

Dissertation

Discovery of polyesterases using proteomics

submitted by

Paal William WALLACE

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Prof. Dr. Ruth Birner-Grünberger

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Eidesstaatliche Erklärung/Declaration

I hereby declare that this thesis is my own original work and that I have fully acknowledged by name all of those individuals and organizations that have contributed to the research of this thesis. Due acknowledgement has been made in the text to all other material used. Throughout this thesis and in all related publications I follow the guidelines of “Good Scientific Practice” 04.01.2017

Preamble

The goal of this project was to identify new enzymes for the biotechnological industry. Specifically we were aiming to identify novel enzymes that could degrade aromatic polyesters. Two different approaches were used; secretome screening of organisms induced with aromatic and co-aliphatic-aromatic polyesters and an approach where we designed new activity based probes targeted towards polyesterases. Most of the data has already been published with me as an author in these three publications: Sturmberger, Wallace et al (1) Leypold et al (2) and Wallace et al. (3)

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Finally it's done.

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Abbreviations

μ	Micro
4-NPB	4-nitrophenyl butyrate
AAC	Azide-alkyne cycloaddition
ABP	Activity based probe
BA	Benzoic acid
BABuTABuBA	bis(4-(benzoyloxybutyl)terephthalate
BHET	bis(2-hydroxyethyl) terephthalate
BSA	Bovine serum albumin
BuTA	4-(4-hydroxybutoxycarbonyl)benzoic acid
C6	hexyl-(4-nitrophenyl)-(azidopropyl)-phosphonate
cDNA	Complementary deoxyribonucleic acid
CID	Collision induced dissociation
CuAAC	Copper(I) catalysed azide-alkyne cycloaddition
Da	Dalton
DBCO	dibenzocyclooctyne
DCM	Dichloromethane
DDBJ	DNA Data Bank of Japan
DIPEA	N,N-diisopropylethylamine
DMEDA	N,N'-dimethylethylenediamine
DMF	Dimethylformamide
DMSO	Dimethyl sulfoxide
DNA	Deoxyribonucleic acid
EDTA	ethylenediaminetetraacetic acid
Eq	Equivalent

ESI	Electron spray ionisation
FDL	Fluorescence detector
FT	Fourier transformation
g	9.81 m/s ²
h	Hour
HPLC	High performance liquid chromatography
Hz	Hertz
IAA	Iodoacetamide
INSDC	International Nucleotide Sequence Database Collaboration
JGI	Joint Genome Institute
k _{cat}	Catalytic constant
K _I	Inhibitory constant
K _M	Michaelis constant
LC	Liquid chromatography
LPL	Lipoprotein lipase from <i>Pseudomonas sp.</i>
M	Molar
m/z	Mass to charge ratio
MALDI	Matrix-assisted laser desorption/ionisation
MHET	mono-(2-hydroxyethyl) terephthalate
mRNA	Messenger ribonucleic acid
MS	Mass spectrometry
MS/MS	Tandem mass spectrometry
n	Nano
NCBI	National Center for Biotechnology Information
NHS	N-hydroxysuccinimid

NMR	Nuclear magnetic resonance
OD ₆₀₀	Optical density at 600 nm
PBAT	Poly(1,4-butylene adipate-co-terephthalate)
PET	Poly(ethylene terephthalate)
PLA	Poly(lactic acid)
PLLA	Poly(L- lactic acid)
PSM	Peptide spectrum match
RI	Refractive Index
RMSD	Minimization root-mean-square deviation
RT	Room temperature
SDS	Sodium dodecyl sulfate
SPAAC	Strain promoted azide-alkyne cycloaddition
TA	Terephthalic acid
TCA	Trichloroacetic acid
TCEP	tris(2-carboxyethyl)phosphine
T _g	Glass transition temperature
THF	Tetrahydrofuran
TLC	Thin layer chromatography
T _m	Melting temperature
UniProtKB	Uniprot Knowledge Database
UV	Ultraviolet

Zusammenfassung

Für die Identifizierung von neuen Polyesterasen, welche für die Hydrolyse und den Abbau von Polyestern verwendet werden sollen, werden hier zwei unterschiedliche Methoden vorgestellt.

Zunächst wurde eine neue Esterase durch proteomisches Screening des *Pseudomonas pseudoalcaligenes* Sekretom's identifiziert. Diese Esterase wurde PpEst genannt. PpEst hydrolysiert den co-aromatisch-aliphatischen Polyester poly(1,4-butylen adipat-co-terephthalat) (PBAT). Das Vorhandensein von PBAT im Wachstumsmedium induziert PpEst, welche eine vorgesehene Arylesterase Aktivität aufweist. Außerdem zeigte PpEst Polyesterase-Aktivität wenn ganzer oder gemahlener PBAT Film zum Medium hinzugefügt wurde, dies ging aus der Erhöhung der Konzentration vom Abbauprodukt 4-(4-hydroxybutoxycarbonyl)benzoic acid hervor, allerdings wurde auch eine Inhibition der Aktivität durch das 4-(4-hydroxybutoxycarbonyl)benzoic acid beobachtet. Die Modellierung von einem PBAT-ähnlichem Oligomer in das aktive Zentrum von PpEst deutet darauf hin, dass die Bindungstasche groß genug sein könnte um große Polymere unterzubringen. Dies ist die erste Untersuchung die ein PBAT abbauendes Enzym durch ein proteomisches Screening identifiziert und verdeutlicht, dass diese Methode großes Potenzial in der Entdeckung neuer Polymer-abbauender Enzyme haben kann. Weiterhin, diese Ergebnisse zeigen, dass Arylesterasen eine relevante Enzymklasse für die Identifizierung von weiteren Polyesterasen sein kann.

Die zweite Methode, die hier verwendet wurde, beinhaltet den Entwurf, die Synthese und die Verwendung von Aktivitäts-basierten Sonden (ABPs - activity based probes), welche auf Polyesterasen gerichtet sind. Im Idealfall können diese ABPs für die Anreicherung von Polyesterasen genutzt werden, z.B. aus Proben von kultivierten Organismen oder Umweltproben, um dann identifiziert zu werden. Der Entwurf der ABPs war so gestaltet, dass sie dem aromatischen Polyester Poly(Ethylen Terephthalat) ähnlich sind, weiterhin sollten sie in Wasser löslich sein und nur Enzyme binden, welche aromatische Ester Bindungen in polymerischen Strukturen spalten können. Sieben neue ABPs wurden synthetisiert, die Serin-Hydrolasen binden. Anschließend wurden diese neuen ABPs auf ihre Aktivität gegen kommerziell erhältliche Lipasen, Esterasen und Polyesterasen getestet. Im Ergebnis wird hier gezeigt, dass diese ABPs nicht genügend Spezifität aufweisen und auch von Enzymen gebunden werden, welche nur kleine, aliphatische Verbindungen

spalten. Daher sollte in Zukunft versucht werden die Spezifität der ABPs zu erhöhen, um sie für die Identifikation von neuen Polyesterasen nützlich zu machen. Nichtsdestotrotz handelt es sich bei ihnen um neue Serin-Hydrolase-ABPs und ihre Spezifität gegen das humane Proteom könnte eine interessante Untersuchung darstellen, da nur wenige ABPs mit aromatischen Bestandteilen bekannt sind.

Abstract

Two approaches to identify novel polyesterases to be used in the hydrolysis and handling of discarded polyesters were pursued.

First a novel esterase, PpEst, that hydrolyses the co-aromatic-aliphatic polyester poly(1,4-butylene adipate-co-terephthalate) (PBAT) was identified by proteomic screening of the *Pseudomonas pseudoalcaligenes* secretome. PpEst was induced by the presence of PBAT in the growth media and had predicted arylesterase (EC 3.1.1.2) activity. PpEst showed polyesterase activity on both whole and milled PBAT film releasing terephthalic acid and 4-(4-hydroxybutoxycarbonyl)benzoic acid while end product inhibition by 4-(4-hydroxybutoxycarbonyl)benzoic acid was observed. Modelling of a PBAT mimicking oligomer into the PpEst active site indicated that the binding pocket could be big enough to accommodate large polymers. This is the first report of a PBAT degrading enzyme being identified by proteomic screening and shows that this approach can contribute to the discovery of new polymer degrading enzymes. Moreover, these results indicate that arylesterases could be an interesting enzyme class for identifications of polyesterases. (3)

The second approach was to design, synthesise and use activity based probes (ABPs) that were directed towards polyesterases. These ABPs are inhibitors that would covalently bind polyesterases and be used to enrich these enzymes from either cultivated organisms or environmental samples. The ABPs were designed to mimic the structure of the aromatic polyester poly(ethylene terephthalate), be soluble in water and target only enzymes capable of hydrolysing aromatic ester bonds in polymeric structures. 7 new ABPs that were active towards serine hydrolases were synthesised and tested on commercially available esterases and lipases as well as on known polyesterases. The new ABPs were determined to target enzymes capable of degrading aromatic polyesters, but also enzymes that have hydrolytic abilities only towards small aliphatic compounds. The specificity of the ABPs would have to be improved for these to be applied to the identification of novel polyesterases, but they are novel serine hydrolase ABPs and their specificity towards the human proteome would be interesting to determine as few ABPs with aromatic components are reported.

Introduction

Plastic: Its uses and disadvantages

Plastics are synthetic polymers that are cheap, inert, non-conductive and resistant compounds that are very useful for packaging, construction, transportation, agriculture, fishing, aquaculture, medical devices, and electronic components. The abilities that make plastic attractive to these industries are unfortunately also part of what makes them problematic later on as they are hard to degrade and thus accumulate in landfills, wastewater or nature as they get discarded or lost. The fact that use and disposal of plastics has increased significantly over the last decades has led to plastic accumulation becoming a major environmental problem (4). The problem is easily seen as increasing amounts of non-biodegradable garbage fill up more and more land or, in perhaps the most famous case: the pacific garbage patch which was identified as early as 1988 to contain large amounts of plastic micro particles (5, 6). These micro plastics, as well as larger plastic debris, have been seen to negatively influence fish, marine mammalian and bird life, contributing to the declining populations of many species (7).

The traditional ways of disposing of plastic waste have been to either bury it and leave it for future generations, dumping it in the ocean, incinerating it (preferably in power plants), or either reusing or recycling the waste. Reuse and recycling depends on infrastructure to collect the plastics and they both rely on the plastics to be of only one kind. Mixing of different polymers most of the time makes the waste unsuitable for any form of reuse or recycling as it changes the composition of the polymer too much (8). Incineration of the plastics is increasing, but still a lot of plastics are being left in garbage dumps or dumped in nature throughout the world.

As plastics have become indispensable and it would be close to impossible to stop using them several companies designed biodegradable polymers to replace the existing plastics. This effort was done to minimize the environmental problems while still producing a product with similar properties as the original plastics. Biodegradation of plastics is done by either purified enzymes or by complete microorganisms that secrete enzymes capable of cleaving the chemical bonds in polymers and thus release smaller polymer fragments, or ideally the monomers the polymer was composed of. If plastics with a high rate of biodegradation were designed it would allow for hydrolysis of plastics both in controlled

environments like wastewater treatment plants and in more uncontrolled environments like garbage dumps or the ocean. This in turn could help prevent plastic accumulation and the dangers this implies.

The aim of this work has been to set up methods to identify new enzymes to hydrolyse these plastics. However, as there are many different kinds of plastics, with different chemical bonds that need to be hydrolysed, a wide variety of enzymes and organisms are needed to hydrolyse them all. In this work we have chosen to focus on aromatic polyesters as these are extensively used and very slow to hydrolyse. Furthermore few enzymes and organisms have been reported to hydrolyse aromatic polyesters.

Aromatic polyester and their hydrolysis

Poly(ethylene terephthalate) (PET) (Structure in Figure 1) is one of the major aromatic polyesters. Aromatic polyesters are harder to hydrolyse than aliphatic polyesters (9) which is mostly due to the reduced accessibility of the ester bonds that are to be hydrolysed. First of all, the ester bonds are next to aromatic rings and thus the enzyme's active site pocket needs to be large enough to be able to accommodate the aromatic ring. And, as is true for all enzymes that hydrolyse polymers, the pocket also needs to be large and open enough to accommodate a large polymeric chain. A second part of the problem is that these polymers usually are large and insoluble in water, the most common solvent used for enzymes, and thus the enzymes will need to be able to attach to the polymer surface to access the ester bonds. This reduces the turnover as the enzyme needs to spend time to adsorb to the polymeric surface. In addition, the motility of the polymeric chain might be low, so that even when the enzyme is adsorbed to the surface it might have problems accessing the chemical bonds it needs to hydrolyse. This polymer surface is usually hydrophobic and the enzymes, which are usually found in aqueous environments, bind poorly. This problem has partially been addressed by covalently linking hydrophobins, proteins that bind hydrophobic surfaces well, to the enzymes, significantly increasing their polyesterase activity (10, 11).

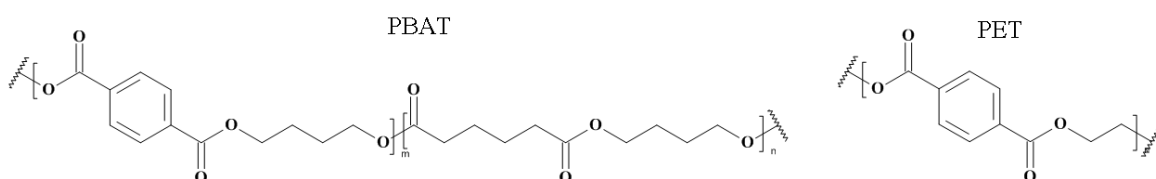


Figure 1: Structure of PBAT and PET. The aromatic-aliphatic co-polyester poly(1,4-butylene adipate-co-terephthalate) (PBAT) and the aromatic polyester poly(ethylene terephthalate) and are examples of commonly used synthetic polyesters that are being targeted for microbial and enzymatic degradation.

In order to increase the biodegradation of aromatic polyesters aromatic-aliphatic co-polyester were designed. One of them is poly(1,4-butylene adipate-co-terephthalate) (PBAT) (Structure in Figure 1) which contains both aliphatic and aromatic ester bonds. This design is a compromise between maintaining the desired properties of the original polyester (PET) and making it more biodegradable. PBAT is a random co-polyester of adipic acid, 1,4-butanediol and dimethyl terephthalate. The introduction of aliphatic ester bonds, which have been seen to be more easily hydrolysed than aromatic ester bonds (9), increases the biodegradability compared to the pure aromatic polyesters like PET, but due to the aromatic components many of the desired properties of PET are maintained. Although polymers are designed to be biodegradable an enzyme or an organism is still needed to hydrolyse them and despite the effort of the biotechnological industry only a limited number of enzymes and organisms with this ability are known.

Enzyme discovery for biotechnology

(The first nine paragraphs of this section are taken from my publication “Synergism of proteomics and mRNA sequencing for enzyme discovery” (1) with minor adaptations).

Enzymes have over the course of the last decade established themselves as useful alternatives to classical organo- and metallo-catalysis (12-15). They are increasingly employed for the manufacturing of a diverse array of chemical products such as pharmaceuticals, agrochemicals, bulk chemicals or biofuels on preparative as well as industrial scale (16). As in our case, this focus also applies to biological degradation of products, such as synthetic polyesters (plastics), biomass, unwanted components in wastewater and xenobiotics (17-23). For all these fields combined about 200 enzymes are industrially used (24), with the majority of those being hydrolytic enzymes and oxidoreductases (25). The importance of enzyme-catalysed synthesis can also be visualized in economic terms. The global enzyme market in 2010 was worth 3.3 billion US dollars and is expected to reach 4.4 billion dollars by the end of 2015 (24, 26).

Due to the need for enzyme-catalysed processes, the biotechnological sector is on a constant quest for new sources of enzymes. The majority of discovered and applied enzymes derive from a limited number of cultivable laboratory organisms, mainly of fungal or bacterial origin (27). Estimates show that less than 1% of all microbes are readily cultivable due to unknown cultivation conditions, slow growth behavior or the absence of

essential nutrients supplied by other organisms (28, 29). This fact presents both a challenge and an opportunity for the discovery of novel enzymes and functions.

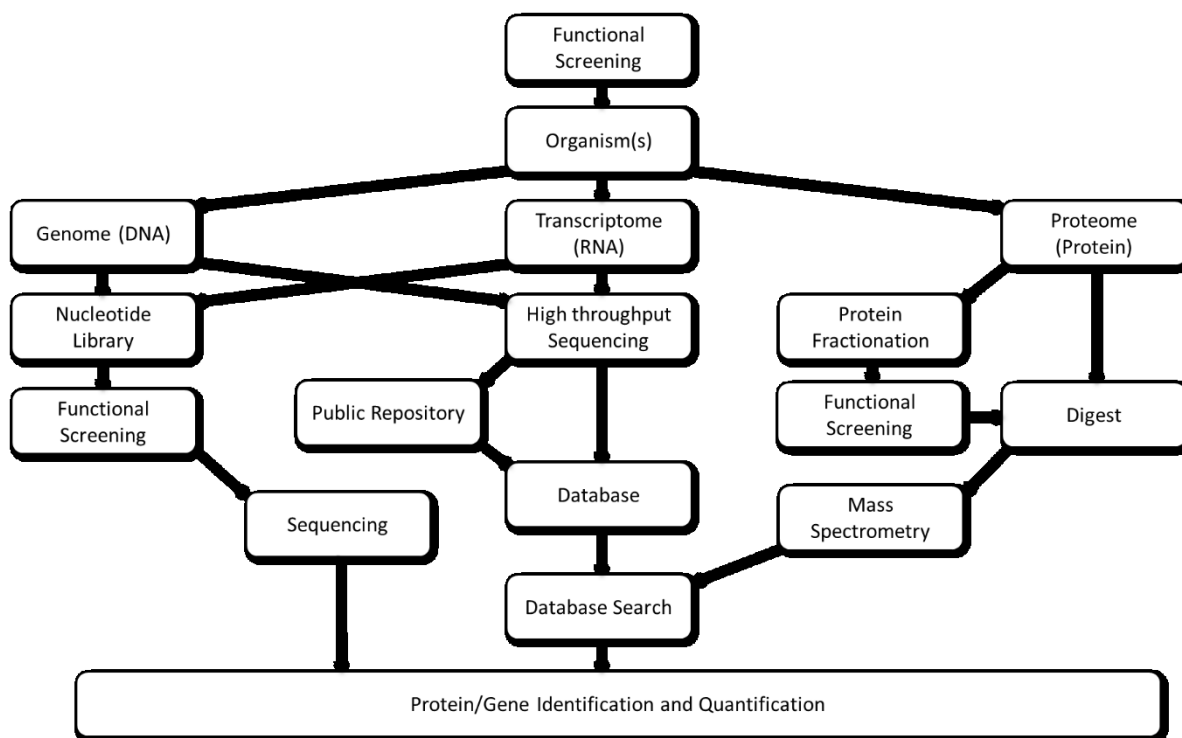


Figure 2: Workflow of -omics experiments for the discovery of novel enzymes. Functional screenings of organisms, tissues or other samples of interest can lead to the identification of desired enzymatic activity. They can be analysed by -omics technologies to identify the gene/protein of interest. Genomic and transcriptomics data can be mined by creating libraries that are cloned, expressed and screened, or it can be integrated into the proteomics workflow, by generating databases, which can improve the number of correct protein identifications from proteomic screenings. (Figure taken from Sturmberger et. al (1))

Most industrially applied enzymes have been found by functional screenings of metagenomic and genomic libraries that have been expressed (30, 31) in host organisms (Figure 2). The advantages of functional screens lie in the immediate identification of enzyme activity whereas methods based solely on sequence (like *in silico* structure guided searches) only give predictions about enzyme function derived from annotations. On the other hand, the complex makeup of eukaryotic genomes, containing many layers of regulatory elements, drastically increases library size, making functional expression and screening of these libraries very challenging. Even though functional screening of bacterial, and to a lesser extent eukaryotic, genomes and metagenomes have been most successful, mere *in silico* methods such as structure guided (32) and sequence similarity-based approaches have also received attention in recent years. They represent a powerful tool by eliminating cost-and labour-intensive wet-laboratory time (32). These in-silico approaches are, however, limited to the discovery of new genes with high similarities to

already deposited sequences, making it impossible to discover truly novel enzymatic functions.

Although genomic screenings have been successful in identifying new enzymes, recent technological advances in the field of transcriptomics and proteomics have made these attractive tools for further discoveries. A major disadvantage of metagenomic or genomic libraries is the high percentage of genomic DNA comprising of non-coding regions (33), which need to be removed in order to produce functional proteins and which unnecessarily increase library size. In addition to problems related to incorrect positioning of the gene relative to its promoters, non-spliceable introns and different codon usage by different organisms, posttranslational modifications are challenging when expressing these genes in hosts other than the original organism (34).

Some of these disadvantages can be circumvented by using either transcriptomic or proteomic approaches. By using transcriptomics instead of genomics the majority of non-coding DNA elements can be removed thereby reducing library size and avoiding non-functional genes arising due to incomplete gene-splicing recognition. Furthermore, the positioning of cDNA transcript sequences in relation to core promoter regions allows for a higher likelihood of successful transcription and translation compared to the majority of sheared genomic DNA fragments. This reduced dramatically the number of enzymes that need to be cloned, expressed and tested, allowing for quicker large-scale screening of e.g. environmental samples. By using transcriptomics rather than genomics, it is also possible to investigate dynamic spatio-temporal gene expression patterns. Therefore, transcriptomics can capture differential gene expression arising due to changes in environmental factors such as the presence of certain chemicals or shifts in cultivation conditions.

These same advantages are also seen when using proteomic approaches. In addition quantitative proteomics has an advantage over transcriptomics as mRNA abundance does not accurately reflect protein abundance (35, 36) and only proteomics can capture posttranslational modifications which can be essential for enzyme activity. Proteomic analysis moreover has the benefit of analysis directly performed on proteins expressed by the original organism. This circumvents problems related to transcription and translation of the gene and the potential subsequent posttranslational modification of the protein in different host organisms.

Importantly proteomics additionally allows the direct elucidation of subcellular localization whereas transcriptomics and genomics rely on predictions to determine these. Proteins can be localized to different sub compartments, such as the cytosol, peroxisomes, mitochondria, endoplasmic reticulum, Golgi vesicles, lipid droplets, lysosomes, and membranes or to the extracellular space by using separation techniques in the sample preparation (37). This information provides valuable cues about the conditions under which the proteins are functional and stable. In turn, it also allows for optimization of the conditions for functional screenings, which can increase the number of hits. This is particularly interesting when the goal is to identify polymer hydrolases as polymers are large and insoluble and thus cannot be taken up by organisms before degradation. In this case the assumption can be made that the enzyme which hydrolyses the polymer must be secreted. Thus the complexity of the sample for the proteomic screening is reduced as it is only necessary to screen the secretome, which can be easily isolated.

Once the secretome is isolated the most commonly used proteomic approach for enzyme discovery is bottom-up shotgun proteomics. In this approach proteins are enzymatically digested into peptides which are analysed either by tandem mass spectrometry after separation on a liquid chromatography system and electrospray ionization (ESI-LC-MS/MS) or by matrix-assisted laser desorption/ionization followed by time of flight mass spectrometry (MALDI-TOF-MS). The identification of proteins is based on the comparison of the measured mass to charge ratios (m/z) of the peptides and their fragments to the respective m/z values for all theoretical peptides and fragments thereof present in the database, which are generated by in silico digestion of the database with the same enzyme. The comparisons are automatically performed by search engines such as MASCOT (38), SEQUEST (39), MaxQuant (40), MS Amanda (41), OMSSA (42), X!Tandem (43), COMET (44), MS-GF+ (45) and MyriMatch (46). All these search engines infer the presence of a protein from identification of at least one peptide that is unique to this protein (within the used database). This however implies that for a protein to be correctly identified it needs to be present in the database. Although the possibility of performing *de-novo* sequencing of proteins exists (47), and could circumvent the problem of a protein not being present in the database, it is time and labour intensive and requires large amounts of highly purified proteins.

The most direct way to construct a high quality database for peptide mapping is by building it from the same sample used for protein identification by either genome or

transcriptome sequencing (Figure 2). For cultivable and, especially, model organisms, genome sequences (and even curated protein databases like SwissProt) are publicly available and present an easy way to obtain a high quality database. Among the most prominent suppliers of sequence databases are the National Center for Biotechnology Information (NCBI), the European Molecular Biology Laboratory (EMBL) and the DNA Data Bank of Japan (DDBJ), which are all integrated through the International Nucleotide Sequence Database Collaboration (INSDC). Other important public database resources are the Uniprot Knowledge database (UniProtKB) (48) or the Joint Genome Institute's genome portal (JGI) (49). However, if public databases lack sequence information of the target organism, which is the case for most complex environmental samples and many cultivable organisms, custom database creation is necessary. If nucleotide sequencing is unfeasible, a reasonable approach is to compile a database consisting of publically available sequences from (more or less) related organisms. This allows acquired MS spectra to be assigned to proteins from closely related organisms, which are assumed to have very similar proteins to the used organism. This has been shown to be less reliable than using databases based on the target organism alone (50) and only allows prediction of protein function but not of the exact sequence, preventing cloning and expression of the protein. Also, by querying against a database not containing the target organism's sequences, potential novel enzymes, that lack any homology with other proteins, cannot be identified.

Once the proteins from the samples have been identified and put into a list they have to be manually curated. To identify proteins that are specific for a condition, e.g. polyester hydrolysing enzymes that are secreted when an organism is cultured together with a polymer, it is necessary to compare it to a control condition, e.g. an organism that is cultured either in standard media with no polyester or to an organism that is cultured with another kind of polymer (e.g. a polyurethane). This differential (and possibly quantitative) approach allows filtering of proteins to remove those that are not specific to the condition (polyester is present in the media), but rather general for the organism (e.g. the organism is grown as a suspension in a flask). This will greatly decrease the number of proteins that need to be considered for cloning, expression and functional testing.

This approach works better the less complex the sample is: thus using an organism's secretome rather than its entire proteome is advantageous. However, an even better way to reduce sample complexity and increase the number of positive hits when looking for active enzymes is to use an enrichment strategy based on activity based probes (ABPs).

Activity based enzyme discovery

Using activity based proteomics is a very direct way to discover enzymes with a desired enzymatic function. This approach relies on enzyme-class specific covalent inhibitors with analytical handles (APBs) that can target enzymatic activities sharing the same reaction mechanism (51, 52). This does however require the development of appropriate ABPs to target the desired enzyme classes. ABPs have been developed for several enzyme classes, among them oxidoreductases and serine hydrolases, enzyme classes that are of high interest to the biotechnological industry. As the enzymes that are known to degrade polyesters are mostly serine hydrolases we will here focus on this enzyme class.

An ABP targeted towards serine hydrolases has a reactive group that is a phosphonate that is designed to mimic the tetrahedral transition state of an ester attacked by the active site serine. However, after the enzyme has cleaved one of the ester bonds of the ABP it remains covalently bound to the phosphonate instead of releasing the substrate as it normally would with a carboxylic ester. The ABP also contains an analytical handle. Traditionally this was either a fluorophore or e.g. a biotin to visualize the enzyme or to purify or enrich it. However, many new ABPs instead use either an azide or an alkyne as the analytical handle. These chemical groups enable, by employing azide-alkyne cycloaddition (AAC) (commonly referred to as click-chemistry), attachment of almost any functionality to the ABP (Figure 3). The advantage of using click chemistry is that it allows the ABPs to be much smaller and thus to be able to e.g. permeate cell walls and access enzymes in their native environment, or to enter enzyme pockets that would not be accessible if e.g. a bulky fluorophore was directly attached to the ABP at the time of binding. The use of azides or alkynes as analytical handles also makes it easier to perform multiplexing of samples as the different tags can be synthesized independently of the ABP and also will not interfere with the reaction between the enzyme and the ABP.

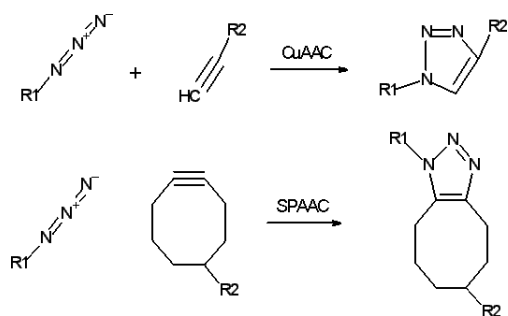


Figure 3: Copper and strain promoted azide-alkyne cycloaddition. Schemes for both the copper(I) catalysed (CuAAC) and the strain promoted (SPAAC) azide-alkyne cycloaddition used in click chemistry. Shown is the simplest example of several different strained alkynes that have been developed.

Click chemistry initially required copper as a catalyst to perform the coupling (CuAAC) (Figure 3). While this was an efficient coupling copper is toxic to living beings and it was thus not suitable for all experiments where live and functional systems were required. A biorthogonal solution was needed and this was remedied by the introduction of strain promoted azide-alkyne cycloaddition (SPAAC) where a copper catalyst is unnecessary. Instead strain promoted alkynes, in the form of cyclooctynes, were used to perform the AAC (Figure 3). A variety of these derivatives have been designed and synthesized with increasing activity and water solubility compared to the original compound (Figure 4).

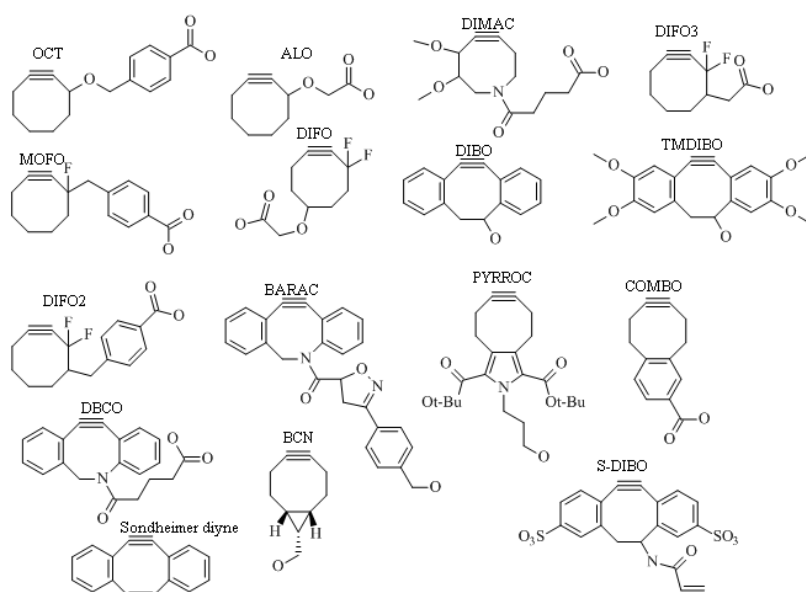


Figure 4: Structures of functionalised cyclooctynes used for SPAAC. (adapted from Dommerholt et al.(53))

Even though serine hydrolases share a reaction mechanism and thus can be targeted by phosphonates, not all ABPs with a reactive group targeting serine hydrolases can react with all serine hydrolases. This is due to specific substrate recognition and needs to be considered in the design of the ABP's binding group. The binding group is the part of the ABP that is designed to mimic the desired substrate of the enzyme. It is possible to develop ABPs that target e.g. only esterases or only lipases or to design ABPs that can target both (Figure 5).

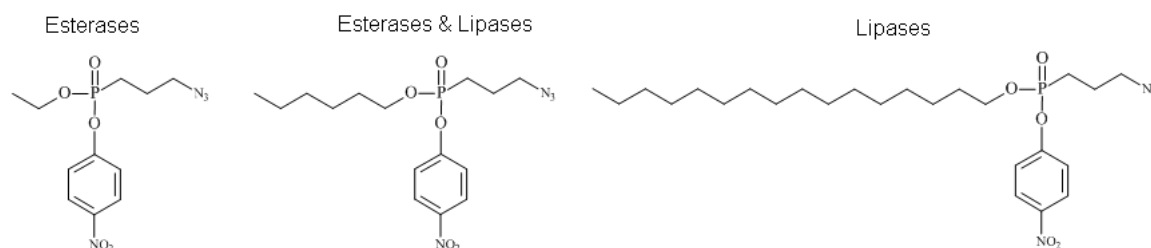


Figure 5: Structures of activity based probes designed to target subclasses of serine hydrolases. The shown compounds are designed to target esterases, lipases or both of them by changing the structure of the binding group of the ABP.

Therefore the design of the binding group is very important if a very specific function is desired. In our case the aim is to identify new enzymes that can degrade the ester bonds next to aromatic rings in polyesters. This means that the binding group should mimic the structure of an aromatic polyester like PET. As PET is a large, aromatic and hydrophilic substance with only aromatic ester bonds it would be important to design the reactive group in a way that it is next to an aromatic ring and to make sure that there are no aliphatic ester bonds for the enzyme to cleave instead of it binding to the reactive group. By tuning the structure and by using e.g. bioisosteres like ethers instead of esters the ABP can be tuned to resemble the desired substrate as closely as possible. A major challenge however when it comes to designing an ABP that mimics polyesters is that polyesters are insoluble in water while the ABPs need to be soluble to readily react with the desired enzymes. Therefore there might need to be a compromise between similarity to the desired substrate and some of the required properties of the ABP.

Identifying a polyesterase that degrades PBAT

(This first six paragraphs of this section are taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with major adaptations).

Microbial biodegradation of PBAT (54-57) and other aromatic-aliphatic co-polyesters like PET/poly(lactic acid) (PET/PLA) (58, 59) has been shown with organisms including species of *Pseudomonas* (58, 60). However, few of the enzymes with the ability to hydrolyse these polyesters have been identified or characterised. Knowing which enzymes are responsible for the degradation would allow for improvement of these enzymes' abilities through engineering and mutations and enable production of genetically modified microorganisms that could be used in large scale degradation of plastic waste. Few enzymes have been identified and employed on an industrial level as identification and production of them is hard and expensive, but the investigation is ongoing.

One of the first biodegradable synthetic aromatic-aliphatic co-polyesters to be introduced to the market on a large scale was PBAT (sold as Ecoflex® by BASF). It is mainly used for packaging, as a breathable film in the health sector or for mulching in agriculture. It is compostable and microbial degradation has been reported by several research groups (54-57). In recent years the focus has shifted into identifying enzymes and organisms that can degrade the polyester reliably. The few enzymes that have been identified originate from typical representatives of compost microbial populations or anaerobic environments. The known PBAT polyesterases are: the serine hydrolase TfH from *Thermobifida fusca* (21, 61), the lipase PfL1 from *Pelosinus fermentans* (62), the esterases Cbotu_EstA and Cbotu_EstB from *Clostridium botulinum* (63) and the cutinases HiC from *Humicola insolens*, The_Cut1 from *Thermobifida cellulosilytica* (9) and Est1 and Est119 from *Thermobifida alba* (64, 65).

There is considerably less known about enzymes from typical aquatic microorganisms that could hydrolyse polyesters. Aquatic microorganisms could be a promising source of polyesterases as more and more polyesters end up in aquatic environments like the ocean or wastewater (66) due to e.g. use in skin care products (67) or lost fishing equipment that is broken down to micro-particles (68). In addition wastewater treatment, which can be done in a closed environment, would be a likely candidate for initial use of enzymatic and microbial degradation of polyesters on a large scale.

All PBAT degrading enzymes previously investigated were identified either through functional screenings followed by chromatographic purification of the enzyme with subsequent peptide analysis for protein identification, or through in-silico screening of publically available databases followed by cloning and expression in a host organism. However, the potential of proteomic screenings of the secretome of microorganisms to identify new PBAT degrading enzymes has not yet been exploited.

Hence, *Pseudomonas pseudoalcaligenes*, as a typical aquatic organism, whose relatives have been reported to be involved in hydrolysis of other aromatic-aliphatic co-polymers (58) and their building blocks (60), was chosen for a proteomic based screening of the secretome to identify new polyesterases.

There are several reasons why this approach would be able to contribute to the discovery of new polyester hydrolysers. Polyesters like PBAT are large water-insoluble polymers and thus cannot be directly taken up by microorganisms. This means that for the polymer to be

hydrolysed and potentially utilised, the polymer has to be hydrolysed outside the organism, which in turn leads to the presumption that the degradation is performed by a secreted enzyme. By exploiting this idea we could reduce the complexity of the sample to be analysed by restricting the search to a microorganism's secretome rather than its entire proteome.(3) It has also previously been reported that polyesterases can be induced by the presence of polymers (69-71) and thus a comparison of the secretome of non-stimulated organisms with the secretome of organism grown with different natural and synthetic polymers might reveal enzymes with a role in polyester hydrolysis.

In the first part of this work we demonstrate how a proteomic screening of the secretome of *Pseudomonas pseudoalcaligenes* led to the identification of an esterase that is induced by the presence of PBAT and that, when recombinantly expressed, can hydrolyse the co-aromatic-aliphatic polyester PBAT.

In the second part we describe the new aromatic ABPs that were designed to target polyesterases that can degrade aromatic polyesters and the initial findings on their specificity.

Materials and Methods

Chemicals and materials

(This section is taken from my publication “PpEst is a novel PBAT degrading polyestherase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

The PBAT film and aromatic polyester mimicking oligomer bis(4-(benzoyloxybutyl)terephthalate (BABuTABuBA) were synthesised as previously described (72) and kindly provided by BASF SE (Germany). BABuTABuBA was designed to contain bonds between aromatic and aliphatic moieties, the hydrolysis of which is known to be the limiting step in hydrolysis of polyesters (9). The properties of the PBAT film were as follow: thickness of 50 μm , glass transition temperature (T_g) of $-34\text{ }^\circ\text{C}$, melting temperature of $125.3\text{ }^\circ\text{C}$, molecular weight of 65,000 g/mol, M_w/M_n of 3.4 and a crystallinity of $\sim 10\%$ (9). Poly(L-lactic acid) PLLA (PLA) film, thickness 0.05 mm (LS373275 M K S) (crystallinity of 60-70 %), and amorphous poly(ethylene terephthalate) (PET) film, thickness 0.25 mm (LS406760) were purchased from Goodfellow (UK). *Pseudomonas pseudoalcaligenes subsp. pseudoalcaligenes* (DSM 50188) was obtained from Leibniz-Institute DSMZ-German Collection of Microorganisms and Cell Cultures in freeze dried form. All solvents used were of HPLC grade. Unless stated otherwise, chemicals were purchased through Sigma-Aldrich.

Induction of *P. pseudoalcaligenes* and collection of supernatant

(This section is taken from my publication “PpEst is a novel PBAT degrading polyestherase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

P. pseudoalcaligenes was cultured in suspension in media consisting of 5 g/L soy bean peptone and 3 g/L meat extract adjusted to pH 7.0. The culture was kept at $28\text{ }^\circ\text{C}$ with orbital shaking at 100 rpm in the dark. For supplementation of media with polymer 0.5 g cellulose (in the form of toothpicks), 1 g milled PBAT or 100 mg of the aromatic polyester mimicking oligomer BABuTABuBA was added to 50 mL of media. Organisms were cultured for either nine hours or three days before the supernatant was collected. 50 mL cultures were transferred to 50 mL conical centrifugation tubes and centrifuged at $4\text{ }^\circ\text{C}$ and $4000 \times g$ for 30 min in a swing-bucket rotor. Supernatant was collected and re-centrifuged as above to yield the final supernatant for analysis.

Sample preparation for proteomic analysis

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

Two millilitres of supernatant from each culture condition was centrifuged for 1 h at 10,000 x g and 4 °C. The supernatant was then transferred to an Amicon Ultra 10 kDa cut-off spin filter (Merck, Germany) and spun at 4,000 x g for 1 h at 4 °C to remove soy bean and bovine peptides originating from the media. Then 4 mL 8 M urea was added to the retentate and spun at 4,000 x g for 30 min at 4 °C to wash the protein suspension. Next, 4 mL 100 mM ammonium bicarbonate was added to the retentate and spun at 4,000 x g for 1 h at 4 °C. Finally the retentate was transferred to a 1.5 mL Eppendorf tube and the proteins were precipitated with 6 volumes of acetone at -20 °C overnight. Proteins were pelleted at 10,000 x g and 4°C, solvent was removed and the pellet was washed once with 100 µL cold acetone. Proteins were reduced and alkylated by dissolving the pellet in 20 µL buffer containing 10 mM tris(2-carboxyethyl)phosphine (TCEP), 20 mM iodoacetamide (IAA), 4 M urea, 2 % sodium dodecyl sulfate (SDS), 0.25 M NaCl and incubated for 1 h at 37 °C at 550 rpm in the dark. 5 µL NuPAGE LDS Sample buffer (4X) and 2 µL NuPAGE Sample Reducing Agent (10X) were added to the sample prior to incubation for 5 min at 95 °C. Sample was loaded on a 20 well NuPAGE 4-12% Bis Tris Midi gel (Invitrogen, USA) and run at a constant 9 W/gel to remove small contaminants. Gel was fixed with 10 % ethanol, 7 % acetic acid in water and stained with Coomassie Brilliant Blue G. The entire lanes were cut out and cut into seven pieces which were destained using repeated incubations in 25 % acetonitrile at 37 °C and 550 rpm. Proteins were digested in-gel by 1.5 µg methylated trypsin (Modified porcine trypsin, Promega, USA) in 120 µL 50 mM ammonium bicarbonate, 10 mM CaCl₂ overnight at 37 °C, 550 rpm. Peptides were extracted from the gel pieces and the extract was dried in a vacuum centrifuge. Dried peptides were redissolved in 20 µL 0.1 % formic acid just before analysis by HPLC-MS/MS.

HPLC-MS/MS analysis

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

Ten microlitres of the sample was injected and separated by nano-HPLC on an Ultimate 3000 system (Dionex) after enrichment on a PepMap100 C18, 5 µm, 300 µm x 5 mm pre-

column (Thermo Scientific, USA) on an Acclaim PepMap RSLC-C18, 2 μ m, 75 μ m x 50 cm nanoviper nano-column (Thermo Scientific, USA) using the following gradient: solvent A: water, 0.1 % formic acid; solvent B: acetonitrile, 0.1 % formic acid; 0-5 min 5 % B; 5-90 min 5-30 % B, 90-90.1 min 30-95 % B, 90.1-105 min 95 % B, 105-105.1 min 95-5 % B, 105.1-120 min re-equilibration at 5 % B. Flow rate was 250 nL/min. The separated peptides were directly analysed in an Orbitrap Velos Pro (Thermo Scientific, USA) in positive ion mode by alternating full scan MS (m/z 300–2000, 60,000 resolution at m/z 200) and MS/MS by CID in the iontrap of the 20 most intense peaks with dynamic exclusion enabled.

