540	STATSLK AAVEEGIVPGGGVALLR
2	M7Y9R2_9RHIZ	RND family efflux transporter MFP subunit OS=Methylobacterium mesophilicum	54574	516	VVAHPVR LSGTSGHDMFK
3	ATPB_BACP2	ATP synthase subunit beta OS=Bacillus pumilus	51812	473	TIAMASTDGVKR FTQAGSEVSALLGR
4	A0A0H3F4R8_RAHSY	Uncharacterized protein OS=Rahnella sp.	66690	596	NEIDILR DVESLTAAAMR
5	A0A0D7FD14_9PSED	Thioredoxin OS=Pseudomonas oryzihabitans	11537	108	SGGLVQR
6	M7XW44_9RHIZ	ABC transporter-like protein OS=Methylobacterium mesophilicum	57159	550	ALLGAVR ASLFAAMAR
7	A0A023XZS8_9GAMM	Cysteine synthase OS=Stenotrophomonas rhizophila	34179	319	VARPDTR
8	A0A0D7FBB2_9PSED	Histidine kinase OS=Pseudomonas oryzihabitans	94191	854	QAEAELR
9	A0A0F0KBP3_9MICO	Uncharacterized protein OS=Microbacterium oxydans	16350	148	LDHDAHR
10	M7Y2T0_9RHIZ	Arginase family OS=Methylobacterium mesophilicum	33634	312	IDDALPR
11	A0A0F0LA20_9MICO	N-acetylglucosaminyl-diphospho-decaprenol L-rhamnosyltransferase OS=Microbacterium oxydans	33171	303	TTAEEAR
12	A0A023Y0J9_9GAMM	DEAD/DEAH box helicase OS=Stenotrophomonas rhizophila	89460	815	AVELDVAGMR
13	J2VW26_9RHIZ	Bifunctional protein PutA OS=Phyllobacterium sp.	111432	1029	LSALHPR KPATDASYMACAK
14	A0A0F0LDH6_9MICO	(3S)-malyl-CoA thioesterase OS=Microbacterium oxydans	27923	267	AVAGLAPDIGIRLPK
15	M7XZQ9_9RHIZ	LacI family transcriptional regulator OS=Methylobacterium mesophilicum	39035	355	RAGVSFQTVSLVLNHPEK
16	HRCA_SPHAL	Heat-inducible transcription repressor HrcA OS=Sphingopyxis alaskensis	36969	347	AAQDLVSR
17	A0A0F0KFK5_9MICO	Putative glutamine synthetase 2 OS=Microbacterium oxydans	49464	445	TIEERGVK
18	A0A0L8AAW6_9GAMM	Selenide, water dikinase OS=[Pseudomonas] geniculata N1	37384	359	LGAGAPGVSVR
19	J2VNI7_9RHIZ	Uncharacterized protein OS=Phyllobacterium sp.	23071	209	SHGGDPDTVPK
20	D5UT44_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	14796	133	VAASAAVIDDR
21	M7XV17_9RHIZ	DNA helicase OS=Methylobacterium mesophilicum	197580	1790	LPPASFEQAGQK
22	A0A0F0KWI8_9MICO	Uncharacterized protein OS=Microbacterium oxydans	78039	730	GGAVRDVR

23	A0A0D7FA34_9PSED	Glucose dehydrogenase OS=Pseudomonas oryzihabitans	86114	799	QIDVNNVK
24	A0A0F0KQ37_9MICO	Mycothiol acetyltransferase OS=Microbacterium oxydans	21030	193	LYESRGFQR
25	A0A0H3FDN7_RAHSY	ABC transporter related protein OS=Rahnella sp.	65575	586	IKYKKMIK
26	M7Y2C5_9RHIZ	Short-chain dehydrogenase/reductase SDR OS=Methylobacterium mesophilicum	28269	268	MDLGISGR VDGGSVMAMGT
27	A0A023Y1Q7_9GAMM	Peptidase OS=Stenotrophomonas rhizophila	76487	704	AGSPMVR
28	ILVC_BACMF	Ketol-acid reductoisomerase OS=Bacillus methylotrophicus	37563	342	EAVVSVAQN
29	J2V6J2_9RHIZ	Phage prohead protease, HK97 family OS=Phyllobacterium sp.	60104	546	LGFVIFESR DAIKAGAFLKSVRER
30	RSMH_BURMS	Ribosomal RNA small subunit methyltransferase H OS=Burkholderia mallei	34126	313	LGDAGRLIAFDK
31	A0A0H3FDA9_RAHSY	Cold-shock protein DNA-binding protein OS=Rahnella sp.	18032	159	IDKENAVLSVGLLMNR
32	ACCA_SPHWW	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha OS=Sphingomonas wittichii	33166	313	GDDTASR
33	A0A0L8ADV3_9GAMM	Coproporphyrinogen-III oxidase OS=[Pseudomonas] geniculata N1	52814	469	QAISDSNQLAR
34	A0A0H3FHH6_RAHSY	Hydro-lyase, Fe-S type, tartrate/fumarate subfamily, beta subunit OS=Rahnella sp.	60484	548	NIKAKINRDGIWIEK
35	M7Y0L7_9RHIZ	Aldose 1-epimerase OS=Methylobacterium mesophilicum	31426	291	LTDGPESR RMRFTGPGK
36	BENB_ACIAD	Benzoate 1,2-dioxygenase subunit beta OS=Acinetobacter baylyi	20118	169	YKNSYSYFGMSR
37	D5URP4_TSUPD	Lycopene beta and epsilon cyclase OS=Tsukamurella paurometabola	37347	351	NPVGDGDVLAHRLR
38	SFSA_AGRRK	Sugar fermentation stimulation protein homolog OS=Agrobacterium radiobacter	27777	249	IDLLLTDPLRTTTYVEVK
39	MURC_RHIL3	UDP-N-acetylmuramate--L-alanine ligase OS=Rhizobium leguminosarum bv. viciae	50987	471	KSNPELIAAREKLLPVVRR
40	J3C7F0_9RHIZ	Non-ribosomal peptide synthase/amino acid adenylation enzyme OS=Phyllobacterium sp.	311281	2833	LVCESIAAVIGMDAVR
41	RRF_BURMS	Ribosome-recycling factor OS=Burkholderia mallei	20886	186	MSVADIKK LVQAKDAEIMTV
42	FLGB_AGRFC	Flagellar basal body rod protein FlgB OS=Agrobacterium fabrum	14911	134	MMLMTVK
43	A0A0F0KPX6_9MICO	Uncharacterized protein OS=Microbacterium oxydans	46419	425	ISGALASGR
44	HFLX_FLAPJ	GTPase HflX OS=Flavobacterium psychrophilum	47776	413	MERPNPK
45	A0A0D7FGT2_9PSED	AraC family transcriptional regulator OS=Pseudomonas oryzihabitans	29269	263	KLPLHDAQGR
46	W0E9H6_9FIRM	Uridylate kinase OS=Desulfitobacterium metallireducens DSM	26266	242	GISGSSQGMDR QVAEPYIRRRAIR

47	FPG_RHOJR	Formamidopyrimidine-DNA glycosylase OS=Rhodococcus jostii	32401	292	CGTAIRR
48	DNAE2_BRASO	Error-prone DNA polymerase OS=Bradyrhizobium sp.	132642	1170	IAIEAAK ASIESIGRR
49	HUTH_AGRVS	Histidine ammonia-lyase OS=Agrobacterium vitis	53603	512	IDAADTATLQR
50	A0A023Y3L3_9GAMM	Chemotaxis protein OS=Stenotrophomonas rhizophila	84465	789	SLVGSMR
51	A0A023Y562_9GAMM	Aspartate 1-decarboxylase OS=Stenotrophomonas rhizophila	13641	126	MHLSLLK
52	J2VH97_9RHIZ	Pseudouridine synthase OS=Phyllobacterium sp.	38715	350	FEAPLPEDMFK
53	M7YL70_9RHIZ	Cytochrome c oxidase subunit III OS=Methylobacterium mesophilicum	24683	219	MSAPLADGVGVAR
54	A0A0D7FBB7_9PSED	Uncharacterized protein OS=Pseudomonas oryzihabitans	136456	1260	TPDPALR DPAAARALLGR
55	RPOC_ARTS2	DNA-directed RNA polymerase subunit beta~ OS=Arthrobacter sp.	144194	1299	MVSSGAR DIIANGK
56	A0A0H3F4H9_RAHSY	Peptidyl-prolyl cis-trans isomerase OS=Rahnella sp.	105208	971	KSQSDYQASQTALSK
57	A0A0D7F835_9PSED	Sugar ABC transporter ATPase OS=Pseudomonas oryzihabitans	40350	366	AVLFDPASGR
58	D5UU71_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	36073	339	TPADLRGR
59	M7Z5P9_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	40288	382	IVAATGLR MARLRAIRAAK
60	ACDH2_NOCSJ	Acetaldehyde dehydrogenase 2 OS=Nocardioides sp.	32761	314	MTASTIPR
61	D5UP34_TSUPD	Mammalian cell entry related domain protein OS=Tsukamurella paurometabola	39659	367	LGAVDGQPLR
62	M7YG83_9RHIZ	Amino acid permease-associated region OS=Methylobacterium mesophilicum	51331	482	MDSSGLMGR
63	A0A023Y0V6_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	15069	135	VLDENYRAER
64	PROB_RHILW	Glutamate 5-kinase OS=Rhizobium leguminosarum bv. trifolii	40689	389	QKKDAAHA
65	D5UMT2_TSUPD	ATP-dependent helicase HrpA OS=Tsukamurella paurometabola	144244	1311	DDRGMATLDR
66	ACSA_AGRFC	Acetyl-coenzyme A synthetase OS=Agrobacterium fabrum	73425	651	SGKIMRRILR SAKIYPVLKSAKAR
67	A0A0F0KTM1_9MICO	Uncharacterized protein OS=Microbacterium oxydans	29399	272	RLAVDAARHDLR ERDAKAASADVRAR
68	A0A0D7FAE4_9PSED	Peptidase S9 OS=Pseudomonas oryzihabitans	75606	673	MTQAPIARR
69	A0A0L8AAC0_9GAMM	Translation elongation factor OS=[Pseudomonas] geniculata N1	70039	643	MIVGTAGHIDHGK
70	A0A0L8AFE5_9GAMM	tRNA (cytidine(34)-2~-O)-methyltransferase OS=[Pseudomonas] geniculata N1	17707	159	RLFALSTRASVR

71	J3HP85_9RHIZ	Alanine dehydrogenase OS=Phyllobacterium sp.	38924	371	EMLSGMK MRVGCPK
72	A0A0D7FCL7_9PSED	Energy transducer TonB OS=Pseudomonas oryzihabitans	32221	292	INAASTQKDK
73	A0A023Y190_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	113474	1055	FRLRDGTRGWR
74	A0A0F0L4I6_9MICO	Signal recognition particle receptor FtsY OS=Microbacterium oxydans	31553	290	LHTKGGLMDELGK
75	A0A0D7QQP3_9MICO	ABC transporter OS=Agreia bicolorata	68463	637	TGALVSR
76	AROK_BRADU	Shikimate kinase OS=Bradyrhizobium diazoefficiens	22445	207	RMAARLK
77	CYSD_RHITR	Sulfate adenylyltransferase subunit 2 OS=Rhizobium tropici	36592	317	DQSGSMEKK
78	A0A0F0LD20_9MICO	Uncharacterized protein OS=Microbacterium oxydans	102148	987	GANATLDSVR
79	J3CF91_9RHIZ	6-phosphogluconate dehydrogenase, decarboxylating OS=Phyllobacterium sp.	49999	471	VAVFNRTVAK
80	A0A023XZ87_9GAMM	Thiol:disulfide interchange protein OS=Stenotrophomonas rhizophila	28700	275	ERAAKGN
81	A0A0D7F5L0_9PSED	Holliday junction resolvase OS=Pseudomonas oryzihabitans	10483	99	GAQLEETLR
82	M7XZB6_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	40751	381	NVGREIVHR
83	J2VHD7_9RHIZ	Non-homologous end joining protein Ku OS=Phyllobacterium sp.	30457	266	KSIASEGK
84	TAM_RHIE6	Trans-aconitate 2-methyltransferase OS=Rhizobium etli	28552	256	MAWSAQQYVK
85	M7Z845_9RHIZ	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Methylobacterium mesophilicum	31031	289	RGGLLLVR
86	A0A0L8AB68_9GAMM	DNA primase OS=[Pseudomonas] geniculata N1	65095	580	SDIVEVVGSR
87	J3HPJ5_9RHIZ	Uracil-xanthine permease OS=Phyllobacterium sp.	51588	496	ITRPMLSAGLR
88	A0A023XZ46_9GAMM	Cation:proton antiporter OS=Stenotrophomonas rhizophila	10424	94	GPTVPDR
89	A0A0F0L7Y7_9MICO	Putative peptidoglycan binding domain protein OS=Microbacterium oxydans	37405	363	ATAKPRR

Phenol-SDS method (MS/MS spectra 10570)

	Accession Name	**Protein Name**	**Protein Mass**	**Length**	**Peptides**
1	CH60_VARPS	60 kDa chaperonin OS=Variovorax paradoxus	57385	550	AIEAPLR AMLEDIAILTGGK
2	J3HQY6_9RHIZ	10 kDa chaperonin OS=Phyllobacterium sp.	10490	98	TAGGIIIPDTAK IGGEDLLIMKESDILGILG

3	CH602_BURTA	60 kDa chaperonin 2 OS=Burkholderia thailandensis	57054	546	ALEEPLR AAVEEGIVPGGGVALIR
4	J3HU93_9RHIZ	50S ribosomal protein L7/L12 OS=Phyllobacterium sp.	12656	124	AVKEGAAK DLVEAAPK
5	A0A0H3FBD0_RAHSY	Oligopeptide/dipeptide ABC transporter, ATPase subunit OS=Rahnella sp.	37934	330	MPLLDIR NLTIEFMTADGPVK
6	J3CCP5_9RHIZ	3,4-dihydroxy-2-butanone 4-phosphate synthase	40512	367	EGGVLMR GEIVVVMDDDGR
7	W0EGQ9_9FIRM	Uncharacterized protein	62451	535	LLGLTEK DRSDPER
8	A0A0D7QR84_9MICO	ATPase OS=Agreia bicolorata GN=TZ00	66245	642	VIAVGGPR AAAWLFWFALGAAVITAIVWSLVGSPNDAIIR
9	W0EBE7_9FIRM	Alanine transporter OS=Desulfitobacterium metallireducens	46053	404	SFLMIGVGR
10	A0A0D7FFG9_9PSED	Electron transfer flavoprotein subunit beta OS=Pseudomonas oryzihabitans	27707	266	QSAFGPAR
11	A0A0H3FC06_RAHSY	Putative agmatine deiminase	39898	361	ITGIPAR TDKQAEK
12	D5UQ45_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	23185	198	DITDIYMK
13	F16PC_BACMF	Fructose-1,6-bisphosphatase class 3	74558	641	NGSGRVK
14	A0A0L8A5M8_9GAMM	Peptidase	79249	703	APFGATR
15	MASZ_BRASO	Malate synthase G OS=Bradyrhizobium sp.	78367	724	GMWAAPDK
16	A0A023Y5S6_9GAMM	UPF0276 protein DX03_13375 OS=Stenotrophomonas rhizophila	32006	290	RALLQTLR
17	A0A023Y783_9GAMM	Elongation factor G OS=Stenotrophomonas rhizophila	78328	713	NFGIMAHIDAGK LASSMAFKQGFQK
18	CLPQ_BACMF	ATP-dependent protease subunit ClpQ OS=Bacillus methylotrophicus	19534	181	ASVELAK SAMSGDGQVTFGQAVVMK
19	SYR_BACP2	Arginine--tRNA ligase	62734	557	AGFDVSR
20	M7YAH2_9RHIZ	Class-III aminotransferase	60954	561	AETEAVR
21	ENGB_BURTA	Probable GTP-binding protein EngB OS=Burkholderia thailandensis	24363	219	AFLLHQAR
22	M7XW44_9RHIZ	ABC transporter-like protein	57080	550	ALLGAVR
23	A0A0H3F999_RAHSY	Transcriptional regulator, GntR family with aminotransferase domain protein	55016	499	TLAPDFR
24	A0A0H3FD19_RAHSY	Phosphotransferase RcsD OS=Rahnella sp.	102296	897	LGGQLEIR
25	M7XP27_9RHIZ	Serine O-acetyltransferase OS=Methylobacterium mesophilicum	30310	283	GVMIGAGAK
26	A0A0D7FG18_9PSED	Lipoprotein	7977	73	DQVRTIK

27	CH604_RHIEC	60 kDa chaperonin 4 OS=Rhizobium etli	57661	542	ALEAPAR
28	A0A0D7QKI9_9MICO	Amidohydrolase OS=Agreia bicolorata	30686	284	DFSAADLR
29	D5USM0_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	15901	146	MAGLMAR
30	D5UWN4_TSUPD	Transcriptional regulator, LysR family OS=Tsukamurella paurometabola	31126	291	GLGVALLPHDDR
31	M7XT82_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	44446	418	SEQRAGAR
32	A0A023Y2Z7_9GAMM	ATPase	37191	352	ILADAHR
33	A0A0D7FIJ6_9PSED	Epimerase	24572	225	DITPLAK AMLNAARK
34	XYLG_BURCH	Xylose import ATP-binding protein XylG OS=Burkholderia cenocepacia	56162	519	HAKLLILDEPSSSLSASETR
35	W0E791_9FIRM	Ribosomal protein S12 methylthiotransferase RimO OS=Desulfitobacterium metallireducens	50926	442	QAMPDIQIR
36	A0A0D7F7I2_9PSED	Deoxyguanosinetriphosphate triphosphohydrolase OS=Pseudomonas oryzihabitans	50126	443	GREPSFKSR LELPLLGPER
37	A0A0F0KZD6_9MICO	Gramicidin S synthase 1 OS=Microbacterium oxydans	54463	511	QPDETAVR
38	J3C5F3_9RHIZ	Porin subfamily OS=Phyllobacterium sp.	38618	360	SETELGTLR
39	A0A023Y5N4_9GAMM	Uncharacterized protein	113787	1074	GEGNELR
40	A0A0H3F760_RAHSY	NAD-dependent epimerase/dehydratase OS=Rahnella sp.	54310	484	IASLARQK QKDRCGR
41	A0A0H3FLE0_RAHSY	ATP-dependent DNA helicase Rep OS=Rahnella sp.	77707	674	LAYVGITR EIGAATLQK
42	M7XXZ2_9RHIZ	Nitrogen regulatory protein P-II OS=Methylobacterium mesophilicum	12204	112	GAEYVVDFLPK IFVSTIEEAIR
43	EFTU_ARTS2	Elongation factor Tu OS=Arthrobacter sp.	43621	396	EGGRTVGSGR
44	A0A0F0L9I6_9MICO	Alkaline phosphatase synthesis sensor protein PhoR OS=Microbacterium oxydans	63508	597	AVEVARMK FTPPGGSVVAR
45	A0A0D7FEY5_9PSED	LysR family transcriptional regulator OS=Pseudomonas oryzihabitans	34386	312	QLASLNAIMSR
46	M7Z4T8_9RHIZ	Ribonucleotide-diphosphate reductase subunit alpha OS=Methylobacterium mesophilicum	135848	1243	SENEKLGGGGK YGSGTGSNFSMLRSENEKLGGGGKSSGLMSFLK
47	A0A0H3FFX2_RAHSY	ABC transporter related protein OS=Rahnella sp.	66622	599	MAEPKKIK
48	M7XZU6_9RHIZ	Putative oxalyl-CoA decarboxylase	61364	581	REANVAK
49	M7YK50_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	24810	233	GHDVRDLHDR
50	CH602_BRASB	60 kDa chaperonin 2 OS=Bradyrhizobium sp.	57222	541	APGFGDR NVLIEKSFGAPRITK