Data analysis

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

The resulting spectra were analysed by searching a custom database. The database contained all protein entries for *Pseudomonas* in the NCBI database (1805231 entries downloaded on Jan. 25th, 2015), a publically available list of common contaminants (<http://www.thegpm.org/crap/>) and a custom protein entry (GI: 012345) for dimethylated trypsin where all lysines were replaced with the custom amino acid J to avoid false positives resulting from autolysis of modified trypsin (73). Searches were performed in Mascot 2.2 (Matrix Science, London, UK). The spectra from the seven gel pieces originating from a single supernatant were analysed together resulting in one protein list per supernatant. Detailed settings: Enzyme: trypsin (with the added specificity of J equal to K) (73); max. missed cleavage sites: 2; N-terminus: hydrogen; C-terminus: free acid; carbamidomethylation on cysteine as fixed modification; oxidized methionine, acetylation of N-terminus, demonomethylation of J and dedimethylation of J as variable modifications (73); maximum precursor charge 3; precursor mass tolerance $\pm$ 10 ppm; product mass tolerance $\pm$ 0.7 Da; acceptance parameters were 1 or more identified distinct peptides after automatic validation; percolator active (decoy search, with a false discovery rate set below 5 %). The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium (<http://proteomecentral.proteomexchange.org>) via the PRIDE partner repository (74) with the dataset identifier PXD004014.

General Recombinant DNA Techniques

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

All DNA manipulations described in this work were performed by standard methods (75). Restriction of DNA was performed using endonucleases *Nde*I and *Hind*III (New England Biolabs, USA). Dephosphorylation with alkaline phosphatase (Roche, Germany) and ligation with T4 DNA-ligase (Fermentas, Germany) were done in accordance to the manufacturer’s instructions. Plasmid DNA was isolated by Wizard® Plus SV Minipreps DNA Purification Systems (Promega, Germany) and plasmids and DNA fragments were purified with Promega DNA purification kits. Vector pET26b(+) (Novagen, Merck KGaA, Germany) was chosen for expression of the constructed fusion proteins carrying a C-terminal 6xHis-tag in *E.coli* BL21-Gold(DE3) (Stratagene, USA).

Expression and purification of PpEst

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

The gene coding for an esterase from *Pseudomonas pseudoalcaligenes* (Genbank accession number WP_003460012) was codon optimized for expression in *E. coli* and commercially synthesized without signal peptide (GeneArt®, Life Technologies, USA). The gene was cloned over the restriction sites *Nde*I and *Hind*III into pET26b(+) and transformed into *E. coli* BL21-Gold(DE3). Freshly transformed *E. coli* BL21-Gold(DE3) cells were used to inoculate 50 mL luria broth (LB) medium supplemented with 40 µg/mL kanamycin that was cultivated at 37 °C and 130 rpm overnight. This culture was used to inoculate 400 mL of fresh medium to an OD₆₀₀ = 0.1 and cultivated at 37 °C and 150 rpm until OD₆₀₀ = 0.6. After cooling down to 25 °C the expression was induced by addition of isopropyl-β-D-thiogalactopyranoside (IPTG) to a final concentration of 0.05 mM. After expression for 20 h at 25 °C and 140 rpm the cells were harvested by centrifugation (20 min, 10 °C, 3,200 x g). Pellets from 400 mL culture were suspended in 30 mL NiNTA Lysis Buffer (20 mM NaH₂PO₄, 500 mM NaCl, 10 mM imidazole, pH 7.4) and sonicated with three-times 30 s pulses under ice cooling (Vibra Cell, Sonics Materials, Meryin/Satigny, Swiss Confederation). Lysates were cleared by centrifugation (60 min, 4 °C, 3,200 x g). PpEst was purified by HisTrap FF (GE Healthcare, Germany). Buffer was exchanged for 100 mM Tris HCl pH 7.0 and purified enzyme stored at –70 °C.

DNA Sequencing, Alignments and Deposition of Sequence Data

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

DNA was sequenced as custom service by Agowa (Germany). DNA analysis was performed with Vector NTI Suite 10 (Invitrogen, USA). BLAST search was performed using the ExPASy (76) proteomics server of the Swiss Institute of Bioinformatics, and sequences of related proteins were aligned using the Clustal W program (Swiss EMBnet node server). The nucleotide sequence of PpEst has been deposited in the GenBank database under accession number KX002004.1.

Hydrolytic activity of non-stimulated and stimulated supernatants

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

Two hundred microliters of supernatant was added to 800 μ L of 0.1 mM 4-nitrophenyl-butyrate (4-NPB) solution pH 8.0 in a 1 mL half-micro cuvette and vortexed briefly before 4-NPB hydrolysis was measured continuously for 10 min by UV-detection of free 4-nitrophenolate at 405 nm on an Agilent Cary 100 UV-Vis Spectrophotometer (USA). Autohydrolysis of 4-NPB was determined by adding 0.2 ml freshly prepared medium instead of supernatant.

Preferred carbon chain length of 4-nitrophenyl carboxylic acid esters

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

One millilitre solutions of 0.1 mM 4-nitrophenyl carboxylic acid esters (with carbon chain lengths from 2 to 14) in 150 mM NaCl, 0.01 % Triton X-100 and 20 mM Tris-HCl pH 8.0 were incubated with 1 μ g PpEst (in 3.75 μ L 100 mM Tris-HCl pH 7.0) at 30 °C for 30 min while the production of 4-nitrophenolate was continuously measured at 405 nm on a Spectramax Omega instrument (BMG-LABTECH, Germany). Autohydrolysis of 4-NPB was determined by addition of 3.75 μ L 100 mM Tris-HCl pH 7.0 without enzyme.

Temperature optimum of enzymatic activity on 4-NPB

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

Assay buffer of 150 mM NaCl, 0.01 % Triton X-100 and 20 mM Tris-HCl pH 8.0 was heated to temperatures between 25 °C and 90 °C in 5-degree increments. 1 µg of PpEst in 7.5 µL 100 mM Tris-HCl was incubated with 1 mL of the buffer solution for 1 min before 4-NPB was added to a final concentration of 0.1 mM. Production of 4-nitrophenolate was measured continuously at 405 nm for 3 min on a Spectramax Plus instrument (BMG-LABTECH, Germany). Autohydrolysis of 4-NPB was determined by addition of 7.5 µL 100 mM Tris-HCl (pH 7.0) without enzyme.

pH optimum of enzymatic activity

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

PpEst was pre-incubated for 1 h in buffers ranging from pH 4 to pH 11 (pH 4-6: 0.1 M citric acid buffer, pH 7-9: 0.1 M Tris-HCl, pH 10-11: 0.1 M borate buffer). 4-NPB was added to the assay buffer (150 mM NaCl, 0.01 % Triton X-100, 20 mM buffer with appropriate pH) to a final concentration of 0.1 mM and the reaction initiated by adding 1 µg enzyme in 7.5 µL to wells in a 96 well plate. Production of 4-nitrophenolate and 4-nitrophenol was measured at 348 nm (their isosbestic point) (77) continuously for 10 min at 30 °C on a Spectramax Plus instrument (BMG-LABTECH, Germany). Autohydrolysis of 4-NPB was determined by addition of 7.5 µL of the corresponding buffer without enzyme.

Influence of Ca²⁺ on PpEst activity and stability

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

First a 65 µM PpEst solution in 100 mM Tris-HCl pH 7.0 was incubated with 10 mM ethylenediaminetetraacetic acid (EDTA) at 4° C for 72 h to remove all bound Ca²⁺ and an aliquot was kept for subsequent activity measurement. Then EDTA was removed from the protein solution by a succession of dilutions in 100 mM Tris-HCl pH 7.0 and ultracentrifugation through an Amicon Ultra 3 kDa cut-off spin filter (Merck, Germany) until EDTA concentration was calculated to be below 10 pM. Subsequently Ca²⁺ was added to aliquots of the protein solution in ratios of mol Ca²⁺: mol PpEst ranging from 0.05 to 20,000 and the enzyme solutions were incubated for 3 h at 25°C prior to activity measurement.

For activity determination 0.5 µg of PpEst (after calcium removal and after readdition of different amounts of calcium) was added to 1 ml 0.1 mM 4-NPB assay buffer (150 mM NaCl, 0.01 % Triton X-100, 20 mM Tris-HCl pH 8.0) and production of 4-nitrophenolate was measured continuously at 405 nm for 3 min on a Spectramax Plus (BMG-LABTECH, Germany). Autohydrolysis of 4-NPB was determined by addition of 3.75 µL 100 mM Tris-HCl pH 7.0 without enzyme. To measure the effect of calcium on protein stability, 50 nM, 10 mM or 200 mM Ca^{2+} was added to solutions of 50 nM PpEst in 100 mM Tris-HCl pH 7.0 after all Ca^{2+} had been removed. The solutions were incubated at 50° C, 65° C or 80° C for 72 h. After 0 h, 24 h, 48 h and 72 h remaining 4-NPB hydrolytic activity was measured as described above.

K_m and K_{cat} determination

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

In a 96 well plate 0.1 µg of PpEst was incubated in 100 µL assay buffer (20 mM Tris-HCl pH 8.0, 150 mM NaCl, 0.1 % Triton- X100) at 25 °C with 4-NPB concentrations ranging from 19 µM to 80 mM and the appearance of 4-nitrophenolate was measured continuously at 405 nm for 3 min on a Spectramax Plus photometer (BMG-LABTECH, Germany). K_m and k_{cat} were determined from functions derived using the Sigmaplot 13.0 (Systat Software Inc, Germany) regression wizard equation ‘Exponential Rise to maximum; Single, 2 Parameter’.

Hydrolysis of polyesters

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

Milled PBAT with particle sizes between 100 - 300 µm and PBAT, PLA and PET films with the size of 10 mm x 5 mm were used for the hydrolysis experiments of polymers. Prior to incubation the films were washed with 5 g/L Triton X-100, followed by 100 mM sodium carbonate and subsequently H_2O . Each washing step was performed at 50 °C in a rotary shaker at 100 rpm for 30 min. To 5 µM PpEst in 1 mL 100 mM potassium phosphate buffer pH 7.0 either 10 mg BABuTABuBA, 10 mg milled PBAT or 100 mm² PBAT, PLA or PET film was added. Polymers were incubated in 2 mL Eppendorf tubes at 50 °C, 65° C or 80° C on a rotary shaker at 100 rpm for 72 h. Samples were taken after 0 h,

24 h and 72 h. Experiments were run in triplicates. In parallel, BABuTABuBA, milled PBAT and PBAT, PLA and PET films were incubated in buffer without enzyme to reveal any autohydrolysis.

Before the analysis of the release products of BABuTABuBA, PBAT and PET the enzyme was precipitated by addition of ice-cold methanol (1:1 volume:volume) and the samples were acidified to pH 3.0 with HCl. The samples were centrifuged for 15 min at 0 °C and 14,000 rpm (Hermle Z300K, MIDSCI, Missouri, US) and the supernatant collected for further analysis.

Before the analysis of the release products of PLA the enzyme was precipitated by a modified Carrez precipitation (78, 79). Samples were acidified to pH 4.0 with HCl, 20 µl of Carrez reagent I was added and samples were mixed and incubated for 1 min at 25 °C. Then 20 µl Carrez reagent II was added; the samples were mixed and incubated for 5 min at 25 °C prior to centrifugation for 30 min at 25 °C and 14,000 rpm (Hermle Z300K, MIDSCI, Missouri, US). Finally, supernatants were filtered through 0.45 µm nylon filters.

Quantitation of hydrolysis products

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

The samples from PBAT and BABuTABuBA hydrolysis were analysed by HPLC-UV on a system consisting of a Dionex UltiMate 181 3000 pump (Dionex Cooperation, USA), a Dionex ASI-100 automated sample injector, a Dionex UltiMate 3000 column compartment and a Dionex UVD 340 U photodiode array detector. The hydrolysis products were separated by a reversed phase column (XTerra® RP18, 3.5 µm, 3.0 mm x 150 mm) with the recommended pre-column (Waters Corporation, USA) using a non-linear gradient: solvent A: H₂O, solvent B: acetonitrile, solvent C: 0.1 % formic acid; solvent C is at 20 % constantly; 0-4.5 min 8 % B, 4.5-5 min 8-20 % B, 5-13 min 20-30 % B, 13-17 min 30-50 % B, 17-17.5 min 50-80 % B, 17.5-18 min 80 % B, 18-19 min 80-8 % B, 19-25 min 8 % B. All eluents were of HPLC grade. The injection volume was 5 µL and the flow rate 0.5 mL/min. The column compartment was kept at 25 °C. The expected release products terephthalic acid (TA), 4-(4-hydroxybutoxycarbonyl)benzoic acid (BuTA) and benzoic acid (BA) were detected via UV spectroscopy at 241 and 228 nm (structures in Figure 6). The release products were qualified and quantified by external calibration curves. The reported values for release of products have had the values from the control samples with

no enzyme subtracted. The values seen in the controls with no enzyme also showed that the acidification by HCl did not lead to hydrolysis of the polymers.

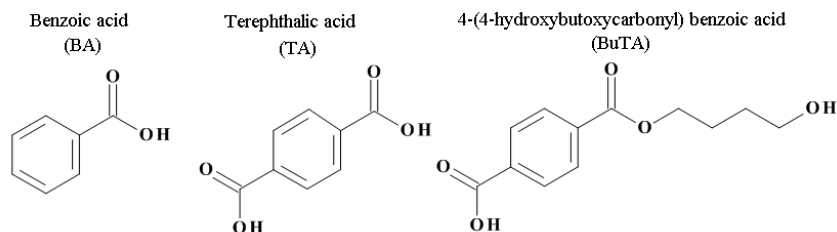


Figure 6: Structure of the PBAT and BABuTABuBA degradation products benzoic acid (BA), terephthalic acid (TA) and 4-(4-hydroxybutoxycarbonyl)benzoic acid (BuTA) that were detected by HPLC-UV.

PLA samples were analysed as described by Pellis et al. (80). LC-Refractive Index (RI) analysis was carried out on a LC system consisting of an HP/Agilent 1100 Series G1310A isocratic pump, an HP/Agilent 1100 Series ALS G1313A automated sample injector, and a HP/Agilent 1100 Series G1316A thermostatic column compartment and refractive index (RI) detector RID G1382A (Agilent Technologies, Santa Clara, USA). Separation of released hydrolysis products were performed over an ICsep ION-300 column (7.8 mm×300 mm, 7 µm) (Transgenomic, Inc., Omaha, USA). 40 µl of the sample was injected and eluted by 0.01 N H₂SO₄ at a flow rate of 0.325 ml/min at 45 °C. The expected release product lactic acid was detected via RI and qualified and quantified by external calibration curve.

PET samples were analysed by a modified version of the method described by Herrero Acero et al. (81). HPLC-UV analysis was carried out on a HPLC system consisting of Dionex UltiMate 181 3000 Pump (Dionex Cooperation, USA), a Dionex ASI-100 automated sample injector, a Dionex UltiMate 3000 column compartment and a Dionex UVD 340U photodiode array detector. Separation of released hydrolysis products was performed over a reversed phase column XTerra® RP18 (3.0×150 mm, 3.5 µm) (Waters Corporation, USA). 10 µl of the sample was injected and eluted by an isocratic method consisting of acetonitrile: 0.01 % formic acid: water (1:1:3 (per volume)) at a flow rate of 0.4 ml/min at 25 °C. The expected release products terephthalic acid (TA), mono-(2-hydroxyethyl) terephthalate (MHET) and bis(2-hydroxyethyl) terephthalate (BHET) were detected by UV spectroscopy. Release molecules were qualified and quantified by external calibration curves, where the calibration curve for TA was used to quantify the amount of released MHET as previously described (82).

Inhibition of PpEst by BuTA

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

0.1 µg PpEst was incubated in 100 µL 100 µM 4-NPB in assay buffer (20 mM Tris-HCl pH 8.0, 150 mM NaCl, 0.1 % Triton-X 100) in a 96 well plate together with BuTA in concentrations ranging from 0 to 1 mM. Activity was determined by the appearance of 4-nitrophenolate at 405 nm on a Spectramax Plus instrument (BMG-LABTECH, Germany) and is given as activity relative to rate when no BuTA was present. K_I was determined from the function derived using the Sigmaplot 13.0 (Systat Software Inc, Germany) regression wizard equation ‘Ligand binding; one site competition’.

Sequence comparisons

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

The amino acid sequence of PpEst was aligned to the sequences of the known PBAT degrading enzymes Tfh, Cbotu_EstA, Cbotu_EstB, HiC and Thc_Cut1 individually using blastp with the BLOSUM62 algorithm with default settings. Protein similarity is given as percentages.

Modelling of PpEst

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

The model of PpEst was generated using the Phyre2 server (83) applying the crystal structure of TesA from *Pseudomonas aeruginosa* (expressed in *E.coli*) (PDB-Code: 4jgg, resolution 1.9 Å) as a template as it has 70 % sequence similarity to PpEst. The tetrahedral intermediate was built using the Phyre2 model and BABuTABuBA as substrate. For the energy minimization YASARA structure (15.10.18) was used (84). Methyl acetate modelled as oxyanion was placed into the active site to form the proposed tetrahedral intermediate by pointing the deprotonated oxygen to the oxyanion hole (main chain of Gly47 and ND2 of Asn76). The active site Ser in the model had to be rotated (The oxygen was positioned at the same location as in the template which was used for modelling). The histidine (His160) was treated as protonated (HIP). Hydrogens were added and the covalently bound intermediate was treated as charged (-1). The model was cleaned and

hydrogen bonding networks were optimized. The AMBER03 force field (85) was used to apply partial charges. This complex was energy minimized using YASARA structure applying the standard energy minimization protocol. The all-atom minimization root-mean-square deviation (RMSD) of the complex after energy minimization was 0.761 Å compared to the Phyre2 model. Additional functional groups of the substrate were then added successively followed by energy minimization steps until the final complex was created.

General analytics for organic synthesis

NMR acquisition

¹H-, ¹³C-NMR spectra were recorded on a Bruker (USA) AVANCE III 300 spectrometer (¹H:300.36 MHz; ¹³C: 75.53 MHz) and 19F (282.47 MHz) and ³¹P (121.58 MHz) NMR spectra were recorded on a Varian (USA) INOVA 300 spectrometer and referenced versus tetramethylsilane (TMS) using the internal 2H-lock signal of the solvent. Chemical shifts were referenced to the residual proton and carbon signal of the deuterated solvent, respectively (DMSO-d6: δ = 2.50 ppm (¹H), 39.52 ppm (¹³C); CDCl3: δ = 7.26 ppm (¹H), 77.16 ppm (¹³C); Pyridine: δ = 8.74 ppm (¹H)). Signal multiplicities are abbreviated as s (singlet), d (doublet), t (triplet), q (quadruplet) p (pentet) and m (multiplet). Deuterated solvents for nuclear resonance spectroscopy were purchased from Euriso-top® (Germany).

HRMS acquisition

Accurate masses were determined using high resolution mass spectrometry (HRMS) by FT-MS on an LTQ FT Ultra instrument (Thermo Scientific (USA)) equipped with an ESI source. Samples were dissolved in 0.01 % FA in dry acetonitrile and directly injected using a syringe pump with a flow of 3 µl/min. Capillary temperature was set to 270 °C and the sheath gas flow to 5. Five spectra per sample were acquired in positive FT-mode with a resolution setting of 1,000,000. Data were analysed with Xcalibur 2.1.0 (Thermo Scientific (USA)).

Synthesis of 3PET

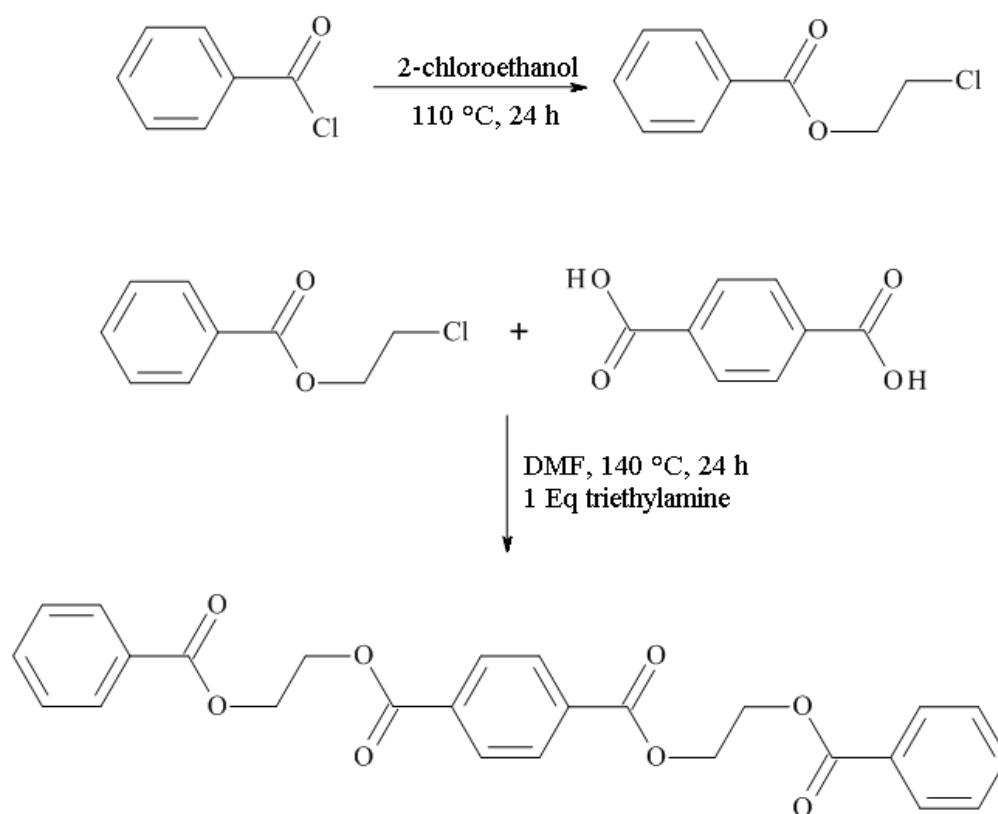


Figure 7: Synthesis scheme of for the PET mimicking oligomer 3PET.

Synthesis bis(2-benzoyloxyethyl) benzene-1,4-dicarboxylate (3PET) is based on the synthetic route published by Heumann et. al (86).

1 Eq (equivalent) benzoyl chloride and 2 Eq 2-chloroethanol were stirred and refluxed for 24 h at 110 °C. ^1H NMR was performed on 2-chloroethyl benzoate and complete conversion of the benzoyl chloride was observed (Supplementary figure 1).

^1H NMR (300 MHz, CDCl_3) δ : 8.07 (2H, d), 7.58 (1H, t), 7.46 (2H, t), 4.58 (2H, t), 3.82 (2H, t)

The product was transferred to an evacuated schlenk and 0.5 Eq of TA was added. The sample was dissolved in dimethylformamid (DMF) and 1 Eq trimethylamine was added before the reaction was stirred at 140 °C for 24 h. All solvent was removed under reduced pressure and the sample dissolved in toluene. A brown precipitate was filtered off before the product was recrystallized in methanol and hot filtered on a hot frit. Product was then dissolved in dichloromethane (DCM) and added to a 10 cm SiO_2 column. 3PET was eluted by ethyl acetate while a brown substance remained on the SiO_2 . All solvent was removed

and the eggshell white product was confirmed by ^1H NMR (Supplementary figure 2). Yield was determined to be 27 %.

^1H NMR (300 MHz, CDCl_3) δ : 8.11 (4H, s), 8.04 (4H, d), 7.57 (2H, t), 7.44 (4H, t), 4.68 (8H, s)

Synthesis of DBCO ATTO fluorophores

One hundred microliters of 10 mM dibenzocyclooctyne (DBCO)-amine (Jena Bioscience, Germany) in tetrahydrofuran (THF):50 mM sodium bicarbonate buffer pH 8.3 (1:1 volume:volume) was added to 250 nmol ATTO-N-hydroxysuccinimide (NHS)-ester (ATTO-TEC (Germany)) and incubated at 37 °C and 550 rpm in the dark overnight. The products (example in Figure 8) were purified on an 1100 Agilent HPLC system with auto sampler, UV, FDL and automatic fraction collector using a ZORBAX Extend-C18, 4.6 x 50 mm, 1.8 μm column (Agilent, USA). Gradient: solvent A: H_2O with 0.1 % acetic acid, solvent B: acetonitrile with 0.1 % acetic acid; 0-10 min 20-95 % B, 10-13 min 95 % B, 13-13.01 min 95-20 % B, 13.01-16 min 20 % B. Yield was determined to be 72 %.

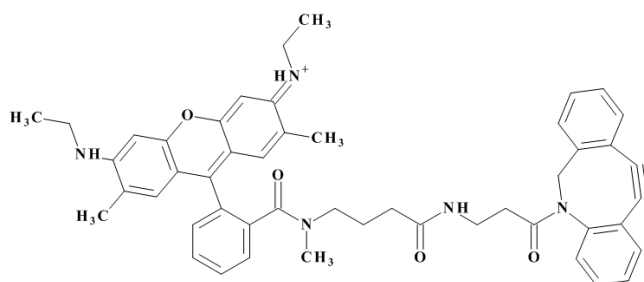


Figure 8: Structure of DBCO-ATTO-Rho6G fluorophore, one of the fluorophores used in click-chemistry experiments. The fluorophore structure (left part of structure) varies between the used fluorophores ATTO-633, ATTO-495 and ATTO-Rho6G (ATTO-TEC (Germany)).

Synthesis of C6 ABP

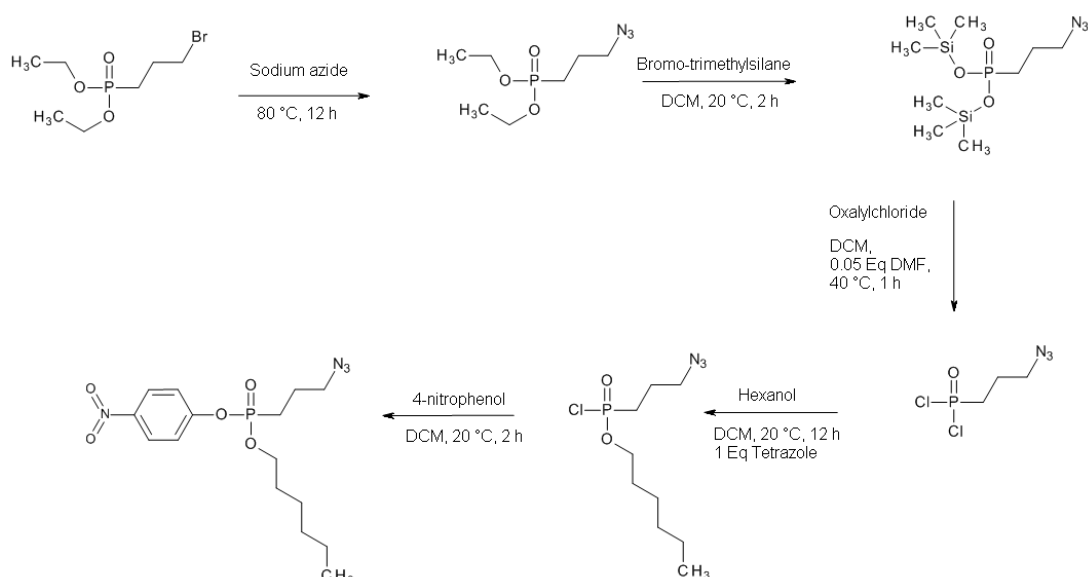


Figure 9: Synthesis scheme for the C6 ABP.

The synthesis is a variation of the route described by Rengachari et al. (87) with the alcohol replaced by 1-hexanol (Figure 9). 1 Eq diethyl-(bromopropyl)-phosphonate in H₂O:THF (1:1) was combined with 2 Eq sodium azide in a round bottom flask. The reaction was refluxed for 12 h at 80° C while stirring slowly. One pellet KOH was added to the solution and the product was extracted three times with diethyl ether (upper phase). The solvent was removed under reduced pressure.

The diethyl-(azidopropyl)-phosphonate was dissolved in dry DCM before 3 Eq bromotrimethylsilane were added and the reaction was stirred at room temperature (RT) for 2 h. Volatiles (ethylbromide, excess bromotrimethylsilane and DCM) were removed under reduced pressure and the product was dissolved in DCM and 0.05 Eq dry DMF was added. Next, 8 Eq oxalylchloride was added dropwise and the reaction was stirred at 40 °C for 1 h. Volatiles were removed under reduced pressure.

A mixture of 1 Eq N,N-diisopropylethylamine (DIPEA), 1 Eq 1-hexanol and 1 Eq tetrazole in dry DCM was added to the dry product and stirred overnight at 25 °C. Next 2 Eq DIPEA and 2 Eq 4-nitrophenol in dry DCM were added and the reaction was stirred at 25 °C for 2 h. The solution was extracted twice with H₂O to remove 1-hexanol, tetrazole and DIPEA.

Purification of the hexyl-(4-nitrophenyl)-(azidopropyl)-phosphonate (C6) was done on an 1100 Agilent HPLC system with an auto sampler, UV, FDL and automatic fraction collector using a C18, 4.6 x 150mm, 5 µm column (Agilent, USA). Retention time for the

product, C6, was 7.1 min. Gradient: solvent A: H₂O with 0.1 % acetic acid, solvent B: acetonitrile with 0.1 % acetic acid; 0-10 min 40-100 % B, 10-12 min 100 % B, 12-12.01 min 100-40 % B, 12.01-16 min 40 % B. Yield was determined to be 38 %.

Synthesis of Azidophenoxyethanol

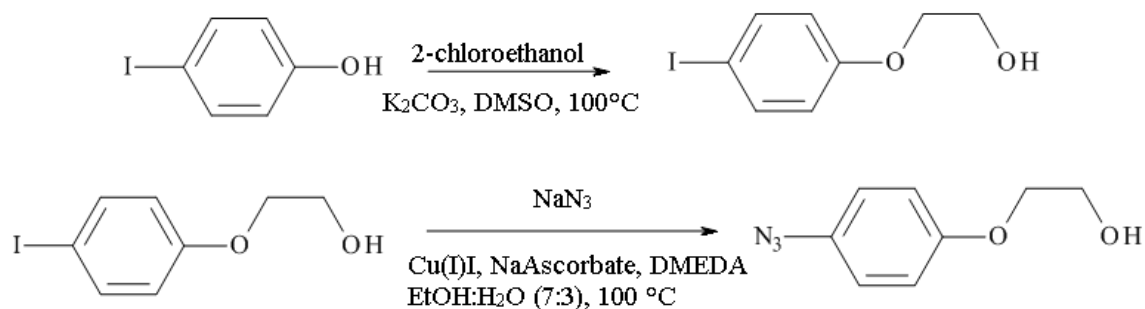


Figure 10: Synthesis scheme for azidophenoxyethanol.

In an evacuated schlenk flask, 1 Eq iodophenol and 3 Eq K₂CO₃ were dissolved in 1 volume dimethyl sulfoxide (DMSO). 1 Eq 2-chloroethanol was added and the reaction was stirred at 100 °C overnight. 2 volumes of H₂O were added and the iodophenoxyethanol was extracted three times with 3 volumes of DCM. The DCM was dried with Na₂SO₄ and the solution was filtered before all solvent was removed under reduced pressure. The product, iodophenoxyethanol, was confirmed by ¹H NMR (Supplementary figure 3). Yield was determined to be < 99 %.

¹H NMR (300 MHz, MeOD) δ : 7.52 (2H, d), 6.73 (2H, d), 3.97 (2H, t), 3.86 (2H, t)

In an evacuated schlenk flask 1 Eq iodophenoxyethanol, 2 Eq NaN₃, 0.1 Eq Cu(I)I and 0.05 Eq sodiumascorbate were dissolved in ethanol:water (7:3 volume:volume) before 0.15 Eq N,N'-dimethylethylenediamine (DMEDA) was added and the reaction left to stir at 100 °C overnight. The solvent was removed under reduced pressure and the sample was dissolved in H₂O. The azidophenoxyethanol was extracted four times with DCM and the solvent was removed under reduced pressure. The product was purified on a silica column (30x weight of the product) by elution with cyclohexane:ethylacetate (2:1). The product was verified by ¹H NMR (Supplementary figure 4). Yield was determined to be 64 %.

¹H NMR (300 MHz, CDCl₃) δ : 6.93 (4H, q), 4.07 (2H, t), 3.96 (2H, t), 1.88 (1H, s)

Synthesis of Tetra-Pål

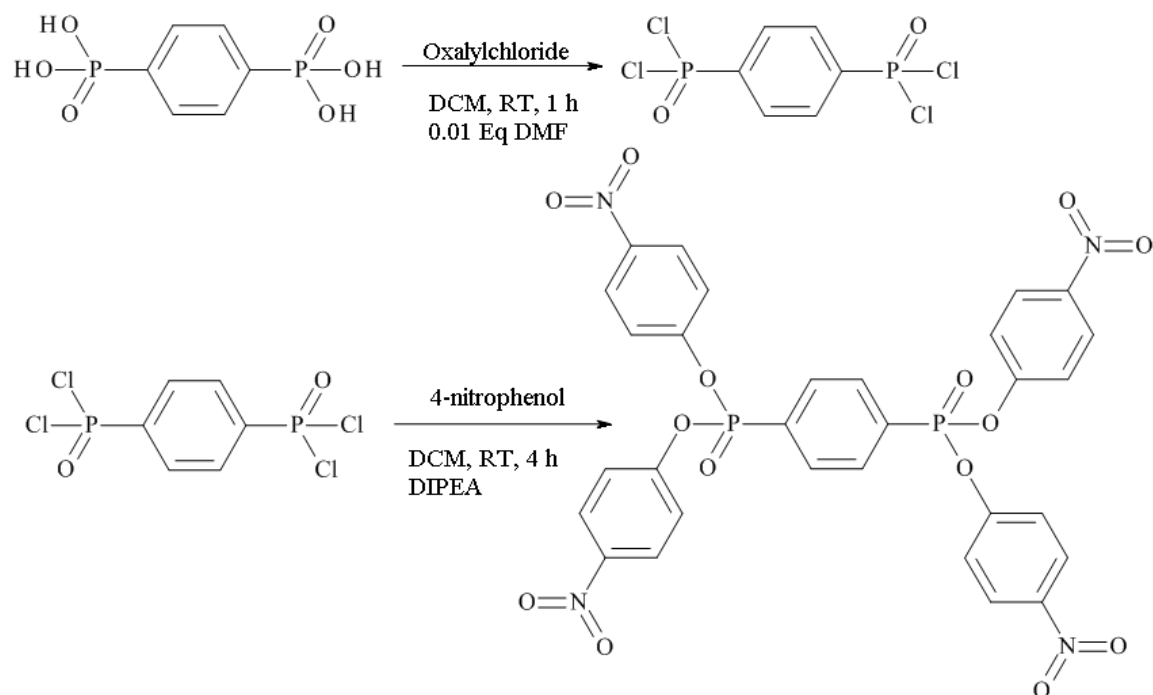


Figure 11: Synthesis scheme for Tetra-Pål.

In an evacuated schlenk flask 1 Eq 1,4-diphosphonic benzene was dissolved in DCM and 8 Eq oxalylchloride were added dropwise while the reaction was stirred on ice. Finally 1 drop of DMF was added and the reaction refluxed for 1 h. Solvent and excess oxalylchloride were removed under reduced pressure and 4 Eq 4-nitrophenol were added. The sample was dissolved in DCM and 4 Eq DIPEA were added before stirring at RT for 4 h. The product precipitated and was collected by filtering through a frit. The product was verified with ^1H NMR (Supplementary figure 5). Yield was determined to be 41 %,

^1H NMR (300 MHz, DMSO) δ : 8.31 (12H, t), 7.54 (8H, d)

Synthesis of PAL 177

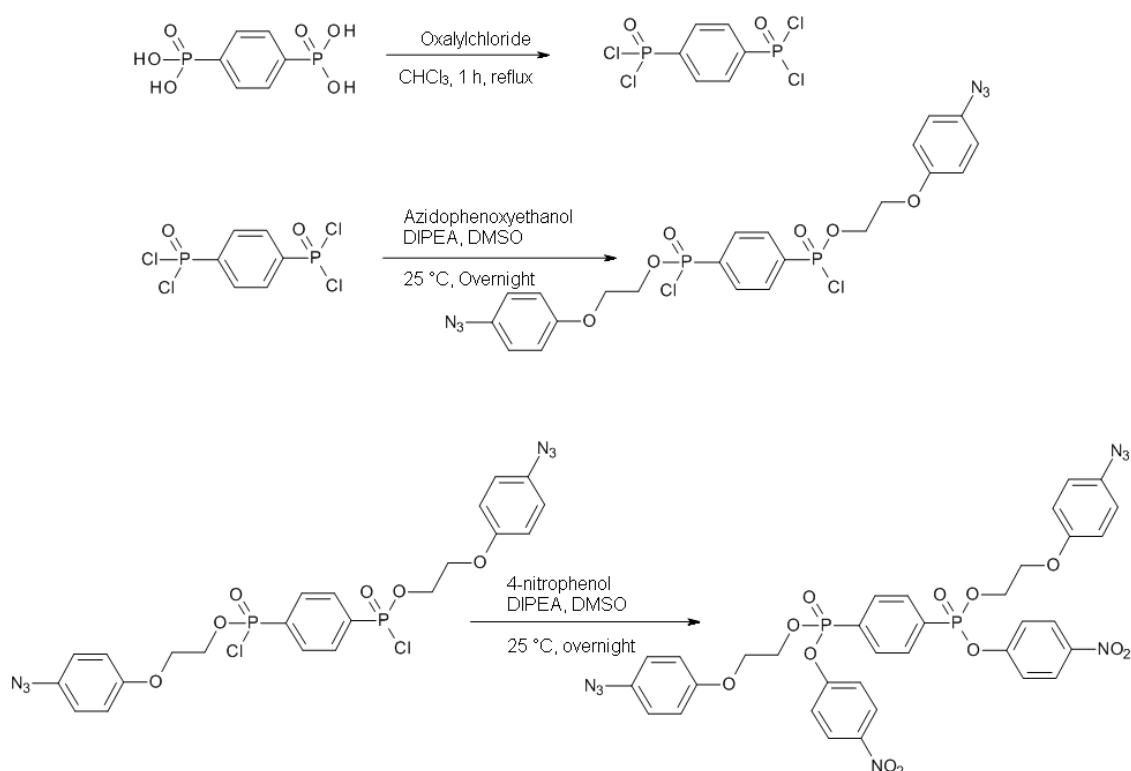


Figure 12: Synthesis scheme for PAL 177.

In an evacuated schlenk 1 Eq 1,4-diphosphonic benzene was dissolved in DCM and 8 Eq oxalylchloride were added dropwise while the reaction was stirred on ice. Finally 1 drop of DMF was added and the reaction refluxed for 1 h. Solvent and excess oxalylchloride were removed under reduced pressure. 2.1 Eq azidophenoxyethanol and 2.1 Eq DIPEA were added and dissolved in DMSO. The reaction was stirred at 25°C overnight and solvents were removed under reduced pressure. Sample was dissolved in DMSO and 4 Eq oxalylchloride were added dropwise while the reaction was stirred on ice. 1 drop DMF was added and the reaction refluxed for 1 h. Excess oxalylchloride and solvent were removed under reduced pressure. 4 Eq 4-nitrophenol and 4 Eq DIPEA were added and dissolved in DMSO. The reaction was stirred at 25°C overnight. A precipitate formed and was filtered off. The precipitate was washed with toluene and then dried under reduced pressure. Sample was dissolved in pyridine and trifluoroacetic acid and ^1H NMR was performed. Even though the product was not pure, ^1H NMR indicated its presence (Supplementary figure 6). The yield was not determined as the product was not pure.

^1H NMR (300 MHz, Pyridine) δ : 8.15 (4H, t), 7.73 (4H, t), 7.55-7.41 (4H, m), 7.19 (8H, q), 4.32 (4H, t), 4.22 (4H, t)

Synthesis of aromatic ABPs

Six aromatic ABPs with fluorine as the leaving group were synthesized by Mario Leypold as described in Leypold et al. (2). A brief summary of the synthesis is shown in Figure 13. The structures and given names of the resulting fluorinated ABPs are shown in Figure 26.

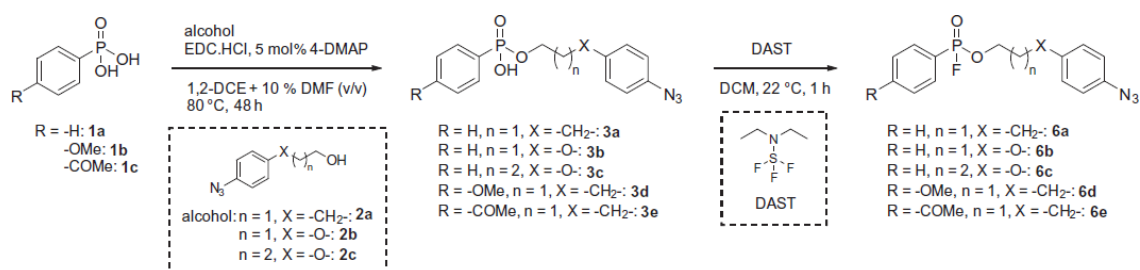


Figure 13: Synthesis scheme for aromatic ABPs copied from Leypold et. al (2). ABPs were synthesised by selective monoesterification using EDC-HCl followed by fluorination using DAST.

In addition a version of LEY 172 was synthesised with 4-nitrophenol as a leaving group instead of fluorine. This was done by replacing the second step of the scheme in Figure 13 by the addition of 2 Eq of oxalylchloride and refluxing for 1 h before removing excess oxalylchloride under reduced pressure. Next 2 Eq 4-nitrophenol in CH₂Cl₂ were added together with 2 Eq DIPEA followed by stirring at room temperature for 2 h. Product was confirmed by ¹H NMR (Supplementary figure 7). The yield was not determined.

¹H NMR (300 MHz, CDCl₃) δ: 8.18 (2H, d), 7.86 (2H, q), 7.64 (1H, t), 7.51 (2H, q), 7.32 (2H, d), 7.11 (2H, d), 6.92 (2H, d), 4.22 (2H, q), 2.69 (2H, t), 2.03 (2H, p)

Determining ABP selectivity against commercial serine hydrolases

1 μg enzyme in 10 μl 100 mM Tris-HCl pH 7.4 was incubated with 10 μM ABP at 25 °C, 550 rpm for 1 h. The ABPs used were LEY 172/197/198/204/206/213 and C6. Heat inactivated enzyme (incubated for 15 min at 95 °C before addition of ABP) was also incubated with 10 μM C6 as a negative control. Samples were reduced and alkylated by incubation for 30 min at 37 °C, 550 rpm in the dark with 10 μL 20 mM TCEP, 60 mM IAA in 0.25 M NaCl, 4 M urea and 2 % SDS. Next, 1 nmol DBCO-ATTO-633 fluorophore (in 1 μl DMSO) was added and samples were incubated for 1 h at 37 °C and 550 rpm in the dark. NuPAGE LDS Sample buffer (from 4X stock) and NuPAGE Sample Reducing Agent (10X stock) were added to the sample prior to incubation for 5 min at 95 °C. Sample was loaded on a 20 well NuPAGE 4-12 % Bis Tris Midi gel (Invitrogen, USA) and run at constant 9 W/gel for 105 min. ABP bound to active enzyme was visualised by laser gel scanner (Bio-Rad FX pro) and intensities of the bands were evaluated using ImageLab v4.1

(Bio-Rad Laboratories, USA). The enzymes used were: Cut1_ThC, Cut2_ThC, Cut2_G65_Thc, Cut_Hum, PpEst (all provided by the Gübitz and Ribitsch groups at BOKU Vienna, Austria (both formerly at TU Graz, Austria)), Amano Lipase, Amano Lipase M, Lipase *Rhizopus Oryzae*, Lipase *Candida Antarctica B*, Esterase *Rhizopus Oryzae*, Esterase *Pseudomonas Fluorescence*, Esterase *Candida Lipolytica*, Amano Lipase A, Lipase *Candida Rugosa* and Lipoprotein lipase from *Pseudomonas species* (LPL) (all from Sigma Aldrich, Germany).