51	PURQ_BRADU	Phosphoribosylformylglycinamidine synthase subunit PurQ OS=Bradyrhizobium diazoefficiens	25260	233	CGAIAAR
52	CH60_KLEOX	60 kDa chaperonin (Fragment) OS=Klebsiella oxytoca	56524	540	APGFGDR SDAPDLGAAGGMGG
53	THIG_ENT38	Thiazole synthase OS=Enterobacter sp.	27116	256	EALGTSWLK
54	ATPG_BRASO	ATP synthase gamma chain OS=Bradyrhizobium sp.	32157	292	QTLVYNR TRQAMITK
55	RBSA3_RHIEC	Ribose import ATP-binding protein RbsA 3 OS=Rhizobium etli	55471	511	AAEEFALAR
56	NODC_RHILV	N-acetylglucosaminyltransferase OS=Rhizobium leguminosarum bv. viciae	46739	424	DPAVGAAMGQMK
57	A0A023Y3F4_9GAMM	3-phosphoglycerate dehydrogenase OS=Stenotrophomonas rhizophila	44070	413	TQLSADVLANAK
58	A0A0D7QP14_9MICO	Uncharacterized protein OS=Agreia bicolorata	104042	965	SLIMMPPHNVAR
59	SYT_BACMF	Threonine--tRNA ligase OS=Bacillus methylotrophicus	73812	643	ELPIRIAELGTMHR
60	A0A0D7QRW1_9MICO	Alanine racemase	37559	361	LDTGLGR
61	J3CBG2_9RHIZ	ABC-type polar amino acid transport system, ATPase component OS=Phyllobacterium sp.	26657	242	SAAVKLNEVIK
62	A0A023Y705_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	18845	174	CTNAAGLEKLWPDMAAAVAK
63	A0A0F0LHL7_9MICO	Uncharacterized protein OS=Microbacterium oxydans	6245	62	GLADVITGRRTS
64	A0A0H3FG34_RAHSY	Uncharacterized protein OS=Rahnella sp.	24171	210	HQLMELMK EVIRLPLKY
65	A0A0D7FIQ2_9PSED	UvrABC system protein B OS=Pseudomonas oryzihabitans	75712	669	DEIQALR SPSEIGKR
66	J2VHZ2_9RHIZ	NAD-specific glutamate dehydrogenase OS=Phyllobacterium sp.	174815	1597	TATTKTK
67	PLSX_BURXL	Phosphate acyltransferase OS=Burkholderia xenovorans	39301	368	KDSSMRVALNRVK AMEENEGSLEQAAR
68	A0A0L8ADS6_9GAMM	Oar protein OS=[Pseudomonas] geniculata N1	118188	1076	AALRYNK
69	RL13_BACMF	50S ribosomal protein L13 OS=Bacillus methylotrophicus	16395	145	SRTALEMR GSLGRQMFKK
70	D5UVA2_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	23964	228	STALAASAGYAK
71	W0EFM0_9FIRM	Chaperone protein DnaJ OS=Desulfitobacterium metallireducens	41285	378	TPFGMVQTAR
72	PUR9_RHIE6	Bifunctional purine biosynthesis protein PurH OS=Rhizobium etli	57247	538	LLSTGGTYK
73	HLYA_PROMI	Hemolysin OS=Proteus mirabilis	165885	1577	QLVGGDISFK INAGNNLAINANK
74	M7Y2Q0_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	8070	69	MIRLARFDLARSERLHR

75	M7YAY0_9RHIZ	TetR family transcriptional regulator	20400	190	RFEGDST
76	GPMI_ENT38	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Enterobacter sp.	56457	514	KKVVNLNFIMLTEYAADIK
77	M7Y615_9RHIZ	Thiamine biosynthesis protein ThiS OS=Methylobacterium mesophilicum	7875	70	VEIVRAMQGG
78	A0A0F0L3A2_9MICO	Isoleucine--tRNA ligase	125607	1129	DGSDAMR DFGTLPR
79	A0A0L8AFK9_9GAMM	Adenylate cyclase	91483	829	RDLPLWR
80	A0A0D7FF74_9PSED	Membrane protein	37998	349	SARLENK
81	J2VJI5_9RHIZ	ABC-type dipeptide transport system, periplasmic component OS=Phyllobacterium sp.	73166	641	VNLWKMTR
82	ASPQ_PSES7	Glutaminase-asparaginase OS=Pseudomonas sp.	36178	337	SSHVNQGGFVLR
83	J3CGC4_9RHIZ	tRNA (guanine-N(7)-)-methyltransferase OS=Phyllobacterium sp.	27109	232	MEIGFGGGEHLLHEAARHPK
84	A0A0F0L5Y0_9MICO	Deoxyguanosinetriphosphate triphosphohydrolase OS=Microbacterium oxydans	51488	467	NRLTHSLEVAQVGR
85	M7Y3W3_9RHIZ	Electron-transferring-flavoprotein dehydrogenase OS=Methylobacterium mesophilicum	60886	557	AIMEGGWQSVPK
86	A0A0D7FGT2_9PSED	AraC family transcriptional regulator OS=Pseudomonas oryzihabitans	29269	263	KLPLHDAQGR
87	A0A0D7FBT3_9PSED	Protein-glutamate methylesterase	36414	339	RLIGKLK
88	Y966_RHIEC	UPF0301 protein RHE_CH00966 OS=Rhizobium etli	22096	201	AISKGAGPK
89	D5UWV0_TSUPD	PPOX class putative F420-dependent enzyme OS=Tsukamurella paurometabola	14766	132	FSGNALK
90	M7YAC4_9RHIZ	Hydrophobe/amphiphile efflux-1 (HAE1) family transporter OS=Methylobacterium mesophilicum	113072	1062	DGYGAVVARIVR
91	D5UYE2_TSUPD	Tex-like protein protein-like protein OS=Tsukamurella paurometabola	85199	796	VLAVLRGEK
92	DAPF_RHOE4	Diaminopimelate epimerase OS=Rhodococcus erythropolis	30434	292	NSDGSIAEMCGNGVR
93	A0A0F0KR00_9MICO	GMP synthase [glutamine-hydrolyzing] OS=Microbacterium oxydans	56746	528	IREQVGDAR
94	A0A0F0L7R0_9MICO	Putative sensor histidine kinase TcrY OS=Microbacterium oxydans	60643	561	MGAIKGEEDTAR
95	A0A023Y2X8_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	109569	1016	SWALRHACK
96	M7YIV7_9RHIZ	2-dehydro-3-deoxyglucarate aldolase OS=Methylobacterium mesophilicum	27666	256	TIEEAVGR
97	UPP_ARTS2	Uracil phosphoribosyltransferase OS=Arthrobacter sp.	23018	211	TLVVDHPLVAHK
98	A0A0H3F8T2_RAHSY	Helicase c2 OS=Rahnella sp.	71566	637	SADRLSQSTMDFR
99	A0A0F0KWM2_9MICO	Putative transcriptional regulatory protein NarL OS=Microbacterium oxydans	90960	836	FATVLKRARLALIDGK

100	M7XPX3_9RHIZ	Aminodeoxychorismate lyase OS=Methylobacterium mesophilicum	50599	471	TVPALSEPTAAPR
101	M7Y1D9_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	19845	183	KARAQNVPGR
102	FMT_RHOE4	Methionyl-tRNA formyltransferase OS=Rhodococcus erythropolis	32400	307	IRDTDTAGDLLGR
103	J3HPK0_9RHIZ	Uncharacterized protein OS=Phyllobacterium sp.	18276	160	KKIVDHEIGK

NoviPureTM method (MS/MS spectra: 11782)

	Accession Name	**Protein Name**	**Protein Mass**	**Length**	**Peptides**
1	D5UPV9_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	25212	241	AADVDTLK KSLSESLVPK
2	M7YE77_9RHIZ	Porin OS=Methylobacterium mesophilicum	58654	553	TQTAYGTLR QFNQGGDSAGYHTRMR
3	A0A0D7QQP3_9MICO	ABC transporter OS=Agreia bicolorata	68463	637	LAGTDVR MPIAFFTRTR
4	A0A0H3FGX0_RAHSY	Transaldolase OS=Rahnella sp.	35328	317	LASTWQGIR
5	A0A023Y0D1_9GAMM	Glyceraldehyde-3-phosphate dehydrogenase OS=Stenotrophomonas rhizophila	36187	334	VGINGFGR ADVEVSGSDLLVNGKK
6	A0A0D7FCJ2_9PSED	Peptidase M48 OS=Pseudomonas oryzihabitans	29380	273	MAQASQGK
7	DHNO_AGRT7	D-nopaline dehydrogenase OS=Agrobacterium tumefaciens	46042	413	VLIIVTR
8	M7YXS4_9RHIZ	Ferredoxin OS=Methylobacterium mesophilicum	11451	106	TVEGSVGATVMETALR
9	A0A0F0L579_9MICO	Putative FAD-linked oxidoreductase OS=Microbacterium oxydans	57344	544	DHENGTVDADR
10	A0A0F0L339_9MICO	ECF RNA polymerase sigma factor SigW OS=Microbacterium oxydans	24342	217	VPVGTVR SRMNRIRTRLNPDR

11	A0A0L8AF63_9GAMM	Cold-shock protein OS=[Pseudomonas] geniculata N1	7716	69	GFGFISR
12	A0A0D7QW45_9MICO	GTP pyrophosphokinase OS=Agreia bicolorata	83697	750	DAIARAMR QWFTKERR
13	XYNA1_PAESJ	Endo-1,4-beta-xylanase A OS=Paenibacillus sp.	157225	1462	LLSPETSTK
14	W0EDD9_9FIRM	7-cyano-7-deazaguanine reductase OS=Desulfitobacterium metallireducens	44399	395	KKRLSTIMSK
15	W0E9A3_9FIRM	(4Fe-4S)-binding protein OS=Desulfitobacterium metallireducens	36443	319	MNYQEMTR
16	A0A0F0L6V3_9MICO	Pectin degradation repressor protein KdgR OS=Microbacterium oxydans	28536	267	SFAMAGR
17	A0A0D7QP09_9MICO	Uncharacterized protein OS=Agreia bicolorata	24402	225	DAGALLR
18	A0A0H3FEQ2_RAHSY	Cell division protein FtsQ OS=Rahnella sp.	31524	278	FIELYPR
19	Y3248_NOCSJ	UPF0102 protein Noca_3248 OS=Nocardioides sp.	13689	124	YGTPHEAVTDIK
20	MNMA_ACIBY	tRNA-specific 2-thiouridylase MnmA OS=Acinetobacter baumannii	42198	377	AETAYNSK
21	A0A023Y246_9GAMM	Stress-responsive transcriptional regulator OS=Stenotrophomonas rhizophila	7293	67	MNATPRTLSR
22	A0A0L8A5F8_9GAMM	Serine protease OS=[Pseudomonas] geniculata N1	116411	1118	VDTNVVMNQK
23	M7XP10_9RHIZ	Type II secretion system protein E OS=Methylobacterium mesophilicum	53191	480	LTLEQLVR
24	J3HSJ8_9RHIZ	ABC-type metal ion transport system, periplasmic component/surface adhesin OS=Phyllobacterium sp.	35230	329	AAIASIPENK
25	D5UXG2_TSUPD	Bifunctional DNA primase/polymerase OS=Tsukamurella paurometabola	87108	808	DANKPLK
26	A0A0D7QRU7_9MICO	Haloacid dehalogenase OS=Agreia bicolorata	84641	761	YSGMPAK
27	PROA_ENT38	Gamma-glutamyl phosphate reductase OS=Enterobacter sp.	45241	417	KLSHGNR
28	UREE_AGRRK	Urease accessory protein UreE OS=Agrobacterium radiobacter	18955	167	VELPHDLR
29	A0A0D7FDU1_9PSED	GTPase Obg OS=Pseudomonas oryzihabitans	44199	403	LKAVVER
30	NOCQ_AGRFC	Nopaline transport system permease protein NocQ OS=Agrobacterium fabrum	25622	236	TAAMGAGSTK
31	M7YCR5_9RHIZ	Hopanoid-associated sugar epimerase OS=Methylobacterium mesophilicum	37218	343	DGTRLMMR
32	A0A0F0KD08_9MICO	Ribosomal RNA small subunit methyltransferase B OS=Microbacterium oxydans	52723	498	GAPANARPRGPR
33	J2VHS1_9RHIZ	Dihydrodipicolinate synthase/N-acetylneuraminate lyase OS=Phyllobacterium sp.	32262	297	ESSDDIRR
34	A0A0D7FD14_9PSED	Thioredoxin OS=Pseudomonas oryzihabitans	11537	108	SGGLVQR
35	D5UM28_TSUPD	Penicillin-binding protein transpeptidase OS=Tsukamurella paurometabola	63061	612	VTAPTTVLDVAGQLTR
36	A0A0D7QLF4_9MICO	Ribonuclease G OS=Agreia bicolorata	92783	865	MVECLSRDR NDDDRPDTSVRRR

37	EFTU_BACMF	Elongation factor Tu OS=Bacillus methylotrophicus	43500	396	EKFDRSK
38	A0A0F0KLZ8_9MICO	Uncharacterized protein OS=Microbacterium oxydans	204140	1971	LVSLGAGAR
39	M7Y7Z5_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	119656	1137	LTGPARAAVAAR
40	A0A0L8AFB7_9GAMM	Histone OS=[Pseudomonas] geniculata	29912	297	KAVAKKTVAAKK
41	J3CGU4_9RHIZ	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin) OS=Phyllobacterium sp.	44346	416	AGSQIVR
42	A0A0H3FIM3_RAHSY	Putative lipoprotein OS=Rahnella sp.	12797	113	TNNSPKP
43	J3CAA5_9RHIZ	Uncharacterized protein OS=Phyllobacterium sp.	7782	64	RFLLQRTMDR
44	A0A0L8AEI2_9GAMM	Bifunctional uridylyltransferase/uridylyl-removing enzyme OS=[Pseudomonas] geniculata N1	97719	875	LRFDYQKTLAAR
45	D5UTY9_TSUPD	Transcriptional regulator, TetR family OS=Tsukamurella paurometabola	23839	218	ETARSLMR
46	A0A023Y5T3_9GAMM	Alpha-glucosidase OS=Stenotrophomonas rhizophila	60752	537	ESRQDRTNPK
47	W0EAM9_9FIRM	(4Fe-4S)-binding protein OS=Desulfitobacterium metallireducens	36871	323	MFKTNYTLPK
48	M7XWH7_9RHIZ	Acetyltransferase (GNAT) domain-containing protein OS=Methylobacterium mesophilicum	43364	405	SPEAAGVR LLIVADR
49	J2VTP8_9RHIZ	Uncharacterized protein OS=Phyllobacterium sp.	13864	125	LHSLGDVMSSSSPTR SYVEAIGGKLELTVK
50	A0A0H3FC57_RAHSY	Apolipoprotein N-acyltransferase OS=Rahnella sp.	56963	509	TVDVALVQGNIPQSMKWDPK
51	TRPC_BACP2	Indole-3-glycerol phosphate synthase OS=Bacillus pumilus	28201	250	MLNQIIARKK
52	A0A0L8ACX5_9GAMM	PTS fructose transporter subunit IIBC OS=[Pseudomonas] geniculata N1	57849	567	KPVTTPA
53	J3CCZ8_9RHIZ	Autotransporter-associated beta strand repeat containing protein (Fragment) OS=Phyllobacterium sp.	76929	724	DGHSEYDR
54	CLPX_SPHAL	ATP-dependent Clp protease ATP-binding subunit ClpX OS=Sphingopyxis alaskensis	46117	423	QIEPEDLLK
55	A0A0D7QRH9_9MICO	DNA helicase OS=Agreia bicolorata	88269	804	ARKRLYLSLAMTR
56	A0A0L8AB49_9GAMM	Phytase OS=[Pseudomonas] geniculata N1	40354	371	RVRQYHVTRDGAK
57	J3HPK5_9RHIZ	Autotransporter adhesin OS=Phyllobacterium sp.	64787	641	INTLRESTDNR
58	A0A0F0KLC3_9MICO	RecBCD enzyme subunit RecD OS=Microbacterium oxydans	125684	1156	LVNEHGFK
59	A0A0D7QNW0_9MICO	ABC transporter substrate-binding protein OS=Agreia bicolorata	40242	375	TYDNGNK MTTRTTKR
60	M7XX55_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	13544	132	VAAKVAAKPAAPKPARASK
61	A0A0D7FLY7_9PSED	Iron-enterobactin ABC transporter substrate-binding protein OS=Pseudomonas oryzihabitans	34326	322	KVVGDFDRR

62	A0A023Y3A7_9GAMM	Histidine kinase OS=Stenotrophomonas rhizophila	231209	2100	GLLARLNPLHLLR
63	MURI_AGRFC	Glutamate racemase OS=Agrobacterium fabrum	30246	273	LMQGFGLSVSSN
64	M7XPK5_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	31148	269	TYALFER
65	A0A023Y718_9GAMM	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase OS=Stenotrophomonas rhizophila	19134	171	KLVMAQADAR
66	M7YYY8_9RHIZ	ATP phosphoribosyltransferase OS=Methylobacterium mesophilicum	34492	327	RLRVATKYVNLTRR
67	A0A0F0L382_9MICO	UvrABC system protein B OS=Microbacterium oxydans	77535	690	MTDSMAK
68	A0A0D7QR47_9MICO	Oxidoreductase OS=Agreia bicolorata	31574	297	ASINTFSK
69	A0A0H3FA72_RAHSY	Formiminoglutamate deiminase OS=Rahnella sp.	50412	457	QLYIEMLK
70	RECX_AMYMU	Regulatory protein RecX OS=Amycolatopsis mediterranei	19805	175	HTTQGLSR LGSLGNVDEQTALR
71	W0EFM5_9FIRM	Elongation factor 4 OS=Desulfitobacterium metallireducens	67051	601	DKADSRGRK
72	GLMS_ACIAD	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Acinetobacter baylyi	67859	612	ELDASVSNASK
73	ODPA_RAT	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Rattus norvegicus	43883	390	EIDVEVRK
74	HSLV_AGRFC	ATP-dependent protease subunit HslV OS=Agrobacterium fabrum	18664	174	AMMDTDK
75	A0A023Y788_9GAMM	Methyltransferase OS=Stenotrophomonas rhizophila	30831	280	ADLAMDGVLAVR
76	M7YZH0_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	32025	291	MNGKVIDLN
77	M7YCA8_9RHIZ	Uncharacterized protein OS=Methylobacterium mesophilicum	21522	203	EVEAWSSR
78	A0A0F0LBB9_9MICO	Aldehyde dehydrogenase PuuC OS=Microbacterium oxydans	53101	496	EALQTELR GSGFGRDKSLHALEK
79	A0A0F0L404_9MICO	Uncharacterized protein OS=Microbacterium oxydans	49229	454	EEVDWKK RTWLNALGG
80	Y3137_ACIAD	UPF0234 protein ACIAD3137 OS=Acinetobacter baylyi	18720	162	NVVQVIKLKDGLDSDTAK
81	A0A023Y3M5_9GAMM	Peptide chain release factor 2 OS=Stenotrophomonas rhizophila	34169	308	DNAMKMLAAK
82	A0A0D7F7B2_9PSED	Penicillin-binding protein 2 OS=Pseudomonas oryzihabitans	70774	635	DIVLTIDSR
83	J2VA23_9RHIZ	NAD-dependent aldehyde dehydrogenase OS=Phyllobacterium sp.	86184	798	ASCGNLK METLRVGDPLDK
84	AZOR_EXISA	FMN-dependent NADH-azoreductase OS=Exiguobacterium sp.	22952	211	AKAEALAK FASGEALTDVEAK
85	D5UMH1_TSUPD	Putative monooxygenase OS=Tsukamurella paurometabola	55347	499	RTSPATV