Time dependant activity of APBs

1 µg PpEst in 7.5 µl 100 mM Tris-HCl pH 7.4 was incubated with 10 µM ABP at 4 °C, 550 rpm for 3, 6, 9 or 60 min. Immediately after incubation samples were flash frozen in liquid nitrogen. To the frozen samples 7.5 µl 10 mM 4-(2-Aminoethyl)benzenesulfonyl fluoride hydrochloride (Pefabloc® SC), 25 mM TCEP, 60 mM IAA in 4 M urea, 2 % SDS, 0.25 M NaCl was added to thaw, inhibit, reduce and alkylate the sample. It was then incubated at 37 °C, 550 rpm for 30 min in the dark. Next, 1 nmol DBCO-ATTO-633 fluorophore (in 1 µl DMSO) was added and samples were incubated for 1 h at 37 °C, 550 rpm in the dark. NuPAGE LDS Sample buffer (4X stock) and NuPAGE Sample Reducing Agent (10X stock) were added to the sample prior to incubation for 5 min at 95 °C. Sample was loaded on a 20 well NuPAGE 4-12 % Bis Tris Midi gel (Invitrogen, USA) and run at constant 9 W/gel for 105 min. ABP bound to active enzyme was visualised by laser gel scanner and intensities of the bands were evaluated using ImageLab v4.1 (Bio-Rad Laboratories, USA).

Reactivity of different leaving groups

1 µg PpEst, LPL or Cut1_Thc in 7.5 µl 100 mM Tris-HCl pH 7.4 were incubated with 10 µM LEY 172, LEY 216 or C6 at 4 °C, 550 rpm for 3 or 15 min. Immediately after incubation samples were flash frozen in liquid nitrogen. To the frozen samples 7.5 µl 10 mM 4-(2-aminoethyl)benzenesulfonyl fluoride hydrochloride (Pefabloc® SC), 25 mM TCEP, 60 mM IAA in 4 M urea, 2 % SDS, 0.25 M NaCl was added to thaw, inhibit, reduce and alkylate the sample. It was then incubated at 37 °C, 550 rpm for 30 min in the dark. Next, 1 nmol DBCO-ATTO-495 fluorophore (in 1 µl DMSO) was added and samples were incubated for 1 h at 37 °C, 550 rpm in the dark. NuPAGE LDS Sample buffer (4X stock) and NuPAGE Sample Reducing Agent (10X stock) were added to the sample prior to incubation for 5 min at 95 °C. Sample was loaded on a 20 well NuPAGE 4-

12 % Bis Tris Midi gel (Invitrogen, USA) and run at constant 9 W/gel for 105 min. ABP bound to active enzyme was visualised by laser gel scanner and intensities of the bands were evaluated using ImageLab v4.1 (Bio-Rad Laboratories, USA).

Targeting polyesterses in secretomes of polyesterase producing organisms

50 mL cultures of *Pseudomonas pseudoalcaligenes* and *Thermobifida cellulosilytica* cultured in standard media with either cellulose, milled PBAT or no supplemental polymer, were transferred to 50 mL conical centrifugation tubes and centrifuged at 4 °C and 4000 x g for 30 min in a swing-bucket rotor. Supernatant was collected and re-centrifuged as above to yield the final supernatant for the experiment. The supernatants were incubated with 10 mM ABP (either LEY 172 or C6) for 1 h at 28 °C before being concentrated down to ~150 µL by an Amicon 3 kDa cut-off spin filter. The protein concentration was determined and 50 µg of protein from each sample was reduced and alkylated by the addition of 1 volume of 20 mM TCEP, 60 mM IAA in 4 M urea, 2 % SDS, 0.25 M NaCl and incubation at 37 °C for 30 min at 550 rpm in the dark. Next 1 nmol DBCO-ATTO-633 fluorophore was linked to the ABP by click chemistry by incubation for 1 h at 37 °C and 550 rpm in the dark. NuPAGE LDS Sample buffer (4X stock) and NuPAGE Sample Reducing Agent (10X stock) were added to the sample prior to incubation for 5 min at 95 °C. Sample was loaded on a 20 well NuPAGE 4-12 % Bis Tris Midi gel (Invitrogen, USA) and run at constant 9 W/gel for 105 min. The gel was scanned by a gel laser scanner (Bio-Rad FX pro) to visualise the labelled enzymes.

Results

Extracellular esterase activity of *Pseudomonas pseudoalcaligenes*

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

To determine if cultivating the organism together with polymers would increase the secretion of hydrolytic enzymes the activity of potential extracellular hydrolases of *Pseudomonas pseudoalcaligenes* cultured with different polymers was measured using 4-NPB as a substrate (Figure 14). Although activity was seen, there was no induction of hydrolytic activity by PBAT when compared to a control without PBAT.

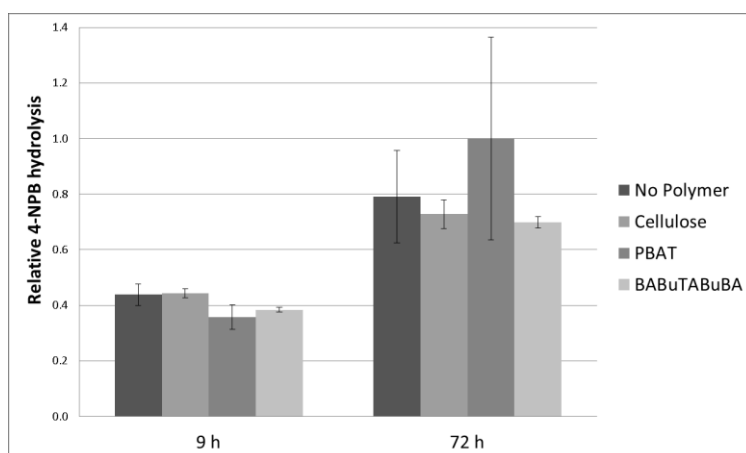


Figure 14: Hydrolytic activity of *Pseudomonas pseudoalcaligenes* supernatants grown with different polymers. An increase in hydrolytic activity can be seen from 24 h to 72 h, but none of the polymers added to stimulate the hydrolytic activity caused a significant increase in activity. Values are means of biological triplicates and standard deviations are shown as bars.

However, addition of PBAT to normal growth medium led to a distinct profile of secreted proteins (Table 1) when compared to the secretome of a culture grown with no polymer added to the medium.

To identify the enzymes responsible for the hydrolytic activity and to determine if there was a distinct secretion profile when polymers were added to the growth medium the supernatants were subjected to proteomic screening. Across the four cultures induced with different polymers a total of 4081 ungrouped proteins were identified (full list in Table S1 in the supplementary data). Based on sequence similarity to known and described enzymes, 25 proteins were predicted to have esterase, lipase, cutinase or depolymerase activity (excluding DNA or RNA depolymerases) (Table 1). These enzyme classes were chosen as they were previously reported to hydrolyse polymers. Several candidates from the list were considered for cloning and expression. As the target enzyme should preferably be able to cleave PBAT a desired ability was to hydrolyse ester bonds adjacent to aromatic rings as well as aliphatic esters. Thioesterases cleave ester bonds next to sulfurs and were thus excluded. Phosphodiesterases and phospholipases were likewise excluded due to high substrate specificity for phospho(di)esters. Two enzymes (GI: 610708963 and GI: 667953879) containing transmembrane segments were excluded as these segments might negatively affect stability in solution. Since the genomic sequence of *Pseudomonas pseudoalcaligenes* is not complete, *in vitro* translated sequences from other *Pseudomonas* strains were included in the database to avoid false positives caused by a mismatch of sample and search space. However, only genes coding for proteins from *Pseudomonas pseudoalcaligenes* were considered for cloning and expression. Of the remaining enzymes,

an esterase (GI: 610711757) (from now on named PpEst) was chosen for cloning and expression due to being identified only in the supernatant induced by PBAT, containing a signal peptide for secretion, originating from the correct organism and having a 70 % sequence similarity to TesA (GI: 530537561) from *Pseudomonas aeruginosa* which is known to have arylesterase activity (88).

Table 1: Esterases and lipases identified from *P. Pseudoalcaligenes*. Listed esterases and lipases were identified in one or more of the supernatants of cultures of *P. pseudoalcaligenes* grown with normal media or with the addition of the polymers cellulose, PBAT or BABuTABuBA. The esterase selected for cloning is in bold. When the protein was identified under the given condition it is indicated by X. (Table taken from Wallace et. al (3))

GI Accession#	Protein name	No polymer	Cellulose	BABuTABuBA	PBAT
667953335	glycerophosphodiester phosphodiesterase [<i>Pseudomonas mendocina</i> S5.2]	X	X	X	X
782988588	ACP phosphodiesterase [<i>Pseudomonas pseudoalcaligenes</i>]	X	X	X	X
610712135	esterase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	X	X	X	X
674101979	acyl-CoA thioesterase [<i>Pseudomonas sp.</i> 1-7]		X	X	X
782988138	glycerophosphodiester phosphodiesterase [<i>Pseudomonas pseudoalcaligenes</i>]	X	X	X	X
667951325	glycerophosphodiester phosphodiesterase [<i>Pseudomonas mendocina</i> S5.2]	X		X	X
782987573	4-hydroxybenzoyl-CoA thioesterase [<i>Pseudomonas pseudoalcaligenes</i>]	X	X	X	X
782987758	thioesterase [<i>Pseudomonas pseudoalcaligenes</i>]	X	X	X	X
610712849	phosphodiesterase [<i>Pseudomonas pseudoalcaligenes</i> AD6]				X
782987757	thioesterase [<i>Pseudomonas pseudoalcaligenes</i>]		X		X
610706739	phosphodiesterase [<i>Pseudomonas pseudoalcaligenes</i> AD6]				X
68345928	arylesterase [<i>Pseudomonas protegens</i> Pf-5]				X
610711757	esterase [<i>Pseudomonas pseudoalcaligenes</i> AD6]				X
641464984	thioesterase superfamily protein [<i>Pseudomonas sp.</i> P482]	X	X	X	
782986630	diguanylate phosphodiesterase [<i>Pseudomonas pseudoalcaligenes</i>]	X	X	X	
939992149	Glycerophosphoryl diester phosphodiesterase [<i>Pseudomonas syringae pv. alisalensis</i>]			X	

564833263	phosphoesterase [<i>Pseudomonas aeruginosa</i> VRFPA07]			X	
610714766	carboxylesterase [<i>Pseudomonas pseudoalcaligenes</i> AD6]		X		
568075804	thioesterase [<i>Pseudomonas sp.</i> M1]		X		
610416967	chemotaxis-specific methylesterase [<i>Pseudomonas aeruginosa</i> PA96]	X			
739188356	acyl-CoA thioesterase [<i>Pseudomonas oleovorans</i>]	X			
610708936	esterase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	X			
757245813	lysophospholipase L2 [<i>Pseudomonas fluorescens</i>]	X		X	
667953879	lipase [<i>Pseudomonas mendocina</i> S5.2]		X		
801164442	lipase [<i>Pseudomonas kilonensis</i>]		X		

Cloning and expression of PpEst

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

The gene coding for the esterase PpEst from *Pseudomonas pseudoalcaligenes* (202 AA) was codon optimized and cloned over restriction sites *NdeI*/ *HindIII* into pET26b(+) for expression in *E.coli* BL21-Gold(DE3) without N-terminal secretion signal peptide (Figure 15). For rapid purification the 6xHis Tag was C-terminally fused to the enzyme. Heterologous expression of PpEst at 25 °C and 28 °C resulted in strong protein bands in the soluble fractions around 20 kDa corresponding well to the calculated mass of 20.3 kDa with higher expression of soluble PpEst at 25 °C than at 28 °C (Figure 16). (Cloning and expression of PpEst was performed by Sabine Zitzenbacher and Doris Ribitsch)

Codon-optimized nucleotide sequence of recombinant PpEst:

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1 atgggcaccc tgcgtgtgt tgggatagc attagcgag catttggtt ggtatgccgt
61 cagggttggg ttgactgct ggaaaaact ctgagcgaag aaggtttga acctagcgt
121 gtaatgcca gattatggg tgataccagt gtcgggtgtg cagcactct gactgcccgt
181 ctggcagaac ataaccgga actggttatt attgaactg gtgtaatga tgcctgcgt
241 ggtcagcctc cggcacagt gtagcagaat ctggcaagca tggttgaaca gggccagcag
301 gcaggcgcaa aagtgtgct gctgggtatg aaactgcctc cgaattatg tgttgttat
361 accacggcat ttgcacagt tttacgat ctggcgaac agaaccaggt tagcctggt
421 ccgtttttc tgaagggtt tgggtgtgt ccgggtatg tgcaggcaga tggattcat
481 cggcagaag cagcacaaga aattctgtg gataatgtt ggcgacctt gaaacgatg
541 ctg
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Protein sequence of recombinant PpEst:

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1 MGTLVVGDS ISAAFGLDSR QGWVALLER LSEBGEFHSV VNASISGDTS AGGAARLSAL
61 LAEHKPELVI IELGGNDGLR GQPPAQLQN LASMVEQSQQ AGAKVLLGM KLPPNYGVRY
121 TTAFQVFTD LAEQKQVSLV PFFLEGVGGV PGMMQADGH PAEAAQEILL DNVWPTLKPM
181 L
```

Figure 15: The codon-optimised nucleotide sequence of the recombinant PpEst and its translated amino acid sequence. The nucleotide sequence was optimised for expression in *E.coli*. The translated amino acid sequence has the predicted catalytic triad in red while the amino acids indicated by large letters are all part of the active site which also includes the oxyanion hole.

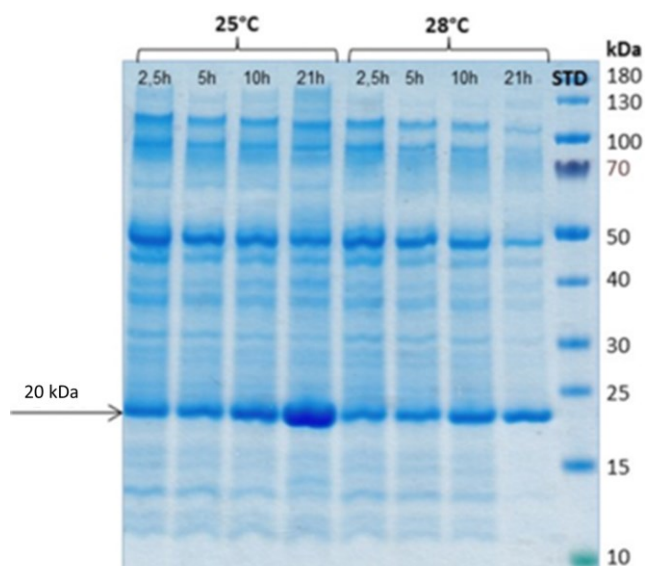


Figure 16: Expression of soluble PpEst in *E.coli* BL21-Gold(DE3). SDS-PAGE (4-12 %) showing the expression of soluble PpEst in *E.coli* BL21-Gold(DE3) at 25 °C and 28 °C. STD: Standard, PageRuler® Prestained Protein Ladder. (Performed by Sabine Zitzenbacher) (Figure is taken from Wallace et. al (3))

Characterisation of PpEst

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

After expression and purification of PpEst from *E.coli* BL21-Gold(DE3) its substrate specificity, pH optimum, temperature optimum and stability and the effects of calcium on activity and stability were determined.

Among 4-nitrophenol esters of increasing carbon chain length (C2 to C14) the highest activity was seen towards 4-nitrophenyl-butyrate and –hexanoate (Figure 17). The pH optimum for 4-NPB hydrolysis was found to be between 7 and 8 (Figure 17). k_{cat} was determined to be 1.98 s^{-1} , while K_{M} was 4.85 mM for 4-NPB.

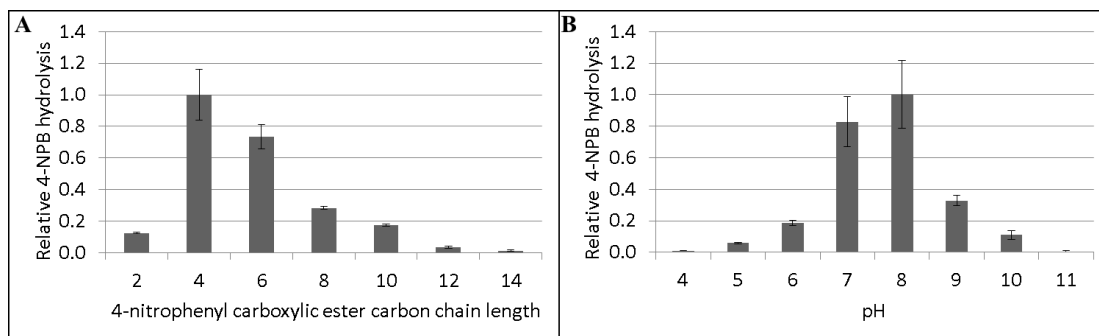


Figure 17: Preferred 4-nitrophenyl carboxylic esters and pH optimum. A: PpEst substrate specificity towards 4-nitrophenyl carboxylic esters with increasing chain lengths. B: PpEst activity towards 4-NPB in buffers ranging from pH 4 to 11. Values are means of triplicates and standard deviations are shown as bars. (Figure is taken from Wallace et. al (3))

These values are in the lower and higher ranges, respectively, of values previously reported (Table 2). However there is not necessarily a direct connection between an enzyme's ability to hydrolyse the soluble 4-NPB and its ability to hydrolyse insoluble polymers (10).

Table 2: Comparison of some known PBAT hydrolysers' K_{M} and k_{cat} towards the soluble substrate 4-NPB (Table taken from Wallace et. al (3))

Enzyme	k_{cat} (s^{-1})	K_{m} (mM)	Reference
PpEst	1.98	4.85	
TfH	220	0.62	Zhang et al.(89)
PlfI	5	6.57	Biundo et al.(62)
Cbotu_EstA	71.86	1.95	Perz et el.(63)
Cbotu_EstB	5.84	1.30	Perz et al.(63)
The_Cut1	325	0.8	Ribitsch et al.(10)

PpEst activity towards 4-NPB was not significantly changed between 25 °C and 80 °C (Figure 18)

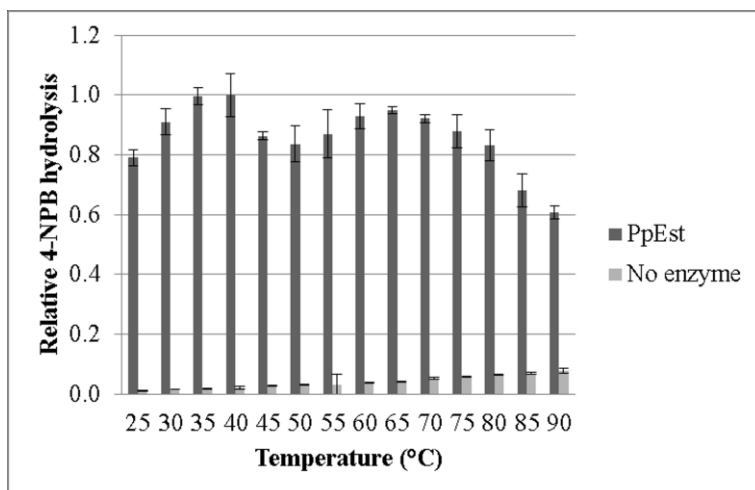


Figure 18: Hydrolysis of 4-NPB under temperatures ranging from 25 °C to 90 °C by PpEst. No significant difference in PpEst activity was seen in the range from 25 °C to 80 °C, but temperatures higher than this decreased the activity. Autohydrolysis (no enzyme) increased slightly with temperature. Values are means of triplicates and standard deviation is shown as a bar. (Figure is taken from Wallace et. al (3))

As other serine hydrolases were found to be stabilised by Ca^{2+} (90-92), this effect was also investigated for PpEst. Removing all Ca^{2+} ions by the addition of EDTA resulted in a complete loss of hydrolytic activity. When Ca^{2+} was reintroduced PpEst activity returned and maximum activity was reached at ~ 1.25 mol Ca^{2+} per mol PpEst (Figure 19). Increasing this ratio further did not increase the activity (Figure 19).

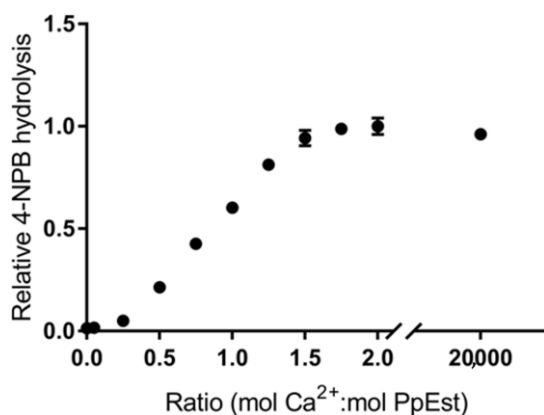


Figure 19: PpEst activity with known Ca^{2+} concentrations. Ca^{2+} was removed from PpEst by complexation to EDTA. Then EDTA was removed and known amounts of Ca^{2+} were added in ratios of mol Ca^{2+} :mol PpEst ranging from 0 to 20,000. Removal of Ca^{2+} completely, but reversibly, abolished PpEst's activity to hydrolyse 4-NPB. Activity was restored by reintroducing Ca^{2+} to the enzyme, reaching a maximum when the ratio of calcium:enzyme was ~ 1.25 and did not significantly change with higher calcium concentrations. Values are means of triplicates and standard deviations are shown as bars. (Figure is taken from Wallace et. al (3))

To test PpEst stability at high temperatures and the effect of increased Ca^{2+} concentrations 50 nM PpEst solutions were incubated over 3 days at 50 °C, 65 °C or 80 °C with either 50 nM, 10 mM or 200 mM Ca^{2+} . At 50 °C 92 % of activity remained after 1 day while 85 % of enzyme activity remained after 3 days. At 65 °C only 5 % of the activity remained after 1 day and finally at 80 °C no activity remained after 1 day (Figure 20). Increasing the

Ca^{2+} above 50 nM (mol Ca^{2+} :mol PpEst=1) did not increase the stability of PpEst at any of the measured temperatures.

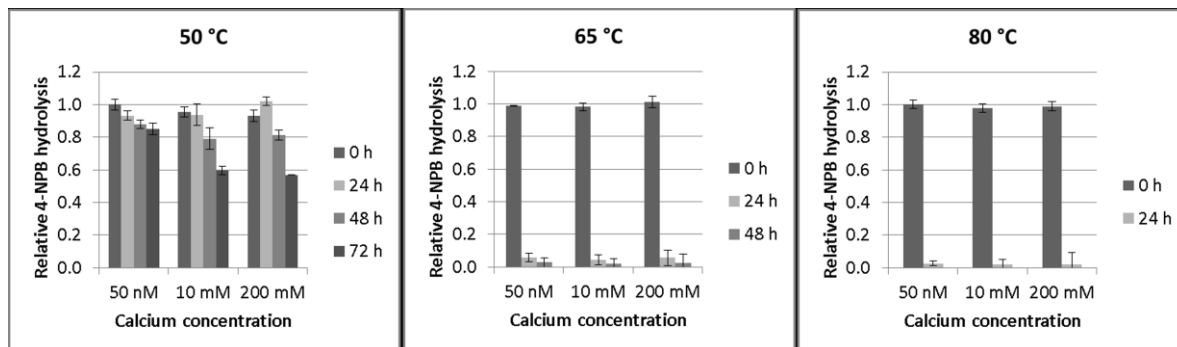


Figure 20: PpEst stability at high temperature and different Ca^{2+} concentrations. PpEst was incubated for 72 h at either 50 °C, 65 °C or 80 °C with Ca^{2+} concentrations of 50 nM, 10 mM or 200 mM. Remaining 4-NPB hydrolytic activity of PpEst was measured at 25 °C every 24 h either until all activity was gone or 72 h had passed. When Ca^{2+} concentration was 50 nM 85 % of the initial activity remained after 72 h at 50 °C while only 5 % activity remained after 24 h at 65 °C, and was completely gone after 48 h. At 80 °C all hydrolytic activity was abolished after 24 h. Higher Ca^{2+} concentrations did not increase PpEst stability. Values are means of triplicates and standard deviations are shown as bars.(Figure is taken from Wallace et. al (3))

PpEst is a polyesterase that can hydrolyse PBAT and BABuTABuBA

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

As PpEst was active on 4-NPB, its activity was tested on the aromatic polyester mimicking oligomer BABuTABuBA (Figure 21A for structure) to determine if PpEst was able to cleave ester bonds next to aromatic rings. After 72 h at 50 °C PpEst had released 22 mol TA per mol PpEst (Figure 21B) demonstrating its esterase activity on an aromatic compound.

Next we investigated whether PpEst could degrade PBAT (Figure 21C for structure). First milled PBAT film which is more easily accessible than whole film was tested due to its higher surface area and because milling of the film might have reduced the crystallinity. Hydrolysis of milled PBAT was observed at 50 °C, 65 °C and 80 °C with the highest activity seen at 65 °C (Figure 21D).

Moreover, PpEst was also able to hydrolyse whole PBAT film at 50 °C, 65 °C and 80 °C, again with the highest activity seen at 65 °C (Figure 21E). The activity at 65 °C was about 7 times higher on the milled film than on the whole film.

Even though only 5 % of initial activity remained after 24 h at 65 °C when the enzyme was incubated in a buffer alone (Figure 20), PpEst clearly had remaining activity after 24 h at

65 °C when the polymer was present. This could perhaps be explained by increased protein stability due to adsorbance to the polymer.

To test if PpEst is active also on other polyesters than PBAT, it was incubated with the aromatic polyester PET and the aliphatic polyester PLA. However no hydrolysis of either polyester could be observed after 7 days of incubation (data not shown). (Polymer degradation data was supplied by Karolina Haernvall)

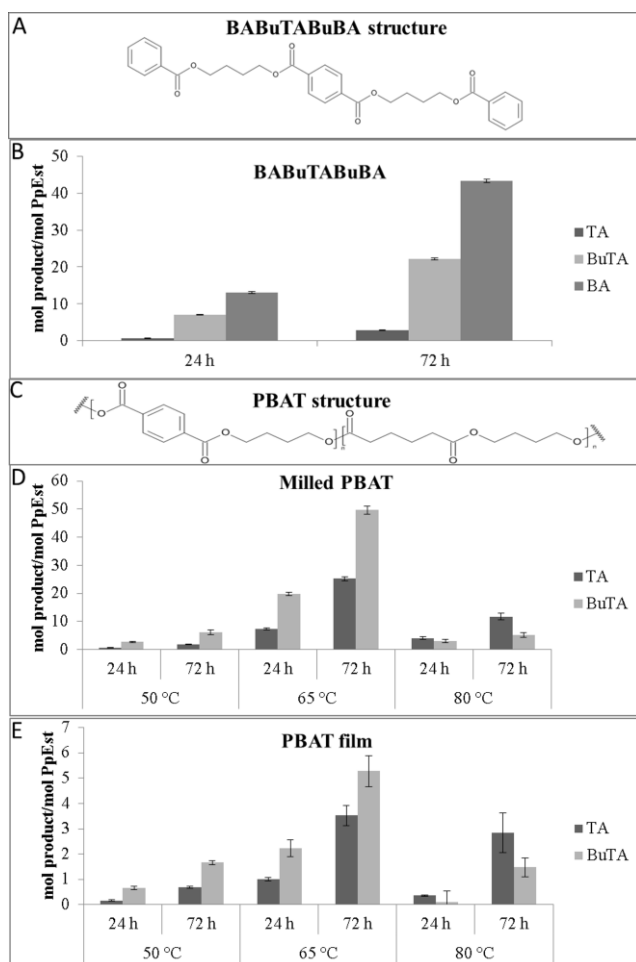


Figure 21: Hydrolysis of BABuTABuBA and PBAT. A: Structure of the aromatic polyester mimicking oligomer BABuTABuBA B: PpEst hydrolysis of BABuTABuTA into its components TA, BuTA and BA at 50 °C after 24 and 72 h. C: Structure of the aromatic-aliphatic co-polyester PBAT. D: PpEst hydrolysis of milled PBAT film into its components TA and BuTA at 50 °C, 65 °C or 80 °C after 24 and 72 h. E: PpEst hydrolysis of whole PBAT film into its components TA and BuTA at 50 °C, 65 °C or 80 °C after 24 and 72 h. Values are means of triplicates and standard deviations are shown as bars. (Data provided by Karolina Haernvall)(Figure is taken from Wallace et. al (3))

PpEst is inhibited by the PBAT hydrolysis product BuTA

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

As the end goal of large scale polyester hydrolysis would be to reduce the polymer to its monomeric components we tested the ability of PpEst to hydrolyse BuTA, one of the

released dimeric degradation products, but no further hydrolysis could be observed (Figure 22).

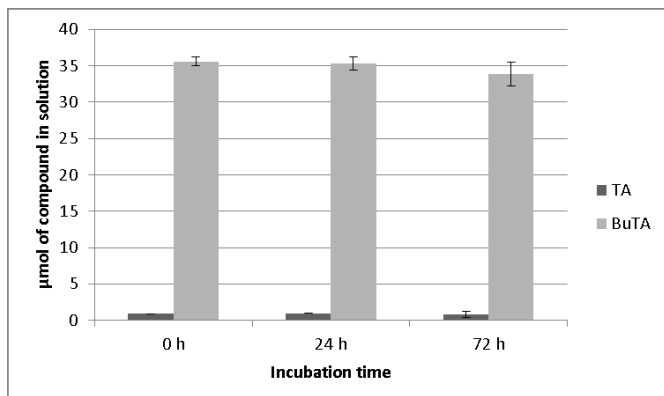


Figure 22: Degradation of BuTA by PpEst. BuTA was incubated with 5 μ M PpEst for 72 h and the degradation was measured by the appearance of TA. Over 72 h no increase in TA was seen and no BuTA hydrolysis was observed. Values are means of triplicates and standard deviations are shown as bars. (Figure is taken from Wallace et. al (3))

We hypothesised that the enzyme might be inhibited by BuTA. Thus we tested the inhibition potential of BuTA and, indeed, BuTA does inhibit PpEst almost completely (10 % activity remaining) at a concentration of 1 mM (Figure 23). K_I was determined to be 0.67 mM.

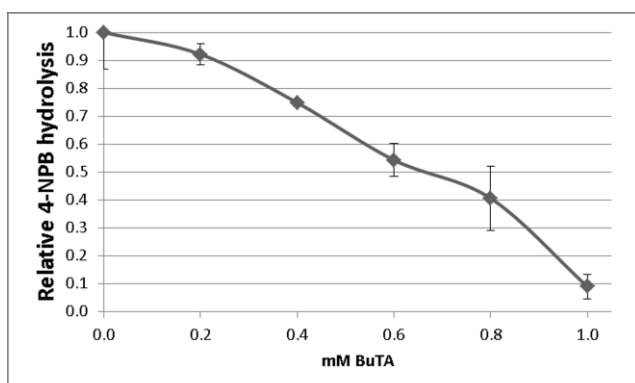


Figure 23: BuTA inhibition of PpEst activity. PpEst hydrolysis of 4-NPB was measured and found to be decreasing with increasing concentrations of BuTA. Values are means of triplicates and standard deviations are shown as bars. (Figure is taken from Wallace et. al (3))

PpEst has low sequence similarity to known PBAT hydrolysers

(This section is taken from my publication “PpEst is a novel PBAT degrading polyestrase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

To determine if PpEst was closely related to any known PBAT hydrolysers its sequence was compared to the amino acid sequence of six known enzymes with this function (Table 3). The sequence similarity is lower than 32 % for all of them, indicating that PpEst is not closely related to any previously known PBAT hydrolysers.

Table 3: Sequence similarity of PpEst from *P. pseudoalcaligenes* aligned to PBAT hydrolysing enzymes. (Table is taken from Wallace et. al (3))

Enzyme	% Similarity towards PpEst
TfH	32
PlfI	18
Cbotu_EstA	24
Cbotu_EstB	16
HiC	32
Thc_Cut1	32

PpEst structure modelled

(This section is taken from my publication “PpEst is a novel PBAT degrading polyesterase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

As the structure of TesA, which has a 70 % sequence similarity to PpEst, has been determined by X-ray diffraction, it was used as a template to create a model of PpEst to predict the structure of the active site and the surrounding cavity. In PBAT degrading enzymes a sufficient size of the cavity is imperative as it allows access of insoluble polyesters to the active site of the enzyme. When the substrate BABuTABuBA was modelled into the active site (Figure 24A) we observed that the pocket was big enough to accommodate it if minor adjustments were made. The aromatic ring of the substrate did not quite fit into the proposed pocket without moving sidechains. Especially Leu79 and Ile159 were moved slightly during the energy minimization to fit the aromatic ring. This region may also open up a groove through the protein together with a loop (Gly149, Gly148) and a turn on the other side (Pro114, Pro113). This may extend the groove even further relaxing the somewhat restricted substrate geometry in the current model. The cavity surrounding the active site would then be relatively accessible for the solvent indicating that the enzyme could potentially allow large polymers to enter (Figure 24B). PpEst was found to be dependent on Ca^{2+} to maintain its activity. However there is no Ca^{2+} binding domain in this model due to the fact that the template (TesA) does not contain a Ca^{2+} binding site. (Modelling was performed by Georg Steinkellner and Karl Gruber)

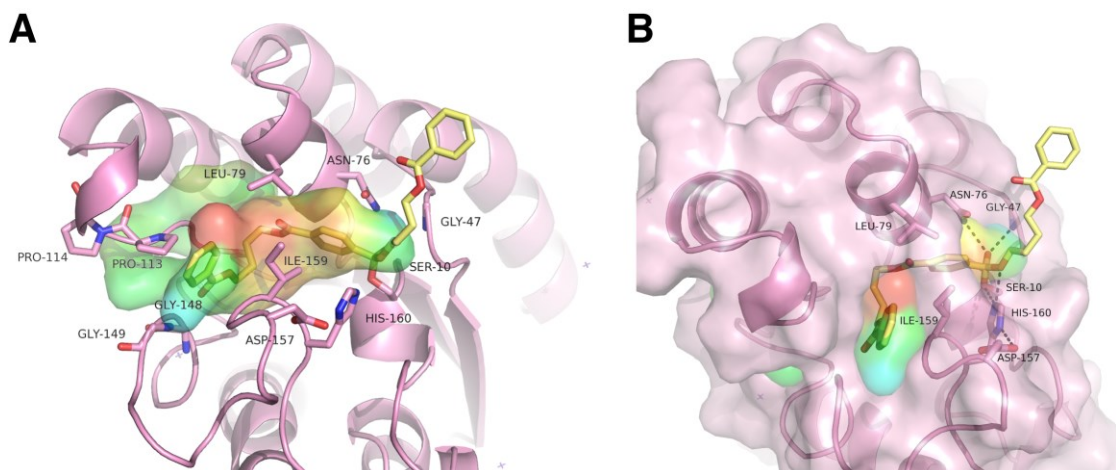


Figure 24: Model of PpEst from *P. pseudoalcaligenes* complexed with BABuTABuBA. A: Cavity of complex model of PpEst. Leu79, Ile156, Pro113 and Pro114 as well as the loop containing Gly149 and Gly148 may widen the groove on the active site. B: PpEst model in complex with BABuTABuBA as a tetrahedral intermediate where the active site groove is shown as cavity surface. The predicted catalytic triad consists of Ser10, Asp157 and His160, while the oxyanion hole encompasses Gly47 and Asn76. (Performed by Karl Gruber and Georg Steinkellner) (Figure is taken from Wallace et. al (3))

The first polyesterase targeting ABP

In order to identify enzymes that specifically degrade plastics we synthesised new ABPs to specifically target these enzymes. These ABPs were designed to have structures that mimic the aromatic polyester PET. The reactive phosphonate was placed next to an aromatic ring to target enzymes with the ability to cleave aromatic ester bonds, and not just aliphatic ones. The initial design of this ABP was a symmetrical compound that very closely resembled PET (Figure 25).

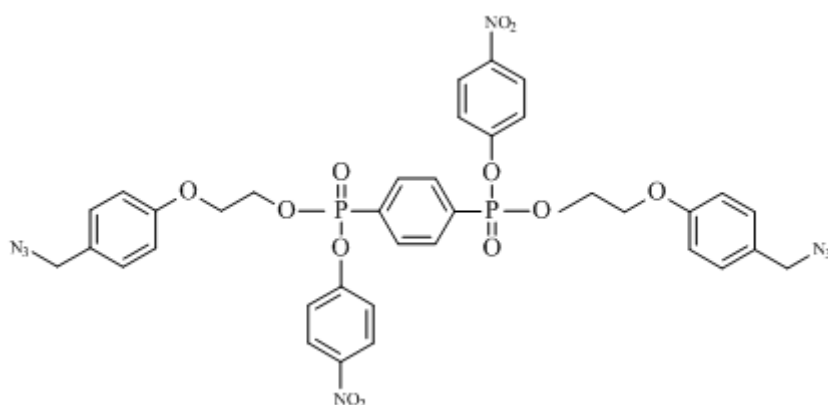


Figure 25: Structure of the initial polyesterase targeting ABP (PAL 177).

Synthesis of PAL 177 was achieved, but the only solvent system it would dissolve in was a mixture of pyridine and trifluoroacetic acid. As this combination might form an ionic liquid several ionic liquids supplied by BASF (Germany) were tested, but it could not be solubilised in anything else. As this combination of solvents is not compatible with enzymatic activity the ABP was redesigned to increase the solubility.

Variety of aromatic ABPs with fluorine as leaving group

In the second design of the polyesterase targeting ABP the compound was no longer symmetrical, it was smaller and it had fluorine as a leaving group instead of 4-nitrophenol. These changes were made to increase the solubility in water to make the ABPs useful in native enzymatic environments. The design still contained a phosphonate next to an aromatic ring (to target enzymes capable of cleaving aromatic ester bonds), but e.g. only one additional aromatic ring was included. The second aromatic ring was kept 5 or 6 bonds away to resemble the distance between two aromatic groups in PET. The ester bond next to the second aromatic ring was either removed or replaced by an ether which acts as a bioisoster of esters. The removal of the second ester bond forces the enzyme to target the phosphonate, cleave an ester bond there and get covalently bound and thus does not allow the enzyme to cleave off part of the ABP, which would change the selectivity of the ABP. Also, to test if the bulkiness or functional group on the para position of the aromatic ring from the phosphonate influences the enzyme binding ethers, esters and ketones were tested. The synthesis effort led to 6 novel aromatic ABPs with fluorine as a leaving group that were designed to mimic aromatic polyesters and thus be able to target polyesterases (Figure 26).

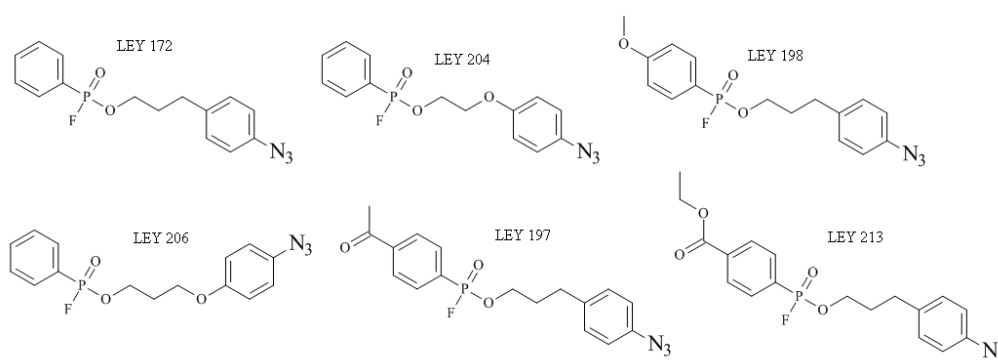


Figure 26: Structure of fluorinated aromatic ABPs. The 6 APBs all have structural similarities to PET, but are distinct from one another in attached functional group, aliphatic chain lengths and the presence of ether bonds next to the second aromatic ring. (Synthesis performed by Mario Leypold)

The selectivity of the aromatic ABP on esterases, lipases and polyesterases

The first 6 ABPs and our lab's standard esterase/lipase probe, C6 (structure is the second ABP in Figure 5), were tested against serine hydrolases in the form of commercially available esterases and lipases as well as recombinantly expressed enzymes known to be polyesterases (Thc_Cut1, Thc_Cut2, Cutinase from *Humicola insolens* (Hum_Cut) and the

mutated Thc_Cut2_G65 which has lost its ability to degrade polymer films while maintaining hydrolytic activity) (Figure 27). No significant difference could be observed between any of the aromatic ABPs, nor against the smaller aliphatic probe, C6.

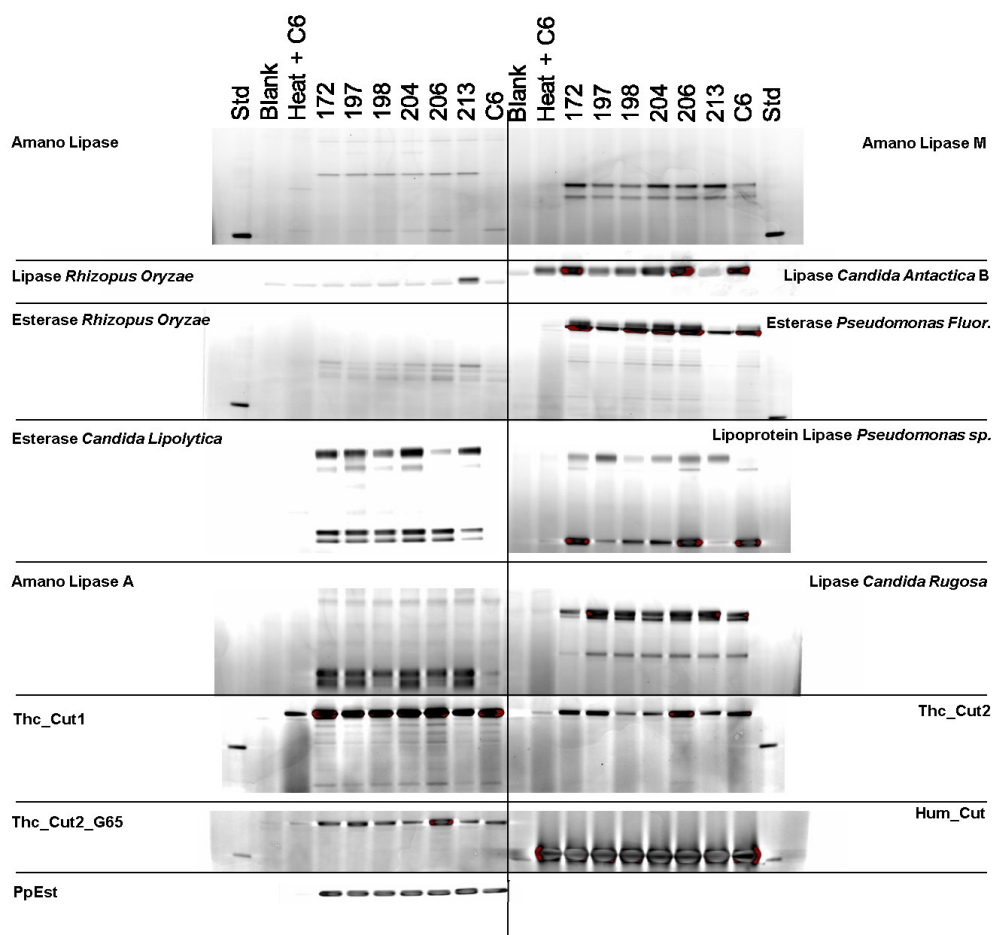


Figure 27: Activity based assays of the aromatic ABPs towards commercially available esterases and lipases as well as known polyesterases. The aromatic ABPs LEY 172, LEY197, LEY 198, LEY204, LEY 206, LEY 213 and the aliphatic ABP C6 were incubated with the enzymes at 25 °C for 1 h , covalently attached to fluorophores by strain promoted click chemistry and visualised by lasers on a gel scanner. The aromatic ABPs showed the same selectivity as the aliphatic C6.

The reaction kinetics of the different ABPs

As we saw high signals for all the ABPs towards most enzymes we tested the kinetics at which the ABPs reacted with the polyesterase PpEst. At 4 °C the aromatic ABPs had fully reacted after 3 min while it took C6 1 h to reach the same degree of enzyme inhibition (Figure 28).

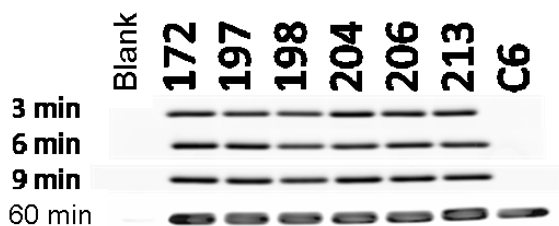


Figure 28: Aromatic ABPs reacted very quickly with PpEst at 4 °C. 1 µg PpEst was incubated with no ABP, 10 µM of aromatic ABP (LEY 172, LEY 197, LEY 198, LEY 204, LEY 206 or LEY 213) or the aliphatic ABP C6 for 3, 6, 9 or 60 min at 4 °C. Based on the fluorescence seen in the resulting gel bands we saw no significant increase in signal from 3 to 60 min at 4 °C for the aromatic ABPs while C6 took 60 min to complete the reaction with PpEst.

Changing the leaving group of the ABP changes selectivity

As the aromatic ABPs reacted very quickly with the enzymes we looked for a way to slow down the reaction to be able to distinguish the ABPs reactivity from one another and thus give us an indication of which structure was the most promising for targeting polyesters. As there were significant differences in reaction kinetics between LEY 172 and C6 we hypothesised that the leaving group could have an influence on probe reactivity. Therefore LEY 236 (Figure 29) was synthesised as a copy of LEY 172, but with 4-nitrophenol as a leaving group rather than fluorine.

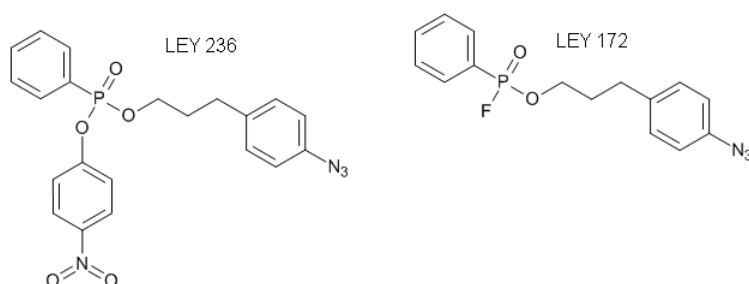


Figure 29: Structure of the ABP LEY 236. LEY 236 has the same structure as LEY 172 except that the leaving group fluorine was replaced with 4-nitrophenol. (Synthesis performed by Mario Leypold)

LEY 172, LEY 236 and C6 were tested on the enzymes PpEst, lipoprotein lipase (LPL) and Thc_Cut1 at 4 °C to see if there was any difference in reactivity (Figure 30). LEY 236 reacted slower than LEY 172 with the polyesters PpEst and Thc_Cut1, while there was no difference observed in their labelling efficiencies of the lipase LPL. Interestingly we saw a difference between PpEst and Thc_Cut1 as they both reacted well with LEY 172, but C6 reacted much quicker with Thc_Cut1 than with PpEst. When we incubated the enzymes with the probes for 1 h at 25 °C they both reached the same level of inhibition (Figure 27).

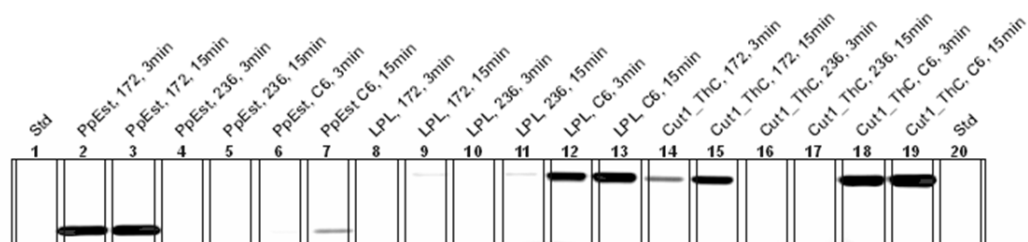


Figure 30: Influence of leaving group on ABP activity. The ABPs LEY 172, LEY 236 and C6 were incubated with the enzymes PpEst, lipoprotein lipase from *Pseudomonas sp.* (LPL) and Thc_Cut1 for either 3 or 15 min at 4 °C. The leaving group had a large effect on the ABP's ability to bind to enzymes. For both PpEst and Thc_Cut1 the 4-nitrophenol as a leaving group significantly decreased the activity compared to fluorine as a leaving group. For LPL no difference was seen between LEY 172 and LEY236, but they were both less reactive than C6. Std: Prestained protein standard (Invitrogen).

Discussion

PpEst discovered in secretome of *Pseudomonas pseudoalcaligenes*

(This first 9 paragraphs of this section are taken from my publication “PpEst is a novel PBAT degrading polyestrase identified by proteomic screening of *Pseudomonas pseudoalcaligenes*” (3) with minor adaptations).

Identification of new enzymes for the degradation of polyesters has mainly been done either by functional screenings followed by protein purification and peptide identification or by in-silico searches of publically available genomic databases. Here we demonstrate that secretome screenings of microorganisms are an efficient way to identify novel polyesterases from under-investigated environments like aquatic eco-systems with *Pseudomonas pseudoalcaligenes* being a typical representative.

We studied the extracellular proteome of this bacterium and found that the supernatants of the cultured organism had hydrolytic abilities. From these supernatants a total of 25 esterases and lipases were identified (Table 1). Only identified proteins predicted to be secreted enzymes were included for further investigation.

Many of the identified proteins (supplementary table 1) have been described to be cytosolic proteins. These have probably been introduced to the supernatant due to cell lysis over the incubation period of three days. This could be due either to natural death or to physical forces originating from the shaking of the flask.

Among the identified esterases and lipases a previously undescribed esterase (PpEst) was found to be induced by the presence of PBAT (as reported with other polyesterases, polymers and organisms (69-71)). PpEst was predicted to be a secreted enzyme and to have arylesterase activity (based on sequence similarity to TesA). This made PpEst a good candidate for cloning and expression as activity towards aromatic esters in an aqueous environment is the desired property for a polyestrase targeting aromatic polyesters. To our knowledge, arylesterases have not been reported to act as polyesterases while, vice versa, several polyester degraders have been shown to be able to use aromatic as well as aliphatic polyesters as substrates. This is the first time, however, that an enzyme was investigated for its polyestrase activity due to its predicted arylesterase activity. We thus suggest that future searches for polyesterases should also include arylesterases in their scope as these enzymes may harbour the desired activities.

PpEst was successfully cloned and expressed in *E.coli*. Its hydrolytic abilities were characterised and the enzyme was modelled. One of the characteristics tested was the role of Ca^{2+} in PpEst activity and stability. Ca^{2+} was necessary for PpEst activity (Figure 19) and it was observed that activity increased until ~ 1.25 mol Ca^{2+} per mole enzyme was added and full activity was reached. Increasing the amount of Ca^{2+} further did not increase PpEst activity indicating that there is a single Ca^{2+} binding site on PpEst. The influence of Ca^{2+} on PpEst stability at higher temperatures was tested and increasing the Ca^{2+} :PpEst ratio above 1.25 did not increase the stability of the enzyme at 50 °C, 65 °C or 80 °C (Figure 20). It has to be noted, however, that our model lacks a binding site for this ion (Figure 24) as the template structure of TesA does not contain a binding site. The model indicates that the active site pocket is relatively open and accessible to the solvent (Figure 24B), which is imperative for the enzyme to be able to accommodate a polymer. This gave us a good hint that PpEst might have an active site pocket large enough for polymers, but did not mean that it necessarily was able to hydrolyse them.

PpEst hydrolysed the aromatic polyester mimicking oligomer (BABuTABuBA) showing that it was capable of degrading aromatic polyester compounds (Figure 21B). It was in turn also able to degrade milled PBAT film (Figure 21D), a polyester substrate that is harder to access due to its size, polymer chain lengths, hydrophobicity and insolubility. Finally PpEst was tested on whole PBAT film which is potentially harder to degrade than milled PBAT film as the surface area is smaller and thus there are fewer easily accessible bonds to cleave. PpEst was able to hydrolyse the polyester PBAT even in this inaccessible form (Figure 21E). This proof of polyester degrading activity demonstrates that proteomic screenings of an organism's extracellular proteome can lead to the identification of novel polyesters.

Even though PpEst was able to degrade the aromatic-aliphatic co-polyester PBAT it was not able to degrade the commercially important aromatic polyester PET, nor the aliphatic polyester PLA. PLA had a much higher crystallinity (60-70 %) than the PBAT film (10 %), which might explain why PpEst did not get access to the polymer chains and thus was unable to hydrolyse them. It is also possible that the active site of PpEst prefers substrates with an aromatic ring coupled to an aliphatic chain of the same length as in PBAT rather than to shorter aliphatic chains (PET), or purely aliphatic polyesters (PLA).

The stability of PpEst at higher temperatures was tested towards 4-NPB after incubation in buffer over 72 h. Only 5 % of the initial activity remained after 24 h at 65 °C (Figure 20). However, when incubated with milled PBAT and PBAT film PpEst displayed the highest hydrolytic activity at 65 °C (Figure 21) and the increasing amount of release products after 24 h indicates that PpEst still remained highly active after this time point. This is in contrast to the data on enzyme stability over time in pure buffer. The increased stability in presence of polymers could be explained by adsorbance of PpEst to the polymer. Also, successful polymer hydrolysis is not only dependant on enzyme stability, but also on e.g. the crystallinity, melting temperature and glass transition temperature of the polymer (9, 93). Therefore it is important to find a compromise between high incubation temperature and enzyme stability as low enzyme stability coupled with high polymer chain mobility (high temperature) might be more effective than high enzyme stability coupled with low polymer chain mobility (low temperature). The increased activity at 65 °C compared to 50 °C could be due to the incubation temperature being closer to the melting temperature of the polymer, resulting in a higher polymer chain motility and thus increased accessibility to the polymeric chains for the enzyme. At 80 °C the hydrolytic activity is lower than at 65 °C suggesting that PpEst is destabilised at this temperature and thus not able to take advantage of the increased polymer chain motility.

The ability of PpEst to degrade PBAT makes it a potential enzyme for use in e.g. waste management plants where polyesters need to be removed, or in recycling schemes where the monomers of the polymers are to be recovered for reuse. However, it was observed that the degradation product BuTA (that results from enzymatic degradation of PBAT) inhibits PpEst (Figure 23). In our incubations of PpEst with PBAT films we only reached concentrations of BuTA that could lead to 10 % inhibition, but this could limit the potential that PpEst has for PBAT degradation on a large scale. This could however be overcome by removing BuTA as soon as it is produced. One way to do this would be by a cascade reaction done by co-incubation with another enzyme that can hydrolyse this dimer as demonstrated in the case of *Ideonella sakaiensis* 201-F6 where PETase and MHETase collaborate to degrade PET, an aromatic polyester similar to PBAT (94). This kind of cascade could then also involve using organisms that use terephthalic acid as a carbon source (95) turning this potentially toxic degradation product into biomass that can be reused.

In this study we identified a polyesterase from the secretome of the organism. We hypothesised that polyesterases should be secreted enzymes as the polymers are large and insoluble and thus cannot be taken up into the organism before they are degraded. However, there is no reason that polyesterases should not be found intracellularly as well. *Pseudomonas oleovorans* is for example known to produce the polyester poly(beta-hydroxyalkanoate) intracellularly (96). To do this it needs enzymes both to synthesise and to degrade large bulky polyesters and to keep these inside the cell (97). This in turn shows that, while secretome screenings are advantageous, as they reduce sample complexity, they might miss novel polyesterases as the entire organism has the potential to contain the enzymes. These enzymes could however then be identified by doing a screening of the whole proteome rather than the secretome, but it would result in a larger list of proteins that would need to be considered for cloning and expression.

Our described method requires relatively large amounts of sample as the concentration of polyesterases is low, but this is possible to obtain as the organism used was cultivable. The bottom-up proteomic approach also requires that sequences for the proteins are known so they can be used in the database search. For cultivable organisms these sequences are often known, and if not they can be acquired by either transcriptomic or genomic sequencing of the organism. However, some of the most interesting places to look for polyesterases are outside the lab, namely in environments where plastics have been stored and composted for decades. The assumption is that these environments have been favourable for organisms that can degrade these plastics and that they thus have thrived, multiplied and evolved. Screening such an environment for new polyesterases could be very productive, but several problems have to be addressed. Most of these organisms are unknown, and even among the ones we know very few have had any genomic, transcriptomic or proteomic sequencing done. This means that if a proteomic screening should be feasible a transcriptomic or genomic screening of the same sample would have to be performed. The resulting metatranscriptome or metagenome could then be used to generate a protein database to be used in combination with bottom-up proteomics. However these approaches have the same problem as the initial proteomic screening, namely limiting amounts of enzymes. The DNA/RNA/Protein amounts originating from each organism or species would be low and might fall below the limit of detection of our methods and as most of these organisms are uncultivable this could be hard to overcome. However, this combination of transcriptomics and proteomics for screening environmental samples holds great promise for the future (1).

Activity based probes

While polyesterase identification using ABPs suffer from the same problems of low sample amounts and lacking databases they are interesting tools that could make a large impact on polyesterase discovery. Currently there are general serine hydrolase ABPs available that could be used to enrich secretomes or environmental samples and lead to the identification of new polyesterases. However the lack of polyesterase specific ABPs is slowing this search down as current approaches would enrich all serine hydrolases and thus still leave a large amount of enzymes to clone, express and functionally test.

Our novel ABPs have been designed to target polyesterases. They resemble the aromatic polyester PET by including aromatic ester bonds, several aromatic rings and a spacing between them that matches the distance between aromatic rings in the polymer. Part of the goal was to make the ABPs so bulky and hydrophobic that enzymes with small active site pockets and enzymes that cannot accept highly hydrophobic substrates like aromatic polyesters would not bind the ABPs.

One of the major issues with polyester mimicking ABPs is solubility. Several of the building blocks and ABPs synthesised were not soluble in solvents appropriate for enzymatic activity. This is to be expected as the substrate the ABP mimics has a very low solubility in water and other solvents of similar polarity. The initial ABP synthesised, PAL 117 (structure in Figure 25), was only soluble in a mixture of pyridine and trifluoroacetic acid, which does not allow for much enzymatic activity.

The six aromatic ABPs synthesised next (Figure 26) were soluble in water and could thus be used to target enzymes in a supernatant. These ABPs were smaller and had fewer aromatic components, but still maintained properties that made them resemble PET so that they could target polyesterases and exclude other serine hydrolases. These aromatic ABPs were tested on commercially available esterases and lipases as well as recombinantly expressed known polyesterases. Their selectivity was seen to be the same as the much smaller aliphatic ABP, C6, indicating that the designs are not yet targeted towards only polyesterases (Figure 27).

The reaction kinetics for the binding of the aromatic ABPs (with fluorine as a leaving group) to the enzymes was very high (Figure 28) and it was higher than the reaction speed of the aliphatic C6 with 4-nitrophenol as leaving group. To test if changing the leaving

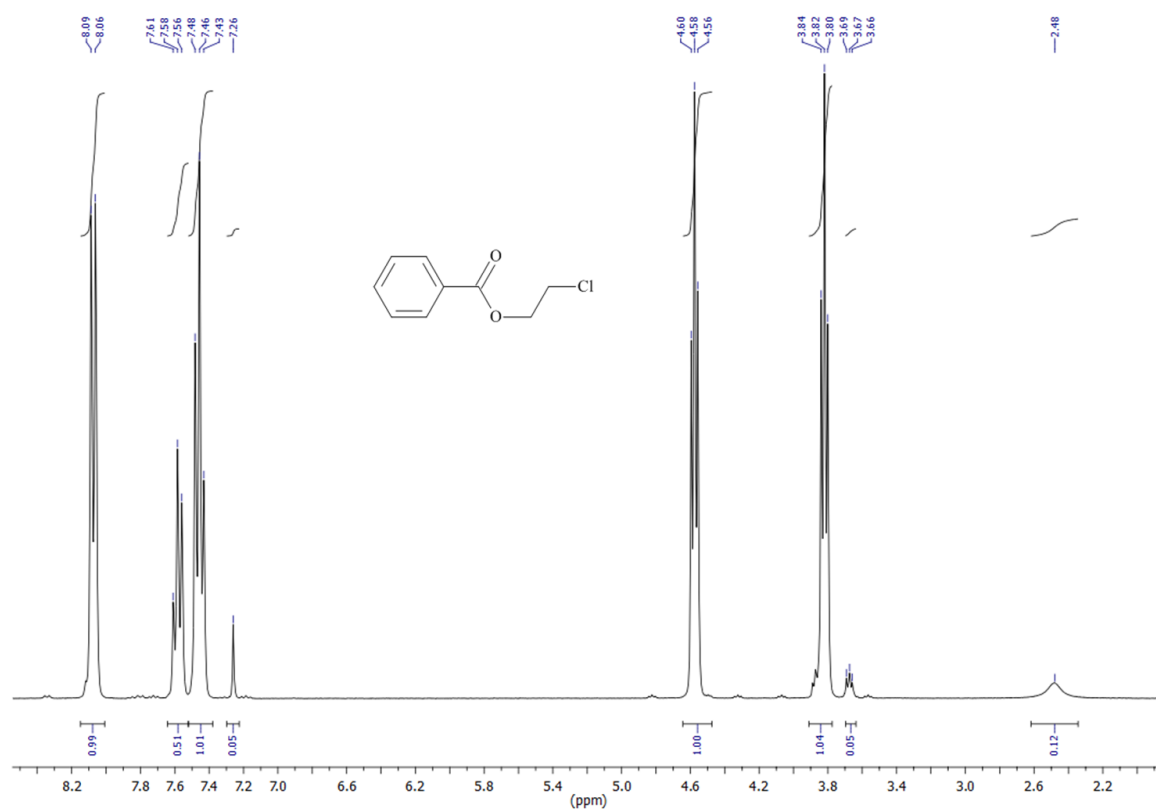
group would slow down the reaction, and reveal possible differences in reactivities of the various aromatic ABPs, a version of LEY 172 was synthesised where the leaving group was replaced with 4-nitrophenol (Figure 29). Changing the leaving group of LEY 172 from fluorine to 4-nitrophenol changed the selectivity (Figure 30). However, whether this was due to the ABP's increased bulkiness or due to different reactivity of the two chemical leaving groups remains to be determined.

The two known polyesterase producing organisms *Pseudomonas pseudoalcaligenes* and *Thermobifida cellulosilytica* were cultured with media supplemented with cellulose or PBAT. When these supernatants were collected and incubated with either LEY 172 or C6 no labelled enzymes were observed after clicking fluorophores to them prior to their separation and visualisation by SDS-PAGE and fluorescence scanning. This indicated that the amounts of enzyme in the supernatants were too low to be observed by this technique. However, if an enrichment system could be set up where the analytical handle of the ABP is used for enrichment rather than visualisation this problem could be overcome as more than 50 µg of total protein could be used. As sensitivity was a problem with cultivable organisms it has to be assumed that enzyme concentrations will be even lower in environmental samples and that for these samples setting up such an enrichment scheme would be more important.

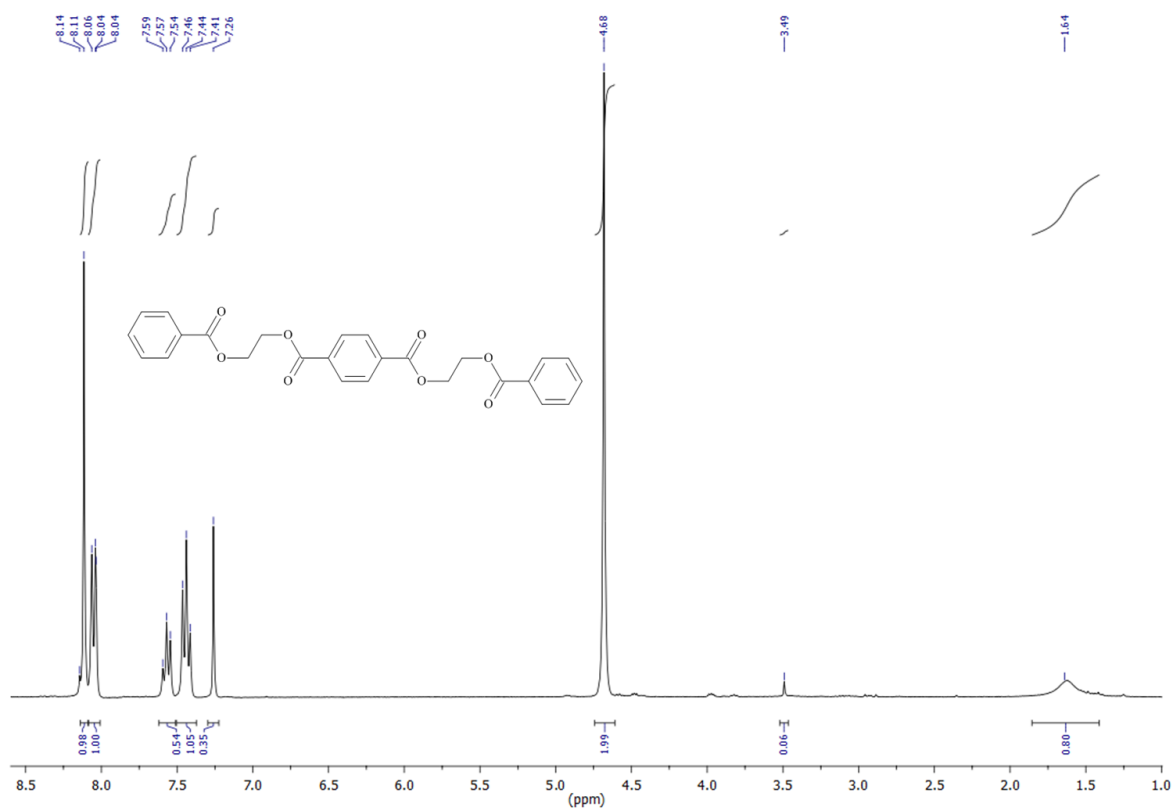
Even though these newly designed and synthesised ABPs are not selective towards polyesterases they are still novel serine hydrolase ABPs with different structures than previously reported ABPs. In particular there are few serine hydrolase ABPs with aromatic components in their structure. This means that it would be interesting to test them on tissues such as liver and brain that are known to contain many serine hydrolases and determine the selectivity of ABPs as they might have the ability to target new serine hydrolases and could thus be used as the basis for developing new targeted inhibitors and drugs.

Supplementary figures and Tables

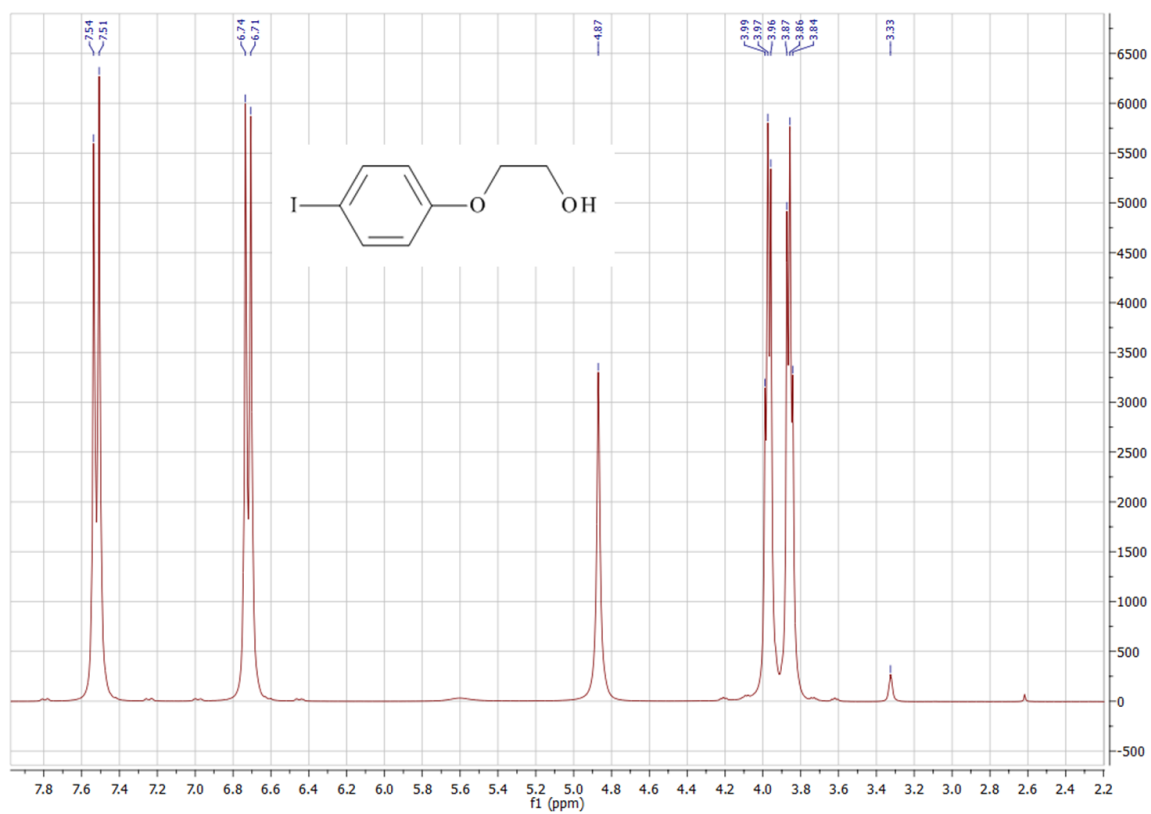
NMR spectra



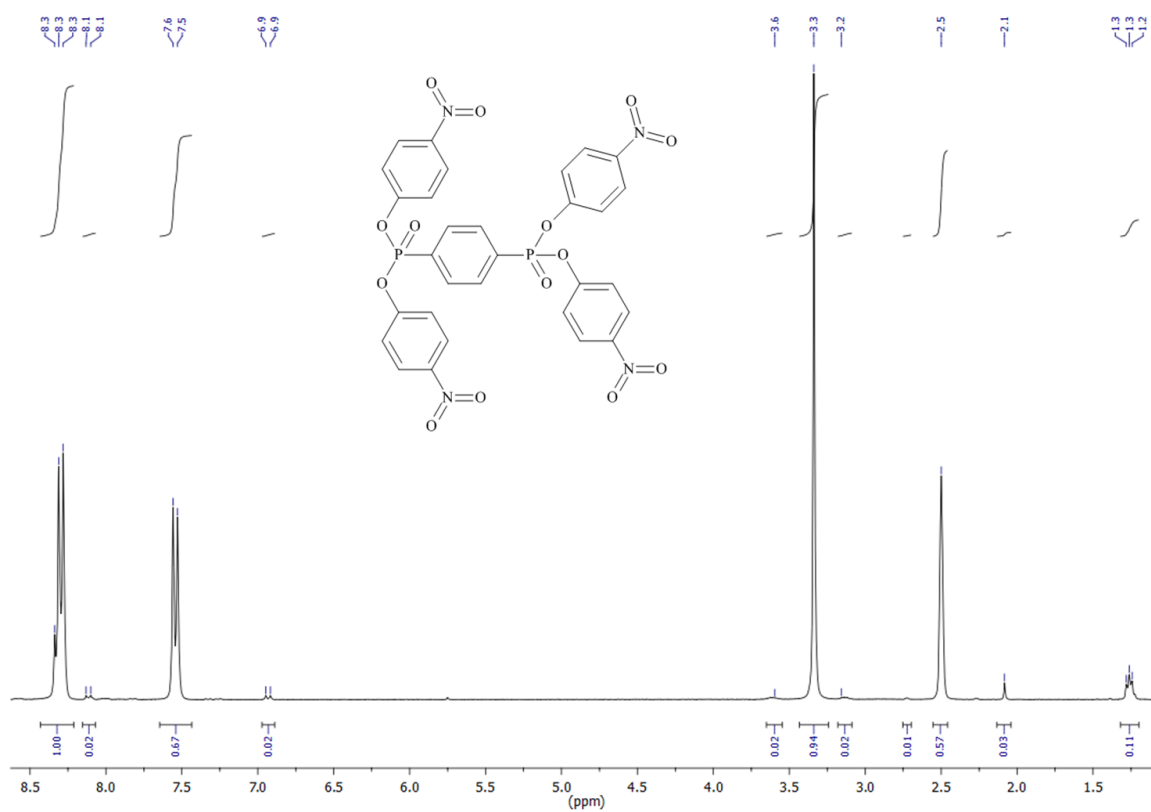
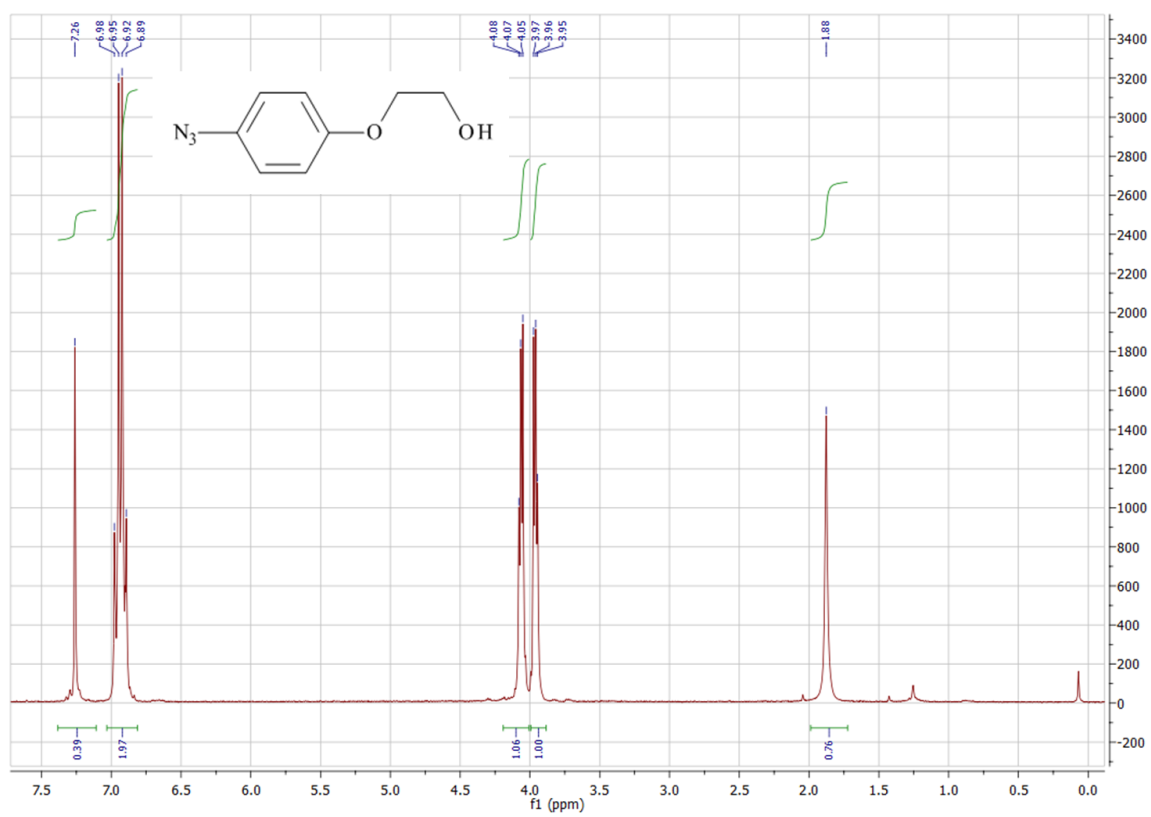
Supplementary figure 1: ^1H NMR of 2-chloroethyl benzoate.

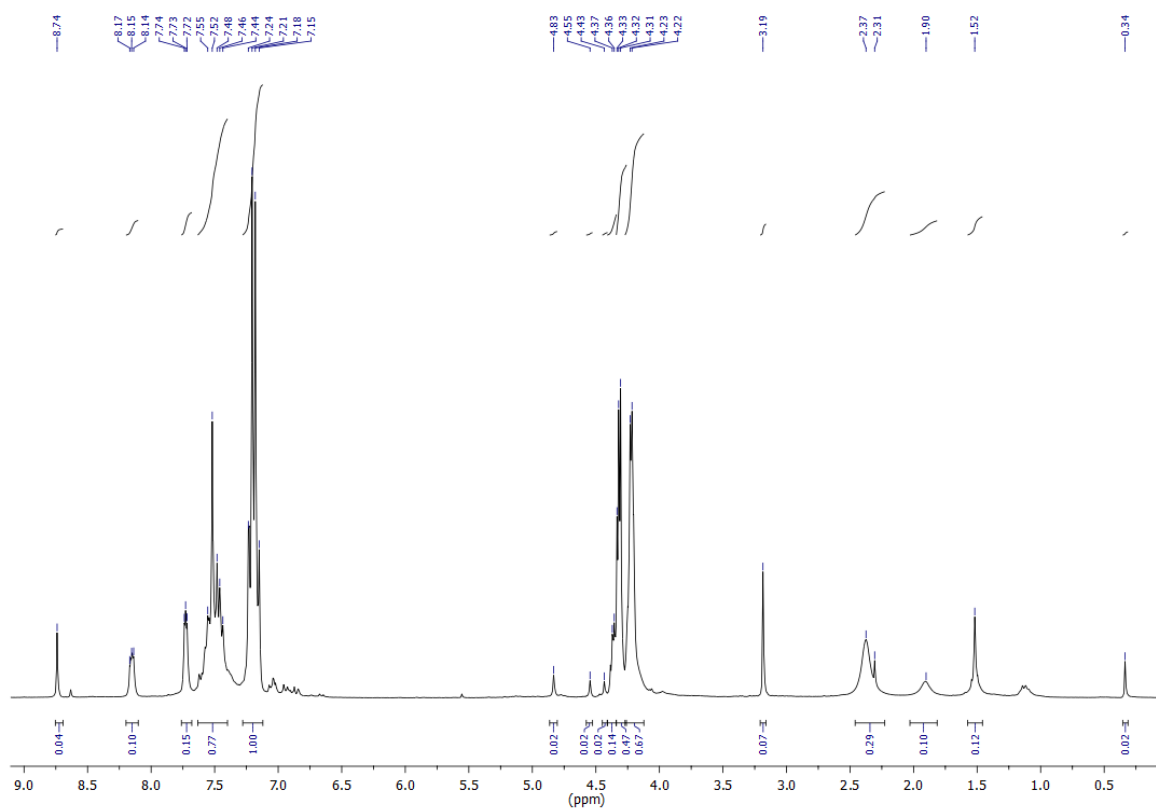


Supplementary figure 2: ¹H NMR of 3PET.

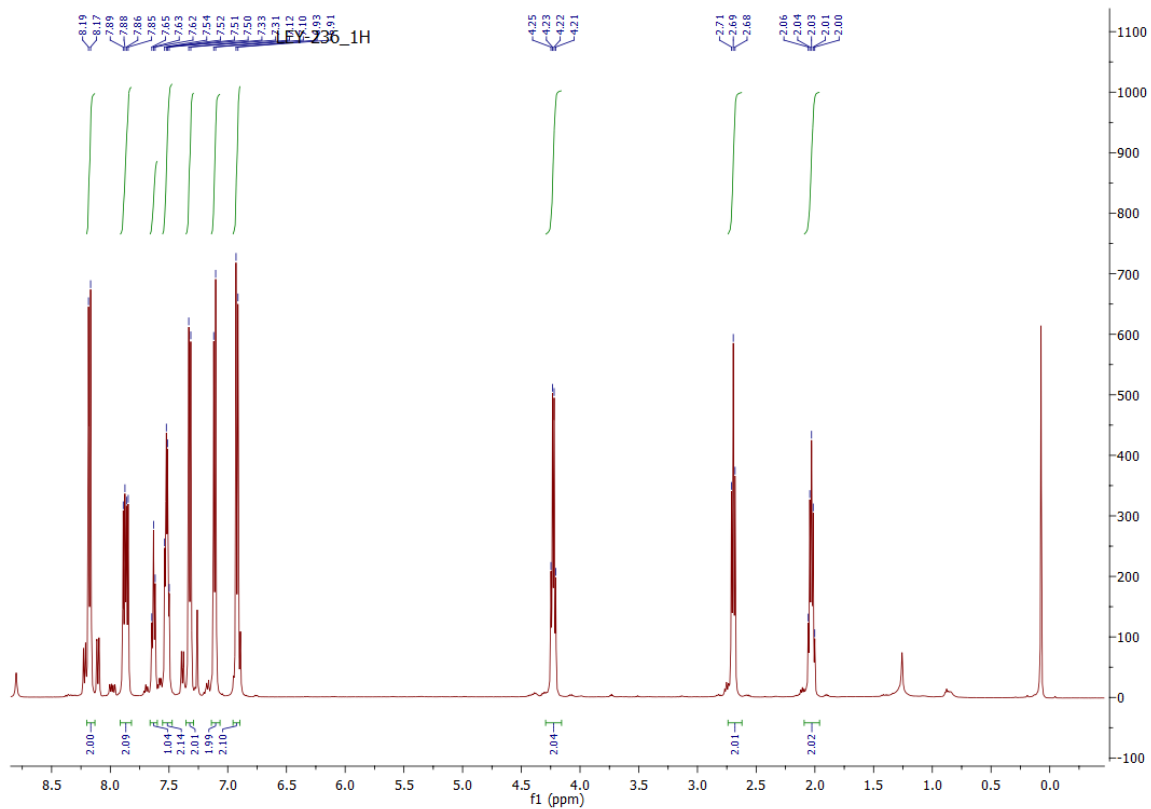


Supplementary figure 3: ¹H NMR of iodophenoxyethanol.





Supplementary figure 6: ¹H NMR of PAL 177.



Supplementary figure 7: ¹H NMR of LEY 236.

Protein lists

Supplementary table I: List of all identified proteins from four *Pseudomonas pseudoalcaligenes* secretomes. When a protein is identified under the given condition this is indicated with “1”.

Accession number	Description	No polymer	Cellulose	BABuTABuB	
				A	PBAT
815974115	Clp protease ClpC [<i>Pseudomonas aeruginosa</i>]	1	1	1	1
953190655	Clp protease ClpC [<i>Pseudomonas aeruginosa</i>]	1	1	1	1
327481005	putative ATPase with chaperone activity, clpB [<i>Pseudomonas stutzeri</i> DSM 4166]	1	1	1	1
782987955	Clp protease ClpC [<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	1
610714292	protein disaggregation chaperone [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
667955352	protein disaggregation chaperone [<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
631781623	Chaperone protein ClpB [<i>Pseudomonas knackmussii</i> B13]	-	-	-	1
735691596	protein disaggregation chaperone [<i>Pseudomonas tuomuerensis</i>]	1	1	1	1
768548465	protein disaggregation chaperone [<i>Pseudomonas stutzeri</i>]	1	1	1	1
296529118	unnamed protein product [<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> 1448A]	1	1	1	1
912970059	protein disaggregation chaperone [<i>Pseudomonas</i> sp. 250J]	1	-	1	1
395807352	ClpB protein [<i>Pseudomonas stutzeri</i> DSM 10701]	1	1	1	1