86	M7YA94_9RHIZ	Succinate dehydrogenase flavoprotein subunit OS=Methylobacterium mesophilicum	66645	605	SMTMEIR ATVGCSEAGLR
87	A0A023Y556_9GAMM	Membrane protein OS=Stenotrophomonas rhizophila	28014	249	HWMAHNAWR HRPLAGSSAAKADR
88	A0A0L8ADV1_9GAMM	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase OS=[Pseudomonas] geniculata N1	23464	208	SRQKKLGN
89	A0A023Y420_9GAMM	Flagellar basal body protein OS=Stenotrophomonas rhizophila	26096	250	SANSLLRLGG
90	SYA_BURP8	Alanine--tRNA ligase OS=Burkholderia phymatum	95452	874	VMAYDEAVK
91	A0A0H3F8F8_RAHSY	Glutamate-ammonia-ligase adenylyltransferase OS=Rahnella sp.	108307	945	GMIAREVRR
92	TMP_BPSPB	Probable tape measure protein OS=Bacillus phage SPbeta	252157	2285	KKLMQEQAK
93	A0A0H3F5T8_RAHSY	DNA topoisomerase 4 subunit B OS=Rahnella sp.	70822	631	KKGKPNVQRFK
94	A0A0D7F850_9PSED	Guanine deaminase OS=Pseudomonas oryzihabitans	47980	436	VVRETYAAGR
95	D5UU39_TSUPD	Uncharacterized protein OS=Tsukamurella paurometabola	39468	340	VLGIHGR
96	J3HLI1_9RHIZ	Methylase involved in ubiquinone/menaquinone biosynthesis OS=Phyllobacterium sp.	28489	250	RTSRRVFVPVLSPQGTAMRR
97	M7YJC1_9RHIZ	Magnesium chelatase, H subunit OS=Methylobacterium mesophilicum	133112	1234	FDMSGTKR
98	HMUV_BURTA	Hemin import ATP-binding protein HmuV OS=Burkholderia thailandensis	28975	272	AIDATRLARLR
99	A0A0D7FIC3_9PSED	DEAD/DEAH box helicase OS=Pseudomonas oryzihabitans	83485	747	EERRRQCPK
100	A0A0D7FBB1_9PSED	Glutamine ABC transporter ATP-binding protein OS=Pseudomonas oryzihabitans	29260	255	WYGQFHVLK
101	G6GEI2_9FIRM	Transposase IS110 OS=Desulfitobacterium metallireducens	48955	427	KQSLIALSCK
102	A0A023Y2X8_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	109569	1016	QADAQGIVK
103	A0A023XYE6_9GAMM	Uncharacterized protein OS=Stenotrophomonas rhizophila	30703	296	TESLDGN
104	A0A0H3FFF8_RAHSY	Potassium-transporting ATPase ATP-binding subunit OS=Rahnella sp.	73222	688	MIAMVEGAKRRK
105	A0A023Y6D3_9GAMM	TonB-dependent receptor OS=Stenotrophomonas rhizophila	106857	977	AVWARDR
106	J3CGD3_9RHIZ	Polyribonucleotide nucleotidyltransferase OS=Phyllobacterium sp.	77311	977	IRDVIGSGGK
107	A0A0L8AE99_9GAMM	Membrane protein OS=[Pseudomonas] geniculata N1	13965	713	GMKWNASAR

On line resource 3. List of proteins belonging to GO terms “response to stimulus”, “small molecule metabolic process”, “oxidation-reduction process”, “transport”, “small molecule binding”, “metal ion binding”, “DNA binding”, and “hydrolase activity” identified from the three soil samples: bulk soil (BS), Biscutella laevigata rhizosphere (BLS) and Noccaea caerulescens rhizosphere (NCS).

	BS					**BLS**					**NCS**			
GO term	**prot ID**	**gene name**	**description**	**species**		**prot ID**	**gene name**	**description**	**species**		**prot ID**	**gene name**	**description**	**species**
response to stimulus														
	J3HN07	mutS	DNA mismatch repair protein MutS	Phyllobacterium sp. YR531		M7YWF3	MmSR116_4062	DNA repair protein RecN	Methylobacterium mesophilicum SR1.6/6		J2VHD7	ku	Non-homologous end joining protein Ku	Phyllobacterium sp. YR531
	A1V6A8	uvrC	UvrABC system protein C	Burkholderia mallei (strain SAVP1)		M7YKY2	tonB	TonB-dependent siderophore receptor	Methylobacterium mesophilicum SR1.6/6		A0A0F0L382	uvrB	UvrABC system protein B	Microbacterium oxydans
	A0A0D7FLL5	UM91_00260	Chemotaxis protein	Pseudomonas oryzihabitans		J2VSM6	mutL	DNA mismatch repair protein MutL	Phyllobacterium sp. YR531		O64046	yomI	Probable tape measure protein	Bacillus phage SPbeta
	J3HQ21	PMI41_03143	Diguanylate cyclase (GGDEF) domain-containing protein	Phyllobacterium sp. YR531		W0E6B0	DESME_03800	DNA mismatch repair protein	Desulfitobacterium metallireducens DSM 15288		A0A0L8ADS6	W7K_04660	Oar protein	[Pseudomonas] geniculata N1
	A0A023Y1S1	DX03_06850	DeoR faimly transcriptional regulator	Stenotrophomonas rhizophila		A0A0H3F4P1	Rahaq_0243	Tex-like protein	Rahnella sp. (strain Y9602)		W0EFM0	dnaJ	Chaperone protein DnaJ	Desulfitobacterium metallireducens DSM 15288
	A0A023XZA6	DX03_02165	Multidrug transporter MatE	Stenotrophomonas rhizophila		A0A0L8AFK9	W7K_01830	Adenylate cyclase	[Pseudomonas] geniculata N1		A0A023Y2Z7	DX03_09635	ATPase	Stenotrophomonas rhizophila
	A0A0D7FEA9	UM91_13305	Peptidase S24	Pseudomonas oryzihabitans		D5UUW6	Tpau_3093	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		Q0S2E0	mutM	Formamidopyrimidine-DNA glycosylase	Rhodococcus jostii (strain RHA1)
	A0A0D7FMA6	ruvB	Holliday junction ATP-dependent DNA helicase RuvB	Pseudomonas oryzihabitans		M7XP91	MmSR116_5619	MCP methyltransferase/methylesterase	Methylobacterium mesophilicum SR1.6/6		A0A0L8AFK9	W7K_01830	Adenylate cyclase	[Pseudomonas] geniculata N1
	A0A0F0KSL8	clpB	Chaperone protein ClpB	Microbacterium oxydans		M7Y663	MmSR116_2370	Integral membrane sensor signal transduction histidine kinase	Methylobacterium mesophilicum SR1.6/6		A0A0F0L9I6	phoR	Alkaline phosphatase synthesis sensor protein PhoR	Microbacterium oxydans
	M7Z301	nth	Endonuclease III	Methylobacterium mesophilicum SR1.6/6		W0E615	DESME_02960	Transposase IS116	Desulfitobacterium metallireducens DSM 15288		A0A0D7FBT3	UM91_11560	Protein-glutamate methylesterase	Pseudomonas oryzihabitans
	W0E620	DESME_032	Sensory histidine	Desulfitobact		M7Y3Y6	MmSR116_	Acid phosphatase	Methylobacte		A4YRD9	dnaE2	Error-prone DNA	Bradyrhizobiu

		00	kinase	erium metallireducens DSM 15288			3375		rium mesophilicum SR1.6/6				polymerase	m sp. (strain ORS278)
	A0A0D7FJ11	UM91_02115	Flagellar rod assembly protein FlgJ	Pseudomonas oryzihabitans		A0A0D7FI45	UM91_00300	ATPase	Pseudomonas oryzihabitans		A0A0H3FD19	rcsD	Phosphotransferase RcsD	Rahnella sp. (strain Y9602)
	D5USV2	Tpau_0601	Transcriptional regulator, CarD family	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		P0C7V2	recA	Protein RecA	Burkholderia cepacia		A0A023Y190	DX03_05200	Uncharacterized protein	Stenotrophomonas rhizophila
	A0A0D7FLN2	relA	(P)ppGpp synthetase	Pseudomonas oryzihabitans		A0A0L8ADW8	uvrB	UvrABC system protein B	[Pseudomonas] geniculata N1		D5UM28	Tpau_1690	Penicillin-binding protein transpeptidase	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
	A0A0L8A5A2	W7K_20575	DNA methylase	[Pseudomonas] geniculata N1		A0A0F0KXV3	tcrY_3	Putative sensor histidine kinase TcrY	Microbacterium oxydans		A0A0D7FIQ2	uvrB	UvrABC system protein B	Pseudomonas oryzihabitans
	A0A0H3F4D0	Rahaq_0416	S-adenosylhomocysteine deaminase	Rahnella sp. (strain Y9602)		A0A023Y216	DX03_08285	TonB-dependent receptor	Stenotrophomonas rhizophila		A0A023Y6D3	DX03_15755	TonB-dependent receptor	Stenotrophomonas rhizophila
	A0A0H3FFX2	Rahaq_3339	ABC transporter related protein	Rahnella sp. (strain Y9602)		O64046	yomI	Probable tape measure protein	Bacillus phage SPbeta		Q9REV5	recX	Regulatory protein RecX	Amycolatopsis mediterranei (strain U-32)
	M7YS07	uvrB	UvrABC system protein B	Methylobacterium mesophilicum SR1.6/6		A0A0H3FEH7	Rahaq_3622	Extracellular solute-binding protein family 3	Rahnella sp. (strain Y9602)		J2VA23	PMI41_02744	NAD-dependent aldehyde dehydrogenase	Phyllobacterium sp. YR531
	Q0BC04	lptD	LPS-assembly protein LptD	Burkholderia ambifaria (strain ATCC BAA-244 / AMMD)		A0A0L8A781	W7K_16285	Histidine kinase	[Pseudomonas] geniculata N1		A0A023Y3L3	DX03_10660	Chemotaxis protein	Stenotrophomonas rhizophila
	A0A023Y6Q8	DX03_16565	Histidine kinase	Stenotrophomonas rhizophila		C0ZXK3	ligA	DNA ligase	Rhodococcus erythropolis (strain PR4 / NBRC 100887)		A0A0F0L7R0	tcrY_2	Putative sensor histidine kinase TcrY	Microbacterium oxydans
						A0A0D7FDR6	UM91_13975	Penicillin-binding protein 1B	Pseudomonas oryzihabitans		A0A0H3FFX2	Rahaq_3339	ABC transporter related protein	Rahnella sp. (strain Y9602)
						M7Z301	nth	Endonuclease III	Methylobacterium mesophilicum SR1.6/6		D5UYE2	Tpau_1628	Tex-like protein protein-like protein	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
						M7Y0L2	MmSR116_4245	Integral membrane sensor signal transduction	Methylobacterium		A0A0D7FBB2	UM91_19110	Histidine kinase	Pseudomonas oryzihabitans

								histidine kinase	mesophilicum SR1.6/6					
						D5USR1	Tpau_2734	Adenylate/guanylate cyclase	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)					
						A0A0F0LD64	RS83_00945	Putative 3-methyladenine DNA glycosylase	Microbacterium oxydans					
						A0A0F0LC60	sbcC	Nuclease SbcCD subunit C	Microbacterium oxydans					
						P45409	cycY	Thiol:disulfide interchange protein CycY	Rhizobium leguminosarum bv. viciae					
						A0A023Y3G2	DX03_10310	Histidine kinase	Stenotrophomonas rhizophila					
small molecule metabolic process														
	A0A023Y227	DX03_07360	Fumarate hydratase	Stenotrophomonas rhizophila		A0A0H3F9X6	dadA	D-amino acid dehydrogenase	Rahnella sp. (strain Y9602)		M7Y2C5	MmSR116_3967	Short-chain dehydrogenase/reductase SDR	Methylobacterium mesophilicum SR1.6/6
	A0A0H3FLE2	ilvD	Dihydroxy-acid dehydratase	Rahnella sp. (strain Y9602)		A0A0F0KI13	kynA	Tryptophan 2,3-dioxygenase	Microbacterium oxydans		W0E9H6	pyrH	Uridylate kinase	Desulfitobacterium metallireducens DSM 15288
	A0A0H3FGG7	gmk	Guanylate kinase	Rahnella sp. (strain Y9602)		A0A0H3FCC4	Rahaq_2124	Cys/Met metabolism pyridoxal-phosphate-dependent protein	Rahnella sp. (strain Y9602)		A0A0H3FA72	Rahaq_2158	Formiminoglutamate deiminase	Rahnella sp. (strain Y9602)
	A0A0F0KI13	kynA	Tryptophan 2,3-dioxygenase	Microbacterium oxydans		M7Y5Y9	atpG	ATP synthase gamma chain	Methylobacterium mesophilicum SR1.6/6		Q89IB6	purQ	Phosphoribosylformylglycinamidine synthase subunit PurQ	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)
	A4W8T4	lpxK	Tetraacyldisaccharide 4'-kinase	Enterobacter sp. (strain 638)		A8GKW1	iolG	Inositol 2-dehydrogenase	Serratia proteamaculans (strain 568)		Q8UBV5	acsA	Acetyl-coenzyme A synthetase	Agrobacterium fabrum (strain C58 / ATCC 33970)
	A0A0D7QLP3	TZ00_14955	Polyphosphate kinase	Agreia bicolorata		M7Y3Y6	MmSR116_3375	Acid phosphatase	Methylobacterium mesophilicum SR1.6/6		B5ZUE4	proB	Glutamate 5-kinase	Rhizobium leguminosarum bv. trifolii (strain WSM2304)

	Q142I6	ilvC	Ketol-acid reductoisomerase	Burkholderia xenovorans (strain LB400)		Q62KW5	valS	Valine--tRNA ligase	Burkholderia mallei (strain ATCC 23344)		B9J8M0	ureE	Urease accessory protein UreE	Agrobacterium radiobacter (strain K84 / ATCC BAA-868)
	J2V752	ilvA	L-threonine dehydratase	Phyllobacterium sp. YR531		J2VDT6	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	Phyllobacterium sp. YR531		B2JK72	alaS	Alanine--tRNA ligase	Burkholderia phymatum (strain DSM 17167 / STM815)
	W0E9X5	nuoC	NADH-quinone oxidoreductase subunit C	Desulfitobacterium metallireducens DSM 15288		J3CEZ8	fhs	Formate--tetrahydrofolate ligase	Phyllobacterium sp. YR531		A0JSM6	upp	Uracil phosphoribosyltransferase	Arthrobacter sp. (strain FB24)
	Q2SYC8	ubiD	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)		A4W6T0	accA	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	Enterobacter sp. (strain 638)		M7XZU6	MmSR116_2042	Putative oxalyl-CoA decarboxylase	Methylobacterium mesophilicum SR1.6/6
	M7Z4T8	MmSR116_1602	Ribonucleotide-diphosphate reductase subunit alpha	Methylobacterium mesophilicum SR1.6/6		M7YCV6	fadJ	NAD-binding 3-hydroxyacyl-CoA dehydrogenase	Methylobacterium mesophilicum SR1.6/6		J3HP85	PMI41_03366	Alanine dehydrogenase	Phyllobacterium sp. YR531
	Q1MG80	lipB	Octanoyltransferase	Rhizobium leguminosarum bv. viciae (strain 3841)		A8FEH5	panD	Aspartate 1-decarboxylase	Bacillus pumilus (strain SAFR-032)		M7Z4T8	MmSR116_1602	Ribonucleotide-diphosphate reductase subunit alpha	Methylobacterium mesophilicum SR1.6/6
	A0A0D7QRP4	TZ00_04945	Glucarate dehydratase	Agreia bicolorata		B2GIA1	alaS	Alanine--tRNA ligase	Kocuria rhizophila (strain ATCC 9341 / DSM 348 / NBRC 103217 / DC2201)		A0A0D7F850	UM91_19705	Guanine deaminase	Pseudomonas oryzihabitans
	Q1GQS5	atpD	ATP synthase subunit beta	Sphingopyxis alaskensis (strain DSM 13593 / LMG 18877 / RB2256)		A8FAD5	pdxS	Pyridoxal 5'-phosphate synthase subunit PdxS	Bacillus pumilus (strain SAFR-032)		A4W6X5	proA	Gamma-glutamyl phosphate reductase	Enterobacter sp. (strain 638)
	A0A0F0KZY1	araD	L-2-keto-3-deoxyarabonate dehydratase	Microbacterium oxydans		Q1MM06	pgi	Glucose-6-phosphate isomerase	Rhizobium leguminosarum bv. viciae (strain 3841)		A0A0L8AAW6	selD	Selenide, water dikinase	[Pseudomonas] geniculata N1
	C1DR19	lpxK	Tetraacyldisaccharide 4'-kinase	Azotobacter vinelandii (strain DJ / ATCC BAA-1303)		Q2K939	gatA	Glutamyl-tRNA(Gln) amidotransferase subunit A	Rhizobium etli (strain CFN 42 / ATCC 51251)		C0ZZD9	fmt	Methionyl-tRNA formyltransferase	Rhodococcus erythropolis (strain PR4 / NBRC 100887)
	A0A0H3FDF9	pgk	Phosphoglycerate kinase	Rahnella sp. (strain Y9602)		A0KAZ7	aceK	Isocitrate dehydrogenase kinase/phosphatase	Burkholderia cenocepacia (strain HI2424)		M7YL70	MmSR116_3766	Cytochrome c oxidase subunit III	Methylobacterium mesophilicum SR1.6/6

	Q9UV64	hxB	Molybdenum cofactor sulfurase	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139)		A0A0H3FCL5	rutE	Probable malonic semialdehyde reductase RutE	Rahnella sp. (strain Y9602)		A0A0F0KR00	guaA_1	GMP synthase [glutamine-hydrolyzing]	Microbacterium oxydans
	M7YA99	amn	AMP nucleosidase	Methylobacterium mesophilicum SR1.6/6		D5USR1	Tpau_2734	Adenylate/guanylate cyclase	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		A0A0F0L5Y0	dgt	Deoxyguanosinetriphosphate triphosphohydrolase	Microbacterium oxydans
	A5V3L0	alaS	Alanine--tRNA ligase	Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)		A0A0L8ACA8	narH	Nitrate reductase	[Pseudomonas] geniculata N1		Q13VL4	plsX	Phosphate acyltransferase	Burkholderia xenovorans (strain LB400)
	A0A0L8A7S1	acnA	Aconitate hydratase	[Pseudomonas] geniculata N1		A0A0D7FKT3	putA	Bifunctional protein PutA	Pseudomonas oryzihabitans		A1SIM4	Noca_2150	Acetaldehyde dehydrogenase 2	Nocardioides sp. (strain BAA-499 / JS614)
	A4JN03	ilvD	Dihydroxy-acid dehydratase	Burkholderia vietnamiensis (strain G4 / LMG 22486)		A0A0H3FD98	Rahaq_3624	Aminotransferase class I and II	Rahnella sp. (strain Y9602)		O33580	cysD	Sulfate adenylyltransferase subunit 2	Rhizobium tropici
	M7Y951	ubiE	Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE	Methylobacterium mesophilicum SR1.6/6		J3CIY2	PMI41_00110	4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate decarboxylase	Phyllobacterium sp. YR531		A0A0D7FA34	UM91_21475	Glucose dehydrogenase	Pseudomonas oryzihabitans
	P06193	pabA	Aminodeoxychorismate synthase component 2	Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)		A4YWZ6	psd	Phosphatidylserine decarboxylase proenzyme	Bradyrhizobium sp. (strain ORS278)		Q89XW7	aroK	Shikimate kinase	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)
	A0A0D7FJ11	UM91_02115	Flagellar rod assembly protein FlgJ	Pseudomonas oryzihabitans		Q39ED2	ilvC	Ketol-acid reductoisomerase	Burkholderia lata (strain ATCC 17760 / LMG 22485 / NCIMB 9086 / R18194 / 383)		M7YIV7	MmSR116_4442	2-dehydro-3-deoxyglucarate aldolase	Methylobacterium mesophilicum SR1.6/6
	A0A0D7FLN2	relA	(P)ppGpp synthetase	Pseudomonas oryzihabitans		A4YJH3	dut	Deoxyuridine 5'-triphosphate nucleotidohydrolase	Bradyrhizobium sp. (strain ORS278)		A7Z7B9	ilvC	Ketol-acid reductoisomerase	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)
	M7Y5N4	MmSR116_2185	Uncharacterized protein	Methylobacterium mesophilicum		A0A0H3FDZ4	Rahaq_2711	Aminotransferase class I and II	Rahnella sp. (strain Y9602)		D5UWV0	Tpau_1343	PPOX class putative F420-dependent enzyme	Tsukamurella paurometabola (strain ATCC

				SR1.6/6										8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
	M7Y916	MmSR116_1529	Cytochrome o ubiquinol oxidase subunit III	Methylobacterium mesophilicum SR1.6/6		J2VD92	PMI41_01567	3-oxoacyl-(Acyl-carrier-protein) synthase	Phyllobacterium sp. YR531		A5V3X0	accA	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)
	J3HTC6	PMI41_01429	Pyridoxamine 5'-phosphate oxidase-related, FMN binding protein	Phyllobacterium sp. YR531		B9K4P2	rutA	Pyrimidine monooxygenase RutA	Agrobacterium vitis (strain S4 / ATCC BAA-846)		A0A0F0LBB9	puuC	Aldehyde dehydrogenase PuuC	Microbacterium oxydans
	M7Z6B1	MmSR116_0403	Bifunctional protein PutA	Methylobacterium mesophilicum SR1.6/6		A0A023Y681	purT	Phosphoribosylglycinamide formyltransferase 2	Stenotrophomonas rhizophila		M7YA94	sdhA	Succinate dehydrogenase flavoprotein subunit	Methylobacterium mesophilicum SR1.6/6
	A4W698	deoC	Deoxyribose-phosphate aldolase	Enterobacter sp. (strain 638)		Q59092	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		J3CGU4	ispG	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin)	Phyllobacterium sp. YR531
	A0A0D7F821	UM91_17905	Formate dehydrogenase	Pseudomonas oryzihabitans		A0A0L8AFK9	W7K_01830	Adenylate cyclase	[Pseudomonas] geniculata N1		A0A0H3FGX0	tal	Transaldolase	Rahnella sp. (strain Y9602)
	A4W777	acpH	Acyl carrier protein phosphodiesterase	Enterobacter sp. (strain 638)		A4W5D0	aceK	Isocitrate dehydrogenase kinase/phosphatase	Enterobacter sp. (strain 638)		M7Z845	MmSR116_0941	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	Methylobacterium mesophilicum SR1.6/6
	A0A0H3FEA3	carA	Carbamoyl-phosphate synthase small chain	Rahnella sp. (strain Y9602)		Q0BJL6	atpG	ATP synthase gamma chain	Burkholderia ambifaria (strain ATCC BAA-244 / AMMD)		M7YYY8	hisG	ATP phosphoribosyltransferase	Methylobacterium mesophilicum SR1.6/6
	A0KBG7	argB	Acetylglutamate kinase	Burkholderia cenocepacia (strain HI2424)		D5UWS2	Tpau_1315	MaoC domain protein dehydratase	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		A4W533	gpmI	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	Enterobacter sp. (strain 638)
	A0JUT1	proS	Proline--tRNA ligase	Arthrobacter sp. (strain FB24)		W0EGI9	glnS	Glutamine--tRNA ligase	Desulfitobacterium metallireducens DSM 15288		J2VW26	PMI41_02060	Bifunctional protein PutA	Phyllobacterium sp. YR531
	Q6FEE5	accD	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		A1V3F2	alaS	Alanine--tRNA ligase	Burkholderia mallei (strain SAVP1)		B3PS36	purH	Bifunctional purine biosynthesis protein PurH	Rhizobium etli (strain CIAT 652)
	Q6F8P2	pckG	Phosphoenolpyruvate carboxykinase [GTP]	Acinetobacter baylyi (strain ATCC 33305 /		A8FHJ0	eno	Enolase	Bacillus pumilus (strain SAFR-		Q8UE93	murI	Glutamate racemase	Agrobacterium fabrum (strain C58 /

				BD413 / ADP1)					032)					ATCC 33970)
	A0A0H3FD69	Rahaq_2468	Pyridoxal phosphate-dependent enzyme, D-cysteine desulfhydrase family	Rahnella sp. (strain Y9602)		A0KBJ7	fmt	Methionyl-tRNA formyltransferase	Burkholderia cenocepacia (strain HI2424)		P26284	Pdha1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	Rattus norvegicus
	Q6FF68	fadB	Fatty acid oxidation complex subunit alpha	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		W0EA48	DESME_02790	Formate acetyltransferase	Desulfitobacterium metallireducens DSM 15288		A0A0D7F7I2	UM91_18625	Deoxyguanosinetriphosphate triphosphohydrolase	Pseudomonas oryzihabitans
	A0A0H3FFW9	Rahaq_4172	Glycyl-radical enzyme activating protein family	Rahnella sp. (strain Y9602)		W0E8G7	DESME_08200	Phosphoribosylformylglycinamidine synthase	Desulfitobacterium metallireducens DSM 15288		J3CGD3	pnp	Polyribonucleotide nucleotidyltransferase	Phyllobacterium sp. YR531
	M7Y045	MmSR116_4626	Precorrin 6A synthase	Methylobacterium mesophilicum SR1.6/6		M7YKT6	MmSR116_3841	Acyl-CoA dehydrogenase type 2	Methylobacterium mesophilicum SR1.6/6		A8FIG8	argS	Arginine--tRNA ligase	Bacillus pumilus (strain SAFR-032)
	Q6FD29	pyrC	Dihydroorotase	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		A0K7U6	pcm	Protein-L-isoaspartate O-methyltransferase	Burkholderia cenocepacia (strain HI2424)		A0JZ92	rpoC	DNA-directed RNA polymerase subunit beta'	Arthrobacter sp. (strain FB24)
	A0A0H3FCY4	Rahaq_3507	D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding protein	Rahnella sp. (strain Y9602)		W0EED3	nuoA	NADH-quinone oxidoreductase subunit A	Desulfitobacterium metallireducens DSM 15288		A0A0L8AFK9	W7K_01830	Adenylate cyclase	[Pseudomonas] geniculata N1
	A6GW77	bioB	Biotin synthase	Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)		Q8UHJ6	ileS	Isoleucine--tRNA ligase	Agrobacterium fabrum (strain C58 / ATCC 33970)		A0A023Y562	panD	Aspartate 1-decarboxylase	Stenotrophomonas rhizophila
	A4WGF4	atpG	ATP synthase gamma chain	Enterobacter sp. (strain 638)		A0A0H3FDP1	Rahaq_3815	Transcriptional regulator, XRE family	Rahnella sp. (strain Y9602)		A0A0F0L3A2	ileS	Isoleucine--tRNA ligase	Microbacterium oxydans
	A0A0D7QWD8	leuA	2-isopropylmalate synthase	Agreia bicolorata		J3CEB9	PMI41_01609	Putative cobalamin binding protein	Phyllobacterium sp. YR531		J3CF91	PMI41_02201	6-phosphogluconate dehydrogenase, decarboxylating	Phyllobacterium sp. YR531
	Q2KDX9	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	Rhizobium etli (strain CFN 42 / ATCC 51251)		A0A023Y6I8	rpoB	DNA-directed RNA polymerase subunit beta	Stenotrophomonas rhizophila		P10182	ansB	Glutaminase-asparaginase	Pseudomonas sp. (strain ATCC 29598 / 7A)
	A5EKP4	gatA	Glutamyl-tRNA(Gln) amidotransferase subunit A	Bradyrhizobium sp. (strain BTAi1 / ATCC BAA-1182)		A7ZAH2	iolJ	6-phospho-5-dehydro-2-deoxy-D-gluconate aldolase	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)		A0A0H3FC06	aguA	Putative agmatine deiminase	Rahnella sp. (strain Y9602)
	A0A0D7QPF6	TZ00_15950	Long-chain fatty acid--CoA ligase	Agreia bicolorata		A8FAK7	leuA2	2-isopropylmalate synthase 2	Bacillus pumilus (strain SAFR-032)		M7XP27	MmSR116_5694	Serine O-acetyltransferase	Methylobacterium mesophilicum SR1.6/6

	M7XYF7	MmSR116_2667	Formate dehydrogenase, alpha subunit	Methylobacterium mesophilicum SR1.6/6		A0A0F0L446	rpoZ	DNA-directed RNA polymerase subunit omega	Microbacterium oxydans		C0ZYN8	dapF	Diaminopimelate epimerase	Rhodococcus erythropolis (strain PR4 / NBRC 100887)
	A0A0H3FGJ4	Rahaq_3588	GDP-mannose 4,6-dehydratase	Rahnella sp. (strain Y9602)							A0A023Y718	fabA	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase	Stenotrophomonas rhizophila
	B2T672	Bphyt_3044	Adenine deaminase	Burkholderia phytofirmans (strain DSM 17436 / PsJN)							P07770	benB	Benzoate 1,2-dioxygenase subunit beta	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)
	A0A0D7FEZ2	gatB	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	Pseudomonas oryzihabitans							J3CCP5	ribB	3,4-dihydroxy-2-butanone 4-phosphate synthase	Phyllobacterium sp. YR531
	A0A0D7F6P7	UM91_20505	Methylmalonate-semialdehyde dehydrogenase	Pseudomonas oryzihabitans							A4YM47	glcB	Malate synthase G	Bradyrhizobium sp. (strain ORS278)
	A4WG52	argB	Acetylglutamate kinase	Enterobacter sp. (strain 638)							B9K288	hutH	Histidine ammonia-lyase	Agrobacterium vitis (strain S4 / ATCC BAA-846)
	B2JF04	aroA	3-phosphoshikimate 1-carboxyvinyltransferase	Burkholderia phymatum (strain DSM 17167 / STM815)							A0A023Y3F4	DX03_10905	3-phosphoglycerate dehydrogenase	Stenotrophomonas rhizophila
	C1DF46	pheS	Phenylalanine--tRNA ligase alpha subunit	Azotobacter vinelandii (strain DJ / ATCC BAA-1303)							J2VHZ2	PMI41_00838	NAD-specific glutamate dehydrogenase	Phyllobacterium sp. YR531
	Q1ME34	murC	UDP-N-acetylmuramate--L-alanine ligase	Rhizobium leguminosarum bv. viciae (strain 3841)							A7ZAK3	fbp	Fructose-1,6-bisphosphatase class 3	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)
	A8GHZ8	prr	Gamma-aminobutyraldehyde dehydrogenase	Serratia proteamaculans (strain 568)							A0A023Y0D1	DX03_04195	Glyceraldehyde-3-phosphate dehydrogenase	Stenotrophomonas rhizophila
	C0ZWI9	iolG	Inositol 2-dehydrogenase	Rhodococcus erythropolis (strain PR4 / NBRC 100887)							A7Z7I1	thrS	Threonine--tRNA ligase	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)
	A7Z6J9	folD	Bifunctional protein FolD	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)							A0A0F0KFK5	glnA_3	Putative glutamine synthetase 2	Microbacterium oxydans

	A0A0L8AEX7	W7K_01815	3-methylcrotonyl-CoA carboxylase	[Pseudomonas] geniculata N1							A0A0D7QRW1	TZ00_06365	Alanine racemase	Agreia bicolorata
	J3HM74	aroE	Shikimate dehydrogenase (NADP(+))	Phyllobacterium sp. YR531							A0A023Y5T3	DX03_14825	Alpha-glucosidase	Stenotrophomonas rhizophila
	A0A0H3F4D0	Rahaq_0416	S-adenosylhomocysteine deaminase	Rahnella sp. (strain Y9602)							A0A0H3FHH6	Rahaq_5029	Hydro-lyase, Fe-S type, tartrate/fumarate subfamily, beta subunit	Rahnella sp. (strain Y9602)
	Q8UIH5	ubiE	Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE	Agrobacterium fabrum (strain C58 / ATCC 33970)							A0A023Y0V6	DX03_05780	Uncharacterized protein	Stenotrophomonas rhizophila
	A0A0F0KHK8	paaJ_2	3-oxoadipyl-CoA/3-oxo-5,6-dehydrosuberyl-CoA thiolase	Microbacterium oxydans							Q6F6U8	glmS	Glutamine--fructose-6-phosphate aminotransferase [isomerizing]	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)
	M7Y2J1	lpd	Dihydrolipoyl dehydrogenase	Methylobacterium mesophilicum SR1.6/6							A4YKD9	atpG	ATP synthase gamma chain	Bradyrhizobium sp. (strain ORS278)
											A8FIB2	atpD	ATP synthase subunit beta	Bacillus pumilus (strain SAFR-032)
											A0A0D7QW45	TZ00_00255	GTP pyrophosphokinase	Agreia bicolorata
											A4W5B3	thiG	Thiazole synthase	Enterobacter sp. (strain 638)
											Q1ME34	murC	UDP-N-acetylmuramate--L-alanine ligase	Rhizobium leguminosarum bv. viciae (strain 3841)
											A8FEK0	trpC	Indole-3-glycerol phosphate synthase	Bacillus pumilus (strain SAFR-032)
											A0A023XZS8	DX03_04250	Cysteine synthase	Stenotrophomonas rhizophila
											J2VA23	PMI41_02744	NAD-dependent aldehyde dehydrogenase	Phyllobacterium sp. YR531
oxidation-reduction process														
	M7Z6B1	MmSR116_0403	Bifunctional protein PutA	Methylobacterium mesophilicum SR1.6/6		A0A0F0KI13	kynA	Tryptophan 2,3-dioxygenase	Microbacterium oxydans		M7Y2C5	MmSR116_3967	Short-chain dehydrogenase/reductase SDR	Methylobacterium mesophilicum SR1.6/6

	A0A023Y227	DX03_07360	Fumarate hydratase	Stenotrophomonas rhizophila		A0A0H3F9X6	dadA	D-amino acid dehydrogenase	Rahnella sp. (strain Y9602)		A0A023Y788	DX03_17790	Methyltransferase	Stenotrophomonas rhizophila
	A0A0D7F821	UM91_17905	Formate dehydrogenase	Pseudomonas oryzihabitans		A1SE34	nuoH	NADH-quinone oxidoreductase subunit H	Nocardioides sp. (strain BAA-499 / JS614)		J2VW26	PMI41_02060	Bifunctional protein PutA	Phyllobacterium sp. YR531
	A0A0F0KI13	kynA	Tryptophan 2,3-dioxygenase	Microbacterium oxydans		B9K4P2	rutA	Pyrimidine monooxygenase RutA	Agrobacterium vitis (strain S4 / ATCC BAA-846)		Q8UBV5	acsA	Acetyl-coenzyme A synthetase	Agrobacterium fabrum (strain C58 / ATCC 33970)
	A0A0H3F6R1	nuoI	NADH-quinone oxidoreductase subunit I	Rahnella sp. (strain Y9602)		D5UUW6	Tpau_3093	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		P26284	Pdha1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	Rattus norvegicus
	Q142I6	ilvC	Ketol-acid reductoisomerase	Burkholderia xenovorans (strain LB400)		A4W5D0	aceK	Isocitrate dehydrogenase kinase/phosphatase	Enterobacter sp. (strain 638)		J3CF91	PMI41_02201	6-phosphogluconate dehydrogenase, decarboxylating	Phyllobacterium sp. YR531
	A8GAB9	nqrA	Na(+)-translocating NADH-quinone reductase subunit A	Serratia proteamaculans (strain 568)		D5UWS2	Tpau_1315	MaoC domain protein dehydratase	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		M7Y3W3	MmSR116_3350	Electron-transferring-flavoprotein dehydrogenase	Methylobacterium mesophilicum SR1.6/6
	Q6F8P2	pckG	Phosphoenolpyruvate carboxykinase [GTP]	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		J3HLY2	PMI41_04100	Putative dehydrogenase	Phyllobacterium sp. YR531		P07770	benB	Benzoate 1,2-dioxygenase subunit beta	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)
	M7YRY0	MmSR116_5495	Oxidoreductase domain-containing protein	Methylobacterium mesophilicum SR1.6/6		M7YVR1	bchL	Light-independent protochlorophyllide reductase iron-sulfur ATP-binding protein	Methylobacterium mesophilicum SR1.6/6		J3HP85	PMI41_03366	Alanine dehydrogenase	Phyllobacterium sp. YR531
	A0A0H3FEK4	nusG	Transcription termination/antitermination protein NusG	Rahnella sp. (strain Y9602)		A8GKW1	iolG	Inositol 2-dehydrogenase	Serratia proteamaculans (strain 568)		W0E791	rimO	Ribosomal protein S12 methylthiotransferase RimO	Desulfitobacterium metallireducens DSM 15288
	A0A0D7FCW5	UM91_12080	tRNA-dihydrouridine synthase	Pseudomonas oryzihabitans		J2VG30	PMI41_01423	FMN-dependent oxidoreductase, nitrilotriacetate monooxygenase family	Phyllobacterium sp. YR531		A4YM47	glcB	Malate synthase G	Bradyrhizobium sp. (strain ORS278)
	W0E9X5	nuoC	NADH-quinone oxidoreductase subunit C	Desulfitobacterium metallireducens DSM 15288		M7YCV6	fadJ	NAD-binding 3-hydroxyacyl-CoA dehydrogenase	Methylobacterium mesophilicum SR1.6/6		A0A023Y3F4	DX03_10905	3-phosphoglycerate dehydrogenase	Stenotrophomonas rhizophila
	M7Y3Q1	MmSR116_3305	Malate/L-lactate dehydrogenase	Methylobacterium mesophilicum SR1.6/6		A0A0D7QLS5	TZ00_14735	Aldo/keto reductase	Agreia bicolorata		J2VHZ2	PMI41_00838	NAD-specific glutamate dehydrogenase	Phyllobacterium sp. YR531