126169242	hypothetical protein PACG_03381 [<i>Pseudomonas aeruginosa</i> C3719]	-	1	1	1
576708363	ATPase AAA-2 domain protein [<i>Pseudomonas</i> sp. GM41(2012)]	1	1	1	1
856770600	Clp protease ClpC, partial [<i>Pseudomonas lundensis</i>]	-	-	-	1
735689814	elongation factor G [<i>Pseudomonas tuomuerensis</i>]	1	1	1	1
500245118	elongation factor G [<i>Pseudomonas protegens</i> CHA0]	1	1	1	1
787858416	elongation factor G (plasmid) [<i>Pseudomonas chlororaphis</i>]	1	1	1	1
942267779	elongation factor G [<i>Pseudomonas aeruginosa</i>]	1	1	1	1

568070319	elongation factor G [Pseudomonas sp. M1]	1	1	1	1
763481883	elongation factor G [Pseudomonas oryzihabitans]	1	1	1	1
758826281	Translation elongation factor G [Pseudomonas sp. FeS53a]	1	1	1	1
747152421	elongation factor G [Pseudomonas balearica DSM 6083]	-	-	1	1
821535467	elongation factor G [Pseudomonas sp. CCOS 191]	1	1	1	1
928533378	elongation factor G [Pseudomonas aeruginosa]	-	1	1	1
758834355	Translation elongation factor G [Pseudomonas sp. FeS53a]	1	1	1	1
544276648	elongation factor G [Pseudomonas putida LF54]	-	1	1	1
641463920	translation elongation factor G [Pseudomonas sp. P482]	-	-	-	1
667951073	DNA-directed RNA polymerase subunit beta [Pseudomonas mendocina S5.2]	1	1	1	1
782989116	DNA-directed RNA polymerase subunit beta [Pseudomonas pseudoalcaligenes]	1	1	1	1
543435917	DNA-directed RNA polymerase subunit beta [Pseudomonas alcaligenes NBRC 14159]	-	-	-	1
747109406	DNA-directed RNA polymerase subunit beta [Pseudomonas fluorescens]	-	-	-	1
452009999	DNA-directed RNA polymerase subunit beta [Pseudomonas stutzeri NF13]	-	-	-	1
330879362	DNA-directed RNA polymerase subunit beta [Pseudomonas savastanoi pv. glycinea str. race 4]	1	1	1	1
212373983	DNA-directed RNA polymerase beta subunit, partial [Pseudomonas sp. R-35717]	1	1	1	1
391224594	RNA polymerase beta subunit, partial [Pseudomonas guguanensis]	1	1	1	1
575875598	DNA-directed RNA polymerase subunit beta [Pseudomonas aeruginosa PA38182]	1	-	1	1
335334556	RNA polymerase beta-subunit, partial [Pseudomonas litoralis]	1	1	1	1
76556260	RNA polymerase beta subunit, partial [Pseudomonas coronafaciens pv. porri]	-	1	1	1
782989457	molecular chaperone GroEL [Pseudomonas pseudoalcaligenes]	1	1	1	1

556073400	chaperonin GroEL [Pseudomonas sp. VLB120]	1	1	1	1
511100327	chaperonin GroEL [Pseudomonas plecoglossicida NB2011]	1	-	1	1
327481869	chaperonin GroEL [Pseudomonas stutzeri DSM 4166]	1	1	-	1
22121798	Cpn60, partial [Pseudomonas pseudoalcaligenes]	1	1	1	1
768456741	molecular chaperone GroEL [Pseudomonas sp. ES3-33]	1	1	-	1
928481789	molecular chaperone GroEL [Pseudomonas psychrophila]	1	1	1	1
387163734	chaperonin GroL [Pseudomonas fluorescens A506]	-	-	-	1
782987739	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase [Pseudomonas pseudoalcaligenes]	1	1	1	1
667953763	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase [Pseudomonas mendocina S5.2]	1	1	1	1
327480661	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase [Pseudomonas stutzeri DSM 4166]	1	1	1	1
928204164	aconitase [Pseudomonas fuscovaginae]	1	1	1	1
873533401	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase [Pseudomonas sp. KG01]	-	-	-	1
747150749	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase, partial [Pseudomonas balearica DSM 6083]	-	-	-	1
511104953	NAD-glutamate dehydrogenase [Pseudomonas plecoglossicida NB2011]	1	1	1	1
782986927	NAD-glutamate dehydrogenase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610712529	NAD-glutamate dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667954600	putative NAD(+)-dependent glutamate dehydrogenase [Pseudomonas alcaligenes]	1	1	1	1
543435870	NAD-specific glutamate dehydrogenase, large form [Pseudomonas sp. FeS53a]	-	1	-	1
856750626	NAD-glutamate dehydrogenase [Pseudomonas sp. NBRC 14159]	-	1	-	1

	[<i>Pseudomonas deceptionensis</i>]				
	NAD-glutamate dehydrogenase				
747151228	[<i>Pseudomonas balearica</i> DSM 6083]	1	1	-	1
	NAD-glutamate dehydrogenase				
768546754	[<i>Pseudomonas stutzeri</i>]	1	1	1	1
	NAD-glutamate dehydrogenase				
763479232	[<i>Pseudomonas oryzihabitans</i>]	1	-	1	1
	NAD-glutamate dehydrogenase				
	[<i>Pseudomonas coronafaciens</i> pv. <i>oryzae</i>				
331023995	str. 1_6]	1	-	-	1
	elongation factor Tu [<i>Pseudomonas</i>				
782989109	pseudoalcaligenes]	-	-	1	1
	elongation factor Tu [<i>Pseudomonas</i>				
390984852	stutzeri CCUG 29243]	1	1	-	1
	elongation factor Tu [<i>Pseudomonas</i>				
543435912	alcaligenes NBRC 14159]	1	-	-	1
	conserved hypothetical protein				
327479310	[<i>Pseudomonas stutzeri</i> DSM 4166]	-	1	-	1
	elongation factor Tu, partial				
404537780	[<i>Pseudomonas aeruginosa</i> CI27]	1	1	-	1
	elongation factor Tu, partial				
823571128	[<i>Pseudomonas aeruginosa</i>]	1	1	1	1
	Translation elongation factor EF-Tu				
443282038	[<i>Pseudomonas syringae</i> pv. <i>syringae</i> B64]	1	1	1	1
	elongation factor Tu [<i>Pseudomonas</i>				
330984350	amygdali pv. <i>lachrymans</i> str. M301315]	-	-	-	1
	DNA-directed RNA polymerase subunit				
667951072	beta' [<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
	DNA-directed RNA polymerase subunit				
	beta' [<i>Pseudomonas plecoglossicida</i>				
511103996	NB2011]	1	1	1	1
	DNA-directed RNA polymerase, beta'				
	subunit, predominant form [<i>Pseudomonas</i>				
928206978	fuscovaginae]	1	-	-	1
	Keratin, type II cytoskeletal 1 OS=Homo				
P04264	sapiens GN=KRT1 PE=1 SV=6	1	1	1	1
	Keratin, type II cytoskeletal 2 epidermal				
	OS=Homo sapiens GN=KRT2 PE=1				
P35908	SV=2	1	1	1	1
	molecular chaperone DnaK				
782989516	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	molecular chaperone DnaK				
747149952	[<i>Pseudomonas balearica</i> DSM 6083]	1	1	1	1
	molecular chaperone DnaK, partial				
756408406	[<i>Pseudomonas fluorescens</i>]	1	1	1	1

	molecular chaperone DnaK				
735691419	[Pseudomonas tuomuerensis]	1	1	1	1
	30S ribosomal protein S1 [Pseudomonas				
610709976	pseudoalcaligenes AD6]	-	1	-	1
	30S ribosomal protein S1 [Pseudomonas				
327480937	stutzeri DSM 4166]	1	1	1	1
	flagellar basal body rod protein FlgF				
610709575	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	Keratin, type I cytoskeletal 10 OS=Homo				
P13645	sapiens GN=KRT10 PE=1 SV=6	1	1	1	1
	Keratin, type I cytoskeletal 9 OS=Homo				
P35527	sapiens GN=KRT9 PE=1 SV=3	1	1	1	1
	Keratin, type I cytoskeletal 15 OS=Ovis				
O77727	aries GN=KRT15 PE=2 SV=1	1	1	1	1
	YfdX protein [Pseudomonas aeruginosa				
575877517	PA38182]	1	1	1	1
	hypothetical protein TU74_12280				
856770604	[Pseudomonas lundensis]	1	1	1	1
	hypothetical protein PACI27_4549				
404531149	[Pseudomonas aeruginosa CI27]	1	1	1	1
	gamma-glutamyl kinase [Pseudomonas				
610714333	pseudoalcaligenes AD6]	1	1	1	1
	aconitate hydratase [Pseudomonas				
782987148	pseudoalcaligenes]	1	1	1	1
	aconitate hydratase [Pseudomonas				
610709439	pseudoalcaligenes AD6]	-	1	-	1
	aconitate hydratase [Pseudomonas				
667954374	mendocina S5.2]	1	1	1	1
	aconitate hydratase [Pseudomonas sp.				
912968514	250J]	1	1	1	1
758535108	aconitate hydratase [Pseudomonas putida]	1	-	1	1
	aconitate hydratase [Pseudomonas sp.				
459958866	Lz4W]	-	-	-	1
	ABC transporter substrate-binding protein				
610709782	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	ABC transporter substrate-binding protein				
782989895	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	succinyl-CoA synthetase subunit beta				
782988855	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	succinyl-CoA ligase subunit beta				
543438865	[Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
	polynucleotide				
	phosphorylase/polyadenylase				
782989545	[Pseudomonas pseudoalcaligenes]	1	1	1	1
667955319	polynucleotide	1	1	1	1

	phosphorylase/polyadenylase				
	[Pseudomonas mendocina S5.2]				
	polynucleotide				
	phosphorylase/polyadenylase				
699968399	[Pseudomonas sp. MT-1]	1	1	1	1
	Polyribonucleotide nucleotidyltransferase				
748444422	[Pseudomonas batumici]	1	1	1	1
	polyribonucleotide nucleotidyltransferase				
512385691	[Pseudomonas putida NBRC 14164]	1	1	1	1
	dihydrolipoamide acetyltransferase				
667952365	[Pseudomonas mendocina S5.2]	1	1	1	1
	dihydrolipoamide acetyltransferase				
692345562	[Pseudomonas rhizosphaerae]	1	1	1	1
	dihydrolipoamide acetyltransferase				
758538474	[Pseudomonas putida]	-	-	-	1
	dihydrolipoamide acetyltransferase				
928533905	[Pseudomonas aeruginosa]	-	1	1	1
	Dihydrolipoamide acetyltransferase				
	component of pyruvate dehydrogenase				
748444666	complex [Pseudomonas batumici]	-	-	1	1
	ATP phosphoribosyltransferase catalytic				
758542066	subunit [Pseudomonas putida]	1	1	1	1
	ATP phosphoribosyltransferase				
26987701	[Pseudomonas putida KT2440]	-	-	-	1
	flagellar basal body rod protein FlgG				
667954517	[Pseudomonas mendocina S5.2]	1	1	1	1
	flagellar basal body rod protein FlgG				
782987015	[Pseudomonas pseudoalcaligenes]	1	1	1	1
404303198	FlgG [Pseudomonas fluorescens R124]	1	-	1	1
	phosphoenolpyruvate synthase				
782988926	[Pseudomonas pseudoalcaligenes]	1	-	-	1
	phosphoenolpyruvate synthase				
324100325	[Pseudomonas sp. TJI-51]	1	1	1	1
	phosphoenolpyruvate synthase				
452008049	[Pseudomonas stutzeri NF13]	-	-	-	1
	Phosphoenolpyruvate synthase				
443284399	[Pseudomonas syringae pv. syringae B64]	1	1	-	1
	trigger factor [Pseudomonas				
782988790	pseudoalcaligenes]	1	1	1	1
	trigger factor [Pseudomonas				
733396240	frederiksborgensis]	-	1	-	1
	trigger factor [Pseudomonas syringae pv.				
213926436	tomato T1]	1	1	1	1
768546999	trigger factor [Pseudomonas stutzeri]	1	1	1	1
747150865	trigger factor [Pseudomonas balearica	1	1	1	1

	DSM 6083]				
	trigger factor [Pseudomonas				
735690524	tuomuerensis]	1	-	-	1
	aldehyde dehydrogenase [Pseudomonas				
742790257	sp. C5pp]	-	-	-	1
	aldehyde dehydrogenase [Pseudomonas				
816237950	stutzeri]	1	1	1	1
	aldehyde dehydrogenase [Pseudomonas				
667954308	mendocina S5.2]	1	-	-	1
	aldehyde dehydrogenase [Pseudomonas				
758546572	putida]	1	1	1	1
	aldehyde dehydrogenase [Pseudomonas				
735690828	tuomuerensis]	1	1	1	1
	aldehyde dehydrogenase [Pseudomonas				
763481822	oryzihabitans]	1	1	1	1
	aldehyde dehydrogenase [Pseudomonas				
426269913	sp. UW4]	1	1	1	1
	aldehyde dehydrogenase [Pseudomonas				
395808883	stutzeri DSM 10701]	1	1	1	1
	aldehyde dehydrogenase [Pseudomonas				
856768668	lundensis]	1	1	1	1
	aldehyde dehydrogenase [Pseudomonas				
949202688	orientalis]	1	1	1	1
	aldehyde dehydrogenase, partial				
816233898	[Pseudomonas stutzeri]	1	1	1	1
	ATP synthase F0F1 subunit beta				
667951708	[Pseudomonas mendocina S5.2]	1	1	1	1
	ATP synthase F0F1 subunit beta				
691225586	[Pseudomonas cremoricolorata]	-	-	-	1
	ATP synthase beta chain [Pseudomonas				
758827087	sp. FeS53a]	1	1	1	1
	glycine dehydrogenase [Pseudomonas				
610707851	pseudoalcaligenes AD6]	1	1	1	1
	glycine dehydrogenase [Pseudomonas				
667953067	mendocina S5.2]	1	1	1	1
	glycine dehydrogenase [Pseudomonas				
954635335	aeruginosa]	-	-	-	1
	pyruvate dehydrogenase [Pseudomonas				
667952366	mendocina S5.2]	-	1	-	1
	pyruvate dehydrogenase [Pseudomonas				
126170206	aeruginosa C3719]	-	1	-	1
	pyruvate dehydrogenase E1 component				
543435959	[Pseudomonas alcaligenes NBRC 14159]	-	1	-	1
	pyruvate dehydrogenase subunit E1				
379066679	[Pseudomonas stutzeri ATCC 14405 =	-	1	-	1

	CCUG 16156]				
	4-aminobutyrate aminotransferase				
610713675	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	4-aminobutyrate aminotransferase				
667952010	[Pseudomonas mendocina S5.2]	-	-	-	1
	4-aminobutyrate aminotransferase				
733475080	[Pseudomonas putida]	-	1	-	1
	isocitrate dehydrogenase [Pseudomonas				
782987855	pseudoalcaligenes]	1	1	1	1
	isocitrate dehydrogenase [Pseudomonas				
929387160	aeruginosa]	1	1	1	1
	isocitrate dehydrogenase [Pseudomonas				
763478485	oryzihabitans]	1	1	1	1
	isocitrate dehydrogenase [Pseudomonas				
298157923	savastanoi pv. savastanoi NCPPB 3335]	-	-	-	1
	flagellin type B [Pseudomonas stutzeri				
452006743	NF13]	1	1	1	1
	branched-chain alpha-keto acid				
	dehydrogenase subunit E2 [Pseudomonas				
816237181	stutzeri]	-	1	-	1
	flagellin type B [Pseudomonas aeruginosa				
115584242	UCBPP-PA14]	1	1	1	1
	A-type flagellin [Pseudomonas stutzeri				
395809336	DSM 10701]	-	1	-	1
	branched-chain alpha-keto acid				
	dehydrogenase subunit E2 [Pseudomonas				
763482566	oryzihabitans]	-	1	1	1
926555844	flagellin [Pseudomonas sp. 655]	1	1	1	1
848256547	flagellin type B [Pseudomonas stutzeri]	1	-	1	1
	flagellin domain-containing protein				
390983549	[Pseudomonas stutzeri CCUG 29243]	1	1	1	1
	amino acid ABC transporter				
667951378	[Pseudomonas mendocina S5.2]	1	1	1	1
	amino acid ABC transporter				
735691098	[Pseudomonas tuomuerensis]	-	-	1	1
	amino acid ABC transporter				
692345046	[Pseudomonas rhizosphaerae]	1	1	1	1
	amino acid ABC transporter				
713119070	[Pseudomonas mediterranea CFBP 5447]	-	-	-	1
	DNA-binding protein HU [Pseudomonas				
327480676	stutzeri DSM 4166]	1	1	1	1
	nucleoid protein HU beta subunit				
699967304	[Pseudomonas sp. MT-1]	1	1	1	1
	transcriptional regulator HU subunit alpha				
763481396	[Pseudomonas oryzihabitans]	-	-	-	1

782989522	carbamoyl phosphate synthase large subunit [Pseudomonas pseudoalcaligenes]	1	1	1	1
543438356	carbamoyl-phosphate synthase large chain [Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
816237951	alcohol dehydrogenase [Pseudomonas stutzeri]	1	1	1	1
703403454	Fe-containing alcohol dehydrogenase [Pseudomonas xanthomarina]	-	-	-	1
667954729	elongation factor Ts [Pseudomonas mendocina S5.2]	1	1	1	1
782985888	multifunctional fatty acid oxidation complex subunit alpha [Pseudomonas pseudoalcaligenes]	1	1	1	1
543438056	fatty acid oxidation complex subunit alpha [Pseudomonas alcaligenes NBRC 14159]	-	1	1	1
782987856	isocitrate dehydrogenase [Pseudomonas pseudoalcaligenes]	1	1	1	1
126167540	isocitrate dehydrogenase [Pseudomonas aeruginosa C3719]	-	-	-	1
782988854	dihydrolipoamide dehydrogenase [Pseudomonas pseudoalcaligenes]	1	1	1	1
631778913	Dihydrolipoamide dehydrogenase [Pseudomonas knackmussii B13]	1	1	-	1
379066824	dihydrolipoamide dehydrogenase [Pseudomonas stutzeri ATCC 14405 = CCUG 16156]	1	-	1	1
699966740	dihydrolipoamide dehydrogenase [Pseudomonas sp. MT-1]	-	-	-	1
756404829	dihydrolipoamide dehydrogenase [Pseudomonas fluorescens]	1	1	1	1
763479278	dihydrolipoamide dehydrogenase [Pseudomonas oryzae]	-	-	1	1
940136548	hypothetical protein ALO69_02750 [Pseudomonas ficuserectae]	1	1	1	1
782988615	malate synthase [Pseudomonas pseudoalcaligenes]	1	1	1	1
667951200	malate synthase [Pseudomonas mendocina S5.2]	-	1	-	1
782984351	malate synthase [Pseudomonas pseudoalcaligenes]	-	1	1	1
749477159	Malate synthase G [Pseudomonas fluorescens]	-	-	1	1
568072297	malate synthase [Pseudomonas sp. M1]	1	1	1	1
856795787	malate synthase [Pseudomonas]	-	-	-	1

	weihenstephanensis]				
	malate synthase [Pseudomonas putida				
816871789	KG-4]	1	1	1	1
	ribonuclease E [Pseudomonas				
782985932	pseudoalcaligenes]	1	1	1	1
	ribonuclease E [Pseudomonas mendocina				
667953350	S5.2]	-	-	-	1
	ribonuclease E [Pseudomonas				
735692781	tuomuerensis]	1	1	1	1
	50S ribosomal protein L1 [Pseudomonas				
667951076	mendocina S5.2]	1	1	-	1
	50S ribosomal protein L1 [Pseudomonas				
610710777	pseudoalcaligenes AD6]	-	-	1	1
	LSU ribosomal protein L1p (L10Ae)				
758826274	[Pseudomonas sp. FeS53a]	-	1	-	1
	pyruvate carboxylase subunit B				
667951591	[Pseudomonas mendocina S5.2]	1	1	1	1
	pyruvate carboxylase subunit B				
747152810	[Pseudomonas balearica DSM 6083]	1	-	1	1
	pyruvate carboxylase subunit B				
390985292	[Pseudomonas stutzeri CCUG 29243]	-	-	1	1
	Pyruvate carboxylase subunit B				
631777071	[Pseudomonas knackmussii B13]	-	-	-	1
782984900	azurin [Pseudomonas pseudoalcaligenes]	1	1	1	1
	50S ribosomal protein L10 [Pseudomonas				
610710778	pseudoalcaligenes AD6]	1	1	1	1
	50S ribosomal protein L6 [Pseudomonas				
667951051	mendocina S5.2]	1	1	1	1
	alkyl hydroperoxide reductase subunit C				
403248708	[Pseudomonas aeruginosa CIG1]	1	1	1	1
	alkyl hydroperoxide reductase subunit C				
543437843	[Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
	ABC transporter substrate-binding protein				
667953780	[Pseudomonas mendocina S5.2]	1	1	1	1
	ABC transporter substrate-binding protein				
782988788	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	dihydrolipoamide succinyltransferase				
667953840	[Pseudomonas mendocina S5.2]	1	1	-	1
	isoleucine--tRNA ligase [Pseudomonas				
782985232	pseudoalcaligenes]	1	1	1	1
	isoleucyl-tRNA synthetase [Pseudomonas				
327479529	stutzeri DSM 4166]	-	-	-	1
	isoleucine--tRNA ligase [Pseudomonas				
667952753	mendocina S5.2]	1	1	1	1
735690967	isoleucine--tRNA ligase [Pseudomonas	-	-	-	1

	tuomuerensis]				
	50S ribosomal protein L14 [Pseudomonas				
310941677	alcaligenes]	-	-	-	1
	hypothetical protein YQ19_29855				
815974110	[Pseudomonas aeruginosa]	1	1	1	1
	hypothetical protein PstZobell_19113				
	[Pseudomonas stutzeri ATCC 14405 =				
379066789	CCUG 16156]	1	1	1	1
	translation initiation factor IF-2				
667955323	[Pseudomonas mendocina S5.2]	1	-	-	1
	translation initiation factor IF-2				
782989540	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	initiation factor 2 [Pseudomonas sp.				
576712172	GM30]	-	-	-	1
	Translation initiation factor 2				
758822864	[Pseudomonas sp. FeS53a]	-	-	-	1
	translation initiation factor IF-2				
735691405	[Pseudomonas tuomuerensis]	-	-	1	1
	C4-dicarboxylate ABC transporter				
782988205	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	C4-dicarboxylate ABC transporter				
	[Pseudomonas fluorescens NCIMB				
913662490	11764]	-	1	1	1
	C4-dicarboxylate ABC transporter				
610712963	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
	C4-dicarboxylate ABC transporter				
735691141	[Pseudomonas tuomuerensis]	1	-	1	1
	C4-dicarboxylate ABC transporter				
782987823	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	phosphonate ABC transporter substrate-				
	binding protein [Pseudomonas				
782986499	pseudoalcaligenes]	1	1	1	1
	phosphonate ABC transporter substrate-				
	binding protein [Pseudomonas mendocina				
667954907	S5.2]	1	1	1	1
	Phosphonate ABC-type transport system,				
	periplasmic substrate-binding protein				
	[Pseudomonas syringae pv. syringae str.				
590455576	B301D-R]	-	-	-	1
	phosphonate ABC transporter substrate-				
699966176	binding protein [Pseudomonas sp. MT-1]	1	-	-	1
	ABC transporter substrate-binding protein				
782985615	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	DNA gyrase subunit A [Pseudomonas				
782987542	pseudoalcaligenes]	1	1	1	1

758829451	DNA gyrase subunit A [Pseudomonas sp. FeS53a]	-	-	1	1
543436257	DNA gyrase subunit A [Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
763482600	DNA gyrase subunit A [Pseudomonas oryzae]	-	-	1	1
667951060	30S ribosomal protein S3 [Pseudomonas mendocina S5.2]	1	1	1	1
213925909	30S ribosomal protein S5 [Pseudomonas syringae pv. tomato T1]	1	1	1	1
782989142	30S ribosomal protein S5 [Pseudomonas pseudoalcaligenes]	1	1	1	1
610709722	50S ribosomal protein L25 [Pseudomonas pseudoalcaligenes AD6]	1	-	1	1
782985318	50S ribosomal protein L25 [Pseudomonas pseudoalcaligenes]	1	1	1	1
667951564	C4-dicarboxylate ABC transporter substrate-binding protein [Pseudomonas mendocina S5.2]	1	1	1	1
610708367	C4-dicarboxylate ABC transporter substrate-binding protein [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782984561	spermidine/putrescine ABC transporter substrate-binding protein [Pseudomonas pseudoalcaligenes]	1	1	1	1
667952309	glutamate synthase [Pseudomonas mendocina S5.2]	1	1	1	1
610712645	glutamate synthase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
26991752	glutamate synthase subunit alpha [Pseudomonas putida KT2440]	1	1	1	1
758546803	glutamate synthase [Pseudomonas putida]	-	1	1	1
641462817	GXGXG motif family protein [Pseudomonas sp. P482]	-	-	-	1
568071993	glutamate synthase subunit alpha [Pseudomonas sp. M1]	-	-	-	1
327479227	glutamate synthase subunit alpha [Pseudomonas stutzeri DSM 4166]	-	-	-	1
782986980	indolepyruvate ferredoxin oxidoreductase [Pseudomonas pseudoalcaligenes]	1	1	1	1
667954557	indolepyruvate ferredoxin oxidoreductase [Pseudomonas mendocina S5.2]	1	1	1	1
327479409	indolepyruvate ferredoxin oxidoreductase [Pseudomonas stutzeri DSM 4166]	-	1	-	1
761540274	hypothetical protein RD00_00020, partial	1	-	1	1

	[<i>Pseudomonas amygdali</i> pv. <i>tabaci</i>]				
	lysyl-tRNA synthetase [<i>Pseudomonas</i>				
782987269	pseudoalcaligenes]	1	1	1	1
	lysyl-tRNA synthetase [<i>Pseudomonas</i> sp.				
761890074	10-1B]	1	1	1	1
	lysyl-tRNA synthetase [<i>Pseudomonas</i>				
856797000	weihenstephanensis]	-	-	-	1
	lysyl-tRNA synthetase [<i>Pseudomonas</i>				
320323151	savastanoi pv. <i>glycinea</i> str. B076]	1	1	1	1
	flagellar basal body rod protein FlgC				
667954521	[<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
	phosphate-binding protein [<i>Pseudomonas</i>				
667951920	mendocina S5.2]	1	1	1	1
	phosphate-binding protein [<i>Pseudomonas</i>				
782984332	pseudoalcaligenes]	1	1	1	1
	phosphate-binding protein [<i>Pseudomonas</i>				
610711003	pseudoalcaligenes AD6]	1	1	1	1
	2-oxoglutarate dehydrogenase				
782988852	[<i>Pseudomonas pseudoalcaligenes</i>]	1	-	1	1
	2-oxoglutarate dehydrogenase				
667953839	[<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
	2-oxoglutarate dehydrogenase				
610712094	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
	ribonucleotide-diphosphate reductase				
	subunit alpha [<i>Pseudomonas</i>				
610712991	pseudoalcaligenes AD6]	1	1	1	1
	ribonucleoside-diphosphate reductase				
	alpha subunit [<i>Pseudomonas alcaligenes</i>				
543439240	NBRC 14159]	1	1	1	1
568075951	isocitrate lyase [<i>Pseudomonas</i> sp. M1]	-	-	1	1
768548004	isocitrate lyase [<i>Pseudomonas stutzeri</i>]	-	-	-	1
	aromatic amino acid aminotransferase				
610709968	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
	aromatic amino acid aminotransferase				
782987563	[<i>Pseudomonas pseudoalcaligenes</i>]	-	1	1	1
	4-hydroxyphenylpyruvate dioxygenase				
782989944	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	flagellar hook-length control protein				
610709537	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	1
	flagellar hook-length control protein				
667954476	[<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
	preprotein translocase subunit SecA				
782985210	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	Protein translocase subunit SecA				
631781358	[<i>Pseudomonas knackmussii</i> B13]	-	1	-	1

	preprotein translocase subunit SecA				
	[Pseudomonas amygdali pv.				
330877125	morsprunorum str. M302280]	-	-	-	1
	preprotein translocase subunit SecA				
556073384	[Pseudomonas sp. VLB120]	-	1	-	1
	preprotein translocase subunit SecA				
692343024	[Pseudomonas rhizosphaerae]	-	-	-	1
404305730	SecA [Pseudomonas fluorescens R124]	1	1	1	1
	hypothetical protein PstZobell_19103				
	[Pseudomonas stutzeri ATCC 14405 =				
379066787	CCUG 16156]	1	1	1	1
	hypothetical protein PACI27_4551				
404531151	[Pseudomonas aeruginosa CI27]	1	-	-	1
	ketol-acid reductoisomerase				
610711129	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	ketol-acid reductoisomerase				
928213318	[Pseudomonas fuscovaginae]	1	-	1	1
	50S ribosomal protein L19 [Pseudomonas				
782986278	pseudoalcaligenes]	1	1	1	1
	aminopeptidase N [Pseudomonas				
782986896	pseudoalcaligenes]	1	1	1	1
	aminopeptidase N [Pseudomonas				
610707824	pseudoalcaligenes AD6]	1	1	1	1
	aminopeptidase N [Pseudomonas				
667954621	mendocina S5.2]	1	1	1	1
	transketolase [Pseudomonas mendocina				
667952215	S5.2]	1	1	1	1
	transketolase [Pseudomonas				
782984659	pseudoalcaligenes]	1	1	1	1
	transketolase [Pseudomonas				
511100703	plecoglossicida NB2011]	1	1	-	1
	flagellar basal body rod modification				
	protein FlgD [Pseudomonas mendocina				
667954520	S5.2]	1	1	1	1
	flagellar basal body rod modification				
	protein FlgD [Pseudomonas				
610709577	pseudoalcaligenes AD6]	1	1	1	1
	Serum albumin OS=Bos taurus GN=ALB				
P02769	PE=1 SV=4	1	1	1	1
	Serum albumin OS=Homo sapiens				
P02768	GN=ALB PE=1 SV=2	1	1	1	1
12345	Trypsin OS=Sus scrofa PE=1 SV=1	1	1	1	1
	30S ribosomal protein S6 [Pseudomonas				
610706380	pseudoalcaligenes AD6]	1	1	1	1
735690928	30S ribosomal protein S6 [Pseudomonas	1	1	1	1

	tuomuerensis]				
	30S ribosomal protein S6 [Pseudomonas				
691225004	cremoricolorata]	-	1	1	1
	transcriptional regulator [Pseudomonas				
667952872	mendocina S5.2]	1	1	1	1
	transcriptional regulator [Pseudomonas				
782985369	pseudoalcaligenes]	1	1	1	1
	proline dehydrogenase/delta-1-pyrroline-				
	5-carboxylate dehydrogenase				
543437478	[Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
	Transcriptional repressor of PutA and				
758823751	PutP [Pseudomonas sp. FeS53a]	-	-	-	1
	bifunctional PutA protein [Pseudomonas				
229359874	fluorescens SBW25]	-	-	-	1
	transcriptional regulator [Pseudomonas				
735691207	tuomuerensis]	1	1	1	1
	pyrroline-5-carboxylate dehydrogenase				
769334675	[Pseudomonas sp. 10B238]	-	1	1	1
	bifunctional proline				
	dehydrogenase/pyrroline-5-carboxylate				
848255251	dehydrogenase [Pseudomonas stutzeri]	-	-	-	1
332651065	OprF, partial [Pseudomonas oleovorans]	1	1	1	1
667954150	porin [Pseudomonas mendocina S5.2]	-	-	-	1
782988933	porin [Pseudomonas pseudoalcaligenes]	1	1	1	1
782985544	ferritin [Pseudomonas pseudoalcaligenes]	1	1	1	1
	ferritin [Pseudomonas balearica DSM				
747151696	6083]	1	1	-	1
568075264	ferritin [Pseudomonas sp. M1]	1	1	1	1
	cytochrome [Pseudomonas				
782984309	pseudoalcaligenes]	1	1	1	1
	spermidine/putrescine ABC transporter				
	substrate-binding protein [Pseudomonas				
610711665	pseudoalcaligenes AD6]	1	1	1	1
	ornithine acetyltransferase [Pseudomonas				
782985211	pseudoalcaligenes]	1	1	1	1
	ornithine acetyltransferase [Pseudomonas				
610708018	pseudoalcaligenes AD6]	-	1	1	1
	ornithine acetyltransferase [Pseudomonas				
691226340	cremoricolorata]	1	1	-	1
	Serine protein kinase (prkA protein), P-				
	loop containing [Pseudomonas sp.				
758833075	FeS53a]	1	-	1	1
	serine/threonine protein kinase				
768549449	[Pseudomonas stutzeri]	1	1	1	1
568076182	PrkA family serine protein kinase	1	1	1	1

	[Pseudomonas sp. M1]				
	glyceraldehyde-3-phosphate				
	dehydrogenase [Pseudomonas				
782985905	pseudoalcaligenes]	1	1	1	1
	glyceraldehyde-3-phosphate				
	dehydrogenase [Pseudomonas				
610712860	pseudoalcaligenes AD6]	-	-	1	1
	glyceraldehyde-3-phosphate				
568071018	dehydrogenase [Pseudomonas sp. M1]	1	1	1	1
	flagellar rod assembly protein FlgJ				
782987017	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	flagellar rod assembly protein FlgJ				
610709571	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	peptidoglycan hydrolase FlgJ				
15596282	[Pseudomonas aeruginosa PAO1]	1	1	1	1
	heat shock protein 90 [Pseudomonas				
327480496	stutzeri DSM 4166]	1	1	1	1
	heat shock protein 90 [Pseudomonas				
667953852	mendocina S5.2]	1	1	1	1
856776237	heat shock protein 90 [Pseudomonas lini]	1	1	1	1
	heat shock protein 90 [Pseudomonas				
610712106	pseudoalcaligenes AD6]	1	1	1	1
	heat shock protein 90 [Pseudomonas				
763479283	oryzihabitans]	1	1	1	1
	succinyl-CoA synthetase alpha chain				
95111644	[Pseudomonas entomophila L48]	1	1	1	1
	succinyl-CoA synthetase subunit alpha				
568073990	[Pseudomonas sp. M1]	1	1	1	1
	succinyl-CoA synthetase (ADP-forming)				
	alpha subunit [Pseudomonas				
928206178	fuscovaginae]	1	1	1	1
	succinyl-CoA synthetase subunit alpha				
747150683	[Pseudomonas balearica DSM 6083]	-	-	-	1
	Succinyl-CoA ligase [ADP-forming]				
	alpha chain [Pseudomonas savastanoi pv.				
298158998	savastanoi NCPPB 3335]	1	1	1	1
	molecular chaperone SurA [Pseudomonas				
782988519	pseudoalcaligenes]	1	1	1	1
	molecular chaperone SurA [Pseudomonas				
761894484	sp. 10-1B]	-	1	-	1
	peptidyl-prolyl cis-trans isomerase SurA				
395807337	[Pseudomonas stutzeri DSM 10701]	-	-	1	1
	peptidyl-prolyl cis-trans isomerase SurA				
327479275	[Pseudomonas stutzeri DSM 4166]	-	-	1	1
667951246	glutamine synthetase [Pseudomonas	1	1	-	1

	mendocina S5.2]				
	aspartyl-tRNA synthetase [Pseudomonas				
782985546	pseudoalcaligenes]	1	1	1	1
	aspartyl-tRNA synthetase [Pseudomonas				
610708667	pseudoalcaligenes AD6]	1	1	1	1
	DNA-directed RNA polymerase subunit				
667951041	alpha [Pseudomonas mendocina S5.2]	1	1	1	1
	xylulose 5-phosphate 3-epimerase				
782985564	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	nitrate reductase [Pseudomonas				
667954660	mendocina S5.2]	1	1	1	1
768548332	nitrate reductase [Pseudomonas stutzeri]	1	1	1	1
	nitrate reductase [Pseudomonas sp.				
780906909	BICA1-14]	1	1	1	1
	phosphoribosylformylglycinamide				
667955153	synthase [Pseudomonas mendocina S5.2]	1	1	1	1
	phosphoribosylformylglycinamide				
691224651	synthase [Pseudomonas cremoricolorata]	1	-	1	1
	phosphoribosylformylglycinamide				
	synthase [Pseudomonas syringae pv.				
817572089	syringae HS191]	-	1	-	1
	phosphoribosylformylglycinamide				
761894131	synthase [Pseudomonas sp. 10-1B]	1	-	1	1
	thiol:disulfide interchange protein				
667951902	[Pseudomonas mendocina S5.2]	1	1	1	1
	thiol:disulfide interchange protein				
782984311	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	hypothetical protein AU05_24515				
610707826	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	hypothetical protein DW68_19215				
667954619	[Pseudomonas mendocina S5.2]	1	1	1	1
	ATP F0F1 synthase subunit alpha				
782984127	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	hypothetical protein N619_04560				
782989618	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	hypothetical protein SZ55_1331				
758835050	[Pseudomonas sp. FeS53a]	1	1	1	1
	hypothetical protein AU05_06355				
610706130	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	putative exported protein [Pseudomonas				
229364397	fluorescens SBW25]	-	-	-	1
	hypothetical protein AU05_20850				
610708714	[Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
	aspartate kinase [Pseudomonas				
782989908	pseudoalcaligenes]	1	1	1	1

940171541	Aspartokinase [<i>Pseudomonas amygdali</i> pv. <i>mori</i>]	1	1	1	1
610708084	electron transporter RnfB [<i>Pseudomonas</i> pseudoalcaligenes AD6]	1	1	1	1
684199038	electron transporter RnfB [<i>Pseudomonas</i> mosselii SJ10]	-	-	-	1
925646618	electron transporter RnfB, partial [<i>Pseudomonas psychrophila</i>]	1	-	-	1
768453996	electron transporter RnfB [<i>Pseudomonas</i> sp. ES3-33]	1	-	-	1
782988791	Clp protease ClpP [<i>Pseudomonas</i> pseudoalcaligenes]	1	1	1	1
610713577	iron ABC transporter substrate-binding protein [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
667952115	iron ABC transporter substrate-binding protein [<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
782984544	iron ABC transporter substrate-binding protein [<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
667953315	DNA topoisomerase I [<i>Pseudomonas</i> mendocina S5.2]	1	1	1	1
782985894	DNA topoisomerase I [<i>Pseudomonas</i> pseudoalcaligenes]	1	-	-	1
684195384	DNA topoisomerase I [<i>Pseudomonas</i> mosselii SJ10]	1	1	1	1
126167915	DNA topoisomerase I [<i>Pseudomonas</i> aeruginosa C3719]	-	-	1	1
395808023	DNA topoisomerase I subunit omega [<i>Pseudomonas stutzeri</i> DSM 10701]	-	-	-	1
667952527	arginine decarboxylase [<i>Pseudomonas</i> mendocina S5.2]	1	1	1	1
782987750	peptidylprolyl isomerase [<i>Pseudomonas</i> pseudoalcaligenes]	1	1	1	1
782984126	ATP F0F1 synthase subunit gamma [<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
782986157	amino acid ABC transporter substrate- binding protein [<i>Pseudomonas</i> pseudoalcaligenes]	1	1	1	1
543439812	fructose-1,6-bisphosphate aldolase [<i>Pseudomonas alcaligenes</i> NBRC 14159]	1	1	1	1
667951054	50S ribosomal protein L5 [<i>Pseudomonas</i> mendocina S5.2]	1	1	1	1
379064301	50S ribosomal protein L5 [<i>Pseudomonas</i> stutzeri ATCC 14405 = CCUG 16156]	-	-	-	1
787852996	50S ribosomal protein L5 [<i>Pseudomonas</i>]	1	1	1	1

	chlororaphis]				
	urocanate hydratase [Pseudomonas				
610708892	pseudoalcaligenes AD6]	1	1	1	1
	urocanate hydratase [Pseudomonas sp.				
768453906	ES3-33]	1	1	1	1
	3-hydroxydecanoyl-ACP dehydratase				
667953876	[Pseudomonas mendocina S5.2]	1	1	1	1
	3-hydroxydecanoyl-ACP dehydratase				
610712129	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	proline--tRNA ligase [Pseudomonas				
610708658	pseudoalcaligenes AD6]	-	-	1	1
	proline--tRNA ligase [Pseudomonas				
543437995	alcaligenes NBRC 14159]	1	-	1	1
	proline--tRNA ligase [Pseudomonas				
692343179	rhizosphaerae]	1	1	1	1
	prolyl-tRNA synthetase [Pseudomonas				
928208468	fuscovaginae]	-	-	-	1
	50S ribosomal protein L22 [Pseudomonas				
500245110	protegens CHA0]	1	1	1	1
	universal stress protein UspA				
610714198	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	universal stress protein UspA				
782985385	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	enoyl-ACP reductase [Pseudomonas				
610712046	pseudoalcaligenes AD6]	1	1	1	1
	hypothetical protein AU05_00025				
610715026	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	hypothetical protein N619_04225				
782989425	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	adenosylhomocysteinase [Pseudomonas				
610708539	pseudoalcaligenes AD6]	1	-	-	1
	adenosylhomocysteinase [Pseudomonas				
568072030	sp. M1]	1	-	1	1
	S-adenosyl-L-homocysteine hydrolase				
	[Pseudomonas stutzeri ATCC 14405 =				
379064885	CCUG 16156]	-	-	-	1
	30S ribosomal protein S4 [Pseudomonas				
667951042	mendocina S5.2]	1	1	1	1
	leucine ABC transporter substrate-binding				
782985672	protein [Pseudomonas pseudoalcaligenes]	1	1	1	1
	leucine ABC transporter substrate-binding				
667953116	protein [Pseudomonas mendocina S5.2]	-	1	1	1
	High-affinity leucine-specific transport				
	system, periplasmic binding protein LivK				
758823082	[Pseudomonas sp. FeS53a]	1	1	1	1

	leucine ABC transporter substrate-binding				
768545796	protein [Pseudomonas stutzeri]	-	-	1	1
568073342	amino acid ABC transporter substrate-binding protein [Pseudomonas sp. M1]	-	-	-	1
674103190	aldehyde dismutase [Pseudomonas sp. 1-7]	1	1	1	1
582006392	glutathione-independent formaldehyde dehydrogenase [Pseudomonas pseudoalcaligenes CECT 5344]	1	1	1	1
148509663	glutathione-independent formaldehyde dehydrogenase [Pseudomonas putida F1]	1	-	1	1
667953469	2-keto-4-pentenoate hydratase [Pseudomonas mendocina S5.2]	1	1	1	1
543438121	hypothetical protein PA6_012_00890 [Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
26987191	30S ribosomal protein S7 [Pseudomonas putida KT2440]	1	1	1	1
782987778	3-oxoacyl-ACP synthase [Pseudomonas pseudoalcaligenes]	1	1	1	1
763482617	3-oxoacyl-ACP synthase [Pseudomonas oryzae]	1	1	1	1
390983520	3-oxoacyl-(acyl carrier protein) synthase I [Pseudomonas stutzeri CCUG 29243]	-	-	-	1
782989539	transcription elongation factor NusA [Pseudomonas pseudoalcaligenes]	1	1	1	1
782989907	alanyl-tRNA synthetase [Pseudomonas pseudoalcaligenes]	1	1	1	1
667953430	alanyl-tRNA synthetase [Pseudomonas mendocina S5.2]	1	1	1	1
641465338	alanine--tRNA ligase [Pseudomonas sp. P482]	1	1	1	1
934020183	alanyl-tRNA synthetase [Pseudomonas viridiflava]	-	-	-	1
390982713	alanyl-tRNA ligase [Pseudomonas stutzeri CCUG 29243]	-	-	-	1
758824086	Alanyl-tRNA synthetase [Pseudomonas sp. FeS53a]	-	-	1	1
782986193	valyl-tRNA synthetase [Pseudomonas pseudoalcaligenes]	1	1	1	1
543437233	valine--tRNA ligase [Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
610710473	valyl-tRNA synthetase [Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
213927026	valyl-tRNA synthetase [Pseudomonas syringae pv. tomato T1]	-	1	1	1

631777905	Valine--tRNA ligase [Pseudomonas knackmussii B13]	-	-	1	1
395807806	valyl-tRNA ligase [Pseudomonas stutzeri DSM 10701]	-	-	-	1
667954112	sulfite reductase [Pseudomonas mendocina S5.2]	1	1	1	1
568073905	sulfite reductase [Pseudomonas sp. M1]	1	-	1	1
327480842	sulfite reductase [Pseudomonas stutzeri DSM 4166]	-	-	-	1
667955185	nucleoside diphosphate kinase [Pseudomonas mendocina S5.2]	1	1	1	1
610708681	quinolinate synthase A [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
327481484	quinolinate synthetase [Pseudomonas stutzeri DSM 4166]	-	1	-	1
769335308	flagellar hook protein FlgK [Pseudomonas sp. 10B238]	1	1	1	1
747150410	flagellar hook protein FlgK [Pseudomonas balearica DSM 6083]	1	1	1	1
390982752	flagellar hook-associated protein FlgK [Pseudomonas stutzeri CCUG 29243]	1	1	-	1
782985563	beta-lactamase [Pseudomonas pseudoalcaligenes]	1	1	1	1
667953011	beta-lactamase [Pseudomonas mendocina S5.2]	1	1	1	1
970755349	DEAD/DEAH box helicase [Pseudomonas aeruginosa]	1	1	1	1
782987548	3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610709978	3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
758829447	Cyclohexadienyl dehydrogenase [Pseudomonas sp. FeS53a]	1	1	1	1
511105003	bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas plecoglossicida NB2011]	1	1	-	1
782984598	phosphoenolpyruvate carboxykinase [ATP] [Pseudomonas pseudoalcaligenes]	1	1	1	1
667952152	hypothetical protein DW68_06340 [Pseudomonas mendocina S5.2]	1	1	1	1
452006446	phosphoenolpyruvate carboxykinase [Pseudomonas stutzeri NF13]	-	-	-	1

68347170	ribosomal protein L24 [Pseudomonas protegens Pf-5]	-	-	-	1
610713676	succinate-semialdehyde dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	1	-	1	1
387161025	succinate-semialdehyde dehydrogenase [Pseudomonas fluorescens A506]	-	-	1	1
856793885	succinate-semialdehyde dehydrogenase [Pseudomonas helleri]	-	-	1	1
667955173	2-isopropylmalate synthase [Pseudomonas mendocina S5.2]	1	1	1	1
568074851	2-isopropylmalate synthase [Pseudomonas sp. M1]	-	-	-	1
768457099	2-isopropylmalate synthase [Pseudomonas sp. ES3-33]	1	-	-	1
610710520	inosine-5-monophosphate dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667955165	inosine-5-monophosphate dehydrogenase [Pseudomonas mendocina S5.2]	-	-	1	1
543438250	inosine-5'-monophosphate dehydrogenase [Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
949218184	inosine-5-monophosphate dehydrogenase [Pseudomonas veronii]	-	-	1	1
327481730	inosine 5'-monophosphate dehydrogenase [Pseudomonas stutzeri DSM 4166]	1	1	1	1
500244517	inosine-5'-monophosphate dehydrogenase GuaB [Pseudomonas protegens CHA0]	-	-	-	1
610713889	NADH dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667953928	NADH dehydrogenase [Pseudomonas mendocina S5.2]	1	1	1	1
782987832	NADH dehydrogenase [Pseudomonas pseudoalcaligenes]	1	1	1	1
689659777	NADH dehydrogenase [Pseudomonas fluorescens LMG 5329]	-	-	1	1
667954796	acetyl-CoA synthetase [Pseudomonas mendocina S5.2]	1	1	1	1
610711160	acetyl-CoA synthetase [Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
768546865	acetyl-CoA synthetase [Pseudomonas stutzeri]	1	-	1	1
735692923	acetyl-CoA synthetase [Pseudomonas tuomuerensis]	1	1	-	1
763479521	acetyl-CoA synthetase [Pseudomonas oryzae]	-	-	1	1
782985025	ABC transporter ATP-binding protein	1	1	1	1

	[Pseudomonas pseudoalcaligenes]				
	acyl carrier protein [Pseudomonas				
610712825	pseudoalcaligenes AD6]	1	1	1	1
	electron transfer flavoprotein subunit beta				
610708083	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	electron transfer flavoprotein subunit beta				
949201026	[Pseudomonas veronii]	1	-	-	1
	Electron transfer flavoprotein, alpha				
800911699	subunit [Pseudomonas fluorescens]	1	1	1	1
	hypothetical protein AU05_23220				
610708211	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	hypothetical protein N619_01370				
782989817	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	enolase [Pseudomonas alcaligenes NBRC				
543437522	14159]	-	1	1	1
	threonine dehydratase [Pseudomonas				
782988153	pseudoalcaligenes]	1	1	1	1
	threonine dehydratase [Pseudomonas				
949192595	poae]	1	-	1	1
	dehydrogenase [Pseudomonas				
782986830	pseudoalcaligenes]	1	1	1	1
	3-methylcrotonyl-CoA carboxylase				
782988771	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	Methylcrotonoyl-CoA carboxylase				
	subunit alpha, mitochondrial				
703403055	[Pseudomonas xanthomarina]	1	-	1	1
	3-methylcrotonyl-CoA carboxylase				
929886228	[Pseudomonas sp. RIT-PI-o]	1	-	-	1
	peptidase S41 [Pseudomonas				
610707194	pseudoalcaligenes AD6]	1	1	1	1
	peptidase S41 [Pseudomonas				
782985604	pseudoalcaligenes]	1	1	1	1
	carboxyl-terminal protease [Pseudomonas				
26988451	putida KT2440]	-	-	-	1
	peptidase S41 [Pseudomonas balearica				
747150418	DSM 6083]	1	1	1	1
	Periplasmic protease [Pseudomonas sp.				
758832589	FeS53a]	-	-	-	1
949188735	peptidase S41 [Pseudomonas poae]	-	1	1	1
	transcription termination factor Rho				
782984526	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	glutamate--tRNA ligase [Pseudomonas				
667953769	mendocina S5.2]	-	-	1	1
	Glutamine--tRNA ligase [Pseudomonas				
631778850	knackmussii B13]	1	1	1	1

928483837	glutamine--tRNA ligase [Pseudomonas psychrophila]	1	1	1	1
610709794	amidase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
556074504	amidase [Pseudomonas sp. VLB120]	1	1	1	1
641462224	amidase family protein [Pseudomonas sp. P482]	-	-	-	1
771843183	amidase [Pseudomonas sp. Os17]	1	-	1	1
610713846	50S ribosomal protein L4 [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
610708088	amidophosphoribosyltransferase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
691228253	amidophosphoribosyltransferase [Pseudomonas cremoricolorata]	-	-	1	1
782987818	peroxidase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610712491	adenylylsulfate kinase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667952691	adenylylsulfate kinase [Pseudomonas mendocina S5.2]	1	1	1	1
126198123	ATP sulfurylase GTP-binding subunit/APS kinase [Pseudomonas aeruginosa 2192]	1	1	1	1
667953955	thioredoxin reductase [Pseudomonas mendocina S5.2]	1	1	1	1
782987340	methionine synthase [Pseudomonas pseudoalcaligenes]	1	1	1	1
733472819	methionine synthase [Pseudomonas putida]	-	-	-	1
856781248	methionine synthase [Pseudomonas helleri]	-	-	-	1
934022585	methionine synthase [Pseudomonas viridiflava]	-	-	-	1
782987473	cysteine synthase [Pseudomonas pseudoalcaligenes]	1	1	1	1
735692685	cysteine synthase [Pseudomonas tuomuerensis]	1	-	1	1
949215443	cysteine synthase [Pseudomonas veronii]	-	-	-	1
667955164	GMP synthase [Pseudomonas mendocina S5.2]	1	1	1	1
747150282	GMP synthase [Pseudomonas balearica DSM 6083]	1	1	1	1
782983995	oligopeptidase A [Pseudomonas pseudoalcaligenes]	1	1	1	1
667951581	oligopeptidase A [Pseudomonas]	1	1	1	1

	mendocina S5.2]				
	oligopeptidase A [Pseudomonas				
610707750	pseudoalcaligenes AD6]	1	-	-	1
	adenylosuccinate synthetase				
667952435	[Pseudomonas mendocina S5.2]	-	-	1	1
	adenylosuccinate synthetase				
610707860	[Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
	adenylosuccinate synthetase				
763481784	[Pseudomonas oryzihabitans]	1	1	1	1
	alcohol dehydrogenase, partial				
825576476	[Pseudomonas sp. TJI-51]	1	1	1	1
	30S ribosomal protein S13 [Pseudomonas				
310941841	mendocina]	1	1	1	1
	phosphoribosylaminoimidazolecarboxami				
	de formyltransferase [Pseudomonas				
667952512	mendocina S5.2]	-	-	-	1
	phosphoribosylaminoimidazolecarboxami				
	de formyltransferase [Pseudomonas				
816873741	putida KG-4]	1	1	1	1
	Bifunctional IMP cyclohydrolase /				
	phosphoribosylaminoimidazolecarboxami				
	de formyltransferase [Pseudomonas				
590456084	syringae pv. syringae str. B301D-R]	-	-	-	1
	RNA polymerase-associated protein				
782985789	RapA [Pseudomonas pseudoalcaligenes]	1	1	1	1
	ATP-dependent helicase HepA				
	[Pseudomonas stutzeri ATCC 14405 =				
379064040	CCUG 16156]	1	1	1	1
	RNA polymerase-associated protein				
666089267	RapA [Pseudomonas fluorescens]	-	-	-	1
	RNA helicase HepA [Pseudomonas				
126168203	aeruginosa C3719]	-	1	1	1
	ferric uptake regulator [Pseudomonas				
361584223	pseudoalcaligenes CECT 5344]	1	1	1	1
	bifunctional glutamine-synthetase				
	adenylyltransferase/deadenyltransferase				
782984808	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	bifunctional glutamine-synthetase				
	adenylyltransferase/deadenyltransferase				
667952367	[Pseudomonas mendocina S5.2]	1	1	1	1
	glutamate-ammonia-ligase				
	adenylyltransferase [Pseudomonas				
327482490	stutzeri DSM 4166]	-	-	1	1
	acetyl-CoA carboxylase [Pseudomonas				
782984976	pseudoalcaligenes]	1	1	1	1

610706198	3-methylcrotonyl-CoA carboxylase [Pseudomonas pseudoalcaligenes AD6]	1	-	1	1
768456667	3-methylcrotonyl-CoA carboxylase [Pseudomonas sp. ES3-33]	-	-	-	1
610707217	peptidylprolyl isomerase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782985576	peptidylprolyl isomerase [Pseudomonas pseudoalcaligenes]	1	1	1	1
443282731	Peptidyl-prolyl cis-trans isomerase A [Pseudomonas syringae pv. syringae B64]	-	-	-	1
782984032	methionine ABC transporter substrate- binding protein [Pseudomonas pseudoalcaligenes]	1	1	1	1
667951609	methionine ABC transporter substrate- binding protein [Pseudomonas mendocina S5.2]	1	1	1	1
782984014	aldehyde oxidase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610712102	hypothetical protein AU05_10185 [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782988808	lysine decarboxylase [Pseudomonas pseudoalcaligenes]	1	1	1	1
758829289	Lysine decarboxylase, inducible [Pseudomonas sp. FeS53a]	1	-	-	1
782984560	aminotransferase [Pseudomonas pseudoalcaligenes]	1	1	-	1
387159919	aminotransferase [Pseudomonas fluorescens A506]	-	1	-	1
782987683	aminotransferase [Pseudomonas pseudoalcaligenes]	1	1	1	1
782985127	glutamyl-tRNA amidotransferase [Pseudomonas pseudoalcaligenes]	1	1	1	1
799196200	glutamyl-tRNA amidotransferase [Pseudomonas fluorescens]	-	-	-	1
692342945	glutamyl-tRNA amidotransferase [Pseudomonas rhizosphaerae]	-	1	1	1
515930653	polyphosphate kinase [Pseudomonas mendocina]	1	1	1	1
674642167	polyphosphate kinase [Pseudomonas sp. 12M76_air]	1	1	1	1
610708512	beta-ketoacyl synthase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782984624	beta-ketoacyl synthase [Pseudomonas pseudoalcaligenes]	1	1	1	1
667952178	beta-ketoacyl synthase [Pseudomonas	1	1	1	1

	mendocina S5.2]				
	pterin-4-alpha-carbinolamine dehydratase				
782986607	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	phenylalanine 4-monooxygenase				
327482209	[Pseudomonas stutzeri DSM 4166]	1	1	1	1
	phenylalanine 4-monooxygenase				
782986608	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	CRISPR-associated protein Cas5				
782983992	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	CRISPR-associated protein Cas5				
610708349	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	leucine--tRNA ligase [Pseudomonas				
782989317	pseudoalcaligenes]	1	1	1	1
	leucine--tRNA ligase [Pseudomonas				
667955498	mendocina S5.2]	-	1	1	1
	leucyl-tRNA synthetase [Pseudomonas				
126168811	aeruginosa C3719]	1	1	1	1
	leucyl-tRNA synthetase [Pseudomonas				
568072690	sp. M1]	1	-	1	1
	UDP-N-acetylglucosamine 1-				
	carboxyvinyltransferase [Pseudomonas				
610712482	pseudoalcaligenes AD6]	1	1	1	1
	phenylalanyl-tRNA synthetase				
782987243	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	phenylalanyl-tRNA synthetase				
667954292	[Pseudomonas mendocina S5.2]	1	1	1	1
	phenylalanyl-tRNA synthetase				
756406923	[Pseudomonas fluorescens]	1	1	1	1
	phenylalanine--tRNA ligase beta subunit				
543437066	[Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
	phenylalanyl-tRNA synthetase				
856769481	[Pseudomonas lundensis]	1	1	1	1
	methylcrotonoyl-CoA carboxylase				
667954212	[Pseudomonas mendocina S5.2]	1	1	-	1
	methylcrotonoyl-CoA carboxylase				
610711738	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
	methylcrotonoyl-CoA carboxylase				
768547568	[Pseudomonas stutzeri]	1	1	1	1
	methylcrotonoyl-CoA carboxylase				
747150045	[Pseudomonas balearica DSM 6083]	-	-	-	1
	50S ribosomal protein L3 [Pseudomonas				
556077032	sp. VLB120]	1	1	1	1
	GTP-binding protein TypA				
782988039	[Pseudomonas pseudoalcaligenes]	1	1	-	1
787857984	GTP-binding protein TypA	-	-	1	1

	[<i>Pseudomonas chlororaphis</i>]				
227482627	unnamed protein product [<i>Pseudomonas</i> protegens Pf-5]	1	1	1	1
610712826	3-ketoacyl-ACP reductase [<i>Pseudomonas</i> pseudoalcaligenes AD6]	1	1	1	1
782988510	spermidine/putrescine ABC transporter substrate-binding protein [<i>Pseudomonas</i> pseudoalcaligenes]	1	1	1	1
782988850	succinate dehydrogenase [<i>Pseudomonas</i> pseudoalcaligenes]	1	1	-	1
782984687	glycine/betaine ABC transporter substrate-binding protein [<i>Pseudomonas</i> pseudoalcaligenes]	1	1	1	1
610707667	glycine/betaine ABC transporter substrate-binding protein [<i>Pseudomonas</i> pseudoalcaligenes AD6]	1	1	1	1
459961199	50S ribosomal protein L2 [<i>Pseudomonas</i> sp. Lz4W]	1	-	1	1
610713844	50S ribosomal protein L2 [<i>Pseudomonas</i> pseudoalcaligenes AD6]	1	1	1	1
782984554	carbon-nitrogen hydrolase [<i>Pseudomonas</i> pseudoalcaligenes]	1	1	1	1
610712089	type II citrate synthase [<i>Pseudomonas</i> pseudoalcaligenes AD6]	1	1	1	1
310941833	30S ribosomal protein S8 [<i>Pseudomonas</i> mendocina]	1	1	1	1
610714148	ornithine decarboxylase [<i>Pseudomonas</i> pseudoalcaligenes AD6]	1	1	1	1
782984739	malate dehydrogenase [<i>Pseudomonas</i> pseudoalcaligenes]	1	1	1	1
610707720	malate dehydrogenase [<i>Pseudomonas</i> pseudoalcaligenes AD6]	1	-	1	1
758832331	NADP-dependent malic enzyme [<i>Pseudomonas</i> sp. FeS53a]	1	1	1	1
747109351	malate dehydrogenase [<i>Pseudomonas</i> fluorescens]	1	1	1	1
713118326	malate dehydrogenase [<i>Pseudomonas</i> mediterranea CFBP 5447]	-	-	1	1
667955188	chaperone protein HscA [<i>Pseudomonas</i> mendocina S5.2]	1	-	1	1
782986215	chaperone protein HscA [<i>Pseudomonas</i> pseudoalcaligenes]	1	1	1	1
229364314	DnaK-homologue chaperone Hsc66 [<i>Pseudomonas fluorescens</i> SBW25]	-	1	1	1
610710492	cysteine desulfurase [<i>Pseudomonas</i> sp.]	1	-	-	1

	pseudoalcaligenes AD6]				
	antitermination protein NusG				
610710775	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	DNA-binding protein [Pseudomonas				
782988793	pseudoalcaligenes]	1	1	1	1
	ATP-dependent protease La				
	[Pseudomonas stutzeri ATCC 14405 =				
379064679	CCUG 16156]	-	-	-	1
	argininosuccinate synthase [Pseudomonas				
782985685	pseudoalcaligenes]	-	-	1	1
	heat-shock protein Hsp20 [Pseudomonas				
856756032	lundensis]	1	1	-	1
	50S ribosomal protein L7/L12				
782989115	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	50S ribosomal protein L7/L12				
543435918	[Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
	50S ribosomal protein L7/L12				
713116582	[Pseudomonas mediterranea CFBP 5447]	1	1	1	1
	methylmalonate-semialdehyde				
	dehydrogenase [Pseudomonas mendocina				
667955407	S5.2]	1	1	-	1
	methylmalonate-semialdehyde				
	dehydrogenase [Pseudomonas putida				
26987335	KT2440]	-	1	1	1
	acyl-CoA dehydrogenase [Pseudomonas				
782983959	pseudoalcaligenes]	1	1	1	1
	glutaryl-CoA dehydrogenase				
699969103	[Pseudomonas sp. MT-1]	-	-	-	1
	acyl-CoA dehydrogenase, partial				
733470969	[Pseudomonas putida]	1	1	1	1
	acyl-CoA dehydrogenase [Pseudomonas				
610708384	pseudoalcaligenes AD6]	1	1	-	1
	acyl-CoA dehydrogenase [Pseudomonas				
751082528	stutzeri]	-	-	1	1
	transcriptional regulator PhoU				
782984335	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	chemotaxis protein CheA [Pseudomonas				
782984636	pseudoalcaligenes]	1	1	1	1
	chemotaxis protein CheA [Pseudomonas				
667952190	mendocina S5.2]	1	1	1	1
	histidine kinase [Pseudomonas mosselii				
684198361	SJ10]	-	-	-	1
	branched-chain amino acid				
	aminotransferase [Pseudomonas				
782984809	pseudoalcaligenes]	-	1	-	1

667955408	omega amino acid--pyruvate aminotransferase [Pseudomonas mendocina S5.2]	1	1	1	1
763482549	omega amino acid--pyruvate aminotransferase [Pseudomonas oryzihabitans]	1	1	1	1
782986291	threonine synthase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610714215	arginine deiminase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
543438645	arginine deiminase [Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
782989565	molecular chaperone DnaK [Pseudomonas pseudoalcaligenes]	1	1	1	1
699968380	RNA polymerase-binding protein DksA [Pseudomonas sp. MT-1]	-	-	-	1
327481006	Hsp20/alpha crystallin family protein [Pseudomonas stutzeri DSM 4166]	1	1	1	1
404531144	small HspC2 heat shock protein [Pseudomonas aeruginosa CI27]	1	1	1	1
856745869	heat-shock protein Hsp20 [Pseudomonas lundensis]	-	-	1	1
782986711	acetyl-CoA carboxylase subunit alpha [Pseudomonas pseudoalcaligenes]	1	1	1	1
667954730	30S ribosomal protein S2 [Pseudomonas mendocina S5.2]	1	1	1	1
758821823	SSU ribosomal protein S2p (SAe) [Pseudomonas sp. FeS53a]	1	-	1	1
610709050	sarcosine oxidase subunit alpha [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782988030	sarcosine oxidase subunit alpha [Pseudomonas pseudoalcaligenes]	-	-	-	1
568072145	dihydroxy-acid dehydratase [Pseudomonas sp. M1]	1	-	1	1
213923351	dihydroxy-acid dehydratase [Pseudomonas syringae pv. tomato T1]	-	-	-	1
556072761	dihydroxy-acid dehydratase [Pseudomonas sp. VLB120]	-	-	-	1
610707202	recombinase RdgC [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
568075323	recombinase RdgC [Pseudomonas sp. M1]	1	1	-	1
691226569	recombinase RdgC [Pseudomonas cremoricolorata]	1	1	-	1
610708014	UDP-3-O-(3-hydroxymyristoyl)	1	1	1	1

	glucosamine N-acyltransferase [Pseudomonas pseudoalcaligenes AD6]				
667951047	50S ribosomal protein L15 [Pseudomonas mendocina S5.2]	1	1	1	1
735689893	50S ribosomal protein L15 [Pseudomonas tuomuerensis]	-	-	-	1
610706962	pyrroline-5-carboxylate reductase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782988055	pyrroline-5-carboxylate reductase [Pseudomonas pseudoalcaligenes]	1	1	1	1
782988471	N-acetyl-gamma-glutamyl-phosphate reductase [Pseudomonas pseudoalcaligenes]	1	1	1	1
782988772	gamma-carboxygeranoyl-CoA hydratase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610714888	ribosome-recycling factor [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667954966	pyruvate kinase [Pseudomonas mendocina S5.2]	1	1	1	1
667954713	CTP synthetase [Pseudomonas mendocina S5.2]	1	1	1	1
692344673	dihydrodipicolinate reductase [Pseudomonas rhizosphaerae]	-	1	1	1
610711186	dihydrodipicolinate reductase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
735691417	dihydrodipicolinate reductase [Pseudomonas tuomuerensis]	1	1	1	1
782984144	DNA gyrase subunit B [Pseudomonas pseudoalcaligenes]	1	1	1	1
151415017	DNA gyrase subunit B, partial [Pseudomonas oleovorans subsp. lubricantis]	1	1	1	1
782987273	beta-D-glucoside glucohydrolase [Pseudomonas pseudoalcaligenes]	-	1	1	1
667954950	beta-D-glucoside glucohydrolase [Pseudomonas mendocina S5.2]	1	-	-	1
782989479	peptidase M48 [Pseudomonas pseudoalcaligenes]	1	1	1	1
782984562	spermidine/putrescine ABC transporter substrate-binding protein [Pseudomonas pseudoalcaligenes]	1	1	1	1
610708799	spermidine/putrescine ABC transporter substrate-binding protein [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
610710960	succinyl-CoA:3-ketoacid-CoA transferase	1	1	1	1

	[Pseudomonas pseudoalcaligenes AD6]				
	50S ribosomal protein L18 [Pseudomonas				
610713831	pseudoalcaligenes AD6]	1	1	1	1
	50S ribosomal protein L18 [Pseudomonas				
310941835	mendocina]	1	1	1	1
	hypothetical protein N619_17410				
782986634	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	dioxygenase [Pseudomonas				
610706548	pseudoalcaligenes AD6]	1	1	1	1
	single-stranded DNA-binding protein				
610713816	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	single-strand DNA-binding protein				
295443570	(plasmid) [Pseudomonas putida]	-	-	-	1
	single-stranded DNA-binding protein				
327479353	[Pseudomonas stutzeri DSM 4166]	1	1	1	1
	single-stranded DNA-binding protein				
758543583	[Pseudomonas putida]	1	1	1	1
	ssDNA-binding protein [Pseudomonas sp.				
556074265	VLB120]	-	-	1	1
	glycine cleavage system protein H				
610707852	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	hypothetical protein N619_16845				
782987275	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	flagellar hook protein FlgE [Pseudomonas				
769335314	sp. 10B238]	1	1	1	1
	alcohol dehydrogenase [Pseudomonas				
782984255	pseudoalcaligenes]	1	1	1	1
	alcohol dehydrogenase [Pseudomonas				
610710327	pseudoalcaligenes AD6]	-	-	-	1
	acetyl-CoA carboxylase [Pseudomonas				
667952519	mendocina S5.2]	1	1	1	1
	pyruvate carboxylase subunit A				
782984013	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	argininosuccinate lyase [Pseudomonas				
782984483	pseudoalcaligenes]	1	1	1	1
	electron transfer flavoprotein-ubiquinone				
	oxidoreductase [Pseudomonas				
610708085	pseudoalcaligenes AD6]	1	1	1	1
	periplasmic binding protein, putative				
327482821	[Pseudomonas stutzeri DSM 4166]	-	-	-	1
	C4-dicarboxylate ABC transporter				
782984076	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	adenylosuccinate lyase [Pseudomonas				
782987846	pseudoalcaligenes]	1	1	1	1
782988810	ferrous iron transporter B [Pseudomonas	1	1	1	1

	pseudoalcaligenes]				
	30S ribosomal protein S19 [Pseudomonas				
310941819	mendocina]	-	-	1	1
	50S ribosomal protein L9 [Pseudomonas				
610706377	pseudoalcaligenes AD6]	1	1	1	1
	50S ribosomal protein L9 [Pseudomonas				
126170284	aeruginosa C3719]	-	-	-	1
	organic solvent tolerance protein OstA				
782985150	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	phosphoenolpyruvate carboxylase				
782986319	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	phosphoenolpyruvate carboxylase				
610709145	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	phosphoenolpyruvate carboxylase				
733394080	[Pseudomonas frederiksbergensis]	1	1	-	1
	phosphoenolpyruvate carboxylase				
816870581	[Pseudomonas putida KG-4]	1	1	1	1
	glucosamine--fructose-6-phosphate				
	aminotransferase [Pseudomonas				
782984120	pseudoalcaligenes]	1	1	1	1
	glucosamine--fructose-6-phosphate				
	aminotransferase [Pseudomonas				
610706661	pseudoalcaligenes AD6]	1	1	1	1
	glucosamine--fructose-6-phosphate				
	aminotransferase [Pseudomonas sp.				
556077571	VLB120]	-	-	-	1
	glucosamine--fructose-6-phosphate				
	aminotransferase, isomerizing				
213926751	[Pseudomonas syringae pv. tomato T1]	-	-	-	1
	chemotaxis protein CheA [Pseudomonas				
782987066	pseudoalcaligenes]	-	-	1	1
	histidine sensor kinase [Pseudomonas				
270160580	pseudoalcaligenes KF707]	-	1	1	1
	phosphoribosylamine--glycine ligase				
782984970	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	phosphoribosylamine--glycine ligase				
667952511	[Pseudomonas mendocina S5.2]	1	-	1	1
	50S ribosomal protein L16 [Pseudomonas				
610713840	pseudoalcaligenes AD6]	1	1	1	1
	Clp protease ATP-binding protein				
782988792	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	spermidine/putrescine ABC transporter				
	substrate-binding protein [Pseudomonas				
782984566	pseudoalcaligenes]	1	1	1	1
610708798	spermidine/putrescine ABC transporter	1	1	1	1

	substrate-binding protein [Pseudomonas pseudoalcaligenes AD6]				
782985782	pyridoxine 5'-phosphate synthase [Pseudomonas pseudoalcaligenes]	1	-	-	1
610713372	pyridoxine 5'-phosphate synthase [Pseudomonas pseudoalcaligenes AD6]	1	-	-	1
489559367	(2Fe-2S)-binding protein [Pseudomonas pseudoalcaligenes]	1	1	1	1
667954728	uridylate kinase [Pseudomonas mendocina S5.2]	-	-	-	1
575877754	3-oxoacyl-ACP reductase [Pseudomonas aeruginosa PA38182]	1	1	1	1
782989154	excinuclease ABC subunit A [Pseudomonas pseudoalcaligenes]	1	1	-	1
641463643	excinuclease ABC subunit A [Pseudomonas sp. P482]	-	-	-	1
928257015	RNA polymerase sigma factor RpoD [Pseudomonas amygdali pv. sesami]	-	-	-	1
782988248	thiosulfate transporter subunit [Pseudomonas pseudoalcaligenes]	-	-	1	1
9951602	nitrogen regulatory protein P-II 2 [Pseudomonas aeruginosa PAO1]	1	1	1	1
782985180	50S ribosomal protein L13 [Pseudomonas pseudoalcaligenes]	1	1	1	1
667953596	prephenate dehydratase [Pseudomonas mendocina S5.2]	1	1	1	1
610709981	prephenate dehydratase [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
98956472	PhaB [Pseudomonas extremaustralis 14-3]	-	-	1	1
564892688	3-ketoacyl-ACP reductase [Pseudomonas aeruginosa VRFPA06]	1	1	1	1
782987126	isochorismatase [Pseudomonas pseudoalcaligenes]	-	1	1	1
610708794	phosphate transport regulator [Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
782985889	3-ketoacyl-CoA thiolase [Pseudomonas pseudoalcaligenes]	-	1	1	1
610713662	endoribonuclease [Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
610711962	glycine-tRNA synthetase subunit beta [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667951769	glycine-tRNA synthetase subunit beta [Pseudomonas mendocina S5.2]	1	1	1	1
940055010	Glycine--tRNA ligase beta subunit	1	-	-	1

	[Pseudomonas syringae pv. coriandricola]				
	50S ribosomal protein L21 [Pseudomonas				
610714336	pseudoalcaligenes AD6]	1	1	1	1
	50S ribosomal protein L21 [Pseudomonas				
390984628	stutzeri CCUG 29243]	-	-	1	1
	Conserved hypothetical protein				
631781650	[Pseudomonas knackmussii B13]	1	-	1	1
	PTS fructose transporter subunit IIA				
782985056	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	PTS fructose transporter subunit IIA				
610712214	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	PTS fructose transporter subunit IIA				
764075615	[Pseudomonas putida S13.1.2]	1	-	1	1
	universal stress protein UspA				
667953765	[Pseudomonas mendocina S5.2]	-	1	1	1
	glycine/betaine ABC transporter				
	substrate-binding protein [Pseudomonas				
610707666	pseudoalcaligenes AD6]	1	1	1	1
	glycine/betaine ABC transporter				
	substrate-binding protein [Pseudomonas				
782984686	pseudoalcaligenes]	1	-	1	1
	histidine ammonia-lyase [Pseudomonas				
782988593	pseudoalcaligenes]	1	1	1	1
	histidine ammonia-lyase [Pseudomonas				
543436411	alcaligenes NBRC 14159]	1	-	1	1
	hypothetical protein PpSQ1_24995				
733469937	[Pseudomonas putida]	-	-	-	1
	enoyl-CoA hydratase [Pseudomonas				
782988945	pseudoalcaligenes]	1	1	1	1
	30S ribosomal protein S10 [Pseudomonas				
610713848	pseudoalcaligenes AD6]	1	1	1	1
	universal stress protein UspA				
782986446	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	universal stress protein UspA				
667954965	[Pseudomonas mendocina S5.2]	1	1	1	1
	acetylglutamate kinase [Pseudomonas				
610714589	pseudoalcaligenes AD6]	-	1	1	1
	aldehyde dehydrogenase [Pseudomonas				
667952014	mendocina S5.2]	1	1	-	1
	gamma-glutamyl-gamma-				
	aminobutyraldehyde dehydrogenase				
568072264	[Pseudomonas sp. M1]	-	-	1	1
	hypothetical protein N619_05925				
782988801	[Pseudomonas pseudoalcaligenes]	1	1	1	1
820908765	hypothetical protein PU99_16310	1	1	1	1

	[<i>Pseudomonas putida</i>]				
782987878	seryl-tRNA synthetase [<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
543438520	serine--tRNA ligase [<i>Pseudomonas alcaligenes</i> NBRC 14159]	-	-	-	1
912966777	seryl-tRNA synthetase [<i>Pseudomonas sp.</i> 250J]	-	-	1	1
568075972	seryl-tRNA synthetase [<i>Pseudomonas sp.</i> M1]	-	-	1	1
545072744	RNA-binding transcriptional accessory protein [<i>Pseudomonas sp.</i> EGD-AK9]	-	-	-	1
328915617	RNA-binding S1 domain-containing protein [<i>Pseudomonas mendocina</i> NK-01]	1	-	-	1
516459737	RNA-binding transcriptional accessory protein [<i>Pseudomonas veronii</i>]	1	1	-	1
610708532	hypothetical protein AU05_21905 [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
379064891	YceI-like family protein [<i>Pseudomonas stutzeri</i> ATCC 14405 = CCUG 16156]	1	1	1	1
782984098	oxidoreductase [<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
544279852	oxidoreductase [<i>Pseudomonas putida</i> LF54]	-	-	-	1
782985899	TetR family transcriptional regulator [<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
511104678	rod shape-determining protein MreC, partial [<i>Pseudomonas plecoglossicida</i> NB2011]	-	-	-	1
610708546	S-adenosylmethionine synthetase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	-	1
543439529	S-adenosylmethionine synthase [<i>Pseudomonas alcaligenes</i> NBRC 14159]	1	1	1	1
610708940	DNA topoisomerase IV subunit A [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
782984832	DNA topoisomerase IV subunit A [<i>Pseudomonas pseudoalcaligenes</i>]	-	1	-	1
610714951	translation initiation factor IF-3 [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
126167652	translation initiation factor IF-3 [<i>Pseudomonas aeruginosa</i> C3719]	-	-	-	1
782987657	dipicolinate synthase [<i>Pseudomonas pseudoalcaligenes</i>]	1	1	-	1
610711382	dihydroorotase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
667953121	dihydroorotase [<i>Pseudomonas mendocina</i>]	1	1	1	1

	S5.2]				
	dihydroorotase [Pseudomonas alcaligenes				
543439151	NBRC 14159]	1	1	1	1
	preprotein translocase subunit SecB				
782988173	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	transcriptional regulator MvaT, P16				
758822944	subunit [Pseudomonas sp. FeS53a]	-	1	-	1
	putative transcriptional regulator protein				
111036203	(plasmid) [Pseudomonas putida]	1	1	1	1
	dihydrodipicolinate synthase				
782986935	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	hypothetical protein PACIG1_5986				
403244311	[Pseudomonas aeruginosa CIG1]	1	1	-	1
	ATP-dependent protease subunit HslV				
691225117	[Pseudomonas cremoricolorata]	-	1	-	1
	methionine--tRNA ligase [Pseudomonas				
667953134	mendocina S5.2]	-	-	1	1
	methionine--tRNA ligase [Pseudomonas				
610711395	pseudoalcaligenes AD6]	1	-	-	1
	methionine--tRNA ligase [Pseudomonas				
735692501	tuomuerensis]	-	-	-	1
	transcription-repair coupling factor				
782985904	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	transcription-repair coupling factor				
667953324	[Pseudomonas mendocina S5.2]	1	-	-	1
	transcription-repair coupling factor				
395809169	[Pseudomonas stutzeri DSM 10701]	-	1	1	1
	transcription-repair coupling factor				
684195393	[Pseudomonas mosselii SJ10]	-	-	-	1
	transcription-repair coupling protein Mfd				
126167907	[Pseudomonas aeruginosa C3719]	-	-	-	1
	Beta-casein OS=Bos taurus GN=CSN2				
P02666	PE=1 SV=2	1	1	1	1
	exoribonuclease R [Pseudomonas				
782984874	pseudoalcaligenes]	1	1	1	1
	exoribonuclease R [Pseudomonas				
667952437	mendocina S5.2]	1	1	1	1
	ribonuclease R [Pseudomonas putida				
26991559	KT2440]	1	1	1	1
	rod shape-determining protein MreB				
667952658	[Pseudomonas mendocina S5.2]	1	1	1	1
	diaminopimelate decarboxylase				
782984469	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	transcriptional regulator PhoB				
610714562	[Pseudomonas pseudoalcaligenes AD6]	1	-	-	1

	RNA polymerase beta subunit D, partial				
292494333	[Pseudomonas indoloxdians]	1	1	1	1
	UTP--glucose-1-phosphate				
	uridylyltransferase [Pseudomonas				
782988953	pseudoalcaligenes]	-	1	-	1
759596999	peroxidase [Pseudomonas sp. PI1]	1	1	-	1
	quinone oxidoreductase [Pseudomonas				
667951805	mendocina S5.2]	1	1	1	1
	quinone oxidoreductase [Pseudomonas				
610710262	pseudoalcaligenes AD6]	1	1	1	1
	DNA polymerase I [Pseudomonas				
782984307	pseudoalcaligenes]	1	1	1	1
	DNA polymerase I [Pseudomonas				
689658980	fluorescens LMG 5329]	-	1	-	1
	DNA polymerase I [Pseudomonas putida				
26986868	KT2440]	1	1	1	1
	DNA polymerase I [Pseudomonas putida				
764076274	S13.1.2]	-	1	-	1
	inorganic pyrophosphatase [Pseudomonas				
667955541	mendocina S5.2]	1	1	1	1
	histidinol dehydrogenase [Pseudomonas				
610712484	pseudoalcaligenes AD6]	-	-	1	1
	Histidinol-phosphate aminotransferase				
748444356	[Pseudomonas batumici]	1	1	1	1
	histidinol-phosphate aminotransferase				
782985163	[Pseudomonas pseudoalcaligenes]	-	1	-	1
	histidinol dehydrogenase [Pseudomonas				
327479609	stutzeri DSM 4166]	1	-	1	1
	Alpha-S1-casein OS=Bos taurus				
P02662	GN=CSN1S1 PE=1 SV=2	1	1	1	1
	phasin [Pseudomonas aeruginosa				
564892686	VRFPA06]	1	1	1	1
	F0F1-type ATP synthase subunit beta				
782985887	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	homoserine dehydrogenase				
667955130	[Pseudomonas mendocina S5.2]	1	1	1	1
	1-deoxy-D-xylulose-5-phosphate synthase				
782989187	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	1-deoxy-D-xylulose-5-phosphate synthase				
667950997	[Pseudomonas mendocina S5.2]	-	1	-	1
	GTP-binding protein LepA [Pseudomonas				
95112252	entomophila L48]	-	-	1	1
	protein-disulfide isomerase				
667955131	[Pseudomonas mendocina S5.2]	1	-	1	1
782985914	pyridine nucleotide-disulfide	1	1	1	1

	oxidoreductase [Pseudomonas pseudoalcaligenes]				
	Major outer membrane lipoprotein				
940026700	[Pseudomonas syringae pv. antirrhini]	-	-	-	1
	30S ribosomal protein S11 [Pseudomonas				
310941843	mendocina]	1	1	1	1
	alkylphosphonate ABC transporter substrate-binding protein [Pseudomonas				
667953443	mendocina S5.2]	1	1	1	1
	alkylphosphonate ABC transporter substrate-binding protein [Pseudomonas				
610706573	pseudoalcaligenes AD6]	1	-	1	1
	ATP-dependent protease ATP-binding subunit HslU [Pseudomonas mendocina				
667952292	S5.2]	1	1	1	1
	phosphoglycerate kinase [Pseudomonas				
543439814	alcaligenes NBRC 14159]	1	1	1	1
	phosphoglycerate kinase [Pseudomonas				
782984661	pseudoalcaligenes]	1	1	1	1
	threonine aldolase [Pseudomonas				
667953429	mendocina S5.2]	1	-	1	1
	Threonine aldolase [Pseudomonas				
404305584	fluorescens R124]	1	1	1	1
	L-allo-threonine aldolase [Pseudomonas				
229364014	fluorescens SBW25]	-	1	1	1
	2-nitropropane dioxygenase				
782988473	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	2-nitropropane dioxygenase				
568076240	[Pseudomonas sp. M1]	1	1	-	1
	copper resistance protein CopC				
403244325	[Pseudomonas aeruginosa CIG1]	1	1	1	1
	twitching motility protein PilH				
758834837	[Pseudomonas sp. FeS53a]	1	1	1	1
404306573	CheY [Pseudomonas fluorescens R124]	-	-	-	1
	chemotaxis protein CheY [Pseudomonas				
666087644	fluorescens]	1	-	1	1
	chemotaxis protein CheY [Pseudomonas				
610712448	pseudoalcaligenes AD6]	1	1	1	1
	chemotaxis protein CheY [Pseudomonas				
667952649	mendocina S5.2]	1	1	1	1
	ribosome hibernation promoting factor HPF [Pseudomonas pseudoalcaligenes				
610712469	AD6]	1	1	1	1
	50S ribosomal protein L17 [Pseudomonas				
459961176	sp. Lz4W]	-	1	-	1

641463640	ribosomal protein L17 [Pseudomonas sp. P482]	1	1	1	1
610712521	phosphoribosylaminoimidazole-succinocarboxamide synthase [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
782989515	heat shock protein GrpE [Pseudomonas pseudoalcaligenes]	1	1	1	1
610713661	alanine racemase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
459963088	alanine racemase [Pseudomonas sp. Lz4W]	1	1	1	1
758833888	LSU ribosomal protein L25p [Pseudomonas sp. FeS53a]	1	1	1	1
667954402	NAD-dependent DNA ligase LigA [Pseudomonas mendocina S5.2]	1	1	1	1
430794344	NAD-dependent DNA ligase LigA [Pseudomonas putida HB3267]	1	-	1	1
949190359	NAD-dependent DNA ligase LigA [Pseudomonas poae]	-	-	-	1
667953640	3-isopropylmalate dehydrogenase [Pseudomonas mendocina S5.2]	1	1	1	1
782985773	RNA polymerase sigma-H factor AlgU [Pseudomonas pseudoalcaligenes]	1	1	1	1
667953198	RNA polymerase sigma-H factor AlgU [Pseudomonas mendocina S5.2]	1	1	1	1
782985190	lipoprotein [Pseudomonas pseudoalcaligenes]	1	1	1	1
799196561	lipoprotein [Pseudomonas fluorescens]	-	-	1	1
576707520	LppC family lipoprotein [Pseudomonas sp. GM41(2012)]	-	-	-	1
782986459	glucan biosynthesis protein G [Pseudomonas pseudoalcaligenes]	1	1	1	1
610709307	glucan biosynthesis protein G [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
856756154	glucan biosynthesis protein G [Pseudomonas lundensis]	-	-	-	1
667953422	acetylornithine aminotransferase [Pseudomonas mendocina S5.2]	-	1	1	1
953163680	histidinol phosphatase [Pseudomonas aeruginosa]	1	1	-	1
970755348	histidinol-phosphatase [Pseudomonas aeruginosa]	1	1	1	1
610712086	oxidoreductase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667953831	oxidoreductase [Pseudomonas mendocina]	1	1	1	1

	S5.2]				
	hypothetical protein PACIG1_5976				
403244301	[Pseudomonas aeruginosa CIG1]	1	-	-	1
	Clp protease ClpX [Pseudomonas				
610713911	pseudoalcaligenes AD6]	1	1	1	1
949205452	ATPase AAA [Pseudomonas orientalis]	-	1	-	1
	acyl-CoA dehydrogenase [Pseudomonas				
610708900	pseudoalcaligenes AD6]	1	1	1	1
	acyl-CoA dehydrogenase [Pseudomonas				
782988602	pseudoalcaligenes]	1	-	1	1
	acyl-CoA dehydrogenase [Pseudomonas				
782988600	pseudoalcaligenes]	-	-	-	1
	acyl-CoA dehydrogenase [Pseudomonas				
610712641	pseudoalcaligenes AD6]	1	1	1	1
	acyl-CoA dehydrogenase [Pseudomonas				
782986037	pseudoalcaligenes]	1	-	1	1
	acyl-CoA dehydrogenase [Pseudomonas				
782989284	pseudoalcaligenes]	1	1	1	1
	acyl-CoA dehydrogenase [Pseudomonas				
395810067	stutzeri DSM 10701]	1	1	1	1
	acyl-CoA dehydrogenase [Pseudomonas				
667955531	mendocina S5.2]	1	1	1	1
	putative acyl-CoA dehydrogenase				
940079994	[Pseudomonas syringae pv. coryli]	-	-	-	1
	acyl-CoA dehydrogenase [Pseudomonas				
856773223	lini]	-	-	-	1
	membrane protein [Pseudomonas				
782987875	pseudoalcaligenes]	-	-	-	1
	deoxycytidine triphosphate deaminase				
610711398	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	acetolactate synthase 3 regulatory subunit				
610711131	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	1
	long-chain fatty acid--CoA ligase				
782989486	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	succinyl-CoA:3-ketoacid-CoA transferase				
667952901	[Pseudomonas mendocina S5.2]	1	1	1	1
	succinyl-CoA:3-ketoacid-CoA transferase				
610710961	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	hypothetical protein N619_11090				
782987453	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	hypothetical protein DW68_13490				