	Q6FF68	fadB	Fatty acid oxidation complex subunit alpha	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		A0A0H3F463	Rahaq_0325	BFD domain protein (2Fe-2S)-binding domain protein	Rahnella sp. (strain Y9602)		M7Z4T8	MmSR116_1602	Ribonucleotide-diphosphate reductase subunit alpha	Methylobacterium mesophilicum SR1.6/6
	A0A0H3FFW9	Rahaq_4172	Glycyl-radical enzyme activating protein family	Rahnella sp. (strain Y9602)		M7YKT6	MmSR116_3841	Acyl-CoA dehydrogenase type 2	Methylobacterium mesophilicum SR1.6/6		A0A0F0L579	RS83_02900	Putative FAD-linked oxidoreductase	Microbacterium oxydans
	A0A0L8A5A2	W7K_20575	DNA methylase	[Pseudomonas] geniculata N1		A5WGD0	mnmG	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	Psychrobacter sp. (strain PRwf-1)		A0A023Y0D1	DX03_04195	Glyceraldehyde-3-phosphate dehydrogenase	Stenotrophomonas rhizophila
	A0A0F0KHJ5	glpD_1	Glycerol-3-phosphate dehydrogenase	Microbacterium oxydans		A0KAZ7	aceK	Isocitrate dehydrogenase kinase/phosphatase	Burkholderia cenocepacia (strain HI2424)		A4W6X5	proA	Gamma-glutamyl phosphate reductase	Enterobacter sp. (strain 638)
	Q2SYC8	ubiD	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)		A0A0H3FCL5	rutE	Probable malonic semialdehyde reductase RutE	Rahnella sp. (strain Y9602)		P00386	nos	D-nopaline dehydrogenase	Agrobacterium tumefaciens (strain T37)
	M7Z4T8	MmSR116_1602	Ribonucleotide-diphosphate reductase subunit alpha	Methylobacterium mesophilicum SR1.6/6		W0EED3	nuoA	NADH-quinone oxidoreductase subunit A	Desulfitobacterium metallireducens DSM 15288		C4L0W8	azoR	FMN-dependent NADH-azoreductase	Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)
	W0E7Z6	DESME_07325	Carbon monoxide dehydrogenase	Desulfitobacterium metallireducens DSM 15288		A0A0L8ACA8	narH	Nitrate reductase	[Pseudomonas] geniculata N1		M7YL70	MmSR116_3766	Cytochrome c oxidase subunit III	Methylobacterium mesophilicum SR1.6/6
	A0A0H3FCY4	Rahaq_3507	D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding protein	Rahnella sp. (strain Y9602)		P45409	cycY	Thiol:disulfide interchange protein CycY	Rhizobium leguminosarum bv. viciae		A0A0H3FHH6	Rahaq_5029	Hydro-lyase, Fe-S type, tartrate/fumarate subfamily, beta subunit	Rahnella sp. (strain Y9602)
	Q8UBM0	mnmG	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	Agrobacterium fabrum (strain C58 / ATCC 33970)		A0A0D7FKT3	putA	Bifunctional protein PutA	Pseudomonas oryzihabitans		Q13VL4	plsX	Phosphate acyltransferase	Burkholderia xenovorans (strain LB400)
	M7XYF7	MmSR116_2667	Formate dehydrogenase, alpha subunit	Methylobacterium mesophilicum SR1.6/6		M7YIM5	MmSR116_4372	Uncharacterized protein	Methylobacterium mesophilicum SR1.6/6		A1SIM4	Noca_2150	Acetaldehyde dehydrogenase 2	Nocardioides sp. (strain BAA-499 / JS614)
	A0A0F0KVB6	dkgA	2,5-diketo-D-gluconic acid reductase A	Microbacterium oxydans		W0EFJ2	DESME_13730	Glycolate oxidase iron-sulfur subunit	Desulfitobacterium metallireducens DSM 15288		A0A023Y0V6	DX03_05780	Uncharacterized protein	Stenotrophomonas rhizophila
	A0A0L8A7S1	acnA	Aconitate hydratase	[Pseudomonas] geniculata N1		W0E7Y1	DESME_07735	Aldehyde ferredoxin oxidoreductase	Desulfitobacterium metallireducens DSM 15288		O33580	cysD	Sulfate adenylyltransferase subunit 2	Rhizobium tropici
	A0A0D7F6P7	UM91_20505	Methylmalonate-semialdehyde dehydrogenase	Pseudomonas oryzihabitans		P96192	dusC	tRNA-dihydrouridine(16) synthase	Azotobacter vinelandii		A0A0D7FA34	UM91_21475	Glucose dehydrogenase	Pseudomonas oryzihabitans

	M7Y951	ubiE	Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE	Methylobacterium mesophilicum SR1.6/6		A0A0H3F5H0	Rahaq_0413	Fumarate reductase flavoprotein subunit	Rahnella sp. (strain Y9602)		D5UMH1	Tpau_3870	Putative monooxygenase	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
	A0A0H3FBR5	Rahaq_3028	Luciferase-like, subgroup	Rahnella sp. (strain Y9602)		Q39ED2	ilvC	Ketol-acid reductoisomerase	Burkholderia lata (strain ATCC 17760 / LMG 22485 / NCIMB 9086 / R18194 / 383)		D5URP4	Tpau_2495	Lycopene beta and epsilon cyclase	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
	A8GHZ8	prr	Gamma-aminobutyraldehyde dehydrogenase	Serratia proteamaculans (strain 568)							A7Z7B9	ilvC	Ketol-acid reductoisomerase	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)
	C0ZWI9	iolG	Inositol 2-dehydrogenase	Rhodococcus erythropolis (strain PR4 / NBRC 100887)							D5UWV0	Tpau_1343	PPOX class putative F420-dependent enzyme	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
	M7Y916	MmSR116_1529	Cytochrome o ubiquinol oxidase subunit III	Methylobacterium mesophilicum SR1.6/6							M7YA94	sdhA	Succinate dehydrogenase flavoprotein subunit	Methylobacterium mesophilicum SR1.6/6
	A7Z6J9	folD	Bifunctional protein FolD	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)							A0A0F0LBB9	puuC	Aldehyde dehydrogenase PuuC	Microbacterium oxydans
	J3HM74	aroE	Shikimate dehydrogenase (NADP(+))	Phyllobacterium sp. YR531							J3CGU4	ispG	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin)	Phyllobacterium sp. YR531
	Q8UIH5	ubiE	Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE	Agrobacterium fabrum (strain C58 / ATCC 33970)							J2VA23	PMI41_02744	NAD-dependent aldehyde dehydrogenase	Phyllobacterium sp. YR531
	A0A023Y9M0	DX03_20425	NADPH:quinone reductase	Stenotrophomonas rhizophila							A0A023XZ87	DX03_03220	Thiol:disulfide interchange protein	Stenotrophomonas rhizophila
	M7Y2J1	lpd	Dihydrolipoyl dehydrogenase	Methylobacterium mesophilicum SR1.6/6							A0A0D7QRU7	TZ00_05865	Haloacid dehalogenase	Agreia bicolorata

	J3HTC6	PMI41_01429	Pyridoxamine 5'-phosphate oxidase-related, FMN binding protein	Phyllobacterium sp. YR531							A0A0L8ADV3	W7K_04370	Coproporphyrinogen-III oxidase	[Pseudomonas] geniculata N1
											A0A0D7QR47	TZ00_05505	Oxidoreductase	Agreia bicolorata
transport														
	A0A0F0KHN1	gsiB_4	Glutathione-binding protein GsiB	Microbacterium oxydans		M7YKY2	tonB	TonB-dependent siderophore receptor	Methylobacterium mesophilicum SR1.6/6		M7YG83	MmSR116_5356	Amino acid permease-associated region	Methylobacterium mesophilicum SR1.6/6
	W0EC19	DESME_06425	Peptide ABC transporter ATP-binding protein	Desulfitobacterium metallireducens DSM 15288		Q8UB30	ugpE	sn-glycerol-3-phosphate transport system permease protein UgpE	Agrobacterium fabrum (strain C58 / ATCC 33970)		A0A0L8ADS6	W7K_04660	Oar protein	[Pseudomonas] geniculata N1
	A0A0H3F951	Rahaq_1836	Flagellar biosynthetic protein FlhB	Rahnella sp. (strain Y9602)		A0A0D7FAY5	secB	Protein-export protein SecB	Pseudomonas oryzihabitans		P35118	nocQ	Nopaline transport system permease protein NocQ	Agrobacterium fabrum (strain C58 / ATCC 33970)
	A8GAB9	nqrA	Na(+)-translocating NADH-quinone reductase subunit A	Serratia proteamaculans (strain 568)		J2VEM8	PMI41_02072	ATPase component of various ABC-type transport systems with duplicated ATPase domain	Phyllobacterium sp. YR531		Q2K0S7	rbsA3	Ribose import ATP-binding protein RbsA 3	Rhizobium etli (strain CFN 42 / ATCC 51251)
	M7Z5B6	MmSR116_1727	Major facilitator superfamily MFS_1	Methylobacterium mesophilicum SR1.6/6		W0EA79	DESME_11995	Molybdenum ABC transporter substrate-binding protein	Desulfitobacterium metallireducens DSM 15288		J3HSJ8	PMI41_02183	ABC-type metal ion transport system, periplasmic component/surface adhesin	Phyllobacterium sp. YR531
	A0A0F0L8E2	nhaA_2	Na(+)/H(+) antiporter NhaA	Microbacterium oxydans		Q0BJL6	atpG	ATP synthase gamma chain	Burkholderia ambifaria (strain ATCC BAA-244 / AMMD)		A0A023Y6D3	DX03_15755	TonB-dependent receptor	Stenotrophomonas rhizophila
	W0E9X5	nuoC	NADH-quinone oxidoreductase subunit C	Desulfitobacterium metallireducens DSM 15288		M7Y5Y9	atpG	ATP synthase gamma chain	Methylobacterium mesophilicum SR1.6/6		A0A0D7QQP3	TZ00_09975	ABC transporter	Agreia bicolorata
	M7Y842	MmSR116_1949	Porin	Methylobacterium mesophilicum SR1.6/6		J3C6R8	PMI41_04073	ABC-type sugar transport system, periplasmic component	Phyllobacterium sp. YR531		J3C5F3	PMI41_04630	Porin subfamily	Phyllobacterium sp. YR531
	A0A0H3FE64	Rahaq_1684	Ribose ABC transporter, periplasmic binding protein	Rahnella sp. (strain Y9602)		J2V3B6	PMI41_03988	RND family efflux transporter, MFP subunit	Phyllobacterium sp. YR531		M7XW44	MmSR116_3014	ABC transporter-like protein	Methylobacterium mesophilicum SR1.6/6
	M7XTI1	secA	Protein translocase subunit SecA	Methylobacterium mesophilicum SR1.6/6		A0A0D7QQR1	TZ00_04355	MFS transporter	Agreia bicolorata		M7YE77	MmSR116_5906	Porin	Methylobacterium mesophilicum SR1.6/6
	M7XW44	MmSR116_3014	ABC transporter-like protein	Methylobacterium mesophilicum SR1.6/6		A0A0F0L713	oppA_6	Oligopeptide-binding protein OppA	Microbacterium oxydans		M7YL70	MmSR116_3766	Cytochrome c oxidase subunit III	Methylobacterium mesophilicum SR1.6/6

	Q1GQS5	atpD	ATP synthase subunit beta	Sphingopyxis alaskensis (strain DSM 13593 / LMG 18877 / RB2256)		A0A0H3FE41	Rahaq_3971	Mammalian cell entry related domain protein	Rahnella sp. (strain Y9602)		A0A0H3FFF8	kdpB	Potassium-transporting ATPase ATP-binding subunit	Rahnella sp. (strain Y9602)
	A4WGF4	atpG	ATP synthase gamma chain	Enterobacter sp. (strain 638)		A0A023Y216	DX03_08285	TonB-dependent receptor	Stenotrophomonas rhizophila		A0A0D7F835	UM91_17450	Sugar ABC transporter ATPase	Pseudomonas oryzihabitans
	D5UXJ5	tig	Trigger factor	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		M7YE77	MmSR116_5906	Porin	Methylobacterium mesophilicum SR1.6/6		A0A0D7QR84	TZ00_03905	ATPase	Agreia bicolorata
	A0A0H3FFF8	kdpB	Potassium-transporting ATPase ATP-binding subunit	Rahnella sp. (strain Y9602)		A0A0D7F8R6	UM91_16215	MFS transporter	Pseudomonas oryzihabitans		J3CBG2	PMI41_03076	ABC-type polar amino acid transport system, ATPase component	Phyllobacterium sp. YR531
	M7XXH1	MmSR116_2367	RND family efflux transporter MFP subunit	Methylobacterium mesophilicum SR1.6/6		A0A0D7QR84	TZ00_03905	ATPase	Agreia bicolorata		A8FIB2	atpD	ATP synthase subunit beta	Bacillus pumilus (strain SAFR-032)
	A0A0D7QR84	TZ00_03905	ATPase	Agreia bicolorata		A0A023Y0X6	DX03_04680	Membrane protein TolA	Stenotrophomonas rhizophila		J3HPJ5	PMI41_03321	Uracil-xanthine permease	Phyllobacterium sp. YR531
	M7YFX3	MmSR116_5404	Drug resistance transporter, EmrB/QacA subfamily	Methylobacterium mesophilicum SR1.6/6		A0A0H3FEH7	Rahaq_3622	Extracellular solute-binding protein family 3	Rahnella sp. (strain Y9602)		A4YKD9	atpG	ATP synthase gamma chain	Bradyrhizobium sp. (strain ORS278)
	Q13TR5	tatA	Sec-independent protein translocase protein TatA	Burkholderia xenovorans (strain LB400)		M7Y8D7	MmSR116_2025	Major facilitator superfamily MFS_1	Methylobacterium mesophilicum SR1.6/6		A0A0H3FBD0	Rahaq_2755	Oligopeptide/dipeptide ABC transporter, ATPase subunit	Rahnella sp. (strain Y9602)
	A0A023XZA6	DX03_02165	Multidrug transporter MatE	Stenotrophomonas rhizophila		J2VYX2	PMI41_01245	Putrescine-binding periplasmic protein	Phyllobacterium sp. YR531		A0A0F0L4I6	ftsY	Signal recognition particle receptor FtsY	Microbacterium oxydans
	A0A023XZI7	DX03_02085	Multidrug transporter	Stenotrophomonas rhizophila		A0A0F0LBN3	cydD	ATP-binding/permease protein CydD	Microbacterium oxydans		M7XP10	MmSR116_5674	Type II secretion system protein E	Methylobacterium mesophilicum SR1.6/6
	M7XP10	MmSR116_5674	Type II secretion system protein E	Methylobacterium mesophilicum SR1.6/6		Q1MCN6	ugpC1	sn-glycerol-3-phosphate import ATP-binding protein UgpC 1	Rhizobium leguminosarum bv. viciae (strain 3841)		A0KE53	xylG	Xylose import ATP-binding protein XylG	Burkholderia cenocepacia (strain HI2424)
	A0KE53	xylG	Xylose import ATP-binding protein XylG	Burkholderia cenocepacia (strain HI2424)		A0A0L8AC50	W7K_08285	Type VI secretion protein	[Pseudomonas] geniculata N1		Q2T3B8	hmuV	Hemin import ATP-binding protein HmuV	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)
	Q0S2Y0	secA	Protein translocase subunit SecA	Rhodococcus jostii (strain RHA1)		W0EED3	nuoA	NADH-quinone oxidoreductase subunit A	Desulfitobacterium metallireduce		M7YAC4	MmSR116_0541	Hydrophobe/amphiphile efflux-1 (HAE1) family transporter	Methylobacterium mesophilicum

									ns DSM 15288					SR1.6/6
	M7XZV6	MmSR116_2052	General substrate transporter	Methylobacterium mesophilicum SR1.6/6		M7YRS7	MmSR116_1948	Porin	Methylobacterium mesophilicum SR1.6/6		A0A0D7FCL7	UM91_11600	Energy transducer TonB	Pseudomonas oryzihabitans
	M7Y916	MmSR116_1529	Cytochrome o ubiquinol oxidase subunit III	Methylobacterium mesophilicum SR1.6/6							A0A0H3FFX2	Rahaq_3339	ABC transporter related protein	Rahnella sp. (strain Y9602)
	M7YWM3	MmSR116_4122	Protein TolR	Methylobacterium mesophilicum SR1.6/6		Q9X7K6	dctA	C4-dicarboxylate transport protein	Rhizobium galegae		A0A0L8ACX5	W7K_05285	PTS fructose transporter subunit IIBC	[Pseudomonas] geniculata N1
	A0A023Y8Q3	DX03_20515	Membrane protein	Stenotrophomonas rhizophila		A0A0H3FDP1	Rahaq_3815	Transcriptional regulator, XRE family	Rahnella sp. (strain Y9602)		M7Y9R2	MmSR116_0371	RND family efflux transporter MFP subunit	Methylobacterium mesophilicum SR1.6/6
	A0A0H3FFX2	Rahaq_3339	ABC transporter related protein	Rahnella sp. (strain Y9602)		A0A0H3FET4	Rahaq_1879	Fusaric acid resistance protein conserved region	Rahnella sp. (strain Y9602)		A0A023XZ46	DX03_01320	Cation:proton antiporter	Stenotrophomonas rhizophila
	M7Y9R2	MmSR116_0371	RND family efflux transporter MFP subunit	Methylobacterium mesophilicum SR1.6/6		A0A0D7F6W1	UM91_19840	Amino acid ABC transporter substrate-binding protein	Pseudomonas oryzihabitans		A0A0D7FBB1	glnQ	Glutamine ABC transporter ATP-binding protein	Pseudomonas oryzihabitans
	Q0BC04	lptD	LPS-assembly protein LptD	Burkholderia ambifaria (strain ATCC BAA-244 / AMMD)										
small molecule binding														
	J3HN07	mutS	DNA mismatch repair protein MutS	Phyllobacterium sp. YR531		W0EA38	DESME_01600	ABC transporter ATP-binding protein	Desulfitobacterium metallireducens DSM 15288		W0E9H6	pyrH	Uridylate kinase	Desulfitobacterium metallireducens DSM 15288
	A0A0D7QQZ5	TZ00_08680	Fis family transcriptional regulator	Agreia bicolorata		J2VSM6	mutL	DNA mismatch repair protein MutL	Phyllobacterium sp. YR531		A0A0L8AAC0	W7K_10235	Translation elongation factor	[Pseudomonas] geniculata N1
	A4W8T4	lpxK	Tetraacyldisaccharide 4'-kinase	Enterobacter sp. (strain 638)		Q89QJ5	glnE	Glutamate-ammonia-ligase adenylyltransferase	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)		A0A0H3F5T8	parE	DNA topoisomerase 4 subunit B	Rahnella sp. (strain Y9602)

	A0A0H3FGG7	gmk	Guanylate kinase	Rahnella sp. (strain Y9602)		W0E6B0	DESME_03800	DNA mismatch repair protein	Desulfitobacterium metallireducens DSM 15288		Q89IB6	purQ	Phosphoribosylformylglycinamidine synthase subunit PurQ	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)
	A0A0D7FCW5	UM91_12080	tRNA-dihydrouridine synthase	Pseudomonas oryzihabitans		J2VEM8	PMI41_02072	ATPase component of various ABC-type transport systems with duplicated ATPase domain	Phyllobacterium sp. YR531		A0A0H3FLE0	rep	ATP-dependent DNA helicase Rep	Rahnella sp. (strain Y9602)
	A0A0H3FF00	Rahaq_3027	ABC transporter related protein	Rahnella sp. (strain Y9602)		M7Y663	MmSR116_2370	Integral membrane sensor signal transduction histidine kinase	Methylobacterium mesophilicum SR1.6/6		A0A023Y783	fusA	Elongation factor G	Stenotrophomonas rhizophila
	D5UN63	Tpau_3987	Amino acid adenylation domain protein	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		M7Y5Y9	atpG	ATP synthase gamma chain	Methylobacterium mesophilicum SR1.6/6		Q8UBV5	acsA	Acetyl-coenzyme A synthetase	Agrobacterium fabrum (strain C58 / ATCC 33970)
	M7XTI1	secA	Protein translocase subunit SecA	Methylobacterium mesophilicum SR1.6/6		M7YVR1	bchL	Light-independent protochlorophyllide reductase iron-sulfur ATP-binding protein	Methylobacterium mesophilicum SR1.6/6		A0A0D7FDU1	obgE	GTPase Obg	Pseudomonas oryzihabitans
	Q2SYC8	ubiD	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)		Q62KW5	valS	Valine--tRNA ligase	Burkholderia mallei (strain ATCC 23344)		B5ZUE4	proB	Glutamate 5-kinase	Rhizobium leguminosarum bv. trifolii (strain WSM2304)
	M7Z4T8	MmSR116_1602	Ribonucleotide-diphosphate reductase subunit alpha	Methylobacterium mesophilicum SR1.6/6							B2JK72	alaS	Alanine--tRNA ligase	Burkholderia phymatum (strain DSM 17167 / STM815)
	Q1GQS5	atpD	ATP synthase subunit beta	Sphingopyxis alaskensis (strain DSM 13593 / LMG 18877 / RB2256)		J2VDT6	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	Phyllobacterium sp. YR531		A0JSM6	upp	Uracil phosphoribosyltransferase	Arthrobacter sp. (strain FB24)
	M7Z2E7	MmSR116_2733	Uncharacterized protein	Methylobacterium mesophilicum SR1.6/6		P0C7V2	recA	Protein RecA	Burkholderia cepacia		J3C7F0	PMI41_03898	Non-ribosomal peptide synthase/amino acid adenylation enzyme	Phyllobacterium sp. YR531
	Q8UBM0	mnmG	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	Agrobacterium fabrum (strain C58 / ATCC 33970)		D5UN63	Tpau_3987	Amino acid adenylation domain protein	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC		M7XZU6	MmSR116_2042	Putative oxalyl-CoA decarboxylase	Methylobacterium mesophilicum SR1.6/6

									16120 / NCTC 13040)					
	C1DR19	lpxK	Tetraacyldisaccharide 4'-kinase	Azotobacter vinelandii (strain DJ / ATCC BAA-1303)		J3CEZ8	fhs	Formate--tetrahydrofolate ligase	Phyllobacterium sp. YR531		W0EFM5	lepA	Elongation factor 4	Desulfitobacterium metallireducens DSM 15288
	A0A0L8A5F9	groS	10 kDa chaperonin	[Pseudomonas] geniculata N1		A4W6T0	accA	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	Enterobacter sp. (strain 638)		A0A023Y0J9	DX03_05600	DEAD/DEAH box helicase	Stenotrophomonas rhizophila
	A0A0H3FDF9	pgk	Phosphoglycerate kinase	Rahnella sp. (strain Y9602)		A0A0H3F867	Rahaq_1451	Cell division protein FtsK/SpoIIIE	Rahnella sp. (strain Y9602)		Q1GPH4	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX	Sphingopyxis alaskensis (strain DSM 13593 / LMG 18877 / RB2256)
	A0A0H3FFF8	kdpB	Potassium-transporting ATPase ATP-binding subunit	Rahnella sp. (strain Y9602)		B2GIA1	alaS	Alanine--tRNA ligase	Kocuria rhizophila (strain ATCC 9341 / DSM 348 / NBRC 103217 / DC2201)		M7Z4T8	MmSR116_1602	Ribonucleotide-diphosphate reductase subunit alpha	Methylobacterium mesophilicum SR1.6/6
	A0A0D7QR84	TZ00_03905	ATPase	Agreia bicolorata		A0A0D7QR84	TZ00_03905	ATPase	Agreia bicolorata		A0A0F0L579	RS83_02900	Putative FAD-linked oxidoreductase	Microbacterium oxydans
	M7Y4H6	dnaK	Chaperone protein DnaK	Methylobacterium mesophilicum SR1.6/6		A0A0D7FDV1	UM91_08500	ATP-dependent protease	Pseudomonas oryzihabitans		A4W6X5	proA	Gamma-glutamyl phosphate reductase	Enterobacter sp. (strain 638)
	A5V3L0	alaS	Alanine--tRNA ligase	Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)		Q2K939	gatA	Glutamyl-tRNA(Gln) amidotransferase subunit A	Rhizobium etli (strain CFN 42 / ATCC 51251)		P00386	nos	D-nopaline dehydrogenase	Agrobacterium tumefaciens (strain T37)
	Q6F823	prfC	Peptide chain release factor 3	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		A0A0F0KNY4	dnaK	Chaperone protein DnaK	Microbacterium oxydans		A0A0L8AAW6	selD	Selenide, water dikinase	[Pseudomonas] geniculata N1
	M7XP10	MmSR116_5674	Type II secretion system protein E	Methylobacterium mesophilicum SR1.6/6		A0A0F0LBN3	cydD	ATP-binding/permease protein CydD	Microbacterium oxydans		A6H294	hflX	GTPase HflX	Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)
	A0KE53	xylG	Xylose import ATP-binding protein XylG	Burkholderia cenocepacia (strain HI2424)							C4L0W8	azoR	FMN-dependent NADH-azoreductase	Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)
	A0A0D7FLN2	relA	(P)ppGpp synthetase	Pseudomonas oryzihabitans		A5WGD0	mnmG	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	Psychrobacter sp. (strain PRwf-1)		A0A0F0KR00	guaA_1	GMP synthase [glutamine-hydrolyzing]	Microbacterium oxydans
	A0A0L8AF72	W7K_03635	Replicative DNA helicase	[Pseudomonas] geniculata		A0KAZ7	aceK	Isocitrate dehydrogenase kinase/phosphatase	Burkholderia cenocepacia		A0A0F0L382	uvrB	UvrABC system protein B	Microbacterium oxydans

				N1					(strain HI2424)					
	M7YS07	uvrB	UvrABC system protein B	Methylobacterium mesophilicum SR1.6/6		A0A0D7FDR6	UM91_13975	Penicillin-binding protein 1B	Pseudomonas oryzihabitans		A0A0H3FFF8	kdpB	Potassium-transporting ATPase ATP-binding subunit	Rahnella sp. (strain Y9602)
	J3HTC6	PMI41_01429	Pyridoxamine 5'-phosphate oxidase-related, FMN binding protein	Phyllobacterium sp. YR531		A0A0H3FEL3	Rahaq_3672	ABC transporter related protein	Rahnella sp. (strain Y9602)		A0A0D7QR84	TZ00_03905	ATPase	Agreia bicolorata
	Q2T3W7	groL2	60 kDa chaperonin 2	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)		J3HM91	PMI41_04061	ATPase component of uncharacterized ABC-type transporter	Phyllobacterium sp. YR531		Q2SU58	engB	Probable GTP-binding protein EngB	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)
	A0KBG7	argB	Acetylglutamate kinase	Burkholderia cenocepacia (strain HI2424)		Q1MCN6	ugpC1	sn-glycerol-3-phosphate import ATP-binding protein UgpC 1	Rhizobium leguminosarum bv. viciae (strain 3841)		A0A0D7FIC3	UM91_01140	DEAD/DEAH box helicase	Pseudomonas oryzihabitans
	A0A0H3FEA3	carA	Carbamoyl-phosphate synthase small chain	Rahnella sp. (strain Y9602)		M7Y0L2	MmSR116_4245	Integral membrane sensor signal transduction histidine kinase	Methylobacterium mesophilicum SR1.6/6		J3CBG2	PMI41_03076	ABC-type polar amino acid transport system, ATPase component	Phyllobacterium sp. YR531
	W0EC19	DESME_06425	Peptide ABC transporter ATP-binding protein	Desulfitobacterium metallireducens DSM 15288		A0A0F0L829	ybeZ_1	PhoH-like protein	Microbacterium oxydans		W0EFM0	dnaJ	Chaperone protein DnaJ	Desulfitobacterium metallireducens DSM 15288
	A0JUT1	proS	Proline--tRNA ligase	Arthrobacter sp. (strain FB24)		M7YIM5	MmSR116_4372	Uncharacterized protein	Methylobacterium mesophilicum SR1.6/6		A1SIM4	Noca_2150	Acetaldehyde dehydrogenase 2	Nocardioides sp. (strain BAA-499 / JS614)
	Q6FEE5	accD	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		C5CPP8	groL	60 kDa chaperonin	Variovorax paradoxus (strain S110)		A0A0D7QRH9	TZ00_06500	DNA helicase	Agreia bicolorata
	Q6F8P2	pckG	Phosphoenolpyruvate carboxykinase [GTP]	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		A0A023Y6K4	DX03_15145	Nucleotide-binding protein DX03_15145	Stenotrophomonas rhizophila		O33580	cysD	Sulfate adenylyltransferase subunit 2	Rhizobium tropici
	D5UZ40	Tpau_4326	Amino acid adenylation domain protein	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		C5CU12	dnaK	Chaperone protein DnaK	Variovorax paradoxus (strain S110)		A0A0H3FDN7	Rahaq_3810	ABC transporter related protein	Rahnella sp. (strain Y9602)
	A0A0F0KSL8	clpB	Chaperone protein ClpB	Microbacterium oxydans		A0A0D7FHJ6	UM91_00135	ATP-dependent DNA helicase	Pseudomonas oryzihabitans		Q89XW7	aroK	Shikimate kinase	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM

														13628 / NBRC 14792 / USDA 110)
	J3HQY6	groS	10 kDa chaperonin	Phyllobacterium sp. YR531		P96192	dusC	tRNA-dihydrouridine(16) synthase	Azotobacter vinelandii		A0A0H3FD19	rcsD	Phosphotransferase RcsD	Rahnella sp. (strain Y9602)
	M7XW44	MmSR116_3014	ABC transporter-like protein	Methylobacterium mesophilicum SR1.6/6		A0A0H3F5H0	Rahaq_0413	Fumarate reductase flavoprotein subunit	Rahnella sp. (strain Y9602)		D5UWV0	Tpau_1343	PPOX class putative F420-dependent enzyme	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
	D5UWB1	Tpau_3325	ABC transporter related protein	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		M7YWF3	MmSR116_4062	DNA repair protein RecN	Methylobacterium mesophilicum SR1.6/6		A0A023Y3A7	DX03_10555	Histidine kinase	Stenotrophomonas rhizophila
	A0A0H3FCY4	Rahaq_3507	D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding protein	Rahnella sp. (strain Y9602)		Q2T3W7	groL2	60 kDa chaperonin 2	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)		A0A0H3F8F8	glnE	Glutamate-ammonia-ligase adenylyltransferase	Rahnella sp. (strain Y9602)
	D5UYF4	Tpau_1640	Uncharacterized protein	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		D3GN19		Uncharacterized protein	Rahnella sp. WMR66 PE=4 SV=1		A5V3X0	accA	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)
	Q6F9W1	miaA	tRNA dimethylallyltransferase	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		A0A023Y681	purT	Phosphoribosylglycinamide formyltransferase 2	Stenotrophomonas rhizophila		M7XP10	MmSR116_5674	Type II secretion system protein E	Methylobacterium mesophilicum SR1.6/6
	A4WGF4	atpG	ATP synthase gamma chain	Enterobacter sp. (strain 638)		A4W5D0	aceK	Isocitrate dehydrogenase kinase/phosphatase	Enterobacter sp. (strain 638)		A0KE53	xylG	Xylose import ATP-binding protein XylG	Burkholderia cenocepacia (strain HI2424)
	M7YAT8	lepA	Elongation factor 4	Methylobacterium mesophilicum SR1.6/6		Q0BJL6	atpG	ATP synthase gamma chain	Burkholderia ambifaria (strain ATCC BAA-244 / AMMD)		C5CPP8	groL	60 kDa chaperonin	Variovorax paradoxus (strain S110)
	A8GIC1	tilS	tRNA(Ile)-lysidine synthase	Serratia proteamaculans (strain 568)		W0EGI9	glnS	Glutamine--tRNA ligase	Desulfitobacterium metallireducens DSM 15288		M7YA94	sdhA	Succinate dehydrogenase flavoprotein subunit	Methylobacterium mesophilicum SR1.6/6
	A5EKP4	gatA	Glutamyl-tRNA(Gln) amidotransferase	Bradyrhizobium sp. (strain		A0A0D7FI45	UM91_00300	ATPase	Pseudomonas oryzihabitans		B0VBY5	mnmA	tRNA-specific 2-thiouridylase MnmA	Acinetobacter baumannii

			subunit A	BTAi1 / ATCC BAA-1182)										(strain AYE)
	A0A0D7FEZ2	gatB	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	Pseudomonas oryzihabitans		A0A0L8ADW8	uvrB	UvrABC system protein B	[Pseudomonas] geniculata N1		A0A0D7FBB2	UM91_19110	Histidine kinase	Pseudomonas oryzihabitans
	Q89IK8	groL6	60 kDa chaperonin 6	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)		Q3JR19	smc	Chromosome partition protein Smc	Burkholderia pseudomallei (strain 1710b)		A0A0D7FBB1	glnQ	Glutamine ABC transporter ATP-binding protein	Pseudomonas oryzihabitans
	A0A0D7FMA6	ruvB	Holliday junction ATP-dependent DNA helicase RuvB	Pseudomonas oryzihabitans		A5WH45	prfC	Peptide chain release factor 3	Psychrobacter sp. (strain PRwf-1)		M7YYY8	hisG	ATP phosphoribosyltransferase	Methylobacterium mesophilicum SR1.6/6
	A4WG52	argB	Acetylglutamate kinase	Enterobacter sp. (strain 638)		A1V3F2	alaS	Alanine--tRNA ligase	Burkholderia mallei (strain SAVP1)		Q2T3W7	groL2	60 kDa chaperonin 2	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)
	W0E620	DESME_03200	Sensory histidine kinase	Desulfitobacterium metallireducens DSM 15288		A0A0F0KXV3	tcrY_3	Putative sensor histidine kinase TcrY	Microbacterium oxydans		A0A0L8AEI2	glnD	Bifunctional uridylyltransferase/uridylyl-removing enzyme	[Pseudomonas] geniculata N1
	A0ZNI0	gyrB	DNA gyrase subunit B (Fragment)	Tsukamurella inchonensis		A0A0D7F8T1	parC	DNA topoisomerase 4 subunit A	Pseudomonas oryzihabitans		O66210	groL	60 kDa chaperonin (Fragment)	Klebsiella oxytoca
	C1DF46	pheS	Phenylalanine--tRNA ligase alpha subunit	Azotobacter vinelandii (strain DJ / ATCC BAA-1303)		M7YKT6	MmSR116_3841	Acyl-CoA dehydrogenase type 2	Methylobacterium mesophilicum SR1.6/6		A0A0H3F8T2	Rahaq_2001	Helicase c2	Rahnella sp. (strain Y9602)
	Q1ME34	murC	UDP-N-acetylmuramate--L-alanine ligase	Rhizobium leguminosarum bv. viciae (strain 3841)		A0A0L8A781	W7K_16285	Histidine kinase	[Pseudomonas] geniculata N1		A7Z0N5	tuf	Elongation factor Tu	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)
	Q0S2Y0	secA	Protein translocase subunit SecA	Rhodococcus jostii (strain RHA1)		A0A0D7FCR0	hslU	ATP-dependent protease ATPase subunit HslU	Pseudomonas oryzihabitans		A8FIG8	argS	Arginine--tRNA ligase	Bacillus pumilus (strain SAFR-032)
	A8GHZ8	prr	Gamma-aminobutyraldehyde dehydrogenase	Serratia proteamaculans (strain 568)		P35864	groS3	10 kDa chaperonin 3	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)		A0A0F0L3A2	ileS	Isoleucine--tRNA ligase	Microbacterium oxydans
	A0A0L8AEX7	W7K_01815	3-methylcrotonyl-CoA carboxylase	[Pseudomonas] geniculata		Q8UHJ6	ileS	Isoleucine--tRNA ligase	Agrobacterium fabrum		A0A0F0L9I6	phoR	Alkaline phosphatase synthesis sensor protein	Microbacterium oxydans