667953529	[Pseudomonas mendocina S5.2]	-	-	-	1
	hypothetical protein NL64_21300				
749417968	[Pseudomonas fluorescens]	-	-	1	1
782986467	polyphosphate kinase [Pseudomonas	1	1	1	1

	pseudoalcaligenes]				
	polyphosphate kinase [Pseudomonas sp.				
324103176	TJI-51]	-	-	-	1
	Chain A, Crystal Structure Of Putative				
	Polyphosphate Kinase 2 From				
193506764	Pseudomonas Aeruginosa Pa01	-	1	-	1
	carbonate dehydratase [Pseudomonas				
782984008	pseudoalcaligenes]	-	1	1	1
	superoxide dismutase [Pseudomonas				
610709187	pseudoalcaligenes AD6]	1	1	1	1
	phosphate acetyltransferase				
667955357	[Pseudomonas mendocina S5.2]	1	1	1	1
	serine hydroxymethyltransferase				
782985024	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	serine hydroxymethyltransferase				
610706941	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	serine hydroxymethyltransferase				
395809975	[Pseudomonas stutzeri DSM 10701]	-	-	-	1
	cell envelope biogenesis protein OmpA				
782989493	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	fumarate hydratase [Pseudomonas				
610709286	pseudoalcaligenes AD6]	1	1	-	1
	fumarate hydratase [Pseudomonas				
782986439	pseudoalcaligenes]	1	1	1	1
	fumarate hydratase [Pseudomonas				
747152036	balearica DSM 6083]	-	-	1	1
	hypothetical protein N619_08530				
782988045	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	type I restriction endonuclease subunit M				
953163675	[Pseudomonas aeruginosa]	1	1	1	1
	hypothetical protein AN901_204448				
940331332	[Pseudomonas syringae pv. theae]	1	1	1	1
	phosphoglycerate mutase [Pseudomonas				
782988176	pseudoalcaligenes]	1	1	1	1
	phosphoglycerate mutase [Pseudomonas				
667951362	mendocina S5.2]	1	1	1	1
	ATP-dependent protease [Pseudomonas				
667952928	mendocina S5.2]	1	1	1	1
	ATP-dependent protease [Pseudomonas				
782985447	pseudoalcaligenes]	1	1	1	1
	putative ATP-dependent protease				
543437672	[Pseudomonas alcaligenes NBRC 14159]	1	-	1	1
	cytosol aminopeptidase [Pseudomonas				
782986195	pseudoalcaligenes]	1	1	1	1
229360462	cytosol aminopeptidase [Pseudomonas	-	-	-	1

	fluorescens SBW25]				
	glutamyl-tRNA synthetase [Pseudomonas				
610709963	pseudoalcaligenes AD6]	1	1	1	1
	glutamyl-tRNA synthetase [Pseudomonas				
667953628	mendocina S5.2]	1	-	1	1
	glutamyl-tRNA synthetase [Pseudomonas				
928538918	aeruginosa]	1	-	-	1
	glutamyl-tRNA synthetase [Pseudomonas				
379066454	stutzeri ATCC 14405 = CCUG 16156]	-	1	1	1
	3-oxoacyl-ACP synthase [Pseudomonas				
782986097	pseudoalcaligenes]	1	1	1	1
	cell division inhibitor MinD				
667952962	[Pseudomonas mendocina S5.2]	1	1	1	1
	peroxiredoxin [Pseudomonas				
782986933	pseudoalcaligenes]	1	1	1	1
	ahpC/TSA family protein [Pseudomonas				
641465166	sp. P482]	-	-	-	1
	putative peroxiredoxin Bcp				
500241122	[Pseudomonas protegens CHA0]	-	-	-	1
	phosphoribosylglycinamide				
	formyltransferase [Pseudomonas				
782986262	pseudoalcaligenes]	1	1	1	1
	shikimate dehydrogenase [Pseudomonas				
667951807	mendocina S5.2]	1	1	1	1
	hypoxanthine-guanine				
	phosphoribosyltransferase [Pseudomonas				
782985226	pseudoalcaligenes]	1	1	1	1
	UDP-N-acetylmuramate--alanine ligase				
782985202	[Pseudomonas pseudoalcaligenes]	-	1	1	1
	UDP-N-acetylmuramate:L-alanyl-				
	gamma-D-glutamyl-meso-				
	diaminopimelate ligase [Pseudomonas				
782989277	pseudoalcaligenes]	1	1	1	1
	phenylalanyl-tRNA synthetase				
610714948	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	imidazolonepropionase [Pseudomonas				
543436414	alcaligenes NBRC 14159]	-	1	1	1
	imidazolonepropionase [Pseudomonas				
667951182	mendocina S5.2]	-	-	-	1
	imidazoleglycerol-phosphate dehydratase				
667951372	[Pseudomonas mendocina S5.2]	1	-	1	1
	imidazoleglycerol-phosphate dehydratase				
758542931	[Pseudomonas putida]	-	-	1	1
	ATP-dependent helicase HrpA				
782985815	[Pseudomonas pseudoalcaligenes]	-	1	1	1

	ATP-dependent RNA helicase hrpA				
631778411	[<i>Pseudomonas knackmussii</i> B13]	1	1	1	1
	ATP-dependent helicase [<i>Pseudomonas</i>				
940722108	endophytica]	-	-	-	1
	CysB family transcriptional regulator				
684197071	[<i>Pseudomonas mosselii</i> SJ10]	1	1	-	1
	CysB family transcriptional regulator				
610708314	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	1
	enoyl-CoA hydratase [<i>Pseudomonas</i>				
782985659	pseudoalcaligenes]	1	1	1	1
	enoyl-CoA hydratase [<i>Pseudomonas</i> sp.				
568075817	M1]	1	-	-	1
	peptide ABC transporter substrate-				
	binding protein [<i>Pseudomonas</i>				
782985117	pseudoalcaligenes]	1	1	1	1
	peptide ABC transporter substrate-				
	binding protein [<i>Pseudomonas</i>				
763481049	oryzihabitans]	1	1	1	1
	ornithine carbamoyltransferase				
782985366	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	ornithine carbamoyltransferase				
799190180	[<i>Pseudomonas fluorescens</i>]	1	1	1	1
	ornithine carbamoyltransferase				
856771793	[<i>Pseudomonas lundensis</i>]	-	-	-	1
	ornithine carbamoyltransferase				
689658524	[<i>Pseudomonas fluorescens</i> LMG 5329]	1	1	1	1
	cytochrome C [<i>Pseudomonas mendocina</i>				
667952029	S5.2]	1	1	1	1
	chemotaxis protein CheY [<i>Pseudomonas</i>				
610708786	pseudoalcaligenes AD6]	1	-	1	1
	chemotaxis protein CheY [<i>Pseudomonas</i>				
747152744	balearica DSM 6083]	-	-	-	1
	chromosome partitioning protein ParA				
667955271	[<i>Pseudomonas mendocina</i> S5.2]	-	1	-	1
	chromosome segregation ATPase				
699966064	[<i>Pseudomonas</i> sp. MT-1]	-	-	-	1
	glutathione reductase [<i>Pseudomonas</i>				
782988955	pseudoalcaligenes]	-	1	1	1
	glutathione reductase [<i>Pseudomonas</i> sp.				
568074329	M1]	-	1	1	1
	glutathione reductase [<i>Pseudomonas</i>				
126193840	aeruginosa 2192]	-	-	1	1
	glutathione reductase [<i>Pseudomonas</i>				
747150817	balearica DSM 6083]	-	-	-	1
610710962	acetyl-CoA acetyltransferase	1	1	1	1

	[<i>Pseudomonas pseudoalcaligenes</i> AD6]				
	acetyl-CoA acetyltransferase				
667952900	[<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
	Acetyl-CoA acetyltransferase				
940285046	[<i>Pseudomonas tremae</i>]	1	-	1	1
	ferrous iron transporter C [<i>Pseudomonas</i>				
782984852	<i>pseudoalcaligenes</i>]	1	1	1	1
	ferrous iron transporter C [<i>Pseudomonas</i>				
667952414	<i>mendocina</i> S5.2]	1	1	1	1
	outer membrane porin OprO precursor				
327481382	[<i>Pseudomonas stutzeri</i> DSM 4166]	1	1	1	1
	outer membrane porin OprO				
699966242	[<i>Pseudomonas</i> sp. MT-1]	-	-	-	1
	betaine-aldehyde dehydrogenase				
782984684	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	NAD/NADP-dependent betaine aldehyde				
	dehydrogenase [<i>Pseudomonas</i>				
749477212	<i>fluorescens</i>]	-	-	-	1
	glycyl-tRNA synthetase [<i>Pseudomonas</i>				
667951770	<i>mendocina</i> S5.2]	1	1	1	1
	bifunctional N-acetylglucosamine-1-				
	phosphate uridyltransferase/glucosamine-				
	1-phosphate acetyltransferase				
782984123	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	ubiquinol-cytochrome C reductase				
667952703	[<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
	D-erythro-7,8-dihydroneopterin				
	triphosphate epimerase [<i>Pseudomonas</i>				
610709254	<i>pseudoalcaligenes</i> AD6]	1	1	1	1
	molybdopterin biosynthesis protein B				
782987407	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	50S ribosomal protein L23 [<i>Pseudomonas</i>				
610713845	<i>pseudoalcaligenes</i> AD6]	1	1	1	1
	phosphomannomutase [<i>Pseudomonas</i>				
667951493	<i>mendocina</i> S5.2]	1	1	-	1
	phosphomannomutase [<i>Pseudomonas</i>				
610714590	<i>pseudoalcaligenes</i> AD6]	1	1	1	1
	phosphomannomutase AlgC				
346060322	[<i>Pseudomonas aeruginosa</i> NCMG1179]	-	-	-	1
	aromatic amino acid aminotransferase				
610712974	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
	aspartate aminotransferase [<i>Pseudomonas</i>				
229363740	<i>fluorescens</i> SBW25]	-	-	1	1
	aromatic-amino-acid aminotransferase				
95111877	[<i>Pseudomonas entomophila</i> L48]	-	-	-	1

	ribose-phosphate pyrophosphokinase				
610714255	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
	2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase				
782986689	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase				
443285028	[<i>Pseudomonas syringae</i> pv. <i>syringae</i> B64]	1	1	1	1
	2,3,4,5-tetrahydropyridine-2,6-carboxylateN-succinyltransferase				
699967924	[<i>Pseudomonas</i> sp. MT-1]	1	-	-	1
	porphobilinogen deaminase				
782984486	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	porphobilinogen deaminase				
667952064	[<i>Pseudomonas mendocina</i> S5.2]	-	1	1	1
	porphobilinogen deaminase				
543438723	[<i>Pseudomonas alcaligenes</i> NBRC 14159]	-	-	-	1
	porphobilinogen deaminase				
735690293	[<i>Pseudomonas tuomuerensis</i>]	-	-	-	1
	MFS transporter [<i>Pseudomonas pseudoalcaligenes</i> AD6]				
610709982		1	1	1	1
	D-alanyl-D-alanine carboxypeptidase				
667955506	[<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
	D-alanyl-D-alanine carboxypeptidase				
782989310	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	-	1
	alcohol dehydrogenase [<i>Pseudomonas balearica</i> DSM 6083]				
747152787		1	1	1	1
	NADPH:quinone reductase				
782989419	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase				
782985196	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diam inopimelate ligase				
748440718	[<i>Pseudomonas batumici</i>]	-	-	-	1
	cysteinyl-tRNA synthetase [<i>Pseudomonas pseudoalcaligenes</i>]				
782987752		1	1	1	1
	cysteinyl-tRNA synthetase [<i>Pseudomonas mendocina</i> S5.2]				
667953770		1	1	1	1
	cysteinyl-tRNA synthetase [<i>Pseudomonas balearica</i> DSM 6083]				
747150756		1	1	1	1
	enoyl-CoA hydratase [<i>Pseudomonas pseudoalcaligenes</i>]				
782988809		-	-	1	1
	enoyl-CoA hydratase [<i>Pseudomonas</i> sp. M1]				
568073892		1	1	-	1

699967287	enoyl-CoA hydratase [Pseudomonas sp. MT-1]	1	1	1	1
667955338	molecular chaperone DnaJ [Pseudomonas mendocina S5.2]	1	1	1	1
610707779	hypothetical protein AU05_24625 [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782985389	beta-lactamase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610710818	hypothetical protein AU05_14000 [Pseudomonas pseudoalcaligenes AD6]	1	-	-	1
667955448	class V aminotransferase [Pseudomonas mendocina S5.2]	1	1	1	1
782989402	class V aminotransferase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610715044	class V aminotransferase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
543437127	putative GTP-binding protein [Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
610711947	DNA polymerase III subunit beta [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667952295	arginyl-tRNA synthetase [Pseudomonas mendocina S5.2]	1	1	1	1
782984734	arginyl-tRNA synthetase [Pseudomonas pseudoalcaligenes]	1	1	-	1
782989160	energy transducer TonB [Pseudomonas pseudoalcaligenes]	1	1	1	1
379064278	chromosome segregation ATPase [Pseudomonas stutzeri ATCC 14405 = CCUG 16156]	-	-	-	1
610715067	alcohol dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
782987010	flagellar basal body rod protein FlgB [Pseudomonas pseudoalcaligenes]	1	1	-	1
667951018	thioredoxin [Pseudomonas mendocina S5.2]	1	1	1	1
379066094	tryptophan synthase subunit beta [Pseudomonas stutzeri ATCC 14405 = CCUG 16156]	1	-	1	1
763481547	tryptophan synthase subunit beta [Pseudomonas oryzae]	-	-	-	1
395808955	tricarboxylate transport protein TctC [Pseudomonas stutzeri DSM 10701]	1	1	1	1
691226450	tricarboxylic transport membrane protein [Pseudomonas cremoricolorata]	1	1	1	1
610708081	amino acid ABC transporter substrate-	1	1	1	1

	binding protein [Pseudomonas pseudoalcaligenes AD6]				
610712479	toluene tolerance protein [Pseudomonas pseudoalcaligenes AD6]	1	-	1	1
543436062	hypothetical protein PA6_038_00060 [Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
346060062	helicase/SNF2 family domain protein [Pseudomonas aeruginosa NCMG1179]	1	1	-	1
782985623	hypothetical protein N619_30365 [Pseudomonas pseudoalcaligenes]	1	1	1	1
543437567	6,7-dimethyl-8-ribityllumazine synthase [Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
782987457	peptidase S9 [Pseudomonas pseudoalcaligenes]	1	1	1	1
610710059	peptidase S9 [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
568075428	peptidase S9 [Pseudomonas sp. M1]	1	-	-	1
782984712	proline iminopeptidase [Pseudomonas pseudoalcaligenes]	1	1	1	1
782987833	NADH dehydrogenase [Pseudomonas pseudoalcaligenes]	1	1	1	1
782986928	peptidase M48 [Pseudomonas pseudoalcaligenes]	1	1	1	1
782987326	RNA helicase [Pseudomonas pseudoalcaligenes]	-	-	1	1
327481186	DEAD-box ATP dependent DNA helicase [Pseudomonas stutzeri DSM 4166]	-	-	1	1
667951923	phosphate ABC transporter ATP-binding protein [Pseudomonas mendocina S5.2]	1	1	-	1
327480020	flagellar basal body FlaE domain- containing protein [Pseudomonas stutzeri DSM 4166]	-	-	-	1
610707191	alkyl hydroperoxide reductase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
543437844	alkyl hydroperoxide reductase subunit F [Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
747113941	alkyl hydroperoxide reductase [Pseudomonas fluorescens]	-	-	-	1
782986710	DNA polymerase III subunit alpha [Pseudomonas pseudoalcaligenes]	1	1	1	1
213926131	DNA polymerase III, alpha subunit [Pseudomonas syringae pv. tomato T1]	-	-	-	1
763481112	DNA polymerase III subunit alpha [Pseudomonas oryzae]	-	-	-	1

667954176	phosphoadenylylsulfate reductase [Pseudomonas mendocina S5.2]	1	1	1	1
610708315	phosphoadenylylsulfate reductase [Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
782988036	threonine aldolase [Pseudomonas pseudoalcaligenes]	1	-	1	1
856779308	threonine aldolase [Pseudomonas psychrophila]	-	-	-	1
324101124	threonine aldolase [Pseudomonas sp. TJI- 51]	-	-	-	1
667955336	carbamoyl phosphate synthase small subunit [Pseudomonas mendocina S5.2]	-	-	1	1
699965998	aldo/keto reductase [Pseudomonas sp. MT-1]	-	-	-	1
667952700	aldo/keto reductase [Pseudomonas mendocina S5.2]	1	1	1	1
970755347	ATP-dependent DNA helicase RecG [Pseudomonas aeruginosa]	1	1	1	1
610709516	chemotaxis protein CheW [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
610710070	glutamate dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
610708676	translocation protein TolB [Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
667953004	translocation protein TolB [Pseudomonas mendocina S5.2]	-	1	1	1
213926189	translocation protein TolB [Pseudomonas syringae pv. tomato T1]	1	1	-	1
610714854	recombinase RecA [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782987468	heme peroxidase [Pseudomonas pseudoalcaligenes]	1	1	1	1
782986724	2-C-methyl-D-erythritol 2,4- cyclodiphosphate synthase [Pseudomonas pseudoalcaligenes]	1	1	1	1
667952268	fructose 1,6-bisphosphatase [Pseudomonas mendocina S5.2]	-	-	-	1
667954162	2-methylisocitrate lyase [Pseudomonas mendocina S5.2]	1	1	1	1
758835609	Methylisocitrate lyase [Pseudomonas sp. FeS53a]	1	1	1	1
115588766	putative oxidoreductase, FMN-binding [Pseudomonas aeruginosa UCBPP-PA14]	-	-	-	1
667952256	N-methylproline demethylase [Pseudomonas mendocina S5.2]	-	-	-	1

782989494	membrane protein [Pseudomonas pseudoalcaligenes]	1	1	1	1
667951366	amino acid ABC transporter substrate-binding protein [Pseudomonas mendocina S5.2]	1	1	1	1
937646635	amino acid ABC transporter substrate-binding protein [Pseudomonas sp. In5]	-	-	-	1
937316229	amino acid ABC transporter substrate-binding protein [Pseudomonas fluorescens]	-	1	1	1
610710207	amino acid ABC transporter substrate-binding protein [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782988179	hemin degrading factor [Pseudomonas pseudoalcaligenes]	1	1	1	1
782989569	peptidoglycan-binding protein LysM [Pseudomonas pseudoalcaligenes]	-	1	1	1
782987584	phosphoribosylaminoimidazole synthetase [Pseudomonas pseudoalcaligenes]	-	1	-	1
782986832	FAD-linked oxidase [Pseudomonas fluorescens]	-	-	-	1
799203839	FAD-linked oxidase [Pseudomonas pseudoalcaligenes]	1	1	1	1
556077338	FAD linked oxidase domain-containing protein [Pseudomonas sp. VLB120]	1	1	-	1
782986260	hypothetical protein N619_15370 [Pseudomonas pseudoalcaligenes]	1	1	1	1
667953589	3-oxoacyl-ACP reductase [Pseudomonas mendocina S5.2]	1	1	1	1
667954297	threonyl-tRNA synthetase [Pseudomonas mendocina S5.2]	1	1	1	1
95110093	threonyl-tRNA synthetase [Pseudomonas entomophila L48]	1	-	1	1
782986683	succinyl-diaminopimelate desuccinylase [Pseudomonas pseudoalcaligenes]	1	1	1	1
667952935	peptidylprolyl isomerase [Pseudomonas mendocina S5.2]	1	1	1	1
335390099	peptidoglycan-associated lipoprotein OprL, partial [Pseudomonas alcaliphila]	1	1	1	1
335390249	peptidoglycan-associated lipoprotein OprL, partial [Pseudomonas straminea]	1	-	-	1

	coproporphyrinogen III oxidase				
667951806	[Pseudomonas mendocina S5.2]	1	1	-	1
	peptidoglycan-binding protein LysM				
782984620	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	peptide chain release factor 3				
667952622	[Pseudomonas mendocina S5.2]	1	1	-	1
	peptide chain release factor 3				
15599098	[Pseudomonas aeruginosa PAO1]	-	1	1	1
	peptide chain release factor 3				
747149918	[Pseudomonas balearica DSM 6083]	1	-	-	1
	3-phosphoglycerate dehydrogenase				
610711623	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
	D-3-phosphoglycerate dehydrogenase				
543439623	[Pseudomonas alcaligenes NBRC 14159]	-	-	-	1
	gamma-glutamyl phosphate reductase				
782989303	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	succinate dehydrogenase [Pseudomonas				
610712093	pseudoalcaligenes AD6]	1	1	1	1
	HIT family hydrolase [Pseudomonas				
782985844	pseudoalcaligenes]	1	1	1	1
	amino acid ABC transporter substrate-				
	binding protein [Pseudomonas				
763478105	oryzihabitans]	1	-	-	1
	O-succinylhomoserine sulfhydrylase				
610708087	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	hypothetical protein AU05_21670				
610708678	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	30S ribosomal protein S16 [Pseudomonas				
610709101	pseudoalcaligenes AD6]	1	1	1	1
	30S ribosomal protein S16 [Pseudomonas				
747151992	balearica DSM 6083]	1	1	1	1
	lactate dehydrogenase [Pseudomonas				
782989504	pseudoalcaligenes]	1	1	1	1
	translation initiation factor IF-1				
968570897	[Pseudomonas aeruginosa AES-1R]	1	1	1	1
	hypothetical protein DW68_23215				
667955384	[Pseudomonas mendocina S5.2]	1	1	1	1
	hypothetical protein PK34_20315, partial				
816235205	[Pseudomonas stutzeri]	1	1	1	1
	type 4 fimbrial biogenesis protein PilB				
848255058	[Pseudomonas stutzeri]	1	-	-	1
	general secretion pathway protein GspE				
768545190	[Pseudomonas stutzeri]	-	-	-	1
	hydroperoxidase [Pseudomonas				
913662753	fluorescens NCIMB 11764]	1	1	1	1

782985536	lipoprotein [Pseudomonas pseudoalcaligenes]	1	1	1	1
575871217	alcohol dehydrogenase [Pseudomonas aeruginosa PA38182]	1	1	-	1
667954404	chromosome segregation protein SMC [Pseudomonas mendocina S5.2]	-	1	-	1
565412986	thiol:disulfide interchange protein [Pseudomonas moraviensis R28-S]	-	-	-	1
782987835	NADH:ubiquinone oxidoreductase [Pseudomonas pseudoalcaligenes]	-	-	-	1
610711169	30S ribosomal protein S15 [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782989936	hypothetical protein N619_00815 [Pseudomonas pseudoalcaligenes]	1	1	1	1
667952404	thiamine biosynthesis protein ThiC [Pseudomonas mendocina S5.2]	1	1	1	1
782985478	Lon protease [Pseudomonas pseudoalcaligenes]	1	1	1	1
667952955	Lon protease [Pseudomonas mendocina S5.2]	1	-	1	1
667951099	peroxiredoxin [Pseudomonas mendocina S5.2]	1	1	1	1
667951369	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase [Pseudomonas mendocina S5.2]	1	1	1	1
782984722	ubiquinone biosynthesis methyltransferase UbiE [Pseudomonas pseudoalcaligenes]	1	1	1	1
667952905	hypothetical protein DW68_10235 [Pseudomonas mendocina S5.2]	1	1	-	1
782986705	3-hydroxyacyl-ACP dehydratase [Pseudomonas pseudoalcaligenes]	1	1	1	1
782989308	lytic transglycosylase [Pseudomonas pseudoalcaligenes]	1	1	1	1
404306255	lytic murein transglycosylase B [Pseudomonas fluorescens R124]	-	1	-	1
610713519	amidotransferase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667953755	amidotransferase [Pseudomonas mendocina S5.2]	-	-	-	1
782986529	peptidylprolyl isomerase [Pseudomonas pseudoalcaligenes]	1	-	1	1
327479689	peptidyl-prolyl cis-trans isomerase, FKBP-type [Pseudomonas stutzeri DSM]	1	-	1	1

	4166]				
	peptidase S41 [Pseudomonas				
782988178	pseudoalcaligenes]	1	1	1	1
	peptidase S41 [Pseudomonas mendocina				
667951364	S5.2]	1	1	1	1
	50S ribosomal protein L30 [Pseudomonas				
310941837	mendocina]	1	1	1	1
	glutamyl-tRNA amidotransferase				
782985125	[Pseudomonas pseudoalcaligenes]	-	-	1	1
	delta-aminolevulinic acid dehydratase				
610713604	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	delta-aminolevulinic acid dehydratase				
543438706	[Pseudomonas alcaligenes NBRC 14159]	-	-	-	1
	Alpha-S2-casein OS=Bos taurus				
P02663	GN=CSN1S2 PE=1 SV=2	1	1	1	1
	peptide ABC transporter substrate-				
	binding protein [Pseudomonas				
782988322	pseudoalcaligenes]	1	1	1	1
	methylcitrate synthase [Pseudomonas				
610708330	pseudoalcaligenes AD6]	1	-	1	1
	glutamate-1-semialdehyde 2,1-				
	aminomutase [Pseudomonas				
610715086	pseudoalcaligenes AD6]	1	1	1	1
	hypothetical protein N619_09150				
782988160	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	OHCU decarboxylase [Pseudomonas				
667954415	mendocina S5.2]	1	1	1	1
	metal-chelation protein CHAD				
782987804	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	triosephosphate isomerase [Pseudomonas				
667955327	mendocina S5.2]	1	1	1	1
	triosephosphate isomerase [Pseudomonas				
782989536	pseudoalcaligenes]	1	-	1	1
	molecular chaperone GroES				
667955396	[Pseudomonas mendocina S5.2]	-	1	1	1
	oxaloacetate decarboxylase				
782984936	[Pseudomonas pseudoalcaligenes]	1	-	-	1
	oxaloacetate decarboxylase				
610706326	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
	carbamoyltransferase [Pseudomonas				
667952376	mendocina S5.2]	1	-	-	1
	long-chain fatty acid--CoA ligase				
782985803	[Pseudomonas pseudoalcaligenes]	-	1	1	1
	long-chain fatty acid--CoA ligase				
610706877	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	1

26991234	long-chain-fatty-acid--CoA ligase [Pseudomonas putida KT2440]	1	-	-	1
28855744	biotin carboxylase/biotin carboxyl carrier protein [Pseudomonas syringae pv. tomato str. DC3000]	-	-	1	1
949198313	acetyl-CoA carboxylase [Pseudomonas trivialis]	1	1	1	1
782984553	agmatine deiminase [Pseudomonas pseudoalcaligenes]	1	1	1	1
26106137	putative tellurite resistant protein (plasmid) [Pseudomonas resinovorans]	1	1	1	1
610710326	N5-carboxyaminoimidazole ribonucleotide mutase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
331025910	2-dehydro-3-deoxyphosphooctonate aldolase [Pseudomonas coronafaciens pv. oryzae str. 1_6]	1	1	-	1
610714872	2-dehydro-3-deoxyphosphooctonate aldolase [Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
782987270	hypothetical protein N619_15760 [Pseudomonas pseudoalcaligenes]	1	1	1	1
667955229	nucleoid-associated protein [Pseudomonas mendocina S5.2]	-	-	-	1
610710488	inositol monophosphatase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
728055315	Chain A, Crystal Structure Of Pseudomonas Oleovorans Pooph Mutant H250i/i263w	1	1	1	1
257070345	MerA (plasmid) [Pseudomonas putida]	1	1	-	1
610712838	3-deoxy-manno-octulosonate cytidyltransferase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667952607	nicotinate-nucleotide pyrophosphorylase [Pseudomonas mendocina S5.2]	1	1	1	1
610712222	nicotinate-nucleotide pyrophosphorylase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
543439136	NH(3)-dependent NAD(+) synthetase [Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
610708628	phosphoheptose isomerase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667952958	phosphoheptose isomerase [Pseudomonas mendocina S5.2]	1	1	1	1
782987547	aspartate aminotransferase [Pseudomonas pseudoalcaligenes]	1	1	1	1

610709979	aspartate aminotransferase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
747150602	aspartate aminotransferase [Pseudomonas balearica DSM 6083]	1	1	1	1
782986320	adenylate kinase [Pseudomonas pseudoalcaligenes]	1	1	1	1
565415797	adenylate kinase [Pseudomonas moraviensis R28-S]	1	1	1	1
782985771	RNA polymerase sigma-H factor [Pseudomonas pseudoalcaligenes]	1	1	1	1
940186434	50S ribosomal protein L33 [Pseudomonas amygdali pv. mori]	-	1	-	1
610706463	exodeoxyribonuclease V subunit gamma [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782987254	exodeoxyribonuclease V subunit gamma [Pseudomonas pseudoalcaligenes]	-	-	-	1
512381674	exodeoxyribonuclease V gamma subunit [Pseudomonas putida NBRC 14164]	-	1	-	1
667955477	AMP nucleosidase [Pseudomonas mendocina S5.2]	1	1	1	1
610714587	orotate phosphoribosyltransferase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667954661	cytochrome C [Pseudomonas mendocina S5.2]	1	1	1	1
667953335	glycerophosphodiester phosphodiesterase [Pseudomonas mendocina S5.2]	1	1	1	1
782987189	transaldolase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610714031	elongation factor P [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782988914	phosphoserine phosphatase [Pseudomonas pseudoalcaligenes]	-	-	-	1
667953938	secretin [Pseudomonas mendocina S5.2]	1	-	1	1
782987287	peptidoglycan-binding protein LysM [Pseudomonas pseudoalcaligenes]	1	1	1	1
782988034	hypothetical protein N619_08465 [Pseudomonas pseudoalcaligenes]	-	1	1	1
782985181	30S ribosomal protein S9 [Pseudomonas pseudoalcaligenes]	1	1	1	1
782985903	hypothetical protein N619_31945 [Pseudomonas pseudoalcaligenes]	1	1	1	1
610714848	50S rRNA methyltransferase [Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
667954688	50S rRNA methyltransferase [Pseudomonas mendocina S5.2]	1	-	1	1

	ABC transporter substrate-binding protein				
610706328	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
	ABC transporter substrate-binding protein				
782984932	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	DNA topoisomerase IV subunit B				
610708937	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	1	1
	DNA topoisomerase IV subunit B				
667952399	[<i>Pseudomonas mendocina</i> S5.2]	-	-	-	1
	ribosomal protein L28 [<i>Pseudomonas</i>				
68348665	protegens Pf-5]	1	1	-	1
	tryptophan--tRNA ligase [<i>Pseudomonas</i>				
782985172	pseudoalcaligenes]	-	1	1	1
	5,10-methylenetetrahydrofolate reductase				
610708538	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	1
	hypothetical protein N619_21160				
782983978	[<i>Pseudomonas pseudoalcaligenes</i>]	-	1	1	1
	hypothetical protein DW68_05800				
667952046	[<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
	hypothetical protein DW68_19210				
667954618	[<i>Pseudomonas mendocina</i> S5.2]	1	1	-	1
	(2Fe-2S)-binding protein [<i>Pseudomonas</i>				
782984015	pseudoalcaligenes]	1	1	1	1
	(2Fe-2S)-binding protein [<i>Pseudomonas</i>				
667951596	mendocina S5.2]	1	1	1	1
	endonuclease I [<i>Pseudomonas</i>				
610708889	pseudoalcaligenes AD6]	1	1	1	1
	endonuclease I [<i>Pseudomonas</i>				
782988591	pseudoalcaligenes]	1	1	1	1
	cysteine synthase [<i>Pseudomonas</i>				
667953485	mendocina S5.2]	-	1	1	1
	hydrolase TatD [<i>Pseudomonas</i>				
610712818	pseudoalcaligenes AD6]	-	1	1	1
	hydrolase, TatD family [<i>Pseudomonas</i>				
928206009	fuscovaginae]	-	-	-	1
	membrane protein [<i>Pseudomonas</i>				
610711430	pseudoalcaligenes AD6]	1	-	1	1
	hypothetical protein PA6_027_00530				
543436913	[<i>Pseudomonas alcaligenes</i> NBRC 14159]	1	-	1	1
	hypothetical protein PP_1131				
26987867	[<i>Pseudomonas putida</i> KT2440]	1	-	1	1
	gamma-glutamyl-gamma-aminobutyrate				
	hydrolase [<i>Pseudomonas</i>				
610714227	pseudoalcaligenes AD6]	-	-	-	1
	copper resistance protein CopA				
953212201	[<i>Pseudomonas aeruginosa</i>]	1	1	1	1

782988588	ACP phosphodiesterase [Pseudomonas pseudoalcaligenes]	1	1	1	1
782989523	transcription elongation factor GreA [Pseudomonas pseudoalcaligenes]	1	1	1	1
543438355	transcription elongation factor GreA [Pseudomonas alcaligenes NBRC 14159]	1	1	-	1
403244308	hypothetical protein PACIG1_5983 [Pseudomonas aeruginosa CIG1]	1	1	1	1
953174994	short-chain dehydrogenase [Pseudomonas aeruginosa]	1	1	1	1
610708214	nucleoprotein/polynucleotide-associated enzyme [Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
610714152	TonB-dependent receptor [Pseudomonas pseudoalcaligenes AD6]	-	-	1	1
735691782	TonB-dependent receptor [Pseudomonas tuomuerensis]	-	-	-	1
782989575	cAMP-binding protein [Pseudomonas pseudoalcaligenes]	1	1	1	1
575877677	luciferase family protein [Pseudomonas aeruginosa PA38182]	1	-	1	1
699968546	luciferase family protein [Pseudomonas sp. MT-1]	-	1	-	1
667953559	MarR family transcriptional regulator [Pseudomonas mendocina S5.2]	1	1	1	1
782987631	glutathione S-transferase [Pseudomonas pseudoalcaligenes]	-	1	1	1
610708544	hypothetical protein AU05_21965 [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782984871	ATP phosphoribosyltransferase regulatory subunit [Pseudomonas pseudoalcaligenes]	1	-	1	1
928211209	ATP phosphoribosyltransferase involved in histidine biosynthesis, partial [Pseudomonas fuscovaginae]	1	-	1	1
782984485	chemotaxis protein CheY [Pseudomonas pseudoalcaligenes]	1	1	1	1
610708385	CoA-transferase [Pseudomonas pseudoalcaligenes AD6]	1	-	1	1
667951542	CoA-transferase [Pseudomonas mendocina S5.2]	1	1	-	1
782989409	palmitoyl-CoA hydrolase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610707218	ferredoxin-NADP reductase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	1

390982753	flagellar hook-associated protein FlgL [Pseudomonas stutzeri CCUG 29243]	-	-	1	1
769335307	flagellar hook protein FlgL [Pseudomonas sp. 10B238]	1	1	1	1
610709569	flagellar hook protein FlgL [Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
782986898	glycine/betaine transmethylase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610707825	glycine/betaine transmethylase [Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
26106256	hypothetical protein (plasmid) [Pseudomonas resinovorans]	1	1	1	1
667955263	saccharopine dehydrogenase [Pseudomonas mendocina S5.2]	-	1	1	1
459960139	saccharopine dehydrogenase [Pseudomonas sp. Lz4W]	-	-	-	1
782985605	NAD(P)H-quinone oxidoreductase [Pseudomonas pseudoalcaligenes]	1	1	1	1
928482145	NAD(P)H-quinone oxidoreductase [Pseudomonas psychrophila]	-	-	-	1
610711625	5-carboxymethyl-2-hydroxymuconate delta-isomerase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667951801	peptide deformylase [Pseudomonas mendocina S5.2]	-	1	1	1
610714012	oxidoreductase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
667954113	oxidoreductase [Pseudomonas mendocina S5.2]	1	1	1	1
782987319	phospho-2-dehydro-3-deoxyheptonate aldolase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610712069	quinone oxidoreductase [Pseudomonas pseudoalcaligenes AD6]	1	-	-	1
782988819	quinone oxidoreductase [Pseudomonas pseudoalcaligenes]	-	1	1	1
403244315	hypothetical protein PACIG1_5990 [Pseudomonas aeruginosa CIG1]	1	1	1	1
610707381	glycine cleavage system protein R [Pseudomonas pseudoalcaligenes AD6]	1	-	-	1
114794740	Chain A, Crystal Structure Of Amidohydrolase From Pseudomonas Aeruginosa	1	1	1	1
666086243	transcriptional regulator [Pseudomonas fluorescens]	-	-	-	1

782989182	GTP cyclohydrolase [Pseudomonas pseudoalcaligenes]	1	-	-	1
782986383	formyltetrahydrofolate deformylase [Pseudomonas pseudoalcaligenes]	1	1	1	1
801170662	acetyl-CoA carboxylase [Pseudomonas kilonensis]	-	1	1	1
P01008	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	1	1	1	1
667955354	glutathione peroxidase [Pseudomonas mendocina S5.2]	1	1	1	1
610706375	alanine racemase [Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
610712984	transcriptional regulator [Pseudomonas pseudoalcaligenes AD6]	-	-	1	1
782987168	GAF domain-containing protein [Pseudomonas pseudoalcaligenes]	1	-	1	1
782988147	phosphoserine phosphatase [Pseudomonas pseudoalcaligenes]	1	1	1	1
782989947	maleylacetoacetate isomerase [Pseudomonas pseudoalcaligenes]	1	1	1	1
782986152	ATP-dependent RNA helicase RhlB [Pseudomonas pseudoalcaligenes]	1	1	1	1
327479207	thioredoxin [Pseudomonas stutzeri DSM 4166]	1	-	-	1
667951161	C4-dicarboxylate ABC transporter [Pseudomonas mendocina S5.2]	-	-	-	1
782989578	hypothetical protein N619_05045 [Pseudomonas pseudoalcaligenes]	1	-	1	1
610711137	hypothetical protein AU05_12705 [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782986309	peptide chain release factor 2 [Pseudomonas pseudoalcaligenes]	-	-	-	1
307752087	peptide chain release factor I [Pseudomonas aeruginosa PAO1]	-	1	-	1
327479377	bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II-like protein [Pseudomonas stutzeri DSM 4166]	-	-	1	1
856761927	3,4-dihydroxy-2-butanone 4-phosphate synthase [Pseudomonas taetrolens]	-	-	-	1
949212538	cupin [Pseudomonas sp. DSM 29167]	-	-	1	1
610712475	D-arabinose 5-phosphate isomerase [Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
940723162	D-arabinose 5-phosphate isomerase [Pseudomonas endophytica]	1	1	1	1

667954278	exodeoxyribonuclease V subunit beta [Pseudomonas mendocina S5.2]	1	1	1	1
782987255	exodeoxyribonuclease V subunit beta [Pseudomonas pseudoalcaligenes]	1	1	1	1
610706462	exodeoxyribonuclease V subunit beta [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
955698346	Exodeoxyribonuclease V beta chain [Pseudomonas brassicacearum]	-	-	-	1
387160323	exodeoxyribonuclease V, beta subunit [Pseudomonas fluorescens A506]	-	-	-	1
764072405	histidine kinase [Pseudomonas putida S13.1.2]	1	1	1	1
782989620	acetolactate synthase 3 catalytic subunit [Pseudomonas pseudoalcaligenes]	-	-	1	1
763479498	acetolactate synthase 3 catalytic subunit [Pseudomonas oryzae]	-	1	-	1
229364470	acetolactate synthase isozyme III large subunit [Pseudomonas fluorescens SBW25]	-	-	-	1
782987067	chemotaxis protein CheY [Pseudomonas pseudoalcaligenes]	-	-	-	1
782988494	indole-3-glycerol-phosphate synthase [Pseudomonas pseudoalcaligenes]	-	1	-	1
610713062	indole-3-glycerol-phosphate synthase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	1
782985702	ATP-binding protein [Pseudomonas pseudoalcaligenes]	-	-	1	1
667952180	aspartate carbamoyltransferase catalytic subunit [Pseudomonas mendocina S5.2]	-	-	1	1
543437514	acyl-[acyl-carrier-protein]-:UDP-N- acetylglucosamine O-acyltransferase [Pseudomonas alcaligenes NBRC 14159]	-	-	-	1
782983990	CRISPR-associated protein Csy2 [Pseudomonas pseudoalcaligenes]	1	1	1	1
379065373	DNA-directed RNA polymerase subunit omega [Pseudomonas stutzeri ATCC 14405 = CCUG 16156]	-	-	-	1
782988053	twitching motility protein PilT [Pseudomonas pseudoalcaligenes]	-	-	-	1
213923756	twitching motility protein [Pseudomonas syringae pv. tomato T1]	-	-	-	1
610712522	hypothetical protein AU05_08710 [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
691226498	Skp [Pseudomonas cremoricolorata]	-	-	1	1
758821814	Outer membrane protein H precursor	1	1	1	1

	[Pseudomonas sp. FeS53a]				
	UDP-3-O-(3-hydroxymyristoyl)				
	glucosamine N-acyltransferase				
667954721	[Pseudomonas mendocina S5.2]	1	1	1	1
	peptidoglycan-binding protein				
768550438	[Pseudomonas stutzeri]	-	-	-	1
	peptidoglycan-binding protein				
610710259	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	acetyl-CoA carboxylase subunit beta				
782987587	[Pseudomonas pseudoalcaligenes]	1	-	1	1
	peptidylprolyl isomerase [Pseudomonas				
782987341	pseudoalcaligenes]	1	1	1	1
	peptidylprolyl isomerase [Pseudomonas				
735693150	tuomuerensis]	-	-	-	1
	fatty acid cistrans isomerase				
576710204	[Pseudomonas sp. GM41(2012)]	-	1	-	1
	CRISPR-associated protein Csy1				
782983989	[Pseudomonas pseudoalcaligenes]	1	1	1	1
949222564	aminotransferase [Pseudomonas veronii]	-	-	1	1
	SCP-2 family sterol carrier protein				
610712066	[Pseudomonas pseudoalcaligenes AD6]	1	-	1	1
	hypothetical protein N619_28420				
782985283	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	pilus assembly protein PilM				
610707722	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
	histidine kinase [Pseudomonas				
610711458	pseudoalcaligenes AD6]	1	1	1	1
	elongation factor Tu [Pseudomonas				
940100172	amygdali pv. dendropanacis]	-	-	-	1
	hypothetical protein AU05_08095				
610712862	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	molybdate ABC transporter, periplasmic				
	molybdate-binding protein [Pseudomonas				
387163587	fluorescens A506]	1	-	1	1
	5'-methylthioadenosine phosphorylase				
782985902	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	protein-PII uridylyltransferase				
782986692	[Pseudomonas pseudoalcaligenes]	1	-	1	1
	metal-binding protein [Pseudomonas				
782985937	pseudoalcaligenes]	1	1	1	1
	ATPase AAA [Pseudomonas				
610707834	pseudoalcaligenes AD6]	1	1	1	1
	propionate kinase [Pseudomonas				