				N1					(strain C58 / ATCC 33970)				PhoR	
	J3HM74	aroE	Shikimate dehydrogenase (NADP(+))	Phyllobacterium sp. YR531		A0A0D7FFL0	UM91_06110	Fis family transcriptional regulator	Pseudomonas oryzihabitans		J3CF91	PMI41_02201	6-phosphogluconate dehydrogenase, decarboxylating	Phyllobacterium sp. YR531
	A0A0H3FFX2	Rahaq_3339	ABC transporter related protein	Rahnella sp. (strain Y9602)		J3CEB9	PMI41_01609	Putative cobalamin binding protein	Phyllobacterium sp. YR531		Q2K0S7	rbsA3	Ribose import ATP-binding protein RbsA 3	Rhizobium etli (strain CFN 42 / ATCC 51251)
	M7Y2J1	lpd	Dihydrolipoyl dehydrogenase	Methylobacterium mesophilicum SR1.6/6		A0A0H3FDP1	Rahaq_3815	Transcriptional regulator, XRE family	Rahnella sp. (strain Y9602)		Q2JYW6	groL4	60 kDa chaperonin 4	Rhizobium etli (strain CFN 42 / ATCC 51251)
	A0A023Y6Q8	DX03_16565	Histidine kinase	Stenotrophomonas rhizophila		A0A023Y6I8	rpoB	DNA-directed RNA polymerase subunit beta	Stenotrophomonas rhizophila		D5UM28	Tpau_1690	Penicillin-binding protein transpeptidase	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
						A0A0L8AD51	W7K_07380	Fis family transcriptional regulator	[Pseudomonas] geniculata N1		A0A0D7FIQ2	uvrB	UvrABC system protein B	Pseudomonas oryzihabitans
											J3HQY6	groS	10 kDa chaperonin	Phyllobacterium sp. YR531
											A0A023Y3F4	DX03_10905	3-phosphoglycerate dehydrogenase	Stenotrophomonas rhizophila
											M7Z5P9	MmSR116_0188	Uncharacterized protein	Methylobacterium mesophilicum SR1.6/6
											A0A0D7QQP3	TZ00_09975	ABC transporter	Agreia bicolorata
											M7XW44	MmSR116_3014	ABC transporter-like protein	Methylobacterium mesophilicum SR1.6/6
											A0A023Y0D1	DX03_04195	Glyceraldehyde-3-phosphate dehydrogenase	Stenotrophomonas rhizophila
											A5EET6	groL2	60 kDa chaperonin 2	Bradyrhizobium sp. (strain BTAi1 / ATCC BAA-1182)
											A7Z7I1	thrS	Threonine--tRNA ligase	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)
											A0A0D7F835	UM91_17450	Sugar ABC transporter ATPase	Pseudomonas oryzihabitans
											A0A023Y2Z7	DX03_09635	ATPase	Stenotrophomonas

														rhizophila
											A4YKD9	atpG	ATP synthase gamma chain	Bradyrhizobium sp. (strain ORS278)
											A8FIB2	atpD	ATP synthase subunit beta	Bacillus pumilus (strain SAFR-032)
											Q0B1N7	groL3	60 kDa chaperonin 3	Burkholderia ambifaria (strain ATCC BAA-244 / AMMD)
											A0JZ88	tuf	Elongation factor Tu	Arthrobacter sp. (strain FB24)
											A0A0H3FBD0	Rahaq_2755	Oligopeptide/dipeptide ABC transporter, ATPase subunit	Rahnella sp. (strain Y9602)
											A0A0F0L4I6	ftsY	Signal recognition particle receptor FtsY	Microbacterium oxydans
											A0A0D7QW45	TZ00_00255	GTP pyrophosphokinase	Agreia bicolorata
											A0A0D7F7B2	UM91_19185	Penicillin-binding protein 2	Pseudomonas oryzihabitans
											Q1ME34	murC	UDP-N-acetylmuramate--L-alanine ligase	Rhizobium leguminosarum bv. viciae (strain 3841)
											Q2T3B8	hmuV	Hemin import ATP-binding protein HmuV	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)
											D5UMT2	Tpau_1811	ATP-dependent helicase HrpA	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
											A0A0H3FFX2	Rahaq_3339	ABC transporter related protein	Rahnella sp. (strain Y9602)
metal ion binding														
	A0A0D7F821	UM91_17905	Formate dehydrogenase	Pseudomonas oryzihabitans		M7YKY2	tonB	TonB-dependent siderophore receptor	Methylobacterium mesophilicum SR1.6/6		A4W533	gpmI	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	Enterobacter sp. (strain 638)
	A0A0H3FLE2	ilvD	Dihydroxy-acid dehydratase	Rahnella sp. (strain Y9602)		Q89QJ5	glnE	Glutamate-ammonia-ligase adenylyltransferase	Bradyrhizobium		A0A0H3F5T8	parE	DNA topoisomerase 4 subunit B	Rahnella sp. (strain Y9602)

									diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)					
	A0A0F0KI13	kynA	Tryptophan 2,3-dioxygenase	Microbacterium oxydans		A0A0F0KI13	kynA	Tryptophan 2,3-dioxygenase	Microbacterium oxydans		Q8UBV5	acsA	Acetyl-coenzyme A synthetase	Agrobacterium fabrum (strain C58 / ATCC 33970)
	M7Y6G0	ccmE	Cytochrome c-type biogenesis protein CcmE	Methylobacterium mesophilicum SR1.6/6		M7XSC1	MmSR116_4465	Peptidase M16 domain-containing protein	Methylobacterium mesophilicum SR1.6/6		A0A0D7F7I2	UM91_18625	Deoxyguanosinetriphosphate triphosphohydrolase	Pseudomonas oryzihabitans
	Q6FEE5	accD	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		A0A023Y681	purT	Phosphoribosylglycinamide formyltransferase 2	Stenotrophomonas rhizophila		A0A0D7FDU1	obgE	GTPase Obg	Pseudomonas oryzihabitans
	A0A0H3F6R1	nuoI	NADH-quinone oxidoreductase subunit I	Rahnella sp. (strain Y9602)		A4WDX1	rlmD	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	Enterobacter sp. (strain 638)		J3CGD3	pnp	Polyribonucleotide nucleotidyltransferase	Phyllobacterium sp. YR531
	B9J8M7	ureD	Urease accessory protein UreD	Agrobacterium radiobacter (strain K84 / ATCC BAA-868)		M7YVR1	bchL	Light-independent protochlorophyllide reductase iron-sulfur ATP-binding protein	Methylobacterium mesophilicum SR1.6/6		Q0S2E0	mutM	Formamidopyrimidine-DNA glycosylase	Rhodococcus jostii (strain RHA1)
	Q6F8P2	pckG	Phosphoenolpyruvate carboxykinase [GTP]	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		J3CHX8	ureD	Urease accessory protein UreD	Phyllobacterium sp. YR531		M7Y2T0	MmSR116_3281	Arginase family	Methylobacterium mesophilicum SR1.6/6
	Q6FD29	pyrC	Dihydroorotase	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		A1V3F2	alaS	Alanine--tRNA ligase	Burkholderia mallei (strain SAVP1)		A7Z4N5	clpQ	ATP-dependent protease subunit ClpQ	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)
	J2VDV4	PMI41_04838	Zinc metalloprotease	Phyllobacterium sp. YR531		A8FHJ0	eno	Enolase	Bacillus pumilus (strain SAFR-032)		A0A0F0L3A2	ileS	Isoleucine--tRNA ligase	Microbacterium oxydans
	M7XTI1	secA	Protein translocase subunit SecA	Methylobacterium mesophilicum SR1.6/6		A0A0F0LAH9	glmM	Phosphoglucosamine mutase	Microbacterium oxydans		B9J8M0	ureE	Urease accessory protein UreE	Agrobacterium radiobacter (strain K84 / ATCC BAA-868)
	Q2SYC8	ubiD	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)		B2GIA1	alaS	Alanine--tRNA ligase	Kocuria rhizophila (strain ATCC 9341 / DSM 348 / NBRC 103217 / DC2201)		B2JK72	alaS	Alanine--tRNA ligase	Burkholderia phymatum (strain DSM 17167 / STM815)

	W0E7Z6	DESME_07325	Carbon monoxide dehydrogenase	Desulfitobacterium metallireducens DSM 15288		A0A0D7QR84	TZ00_03905	ATPase	Agreia bicolorata		A0JSM6	upp	Uracil phosphoribosyltransferase	Arthrobacter sp. (strain FB24)
	M7Z4T8	MmSR116_1602	Ribonucleotide-diphosphate reductase subunit alpha	Methylobacterium mesophilicum SR1.6/6		A0A0H3F463	Rahaq_0325	BFD domain protein (2Fe-2S)-binding domain protein	Rahnella sp. (strain Y9602)		J3HSJ8	PMI41_02183	ABC-type metal ion transport system, periplasmic component/surface adhesin	Phyllobacterium sp. YR531
	A0A0D7QRP4	TZ00_04945	Glucarate dehydratase	Agreia bicolorata		A0A023Y292	nfuA	Fe/S biogenesis protein NfuA	Stenotrophomonas rhizophila		M7XZU6	MmSR116_2042	Putative oxalyl-CoA decarboxylase	Methylobacterium mesophilicum SR1.6/6
	A0A0D7QMN7	rnc	Ribonuclease 3	Agreia bicolorata		Q13QH6	Bxeno_B0695	4-hydroxy-2-oxovalerate aldolase 3	Burkholderia xenovorans (strain LB400)		W0E791	rimO	Ribosomal protein S12 methylthiotransferase RimO	Desulfitobacterium metallireducens DSM 15288
	A6GW77	bioB	Biotin synthase	Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)		C0ZXK3	ligA	DNA ligase	Rhodococcus erythropolis (strain PR4 / NBRC 100887)		Q1GPH4	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX	Sphingopyxis alaskensis (strain DSM 13593 / LMG 18877 / RB2256)
	Q9UV64	hxB	Molybdenum cofactor sulfurase	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139)		M7Z301	nth	Endonuclease III	Methylobacterium mesophilicum SR1.6/6		J3CCP5	ribB	3,4-dihydroxy-2-butanone 4-phosphate synthase	Phyllobacterium sp. YR531
	A0A0H3FFF8	kdpB	Potassium-transporting ATPase ATP-binding subunit	Rahnella sp. (strain Y9602)		D5UT97	Tpau_2784	Peptidyl-dipeptidase Dcp	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		A0A0L8AB68	dnaG	DNA primase	[Pseudomonas] geniculata N1
	A0A0D7QR84	TZ00_03905	ATPase	Agreia bicolorata		J3CEB9	PMI41_01609	Putative cobalamin binding protein	Phyllobacterium sp. YR531		A4YM47	glcB	Malate synthase G	Bradyrhizobium sp. (strain ORS278)
	A5V3L0	alaS	Alanine--tRNA ligase	Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)		W0EFJ2	DESME_13730	Glycolate oxidase iron-sulfur subunit	Desulfitobacterium metallireducens DSM 15288		M7Z5P9	MmSR116_0188	Uncharacterized protein	Methylobacterium mesophilicum SR1.6/6
	M7XYF7	MmSR116_2667	Formate dehydrogenase, alpha subunit	Methylobacterium mesophilicum SR1.6/6		M7Z0G6	MmSR116_2127	ApbE family lipoprotein	Methylobacterium mesophilicum SR1.6/6		A0A0D7F850	UM91_19705	Guanine deaminase	Pseudomonas oryzihabitans
	B2T672	Bphyt_3044	Adenine deaminase	Burkholderia phytofirmans (strain DSM 17436 / PsJN)		A7ZAH2	iolJ	6-phospho-5-dehydro-2-deoxy-D-gluconate aldolase	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 /		M7Z4T8	MmSR116_1602	Ribonucleotide-diphosphate reductase subunit alpha	Methylobacterium mesophilicum SR1.6/6

									FZB42)					
	M7XSW0	MmSR116_4226	Beta-lactamase domain-containing protein	Methylobacterium mesophilicum SR1.6/6		A4YJH3	dut	Deoxyuridine 5'-triphosphate nucleotidohydrolase	Bradyrhizobium sp. (strain ORS278)		A0A0L8AAW6	selD	Selenide, water dikinase	[Pseudomonas] geniculata N1
	A4YUF4	glmU	Bifunctional protein GlmU	Bradyrhizobium sp. (strain ORS278)		M7YXS4	MmSR116_3815	Ferredoxin	Methylobacterium mesophilicum SR1.6/6		A6H294	hflX	GTPase HflX	Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)
	Q44493	algE4	Poly(beta-D-mannuronate) C5 epimerase 4	Azotobacter vinelandii							A7Z7I1	thrS	Threonine--tRNA ligase	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)
	A4JN03	ilvD	Dihydroxy-acid dehydratase	Burkholderia vietnamiensis (strain G4 / LMG 22486)							A0A0F0LDH6	mcl2	(3S)-malyl-CoA thioesterase	Microbacterium oxydans
	M7Z301	nth	Endonuclease III	Methylobacterium mesophilicum SR1.6/6							A0A0F0L5Y0	dgt	Deoxyguanosinetriphosphate triphosphohydrolase	Microbacterium oxydans
	A0ZNI0	gyrB	DNA gyrase subunit B (Fragment)	Tsukamurella inchonensis							A0A0H3FFF8	kdpB	Potassium-transporting ATPase ATP-binding subunit	Rahnella sp. (strain Y9602)
	C1DF46	pheS	Phenylalanine--tRNA ligase alpha subunit	Azotobacter vinelandii (strain DJ / ATCC BAA-1303)							Q2SU58	engB	Probable GTP-binding protein EngB	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)
	A0A0L8AEX7	W7K_01815	3-methylcrotonyl-CoA carboxylase	[Pseudomonas] geniculata N1							A0A0D7QR84	TZ00_03905	ATPase	Agreia bicolorata
	B2SZR6	glmM	Phosphoglucosamine mutase	Burkholderia phytofirmans (strain DSM 17436 / PsJN)							W0EFM0	dnaJ	Chaperone protein DnaJ	Desulfitobacterium metallireducens DSM 15288
	A0A023Y9M0	DX03_20425	NADPH:quinone reductase	Stenotrophomonas rhizophila							Q8UJ88	hslV	ATP-dependent protease subunit HslV	Agrobacterium fabrum (strain C58 / ATCC 33970)
	M7YXS4	MmSR116_3815	Ferredoxin	Methylobacterium mesophilicum SR1.6/6							Q89XW7	aroK	Shikimate kinase	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)
											M7YIV7	MmSR116_	2-dehydro-3-	Methylobacte

												4442	deoxyglucarate aldolase	rium mesophilicum SR1.6/6
											A0A0H3F8F8	glnE	Glutamate-ammonia-ligase adenylyltransferase	Rahnella sp. (strain Y9602)
											J3CGU4	ispG	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin)	Phyllobacterium sp. YR531
											A0A0L8ADV3	W7K_04370	Coproporphyrinogen-III oxidase	[Pseudomonas] geniculata N1
											M7YYY8	hisG	ATP phosphoribosyltransferase	Methylobacterium mesophilicum SR1.6/6
											M7YXS4	MmSR116_3815	Ferredoxin	Methylobacterium mesophilicum SR1.6/6
DNA binding														
	M7Z6B1	MmSR116_0403	Bifunctional protein PutA	Methylobacterium mesophilicum SR1.6/6		J2VSM6	mutL	DNA mismatch repair protein MutL	Phyllobacterium sp. YR531		A0A0H3FDA9	Rahaq_3639	Cold-shock protein DNA-binding protein	Rahnella sp. (strain Y9602)
	J3HN07	mutS	DNA mismatch repair protein MutS	Phyllobacterium sp. YR531		W0E6B0	DESME_03800	DNA mismatch repair protein	Desulfitobacterium metallireducens DSM 15288		M7XZQ9	MmSR116_4801	LacI family transcriptional regulator	Methylobacterium mesophilicum SR1.6/6
	A1V6A8	uvrC	UvrABC system protein C	Burkholderia mallei (strain SAVP1)		A0A0D7FED5	UM91_07650	DNA-directed DNA polymerase	Pseudomonas oryzihabitans		A0A0F0L6V3	kdgR_2	Pectin degradation repressor protein KdgR	Microbacterium oxydans
	A0A0D7QQZ5	TZ00_08680	Fis family transcriptional regulator	Agreia bicolorata		A0A0H3F4P1	Rahaq_0243	Tex-like protein	Rahnella sp. (strain Y9602)		A0A0H3F5T8	parE	DNA topoisomerase 4 subunit B	Rahnella sp. (strain Y9602)
	A0A0D7QNY7	TZ00_07235	Uncharacterized protein	Agreia bicolorata		A0A0D7FMB2	UM91_01620	Cold-shock protein	Pseudomonas oryzihabitans		A0A0H3F999	Rahaq_0038	Transcriptional regulator, GntR family with aminotransferase domain protein	Rahnella sp. (strain Y9602)
	A0A0D7QNE7	TZ00_10950	Uncharacterized protein	Agreia bicolorata		A0A069AW52	vdlC	Putative short-chain type dehydrogenase/reductase VdlC	Micrococcus sp. A1		A0A0H3FLE0	rep	ATP-dependent DNA helicase Rep	Rahnella sp. (strain Y9602)
	A0A023Y141	DX03_05495	RNA polymerase sigma factor RpoE	Stenotrophomonas rhizophila		D5UT46	Tpau_0696	Transcriptional regulator, MarR family	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		A0A0H3F8T2	Rahaq_2001	Helicase c2	Rahnella sp. (strain Y9602)
	W0EFY0	DESME_14585	GntR family transcriptional regulator	Desulfitobacterium metallireducens DSM 15288		M7Y7Y5	MmSR116_1435	Phage integrase family	Methylobacterium mesophilicum SR1.6/6		Q0S2E0	mutM	Formamidopyrimidine-DNA glycosylase	Rhodococcus jostii (strain RHA1)

	A0A0D7FEA9	UM91_13305	Peptidase S24	Pseudomonas oryzihabitans		W0E615	DESME_02960	Transposase IS116	Desulfitobacterium metallireducens DSM 15288		A0JZ92	rpoC	DNA-directed RNA polymerase subunit beta'	Arthrobacter sp. (strain FB24)
	J2V021	PMI41_04659	Transcriptional regulator	Phyllobacterium sp. YR531		P0C7V2	recA	Protein RecA	Burkholderia cepacia		D5UTY9	Tpau_2894	Transcriptional regulator, TetR family	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
	A0A0D7FMA6	ruvB	Holliday junction ATP-dependent DNA helicase RuvB	Pseudomonas oryzihabitans		A0A0L8ADW8	uvrB	UvrABC system protein B	[Pseudomonas] geniculata N1		A4YRD9	dnaE2	Error-prone DNA polymerase	Bradyrhizobium sp. (strain ORS278)
	M7Z301	nth	Endonuclease III	Methylobacterium mesophilicum SR1.6/6		Q3JR19	smc	Chromosome partition protein Smc	Burkholderia pseudomallei (strain 1710b)		Q1GWJ6	hrcA	Heat-inducible transcription repressor HrcA	Sphingopyxis alaskensis (strain DSM 13593 / LMG 18877 / RB2256)
	J2VIU6	PMI41_00554	DNA-binding domain-containing protein, AraC-type	Phyllobacterium sp. YR531		A0A023XZP1	DX03_02315	RNA polymerase subunit sigma-24	Stenotrophomonas rhizophila		A0A0D7FIQ2	uvrB	UvrABC system protein B	Pseudomonas oryzihabitans
	A0A0D7FGT2	UM91_05450	AraC family transcriptional regulator	Pseudomonas oryzihabitans		D5UWH8	Tpau_3393	Transcriptional regulator, MerR family	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		A0A0F0L339	sigW_2	ECF RNA polymerase sigma factor SigW	Microbacterium oxydans
	A0ZNI0	gyrB	DNA gyrase subunit B (Fragment)	Tsukamurella inchonensis		A0A0H3F867	Rahaq_1451	Cell division protein FtsK/SpoIIIE	Rahnella sp. (strain Y9602)		A0A0L8AF63	W7K_03575	Cold-shock protein	[Pseudomonas] geniculata N1
	A0A023Y2G8	DX03_08015	Uncharacterized protein	Stenotrophomonas rhizophila		A0A0D7F8T1	parC	DNA topoisomerase 4 subunit A	Pseudomonas oryzihabitans		A0A0L8AB68	dnaG	DNA primase	[Pseudomonas] geniculata N1
	A0A0D7QSV4	TZ00_07540	GntR family transcriptional regulator	Agreia bicolorata		A0A0F0LD33	rbsR_3	Ribose operon repressor	Microbacterium oxydans		M7YAY0	MmSR116_0774	TetR family transcriptional regulator	Methylobacterium mesophilicum SR1.6/6
	M7XXR7	MmSR116_5260	Uncharacterized protein	Methylobacterium mesophilicum SR1.6/6		C0ZXK3	ligA	DNA ligase	Rhodococcus erythropolis (strain PR4 / NBRC 100887)		J2VTP8	PMI41_02514	Uncharacterized protein	Phyllobacterium sp. YR531
	A0A0L8AF72	W7K_03635	Replicative DNA helicase	[Pseudomonas] geniculata N1		M7Z301	nth	Endonuclease III	Methylobacterium mesophilicum SR1.6/6		J2VHD7	ku	Non-homologous end joining protein Ku	Phyllobacterium sp. YR531
	J3CEW5	PMI41_01994	Transcriptional regulator	Phyllobacterium sp. YR531		A0A0F0LD64	RS83_00945	Putative 3-methyladenine DNA glycosylase	Microbacterium oxydans		A0A0F0L382	uvrB	UvrABC system protein B	Microbacterium oxydans
	P06665	virC1	Protein virC1	Rhizobium radiobacter		A0A0L8A899	W7K_14015	HupB	[Pseudomonas] geniculata N1		D5UWN4	Tpau_1275	Transcriptional regulator, LysR family	Tsukamurella paurometabola (strain ATCC

														8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
	M7YS07	uvrB	UvrABC system protein B	Methylobacterium mesophilicum SR1.6/6		A0A0D7QT09	sigA	RNA polymerase sigma factor SigA	Agreia bicolorata		A0A0D7FIC3	UM91_01140	DEAD/DEAH box helicase	Pseudomonas oryzihabitans
						A0A0H3FDP1	Rahaq_3815	Transcriptional regulator, XRE family	Rahnella sp. (strain Y9602)		A0A0D7QRH9	TZ00_06500	DNA helicase	Agreia bicolorata
						A0A0D7FFL0	UM91_06110	Fis family transcriptional regulator	Pseudomonas oryzihabitans		A0A0D7FGT2	UM91_05450	AraC family transcriptional regulator	Pseudomonas oryzihabitans
						A0A0D7FKT3	putA	Bifunctional protein PutA	Pseudomonas oryzihabitans		A0A0F0KWM2	narL	Putative transcriptional regulatory protein NarL	Microbacterium oxydans
						A0A023Y6I8	rpoB	DNA-directed RNA polymerase subunit beta	Stenotrophomonas rhizophila		G6GEI2	DESME_03165	Transposase IS110	Desulfitobacterium metallireducens DSM 15288
						A0A0F0L547	RS83_03358	Uncharacterized protein	Microbacterium oxydans		B9JEJ1	sfsA	Sugar fermentation stimulation protein homolog	Agrobacterium radiobacter (strain K84 / ATCC BAA-868)
						M7XXR7	MmSR116_5260	Uncharacterized protein	Methylobacterium mesophilicum SR1.6/6		D5UYE2	Tpau_1628	Tex-like protein protein-like protein	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
						A0A023XZW6	DX03_03370	LysR family transcriptional regulator	Stenotrophomonas rhizophila					
						A0A0D7QNM3	TZ00_11045	Uncharacterized protein	Agreia bicolorata					
						J3HVE7	PMI41_00064	Site-specific recombinase XerC	Phyllobacterium sp. YR531					
						A0A0L8AD51	W7K_07380	Fis family transcriptional regulator	[Pseudomonas] geniculata N1					
						A0A0F0L446	rpoZ	DNA-directed RNA polymerase subunit omega	Microbacterium oxydans					
hydrolase activity														
	A1V6A8	uvrC	UvrABC system protein C	Burkholderia mallei (strain SAVP1)		W0EA38	DESME_01600	ABC transporter ATP-binding protein	Desulfitobacterium metallireducens DSM 15288		A0A023Y1Q7	DX03_06050	Peptidase	Stenotrophomonas rhizophila
	A4W777	acpH	Acyl carrier protein phosphodiesterase	Enterobacter sp. (strain 638)		A0A023Y1Q7	DX03_06050	Peptidase	Stenotrophomonas rhizophila		A0A0L8AAC0	W7K_10235	Translation elongation factor	[Pseudomonas] geniculata N1

	A0JUT1	proS	Proline--tRNA ligase	Arthrobacter sp. (strain FB24)		A0A0D7FED5	UM91_07650	DNA-directed DNA polymerase	Pseudomonas oryzihabitans		A0A0H3FA72	Rahaq_2158	Formiminoglutamate deiminase	Rahnella sp. (strain Y9602)
	W0EC19	DESME_06425	Peptide ABC transporter ATP-binding protein	Desulfitobacterium metallireducens DSM 15288		M7XSC1	MmSR116_4465	Peptidase M16 domain-containing protein	Methylobacterium mesophilicum SR1.6/6		A0A0H3F5T8	parE	DNA topoisomerase 4 subunit B	Rahnella sp. (strain Y9602)
	A0A0H3FIM7	Rahaq_3185	N-acetylglucosamine-6-phosphate deacetylase	Rahnella sp. (strain Y9602)		A0A0H3F4P1	Rahaq_0243	Tex-like protein	Rahnella sp. (strain Y9602)		Q89IB6	purQ	Phosphoribosylformylglycinamidine synthase subunit PurQ	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)
	D5UP01	Tpau_4141	Carboxylic ester hydrolase	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		Q0BJL6	atpG	ATP synthase gamma chain	Burkholderia ambifaria (strain ATCC BAA-244 / AMMD)		A0A023Y783	fusA	Elongation factor G	Stenotrophomonas rhizophila
	A0A0F0L6L9	RS83_02303	Calcineurin-like phosphoesterase superfamily domain protein	Microbacterium oxydans		A4W5D0	aceK	Isocitrate dehydrogenase kinase/phosphatase	Enterobacter sp. (strain 638)		A0A0H3FLE0	rep	ATP-dependent DNA helicase Rep	Rahnella sp. (strain Y9602)
	A0A0L8AD80	W7K_04990	Uncharacterized protein	[Pseudomonas] geniculata N1		J2VEM8	PMI41_02072	ATPase component of various ABC-type transport systems with duplicated ATPase domain	Phyllobacterium sp. YR531		A0A0L8AB49	W7K_08590	Phytase	[Pseudomonas] geniculata N1
	A0A0H3FF00	Rahaq_3027	ABC transporter related protein	Rahnella sp. (strain Y9602)		W0EA79	DESME_11995	Molybdenum ABC transporter substrate-binding protein	Desulfitobacterium metallireducens DSM 15288		A0A0D7FDU1	obgE	GTPase Obg	Pseudomonas oryzihabitans
	Q6FD29	pyrC	Dihydroorotase	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		M7XP91	MmSR116_5619	MCP methyltransferase/methylesterase	Methylobacterium mesophilicum SR1.6/6		A1SLR5	Noca_3248	UPF0102 protein Noca_3248	Nocardioides sp. (strain BAA-499 / JS614)
	D5UN63	Tpau_3987	Amino acid adenylation domain protein	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		M7Y5Y9	atpG	ATP synthase gamma chain	Methylobacterium mesophilicum SR1.6/6		Q0S2E0	mutM	Formamidopyrimidine-DNA glycosylase	Rhodococcus jostii (strain RHA1)
	J2VDV4	PMI41_04838	Zinc metalloprotease	Phyllobacterium sp. YR531		D5UPW3	Tpau_0077	Glycoside hydrolase family 5	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC		M7Y2T0	MmSR116_3281	Arginase family	Methylobacterium mesophilicum SR1.6/6

									13040)					
	M7XW44	MmSR116_3014	ABC transporter-like protein	Methylobacterium mesophilicum SR1.6/6		M7Y3Y6	MmSR116_3375	Acid phosphatase	Methylobacterium mesophilicum SR1.6/6		A4YRD9	dnaE2	Error-prone DNA polymerase	Bradyrhizobium sp. (strain ORS278)
	A0A0D7QMN7	rnc	Ribonuclease 3	Agreia bicolorata		Q62KW5	valS	Valine--tRNA ligase	Burkholderia mallei (strain ATCC 23344)		J3CCZ8	PMI41_02736	Autotransporter-associated beta strand repeat containing protein (Fragment)	Phyllobacterium sp. YR531
	P06665	virC1	Protein virC1	Rhizobium radiobacter		P0C7V2	recA	Protein RecA	Burkholderia cepacia		J3C7F0	PMI41_03898	Non-ribosomal peptide synthase/amino acid adenylation enzyme	Phyllobacterium sp. YR531
	D5UWB1	Tpau_3325	ABC transporter related protein	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		A0A0L8ADW8	uvrB	UvrABC system protein B	[Pseudomonas] geniculata N1		W0EFM5	lepA	Elongation factor 4	Desulfitobacterium metallireducens DSM 15288
	Q1GQS5	atpD	ATP synthase subunit beta	Sphingopyxis alaskensis (strain DSM 13593 / LMG 18877 / RB2256)		A5WH45	prfC	Peptide chain release factor 3	Psychrobacter sp. (strain PRwf-1)		A0A023Y0J9	DX03_05600	DEAD/DEAH box helicase	Stenotrophomonas rhizophila
	A4WGF4	atpG	ATP synthase gamma chain	Enterobacter sp. (strain 638)		A0A0F0KY75	malL_1	Oligo-1,6-glucosidase	Microbacterium oxydans		Q1GPH4	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX	Sphingopyxis alaskensis (strain DSM 13593 / LMG 18877 / RB2256)
	M7YAT8	lepA	Elongation factor 4	Methylobacterium mesophilicum SR1.6/6		D5UN63	Tpau_3987	Amino acid adenylation domain protein	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		A0A0D7F850	UM91_19705	Guanine deaminase	Pseudomonas oryzihabitans
	A0A0H3FFF8	kdpB	Potassium-transporting ATPase ATP-binding subunit	Rahnella sp. (strain Y9602)		A0A0D7F8T1	parC	DNA topoisomerase 4 subunit A	Pseudomonas oryzihabitans		A6H294	hflX	GTPase HflX	Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)
	A0A0D7QR84	TZ00_03905	ATPase	Agreia bicolorata		A0A0D7QR84	TZ00_03905	ATPase	Agreia bicolorata		A0A0F0KR00	guaA_1	GMP synthase [glutamine-hydrolyzing]	Microbacterium oxydans
	M7YA99	amn	AMP nucleosidase	Methylobacterium mesophilicum SR1.6/6		A0A0H3F982	Rahaq_2180	Polysaccharide deacetylase	Rahnella sp. (strain Y9602)		A0A0F0L382	uvrB	UvrABC system protein B	Microbacterium oxydans
	A0A023Y8A7	DX03_18100	Uncharacterized protein	Stenotrophomonas		A0A0D7FDV1	UM91_08500	ATP-dependent protease	Pseudomonas oryzihabitans		A0A0H3FFF8	kdpB	Potassium-transporting ATPase ATP-binding	Rahnella sp. (strain Y9602)

				rhizophila									subunit	
	Q6F823	prfC	Peptide chain release factor 3	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		A0A0F0LBN3	cydD	ATP-binding/permease protein CydD	Microbacterium oxydans		A0A0L8A5F8	W7K_19260	Serine protease	[Pseudomonas] geniculata N1
	B2T672	Bphyt_3044	Adenine deaminase	Burkholderia phytofirmans (strain DSM 17436 / PsJN)		A0A0D7FCR0	hslU	ATP-dependent protease ATPase subunit HslU	Pseudomonas oryzihabitans		A0A0F0L5Y0	dgt	Deoxyguanosinetriphosphate triphosphohydrolase	Microbacterium oxydans
	M7XSW0	MmSR116_4226	Beta-lactamase domain-containing protein	Methylobacterium mesophilicum SR1.6/6		A0A0D7FDR6	UM91_13975	Penicillin-binding protein 1B	Pseudomonas oryzihabitans		Q2SU58	engB	Probable GTP-binding protein EngB	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)
	A0A0D7FEA9	UM91_13305	Peptidase S24	Pseudomonas oryzihabitans		A0KAZ7	aceK	Isocitrate dehydrogenase kinase/phosphatase	Burkholderia cenocepacia (strain HI2424)		A0A0D7QR84	TZ00_03905	ATPase	Agreia bicolorata
	A0A023Y171	DX03_05720	Phosphonoacetate hydrolase	Stenotrophomonas rhizophila		Q1MCN6	ugpC1	sn-glycerol-3-phosphate import ATP-binding protein UgpC 1	Rhizobium leguminosarum bv. viciae (strain 3841)		A0A0D7FIC3	UM91_01140	DEAD/DEAH box helicase	Pseudomonas oryzihabitans
	D5UT34	Tpau_0684	Carboxylic ester hydrolase	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		M7Z301	nth	Endonuclease III	Methylobacterium mesophilicum SR1.6/6		J3CBG2	PMI41_03076	ABC-type polar amino acid transport system, ATPase component	Phyllobacterium sp. YR531
	A0A0D7FMA6	ruvB	Holliday junction ATP-dependent DNA helicase RuvB	Pseudomonas oryzihabitans		A0A0H3FEL3	Rahaq_3672	ABC transporter related protein	Rahnella sp. (strain Y9602)		Q8UJ88	hslV	ATP-dependent protease subunit HslV	Agrobacterium fabrum (strain C58 / ATCC 33970)
	M7Z301	nth	Endonuclease III	Methylobacterium mesophilicum SR1.6/6		J3HM91	PMI41_04061	ATPase component of uncharacterized ABC-type transporter	Phyllobacterium sp. YR531		A0A0D7QRH9	TZ00_06500	DNA helicase	Agreia bicolorata
	A5WI39	rnpA	Ribonuclease P protein component	Psychrobacter sp. (strain PRwf-1)		D5UT97	Tpau_2784	Peptidyl-dipeptidase Dcp	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)		A0A0H3FDN7	Rahaq_3810	ABC transporter related protein	Rahnella sp. (strain Y9602)
	A0ZNI0	gyrB	DNA gyrase subunit B (Fragment)	Tsukamurella inchonensis		Q8UHJ6	ileS	Isoleucine--tRNA ligase	Agrobacterium fabrum (strain C58 / ATCC 33970)		A0A023Y3A7	DX03_10555	Histidine kinase	Stenotrophomonas rhizophila
	M7XP10	MmSR116_5674	Type II secretion system protein E	Methylobacterium		A0A0F0LD64	RS83_00945	Putative 3-methyladenine DNA glycosylase	Microbacterium oxydans		A0A0F0LD20	RS83_00648	Uncharacterized protein	Microbacterium oxydans

				mesophilicum SR1.6/6										
	W0E604	DESME_03870	Cell wall-binding protein	Desulfitobacterium metallireducens DSM 15288		A0A0F0LC60	sbcC	Nuclease SbcCD subunit C	Microbacterium oxydans		M7XP10	MmSR116_5674	Type II secretion system protein E	Methylobacterium mesophilicum SR1.6/6
	A0KE53	xylG	Xylose import ATP-binding protein XylG	Burkholderia cenocepacia (strain HI2424)		A0A0D7FHJ6	UM91_00135	ATP-dependent DNA helicase	Pseudomonas oryzihabitans		A0KE53	xylG	Xylose import ATP-binding protein XylG	Burkholderia cenocepacia (strain HI2424)
	A0A0H3FCR4	Rahaq_2285	Protein HflC	Rahnella sp. (strain Y9602)		A4YJH3	dut	Deoxyuridine 5'-triphosphate nucleotidohydrolase	Bradyrhizobium sp. (strain ORS278)		J3CGU4	ispG	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin)	Phyllobacterium sp. YR531
	A0A0D7FJ11	UM91_02115	Flagellar rod assembly protein FlgJ	Pseudomonas oryzihabitans		A8GAD1	Spro_0965	UPF0255 protein Spro_0965	Serratia proteamaculans (strain 568)		A0A0D7FBB1	glnQ	Glutamine ABC transporter ATP-binding protein	Pseudomonas oryzihabitans
	Q0S2Y0	secA	Protein translocase subunit SecA	Rhodococcus jostii (strain RHA1)							A0A0L8AEI2	glnD	Bifunctional uridylyltransferase/uridylyl-removing enzyme	[Pseudomonas] geniculata N1
	A0A0D7QPE3	TZ00_08055	NTP pyrophosphohydrolase	Agreia bicolorata							B3PS36	purH	Bifunctional purine biosynthesis protein PurH	Rhizobium etli (strain CIAT 652)
	A0A0D7FLN2	relA	(P)ppGpp synthetase	Pseudomonas oryzihabitans							A0A0H3F8T2	Rahaq_2001	Helicase c2	Rahnella sp. (strain Y9602)
	A7Z6J9	folD	Bifunctional protein FolD	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)							J3CGD3	pnp	Polyribonucleotide nucleotidyltransferase	Phyllobacterium sp. YR531
	A0A0D7QSY9	TZ00_02585	Glycoside hydrolase	Agreia bicolorata							A7Z0N5	tuf	Elongation factor Tu	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)
	A0A0L8AF72	W7K_03635	Replicative DNA helicase	[Pseudomonas] geniculata N1							A0A0D7F7I2	UM91_18625	Deoxyguanosinetriphosphate triphosphohydrolase	Pseudomonas oryzihabitans
	A0A0H3F4D0	Rahaq_0416	S-adenosylhomocysteine deaminase	Rahnella sp. (strain Y9602)							A7Z4N5	clpQ	ATP-dependent protease subunit ClpQ	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)
	A0A0H3FFX2	Rahaq_3339	ABC transporter related protein	Rahnella sp. (strain Y9602)							A0A0F0L3A2	ileS	Isoleucine--tRNA ligase	Microbacterium oxydans
	M7YS07	uvrB	UvrABC system protein B	Methylobacterium mesophilicum SR1.6/6							P10182	ansB	Glutaminase-asparaginase	Pseudomonas sp. (strain ATCC 29598 / 7A)
											Q2K0S7	rbsA3	Ribose import ATP-binding protein RbsA 3	Rhizobium etli (strain CFN 42 / ATCC 51251)

											A0A0H3FC06	aguA	Putative agmatine deiminase	Rahnella sp. (strain Y9602)
											A0A0D7QLF4	TZ00_15130	Ribonuclease G	Agreia bicolorata
											A0A0L8AFB7	W7K_02470	Histone	[Pseudomonas] geniculata N1
											A0A0D7FIQ2	uvrB	UvrABC system protein B	Pseudomonas oryzihabitans
											A0A0D7FAE4	UM91_16170	Peptidase S9	Pseudomonas oryzihabitans
											J3CCP5	ribB	3,4-dihydroxy-2-butanone 4-phosphate synthase	Phyllobacterium sp. YR531
											A0A0L8A5M8	W7K_19605	Peptidase	[Pseudomonas] geniculata N1
											A0A0D7QQP3	TZ00_09975	ABC transporter	Agreia bicolorata
											M7XW44	MmSR116_3014	ABC transporter-like protein	Methylobacterium mesophilicum SR1.6/6
											A7ZAK3	fbp	Fructose-1,6-bisphosphatase class 3	Bacillus methylotrophicus (strain DSM 23117 / BGSC 10A6 / FZB42)
											J2V6J2	PMI41_03484	Phage prohead protease, HK97 family	Phyllobacterium sp. YR531
											A0A0F0LDH6	mcl2	(3S)-malyl-CoA thioesterase	Microbacterium oxydans
											A0A023Y5T3	DX03_14825	Alpha-glucosidase	Stenotrophomonas rhizophila
											A0A0D7F835	UM91_17450	Sugar ABC transporter ATPase	Pseudomonas oryzihabitans
											A4YKD9	atpG	ATP synthase gamma chain	Bradyrhizobium sp. (strain ORS278)
											A8FIB2	atpD	ATP synthase subunit beta	Bacillus pumilus (strain SAFR-032)
											A0JZ88	tuf	Elongation factor Tu	Arthrobacter sp. (strain FB24)
											A0A0D7FBT3	UM91_11560	Protein-glutamate methylesterase	Pseudomonas oryzihabitans
											A0A0H3FBD0	Rahaq_2755	Oligopeptide/dipeptide ABC transporter, ATPase subunit	Rahnella sp. (strain Y9602)
											A0A0F0L4I6	ftsY	Signal recognition particle receptor FtsY	Microbacterium oxydans

											C6CRV0	xynA1	Endo-1,4-beta-xylanase A	Paenibacillus sp. (strain JDR-2)
											A0A0D7QKI9	TZ00_17035	Amidohydrolase	Agreia bicolorata
											A0A0D7FCJ2	UM91_11475	Peptidase M48	Pseudomonas oryzihabitans
											A0A0F0KLC3	recD_1	RecBCD enzyme subunit RecD	Microbacterium oxydans
											A0A0H3FC57	lnt	Apolipoprotein N-acyltransferase	Rahnella sp. (strain Y9602)
											Q2T3B8	hmuV	Hemin import ATP-binding protein HmuV	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)
											D5UMT2	Tpau_1811	ATP-dependent helicase HrpA	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040)
											A0A0H3FFX2	Rahaq_3339	ABC transporter related protein	Rahnella sp. (strain Y9602)