610714297	pseudoalcaligenes AD6]	1	1	1	1
28854238	ribosomal protein L32 [Pseudomonas	1	1	1	1

	syringae pv. tomato str. DC3000]				
	2-keto-3-deoxy-D-arabino-heptulosonate-				
	7- phosphate synthase I alpha				
758835586	[Pseudomonas sp. FeS53a]	-	-	-	1
	ribulose-phosphate 3-epimerase				
610713067	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	N-ethylammeline chlorohydrolase				
782987540	[Pseudomonas pseudoalcaligenes]	-	1	1	1
	hypothetical protein DW68_02990				
667951502	[Pseudomonas mendocina S5.2]	-	1	-	1
	bacterial regulatory s, tetR family protein				
641461592	[Pseudomonas sp. P482]	-	-	-	1
	ABC transporter substrate-binding protein				
782988802	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	nucleotide-binding protein [Pseudomonas				
663683376	mendocina]	1	1	1	1
	malonyl CoA-ACP transacylase				
667953358	[Pseudomonas mendocina S5.2]	1	-	-	1
	fumarate hydratase [Pseudomonas				
782989933	pseudoalcaligenes]	-	-	-	1
	glutamine amidotransferase				
782986423	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	glutamine synthetase [Pseudomonas				
610706805	pseudoalcaligenes AD6]	1	1	-	1
	glutamine synthetase [Pseudomonas				
735690283	tuomuerensis]	-	-	-	1
	3-dehydroquinate dehydratase				
610706291	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	3-dehydroquinate dehydratase				
126170363	[Pseudomonas aeruginosa C3719]	1	-	-	1
	transcriptional regulator [Pseudomonas				
610707788	pseudoalcaligenes AD6]	1	-	1	1
	hypothetical protein N619_09200				
782988168	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	sulfoxide reductase catalytic subunit				
782989586	YedY [Pseudomonas pseudoalcaligenes]	-	1	1	1
	GntR family transcriptional regulator				
667955046	[Pseudomonas mendocina S5.2]	1	1	1	1
	transcriptional regulator [Pseudomonas				
782986384	pseudoalcaligenes]	-	-	-	1
	GntR family transcriptional regulator				
937315665	[Pseudomonas fluorescens]	-	1	1	1
	xanthine dehydrogenase [Pseudomonas				
782987113	pseudoalcaligenes]	1	1	1	1
610709473	xanthine dehydrogenase [Pseudomonas	-	-	-	1

	pseudoalcaligenes AD6]				
	RecT protein [Pseudomonas				
928288052	coronafaciens pv. oryzae]	1	1	1	1
	Helicase domain protein [Pseudomonas				
327478901	stutzeri DSM 4166]	1	-	-	1
	Helicase domain protein [Pseudomonas				
703405723	xanthomarina]	-	-	1	1
	PEP synthetase regulatory protein				
667954158	[Pseudomonas mendocina S5.2]	-	-	-	1
	tyrosine--tRNA ligase [Pseudomonas				
667951084	mendocina S5.2]	1	-	-	1
	tyrosyl-tRNA synthetase [Pseudomonas				
404306382	fluorescens R124]	-	-	-	1
	5-oxo-L-prolinase [Pseudomonas				
782987771	pseudoalcaligenes]	1	1	1	1
	5-oxo-L-prolinase [Pseudomonas				
610712117	pseudoalcaligenes AD6]	1	1	1	1
	3-oxoacyl-ACP synthase [Pseudomonas				
782985943	pseudoalcaligenes]	-	-	1	1
	LuxR family transcriptional regulator				
667953017	[Pseudomonas mendocina S5.2]	-	-	-	1
	DNA-binding response regulator, LuxR				
	family [Pseudomonas syringae pv. tomato				
213926157	T1]	-	-	-	1
	TetR family transcriptional regulator				
667955411	[Pseudomonas mendocina S5.2]	-	-	-	1
	peptidylprolyl isomerase [Pseudomonas				
610707201	pseudoalcaligenes AD6]	-	-	1	1
	tricarboxylic transport membrane protein				
610711453	[Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
	alpha/beta hydrolase [Pseudomonas				
610712493	pseudoalcaligenes AD6]	1	1	1	1
	phospholipid-binding protein				
782985187	[Pseudomonas pseudoalcaligenes]	-	-	-	1
782988329	keratin [Pseudomonas pseudoalcaligenes]	1	1	1	1
	pseudouridine synthase [Pseudomonas				
782989542	pseudoalcaligenes]	1	1	1	1
	RNA polymerase factor sigma-54				
782985148	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	flagellar biosynthesis sigma factor				
667954464	[Pseudomonas mendocina S5.2]	-	-	1	1
	flagellar motor switch protein FliN				
576705903	[Pseudomonas sp. GM41(2012)]	-	-	-	1
	pyrroloquinoline quinone biosynthesis				
610709356	protein PqqE [Pseudomonas	1	1	1	1

	pseudoalcaligenes AD6]				
	hypothetical protein DW68_13310				
667953494	[Pseudomonas mendocina S5.2]	1	1	-	1
	ferredoxin [Pseudomonas mendocina				
667954697	S5.2]	1	1	1	1
	D-serine dehydratase [Pseudomonas				
667954972	mendocina S5.2]	1	1	1	1
	cell division protein FtsZ [Pseudomonas				
610708013	pseudoalcaligenes AD6]	1	1	-	1
	peptidylprolyl isomerase [Pseudomonas				
667952755	mendocina S5.2]	1	1	-	1
	riboflavin synthase subunit alpha				
667951013	[Pseudomonas mendocina S5.2]	-	-	-	1
	Riboflavin synthase [Pseudomonas				
749476990	fluorescens]	-	-	-	1
	mannose-1-phosphate guanylyltransferase				
610713080	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	protein phosphatase [Pseudomonas				
667954462	mendocina S5.2]	-	1	1	1
	chemotaxis phosphatase [Pseudomonas				
270160584	pseudoalcaligenes KF707]	-	1	1	1
	membrane protein [Pseudomonas				
610714883	pseudoalcaligenes AD6]	-	-	-	1
	diguanylate cyclase [Pseudomonas				
782984315	pseudoalcaligenes]	1	-	-	1
	peptidase [Pseudomonas				
610707993	pseudoalcaligenes AD6]	1	1	1	1
	aminopeptidase [Pseudomonas				
782985488	pseudoalcaligenes]	1	1	1	1
	ABC transporter permease [Pseudomonas				
782988299	pseudoalcaligenes]	-	-	1	1
	isocitrate dehydrogenase [Pseudomonas				
782987480	pseudoalcaligenes]	-	-	-	1
	anthranilate synthase component II				
667951103	[Pseudomonas mendocina S5.2]	1	1	1	1
	NADH:flavin oxidoreductase				
667952882	[Pseudomonas mendocina S5.2]	1	1	1	1
	NADH:flavin oxidoreductase				
782985381	[Pseudomonas pseudoalcaligenes]	-	1	1	1
	sulfoacetaldehyde reductase				
782984949	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	SAM-dependent methyltransferase				
799189818	[Pseudomonas fluorescens]	-	1	1	1
	hypothetical protein N619_15710				
782986323	[Pseudomonas pseudoalcaligenes]	1	1	1	1

	stress-induced protein YgiW				
610711627	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
	gamma-glutamylputrescine synthetase				
667952127	[<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
	glutamine synthetase [<i>Pseudomonas</i>				
213923244	<i>syringae</i> pv. tomato T1]	-	-	-	1
	S-formylglutathione hydrolase				
667954705	[<i>Pseudomonas mendocina</i> S5.2]	1	1	-	1
	putative LysR family transcriptional				
	regulator [<i>Pseudomonas alcaligenes</i>				
543436563	NBRC 14159]	-	-	-	1
	cold-shock protein [<i>Pseudomonas</i>				
949203754	<i>orientalis</i>]	-	-	-	1
	histidinol dehydrogenase [<i>Pseudomonas</i>				
782986223	<i>pseudoalcaligenes</i>]	1	1	1	1
	UDP-N-acetylmuramoyl-tripeptide--D-				
	alanyl-D-alanine ligase [<i>Pseudomonas</i>				
782985197	<i>pseudoalcaligenes</i>]	1	1	1	1
	dTDP-4-dehydrorhamnose 3,5-epimerase				
610713268	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
	flagellar biosynthesis anti-sigma factor				
667954526	FlgM [<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
	malate:quinone oxidoreductase				
667955386	[<i>Pseudomonas mendocina</i> S5.2]	-	1	1	1
	hypothetical protein TU79_11920				
949199339	[<i>Pseudomonas trivialis</i>]	1	-	-	1
	hypothetical protein UF78_07745				
768547931	[<i>Pseudomonas stutzeri</i>]	-	-	-	1
	endoribonuclease [<i>Pseudomonas</i>				
782988340	<i>pseudoalcaligenes</i>]	-	-	-	1
	endoribonuclease [<i>Pseudomonas balearica</i>				
747149529	DSM 6083]	1	-	1	1
	oligoribonuclease [<i>Pseudomonas</i>				
667952423	<i>mendocina</i> S5.2]	-	1	1	1
	5-hydroxyisourate hydrolase				
782987108	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	FMN adenylyltransferase [<i>Pseudomonas</i>				
782985231	<i>pseudoalcaligenes</i>]	1	1	1	1
	phosphoserine phosphatase SerB				
928207827	[<i>Pseudomonas fuscovaginae</i>]	-	1	-	1
	phosphoserine phosphatase				
327482433	[<i>Pseudomonas stutzeri</i> DSM 4166]	-	1	-	1
	glutamate synthase small chain				
543439851	[<i>Pseudomonas alcaligenes</i> NBRC 14159]	1	1	1	1
610707147	NADPH-dependent FMN reductase	1	-	-	1

	[Pseudomonas pseudoalcaligenes AD6]				
	ATP synthase F0F1 subunit epsilon				
782984124	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	hypothetical protein AN920_04700				
928538525	[Pseudomonas aeruginosa]	-	-	1	1
	histidine kinase [Pseudomonas				
782988631	pseudoalcaligenes]	1	1	1	1
	molybdopterin-synthase				
	adenylyltransferase [Pseudomonas				
610714248	pseudoalcaligenes AD6]	1	1	-	1
	molybdopterin biosynthesis MoeB protein				
126170528	[Pseudomonas aeruginosa C3719]	-	1	-	1
	GntR family transcriptional regulator				
610709476	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	GntR family transcriptional regulator				
940725874	[Pseudomonas endophytica]	1	-	1	1
	thiosulfate sulfurtransferase				
782984855	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	NADH dehydrogenase [Pseudomonas				
610713891	pseudoalcaligenes AD6]	-	-	-	1
	flagellar motor switch protein FlIM				
610709535	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
	flagellar motor switch protein FlIM				
856775977	[Pseudomonas lini]	-	-	-	1
	putative MerR family transcriptional				
	regulator [Pseudomonas alcaligenes				
543437064	NBRC 14159]	-	1	1	1
	ribose 5-phosphate isomerase				
610711633	[Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
	imidazole glycerol phosphate synthase				
610710201	[Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
	glutathione synthetase [Pseudomonas				
782984631	pseudoalcaligenes]	1	1	1	1
	glutathione synthetase [Pseudomonas sp.				
324101796	TJI-51]	1	1	1	1
	3-methyl-2-oxobutanoate				
	hydroxymethyltransferase [Pseudomonas				
610711157	pseudoalcaligenes AD6]	1	1	-	1
	3-isopropylmalate dehydratase small				
758829426	subunit [Pseudomonas sp. FeS53a]	-	-	-	1
	LOG family protein [Pseudomonas				
782984646	pseudoalcaligenes]	1	1	1	1
	Protein of unknown function DUF3412				
576710085	[Pseudomonas sp. GM41(2012)]	1	1	1	1
610712135	esterase [Pseudomonas pseudoalcaligenes	1	1	1	1

	AD6]				
	RNA-binding protein Hfq [Pseudomonas				
610707866	pseudoalcaligenes AD6]	1	1	1	1
	signal recognition particle receptor				
	protein FtsY, alpha subunit [Pseudomonas				
748439697	batumici]	-	-	-	1
	cell division protein FtsY [Pseudomonas				
667951283	mendocina S5.2]	-	1	1	1
	Signal recognition particle receptor FtsY				
940244982	[Pseudomonas amygdali pv. sesami]	-	-	-	1
799199837	cytochrome C [Pseudomonas fluorescens]	-	-	-	1
	aminomethyltransferase [Pseudomonas				
782985767	pseudoalcaligenes]	-	-	1	1
	glucose-1-phosphate				
	thymidyltransferase [Pseudomonas				
782988201	pseudoalcaligenes]	1	1	1	1
	thymidylate kinase [Pseudomonas				
782985946	pseudoalcaligenes]	-	1	-	1
	hypothetical protein AU05_22020				
610708554	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	aromatic acid decarboxylase				
735690826	[Pseudomonas tuomuerensis]	-	-	-	1
	ribosome-binding factor A [Pseudomonas				
610711171	pseudoalcaligenes AD6]	1	1	-	1
	alcohol dehydrogenase [Pseudomonas				
667954902	mendocina S5.2]	1	1	1	1
	hypothetical protein AU05_02355				
610707190	[Pseudomonas pseudoalcaligenes AD6]	1	-	1	1
	pyrophosphatase [Pseudomonas				
782985523	pseudoalcaligenes]	1	1	1	1
	16S rRNA methyltransferase				
610708000	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	16S rRNA methyltransferase				
667952714	[Pseudomonas mendocina S5.2]	1	1	1	1
	16S rRNA methyltransferase				
747152101	[Pseudomonas balearica DSM 6083]	1	1	1	1
	hypothetical protein N619_08215				
782988603	[Pseudomonas pseudoalcaligenes]	1	1	-	1
	acyl-CoA thioesterase [Pseudomonas sp.				
674101979	1-7]	-	1	1	1
	dehydratase [Pseudomonas				
782989297	pseudoalcaligenes]	1	1	1	1
	peptidase M22 family protein				
543437470	[Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
610707279	anti-anti-sigma factor [Pseudomonas	1	1	1	1

	pseudoalcaligenes AD6]				
	TldD protein [Pseudomonas syringae pv.				
940049398	coriandricola]	-	-	-	1
	peptidase U62, modulator of DNA gyrase				
	[Pseudomonas stutzeri ATCC 14405 =				
379063980	CCUG 16156]	-	-	-	1
	3-ketoacyl-ACP reductase [Pseudomonas				
667955393	mendocina S5.2]	1	1	1	1
	ribosomal protein L20 [Pseudomonas				
4972786	protegens]	-	-	-	1
	tRNA uridine 5-				
	carboxymethylaminomethyl modification				
	protein [Pseudomonas pseudoalcaligenes				
610711940	AD6]	1	-	-	1
	3-deoxy-D-manno-octulosonate 8-				
	phosphate phosphatase [Pseudomonas				
782985152	pseudoalcaligenes]	-	-	1	1
	GNAT family acetyltransferase				
782984280	[Pseudomonas pseudoalcaligenes]	-	1	1	1
	membrane protein [Pseudomonas				
782986312	pseudoalcaligenes]	-	-	-	1
	thiopurine S-methyltransferase				
782988824	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	anthranilate synthase component II				
543436126	[Pseudomonas alcaligenes NBRC 14159]	1	-	1	1
	nitrogen regulation protein NR(I)				
667951250	[Pseudomonas mendocina S5.2]	1	-	-	1
	hypothetical protein N619_27625				
782985136	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	LPS biosynthesis protein [Pseudomonas				
782988518	pseudoalcaligenes]	1	1	1	1
	gamma-glutamylputrescine				
	oxidoreductase [Pseudomonas				
782987237	pseudoalcaligenes]	1	1	1	1
	30S ribosomal protein S18 [Pseudomonas				
610706379	pseudoalcaligenes AD6]	-	1	-	1
	peptidase PmbA [Pseudomonas				
667952667	mendocina S5.2]	1	1	1	1
	gamma-glutamyltransferase				
782988103	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	pilus assembly protein [Pseudomonas				
667952584	mendocina S5.2]	1	1	1	1
	tRNA 2-thiouridylase [Pseudomonas				
667953945	mendocina S5.2]	-	1	1	1
782986722	S-(hydroxymethyl)glutathione	1	1	1	1

	dehydrogenase [Pseudomonas pseudoalcaligenes]				
	ribosomal large subunit pseudouridine synthase D [Pseudomonas mendocina S5.2]	667952770	-	1	- 1
	phosphoglycolate phosphatase [Pseudomonas pseudoalcaligenes]	782987538	-	1	- 1
	lipoprotein [Pseudomonas pseudoalcaligenes]	782986311	1	1	1 1
	amino acid dehydrogenase [Pseudomonas mendocina S5.2]	667952024	1	-	1 1
	formimidoylglutamase [Pseudomonas mendocina S5.2]	667951181	1	1	1 1
	formimidoylglutamase [Pseudomonas pseudoalcaligenes AD6]	610708894	1	1	1 1
	oxidoreductase, molybdopterin-binding protein [Pseudomonas syringae pv. tomato str. DC3000]	28854555	-	-	- 1
	beta-lactamase [Pseudomonas pseudoalcaligenes]	782989492	-	-	- 1
	choline dehydrogenase [Pseudomonas aeruginosa PAO1]	9951694	-	-	- 1
	choline dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	610707663	1	1	1 1
	choline dehydrogenase [Pseudomonas mendocina S5.2]	667952240	-	1	- 1
	choline dehydrogenase [Pseudomonas amygdali pv. aesculi str. 0893_23]	330871147	-	-	- 1
	chorismate synthase [Pseudomonas pseudoalcaligenes AD6]	610709458	-	1	1 1
	molecular chaperone Hsp33 [Pseudomonas pseudoalcaligenes AD6]	610706456	1	1	1 1
	dTDP-glucose 4,6-dehydratase [Pseudomonas pseudoalcaligenes]	782988200	1	1	1 1
	dTDP-glucose 4,6-dehydratase [Pseudomonas mendocina S5.2]	667951382	1	1	- 1
	pseudouridine synthase [Pseudomonas pseudoalcaligenes]	782987535	-	-	- 1
	16S rRNA methyltransferase [Pseudomonas pseudoalcaligenes AD6]	610711939	1	-	- 1
	peptide chain release factor 1 [Pseudomonas putida HB3267]	430791553	-	1	- 1
	peptide chain release factor 1 [Pseudomonas mendocina S5.2]	667952830	-	1	1 1
	peptide chain release factor 1	641465463	1	-	1 1

	[Pseudomonas sp. P482]				
	diguanylate cyclase [Pseudomonas				
667952738	mendocina S5.2]	-	1	1	1
	uracil phosphoribosyltransferase				
782985225	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	nitroreductase [Pseudomonas				
782987522	pseudoalcaligenes]	1	1	1	1
881082675	endonuclease [Pseudomonas aeruginosa]	1	1	1	1
	hydrolase or acyltransferase				
782988514	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	ABC transporter ATP-binding protein				
395806951	[Pseudomonas stutzeri DSM 10701]	1	1	-	1
	pilus assembly protein PilG				
610708520	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	1
	isopropylmalate isomerase [Pseudomonas				
610708476	pseudoalcaligenes AD6]	-	-	-	1
	isopropylmalate isomerase [Pseudomonas				
928483180	psychrophila]	1	-	-	1
	scaffolding protein [Pseudomonas				
782986212	pseudoalcaligenes]	1	1	1	1
	FeS cluster assembly scaffold IscU				
568074827	[Pseudomonas sp. M1]	-	1	-	1
	hypothetical protein PP_2500				
26989223	[Pseudomonas putida KT2440]	1	1	1	1
	hypothetical protein AU05_24960				
610707677	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	chromosome partitioning protein ParB				
667951716	[Pseudomonas mendocina S5.2]	1	1	1	1
	1,2-oxophytodienoate reductase				
610708057	[Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
	ATP-dependent metalloprotease				
747149961	[Pseudomonas balearica DSM 6083]	1	1	-	1
	Phosphonate metabolism PhnJ				
940116713	[Pseudomonas coronafaciens pv. garcae]	-	-	-	1
	glucose-6-phosphate isomerase				
610711159	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	hypothetical protein DW68_01745				
667951257	[Pseudomonas mendocina S5.2]	1	1	-	1
	peptidyl-tRNA hydrolase [Pseudomonas				
610709721	pseudoalcaligenes AD6]	1	1	1	1
	conserved membrane protein (plasmid)				
295443587	[Pseudomonas putida]	1	1	1	1
	outer membrane protein OprG				
390984782	[Pseudomonas stutzeri CCUG 29243]	1	-	1	1
379064279	outer membrane protein OprG	-	1	1	1

[Pseudomonas stutzeri ATCC 14405 = CCUG 16156]					
SsrA-binding protein [Pseudomonas					
782989508	pseudoalcaligenes]	1	1	1	1
tRNA hydroxylase [Pseudomonas					
782987742	pseudoalcaligenes]	-	1	1	1
tRNA hydroxylase [Pseudomonas					
667953766	mendocina S5.2]	1	-	-	1
30S ribosomal protein S17 [Pseudomonas					
848254747	stutzeri]	1	-	-	1
2Fe-2S ferredoxin [Pseudomonas					
610710497	pseudoalcaligenes AD6]	1	1	1	1
anhydrase [Pseudomonas mendocina					
667951580	S5.2]	1	1	1	1
serine dehydratase [Pseudomonas					
610710812	pseudoalcaligenes AD6]	1	-	1	1
serine dehydratase [Pseudomonas					
749422383	fluorescens]	-	-	-	1
periplasmic/secreted protein					
782985118	[Pseudomonas pseudoalcaligenes]	1	1	1	1
anthranilate phosphoribosyltransferase					
782988495	[Pseudomonas pseudoalcaligenes]	1	1	1	1
poly(3-hydroxyalkanoate) granule-					
associated protein PhaF [Pseudomonas					
610707706	pseudoalcaligenes AD6]	1	-	1	1
polyhydroxyalkanoate synthesis protein					
95112975	PhaF [Pseudomonas entomophila L48]	-	-	-	1
928538031	flavodoxin [Pseudomonas aeruginosa]	-	-	-	1
outer membrane heme receptor					
[Pseudomonas pseudoalcaligenes CECT					
582003469	5344]	1	-	1	1
bacterioferritin [Pseudomonas					
610709156	pseudoalcaligenes AD6]	1	1	1	1
signal recognition particle protein					
699968269	[Pseudomonas sp. MT-1]	-	-	1	1
dihydropyrimidinase [Pseudomonas					
68344215	protegens Pf-5]	-	-	-	1
phenylhydantoinase [Pseudomonas					
799192778	fluorescens]	-	-	-	1
phosphogluconate dehydratase					
782985591	[Pseudomonas pseudoalcaligenes]	1	1	1	1
phosphogluconate dehydratase					
610707203	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
phosphogluconate dehydratase					
26987746	[Pseudomonas putida KT2440]	-	1	1	1

	hypothetical protein AU05_12175				
610711439	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	1
	chemotaxis protein CheW [<i>Pseudomonas</i>				
610709581	<i>pseudoalcaligenes</i> AD6]	-	1	1	1
	arginine N-succinyltransferase				
782989902	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	glycine cleavage system protein T				
667953065	[<i>Pseudomonas mendocina</i> S5.2]	-	-	-	1
	stringent starvation protein A				
782985185	[<i>Pseudomonas pseudoalcaligenes</i>]	-	1	-	1
	hypothetical protein AU05_19065				
610709123	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	1	1
	hypothetical protein DW68_21805				
667955117	[<i>Pseudomonas mendocina</i> S5.2]	1	-	1	1
	NADH dehydrogenase subunit I				
565415128	[<i>Pseudomonas moraviensis</i> R28-S]	1	-	-	1
953199533	endonuclease [<i>Pseudomonas aeruginosa</i>]	1	1	1	1
	PAS domain S-box/diguanylate cyclase				
	(GGDEF) domain-containing protein				
	[<i>Pseudomonas stutzeri</i> ATCC 14405 =				
379066784	CCUG 16156]	-	1	1	1
	GTP-binding protein [<i>Pseudomonas</i>				
782985019	<i>pseudoalcaligenes</i>]	1	1	1	1
	aldose epimerase [<i>Pseudomonas</i>				
610710297	<i>pseudoalcaligenes</i> AD6]	1	1	1	1
	ribosomal protein L11 methyltransferase				
390982120	[<i>Pseudomonas stutzeri</i> CCUG 29243]	-	-	-	1
	Peptide methionine sulfoxide reductase				
940031784	MsrA [<i>Pseudomonas caricapapayae</i>]	-	-	-	1
	putative lipoprotein [<i>Pseudomonas</i> sp.				
758833011	FeS53a]	1	-	1	1
	NADPH quinone reductase MdaB				
782986536	[<i>Pseudomonas pseudoalcaligenes</i>]	-	-	-	1
	heat-shock protein [<i>Pseudomonas</i>				
610708473	<i>pseudoalcaligenes</i> AD6]	1	1	1	1
	peptidase [<i>Pseudomonas</i>				
782987726	<i>pseudoalcaligenes</i>]	1	-	1	1
	Fis family transcriptional regulator				
667951388	[<i>Pseudomonas mendocina</i> S5.2]	-	-	-	1
	integrase (int) [<i>Pseudomonas aeruginosa</i>				
575877904	PA38182]	1	1	-	1
	hypothetical protein DW68_00490				
667951020	[<i>Pseudomonas mendocina</i> S5.2]	1	-	-	1
	anti-anti-sigma factor [<i>Pseudomonas</i>				
610709540	<i>pseudoalcaligenes</i> AD6]	1	-	-	1

782985898	LexA family transcriptional regulator [Pseudomonas pseudoalcaligenes]	-	-	1	1
735691260	ribonuclease PH [Pseudomonas tuomuerensis]	-	-	-	1
610714052	ribonuclease activity regulator protein RraA [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
856790994	ribonuclease activity regulator protein RraA [Pseudomonas helleri]	1	1	1	1
610708630	pseudouridine synthase [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
610712816	TetR family transcriptional regulator [Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
667954400	GTP cyclohydrolase [Pseudomonas mendocina S5.2]	1	-	1	1
667953069	superoxide dismutase [Pseudomonas mendocina S5.2]	1	1	1	1
667952311	uroporphyrinogen decarboxylase [Pseudomonas mendocina S5.2]	1	1	-	1
610710046	ATPase AAA [Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
782984050	aminotransferase [Pseudomonas pseudoalcaligenes]	-	1	-	1
782985168	sulfate adenylyltransferase subunit 2 [Pseudomonas pseudoalcaligenes]	1	1	1	1
782989438	hypothetical protein N619_04290 [Pseudomonas pseudoalcaligenes]	-	1	1	1
761892952	ATP-binding protein [Pseudomonas sp. 10-1B]	1	1	1	1
610711739	isovaleryl-CoA dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
782987630	GntR family transcriptional regulator [Pseudomonas pseudoalcaligenes]	1	1	1	1
610711740	MerR family transcriptional regulator [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782985884	ABC transporter ATPase [Pseudomonas pseudoalcaligenes]	1	-	1	1
691228129	ABC transporter ATPase [Pseudomonas cremoricolorata]	-	-	-	1
568070998	heme ABC transporter ATPase [Pseudomonas sp. M1]	1	1	1	1
667953441	DNA-binding protein [Pseudomonas mendocina S5.2]	1	1	-	1
610709269	glutamine amidotransferase [Pseudomonas pseudoalcaligenes AD6]	-	1	1	1

	hypothetical protein ALO83_00965				
939987842	[Pseudomonas syringae pv. alisalensis]	1	-	1	1
	50S ribosomal protein L11 [Pseudomonas				
543435921	alcaligenes NBRC 14159]	-	1	1	1
	50S ribosomal protein L11 [Pseudomonas				
126169065	aeruginosa C3719]	-	1	1	1
	phosphoenolpyruvate-protein				
	phosphotransferase [Pseudomonas				
763480210	oryzihabitans]	1	1	1	1
	phosphoenolpyruvate-protein				
	phosphotransferase [Pseudomonas				
610711638	pseudoalcaligenes AD6]	-	-	-	1
	hydroxyacylglutathione hydrolase				
782988805	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	ribonucleotide-diphosphate reductase				
	subunit beta [Pseudomonas				
610712992	pseudoalcaligenes AD6]	1	1	1	1
	ribonucleotide-diphosphate reductase				
	subunit beta [Pseudomonas amygdali pv.				
330880140	morsprunorum str. M302280]	-	1	-	1
	lipoprotein [Pseudomonas				
782989316	pseudoalcaligenes]	1	1	1	1
	glycerate dehydrogenase [Pseudomonas				
782989483	pseudoalcaligenes]	-	-	-	1
	ABC transporter substrate-binding protein				
782984025	[Pseudomonas pseudoalcaligenes]	1	1	-	1
	amino acid ABC transporter substrate-				
	binding protein [Pseudomonas				
782986685	pseudoalcaligenes]	-	-	-	1
	3-hydroxyisobutyrate dehydrogenase				
610714483	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
	siroheme synthase [Pseudomonas				
582004360	pseudoalcaligenes CECT 5344]	1	-	-	1
	isoprenoid biosynthesis protein				
782984503	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	excinuclease ABC subunit B				
610709967	[Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
	short-chain dehydrogenase [Pseudomonas				
610713459	pseudoalcaligenes AD6]	-	1	-	1
	3-dehydroquinate synthase [Pseudomonas				
782984746	pseudoalcaligenes]	1	1	1	1
	3-dehydroquinate synthase [Pseudomonas				
667952307	mendocina S5.2]	-	1	1	1
	cytochrome D ubiquinol oxidase subunit				
610707228	II [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1

	cytochrome D ubiquinol oxidase subunit				
667953010	II [Pseudomonas mendocina S5.2]	1	-	1	1
	putative lysine decarboxylase				
115586833	[Pseudomonas aeruginosa UCBBP-PA14]	-	-	1	1
	cytochrome D ubiquinol oxidase subunit				
747151568	II [Pseudomonas balearica DSM 6083]	-	-	1	1
	peptidylprolyl isomerase [Pseudomonas				
782988795	pseudoalcaligenes]	1	1	1	1
	peptidase inhibitor I78 family protein				
782987688	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	hypothetical protein DW68_06285				
667952142	[Pseudomonas mendocina S5.2]	-	1	-	1
	methionyl-tRNA formyltransferase				
667951800	[Pseudomonas mendocina S5.2]	1	1	1	1
691226141	CreA [Pseudomonas cremoricolorata]	-	-	-	1
	glycine/betaine ABC transporter				
	substrate-binding protein [Pseudomonas				
768548889	stutzeri]	-	-	-	1
	hypothetical protein PACI27_2935				
404533817	[Pseudomonas aeruginosa CI27]	-	1	1	1
	ABC transporter substrate-binding protein				
782984219	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	carboxynorspermidine decarboxylase				
610714740	[Pseudomonas pseudoalcaligenes AD6]	1	-	1	1
	aspartate-semialdehyde dehydrogenase				
782987582	[Pseudomonas pseudoalcaligenes]	-	-	1	1
	glutamate--cysteine ligase [Pseudomonas				
782984587	pseudoalcaligenes]	1	1	1	1
	glutamate--cysteine ligase [Pseudomonas				
691225379	cremoricolorata]	-	-	1	1
	sulfurtransferase [Pseudomonas				
782987885	pseudoalcaligenes]	-	-	-	1
	hypothetical protein AU05_02540				
610707225	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
	glutamine amidotransferase				
782987459	[Pseudomonas pseudoalcaligenes]	-	1	-	1
	hypothetical protein AU05_12280				
610711460	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	type 4 fimbriae expression regulatory				
	protein PilR [Pseudomonas				
610708050	pseudoalcaligenes AD6]	1	-	-	1
	MutT/nudix family protein [Pseudomonas				
395809037	stutzeri DSM 10701]	-	-	1	1
	flagellar basal body rod modification				
379063101	protein [Pseudomonas stutzeri ATCC	1	1	1	1

	14405 = CCUG 16156]				
	guanylate kinase [Pseudomonas				
782988336	pseudoalcaligenes]	1	1	1	1
	ribonuclease T [Pseudomonas				
610711381	pseudoalcaligenes AD6]	1	1	-	1
	flagellar assembly protein FliH				
667954482	[Pseudomonas mendocina S5.2]	-	-	1	1
	hypothetical protein N619_12430				
782987689	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	IMP dehydrogenase [Pseudomonas				
782984897	pseudoalcaligenes]	1	-	1	1
	hypothetical protein DW68_11530				
667953153	[Pseudomonas mendocina S5.2]	-	1	1	1
	antitermination protein NusB				
610712419	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	N utilization substance protein B				
500245050	[Pseudomonas protegens CHA0]	-	-	-	1
	hypothetical protein AU05_18720				
610714499	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	inorganic polyphosphate kinase				
667954626	[Pseudomonas mendocina S5.2]	-	1	1	1
	DNA polymerase III subunit epsilon				
782989074	[Pseudomonas pseudoalcaligenes]	-	-	1	1
	nucleoside diphosphate kinase regulator				
782984474	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	membrane protein [Pseudomonas				
782988470	pseudoalcaligenes]	1	-	1	1
	BetI family transcriptional regulator				
782984685	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	alpha/beta hydrolase [Pseudomonas				
667953225	mendocina S5.2]	-	-	1	1
	alpha/beta hydrolase [Pseudomonas				
684194968	mosselii SJ10]	-	-	-	1
	ADP-ribose diphosphatase [Pseudomonas				
610708510	pseudoalcaligenes AD6]	-	1	-	1
	succinylglutamate-semialdehyde				
	dehydrogenase [Pseudomonas mendocina				
667953425	S5.2]	-	-	1	1
	dihydroorotate dehydrogenase				
782986814	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	dihydroorotate dehydrogenase				
747110230	[Pseudomonas fluorescens]	-	-	-	1
	FKBP-type peptidyl-prolyl cis-trans				
	isomerase FkpB [Pseudomonas				
543435655	alcaligenes NBRC 14159]	1	1	1	1

	AsnC family transcriptional regulator				
763478062	[Pseudomonas oryzihabitans]	-	1	-	1
	membrane protein [Pseudomonas				
782985320	pseudoalcaligenes]	1	1	-	1
	hypothetical protein AU05_15930				
610714569	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	RNA methyltransferase [Pseudomonas				
667955195	mendocina S5.2]	-	-	1	1
	aminotransferase [Pseudomonas				
782986227	pseudoalcaligenes]	1	1	1	1
	adenosylmethionine--8-amino-7-				
	oxononanoate aminotransferase BioA				
759597526	[Pseudomonas sp. P11]	-	1	1	1
	DNA repair protein [Pseudomonas				
610713904	pseudoalcaligenes AD6]	1	1	-	1
	Cysteine desulfurase CsdA-CsdE, main				
758821831	protein CsdA [Pseudomonas sp. FeS53a]	-	-	-	1
	ErfK/YbiS/YcfS/YnhG family protein				
782988901	[Pseudomonas pseudoalcaligenes]	-	1	-	1
	Chain A, Structure Of A Putative Tetr				
	Transcriptional Regulator (Pa3699) From				
281307402	Pseudomonas Aeruginosa Pa01	-	1	-	1
	bacterioferritin [Pseudomonas mendocina				
667951038	S5.2]	1	1	1	1
	glycerophosphodiester phosphodiesterase				
782988138	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	cell division protein FtsE [Pseudomonas				
610706980	pseudoalcaligenes AD6]	1	1	1	1
	DeoR family transcriptional regulator				
	[Pseudomonas amygdali pv. mori str.				
330890270	301020]	-	-	-	1
	isochorismatase [Pseudomonas				
610714787	pseudoalcaligenes AD6]	1	1	1	1
	DEAD/DEAH box helicase				
782984644	[Pseudomonas pseudoalcaligenes]	1	-	-	1
	iojap family protein [Pseudomonas				
667955512	mendocina S5.2]	-	-	-	1
	D-amino acid dehydrogenase small				
	subunit [Pseudomonas alcaligenes NBRC				
543436597	14159]	1	1	1	1
	tRNA threonylcarbamoyladenosine				
	biosynthesis protein RimN [Pseudomonas				
667951804	mendocina S5.2]	-	1	1	1
	organic hydroperoxide resistance protein				
782987686	[Pseudomonas pseudoalcaligenes]	1	1	1	1

782984676	glutathione S-transferase [Pseudomonas pseudoalcaligenes]	-	1	-	1
610709160	glycerol kinase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	1
610714607	Crp/Fnr family transcriptional regulator [Pseudomonas pseudoalcaligenes AD6]	1	-	1	1
610714862	stationary phase survival protein SurE [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
327478907	type III restriction enzyme, res subunit [Pseudomonas stutzeri DSM 4166]	-	-	-	1
856771595	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Pseudomonas lini]	1	1	1	1
P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	1	1	1	1
782988605	dethiobiotin synthetase [Pseudomonas pseudoalcaligenes]	1	-	-	1
667954630	chromosome partitioning protein ParA [Pseudomonas mendocina S5.2]	1	-	1	1
692343684	virulence factor SrfB [Pseudomonas rhizosphaerae]	1	1	1	1
610710596	hypothetical protein AU05_14380 [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
575876748	hypothetical protein BN889_05912 [Pseudomonas aeruginosa PA38182]	1	1	1	1
667953357	phosphate acyltransferase [Pseudomonas mendocina S5.2]	-	-	-	1
610709488	TetR family transcriptional regulator [Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
782987076	flagellar hook-length control protein FliK [Pseudomonas pseudoalcaligenes]	1	1	1	1
667954488	ATPase AAA [Pseudomonas mendocina S5.2]	-	1	1	1
782986341	isomerase [Pseudomonas pseudoalcaligenes]	-	-	-	1
782987167	ATPase AAA [Pseudomonas pseudoalcaligenes]	1	1	1	1
820914999	hydroperoxidase [Pseudomonas putida]	1	-	1	1
782985580	FMN-dependent NADH-azoreductase [Pseudomonas pseudoalcaligenes]	1	1	1	1
782984262	spermidine/putrescine ABC transporter substrate-binding protein [Pseudomonas pseudoalcaligenes]	1	-	-	1
667951855	spermidine/putrescine ABC transporter	-	1	1	1

	substrate-binding protein [Pseudomonas mendocina S5.2]				
667951322	lactoylglutathione lyase [Pseudomonas mendocina S5.2]	1	1	1	1
782984796	hypothetical protein N619_25695 [Pseudomonas pseudoalcaligenes]	1	-	-	1
26987190	30S ribosomal protein S12 [Pseudomonas putida KT2440]	-	-	-	1
667954272	transcriptional regulator [Pseudomonas mendocina S5.2]	-	1	1	1
610708797	transporter [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
667953909	membrane protein [Pseudomonas mendocina S5.2]	1	1	1	1
610709282	Isochorismatase [Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
782986222	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase [Pseudomonas pseudoalcaligenes]	1	1	1	1
610706974	thiazole synthase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
610708269	DNA polymerase III subunit gamma/tau [Pseudomonas pseudoalcaligenes AD6]	1	-	-	1
403244303	hypothetical protein PACIG1_5978 [Pseudomonas aeruginosa CIG1]	1	1	1	1
667955525	hypothetical protein DW68_23925 [Pseudomonas mendocina S5.2]	1	1	1	1
782988080	peptidase M16 [Pseudomonas pseudoalcaligenes]	-	-	-	1
95108567	putative zinc-dependent peptidase, M16 family [Pseudomonas entomophila L48]	-	1	-	1
667953428	succinylglutamate desuccinylase [Pseudomonas mendocina S5.2]	1	-	-	1
782988497	anthranilate synthase component I [Pseudomonas pseudoalcaligenes]	1	-	-	1
310941831	30S ribosomal protein S14 [Pseudomonas mendocina]	1	1	1	1
782986466	FAD-dependent cmnm(5)s(2)U34 oxidoreductase [Pseudomonas pseudoalcaligenes]	1	-	1	1
782987424	alpha-ribazole phosphatase [Pseudomonas pseudoalcaligenes]	-	-	-	1
71558228	sigma-54 dependent DNA-binding response regulator [Pseudomonas savastanoi pv. phaseolicola 1448A]	-	-	-	1

782987781	glycerol-3-phosphate dehydrogenase [Pseudomonas pseudoalcaligenes]	1	-	1	1
610706609	GntR family transcriptional regulator [Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
782984051	glutamine synthetase [Pseudomonas pseudoalcaligenes]	1	1	-	1
667951625	glutamine synthetase [Pseudomonas mendocina S5.2]	1	-	1	1
667953910	exonuclease III [Pseudomonas mendocina S5.2]	-	-	1	1
543435585	exodeoxyribonuclease III [Pseudomonas alcaligenes NBRC 14159]	1	-	-	1
782985287	molybdenum cofactor biosynthesis protein MoaE [Pseudomonas pseudoalcaligenes]	-	1	-	1
820916328	TetR family transcriptional regulator [Pseudomonas putida]	1	1	1	1
667953673	TetR family transcriptional regulator [Pseudomonas mendocina S5.2]	-	-	-	1
667953162	beta-lactamase [Pseudomonas mendocina S5.2]	1	1	1	1
667951627	hypothetical protein DW68_03665 [Pseudomonas mendocina S5.2]	1	1	1	1
95112804	conserved hypothetical protein; putative signal peptide [Pseudomonas entomophila L48]	-	1	-	1
327481343	Na(+)-translocating NADH-quinone reductase subunit C [Pseudomonas stutzeri DSM 4166]	-	1	-	1
610713091	SpoVR family protein [Pseudomonas pseudoalcaligenes AD6]	1	-	1	1
782984039	glyoxalase [Pseudomonas pseudoalcaligenes]	1	-	-	1
928204977	putative dioxygenase of extradiol dioxygenase family [Pseudomonas fuscovaginae]	1	1	1	1
426267739	enoyl-CoA hydratase/isomerase [Pseudomonas sp. UW4]	1	1	-	1
610712468	PTS fructose transporter subunit IIA [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
610708215	nucleoside triphosphate hydrolase [Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
782985041	toxin-antitoxin antitoxin component [Pseudomonas pseudoalcaligenes]	-	1	1	1
26106140	replication terminus site binding protein	1	1	1	1

	(plasmid) [<i>Pseudomonas resinovorans</i>]				
	lipoprotein [<i>Pseudomonas</i>				
782987790	pseudoalcaligenes]	1	1	1	1
	2-aminoethylphosphonate uptake and				
	metabolism regulator [<i>Pseudomonas</i> sp.				
758829500	FeS53a]	-	-	-	1
	hypothetical protein DW68_06100				
667952106	[<i>Pseudomonas mendocina</i> S5.2]	-	1	-	1
	hemolysin D [<i>Pseudomonas</i>				
610707288	pseudoalcaligenes AD6]	-	-	1	1
	iron ABC transporter periplasmic iron-				
	binding protein [<i>Pseudomonas stutzeri</i>				
379065016	ATCC 14405 = CCUG 16156]	1	1	1	1
	NADH dehydrogenase subunit B				
928206365	[<i>Pseudomonas fuscovaginae</i>]	-	-	-	1
	hypothetical protein (plasmid)				
26106255	[<i>Pseudomonas resinovorans</i>]	1	1	1	1
	glycerophosphodiester phosphodiesterase				
667951325	[<i>Pseudomonas mendocina</i> S5.2]	1	-	1	1
	conserved hypothetical protein				
327478905	[<i>Pseudomonas stutzeri</i> DSM 4166]	1	1	1	1
	transposon DNA-invertase [<i>Pseudomonas</i>				
733391907	frederiksbergensis]	-	-	-	1
	GntR family transcriptional regulator				
610709470	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	1
	L-aspartate oxidase [<i>Pseudomonas</i>				
782985770	pseudoalcaligenes]	1	1	1	1
	ATP-binding protein [<i>Pseudomonas</i>				
610715091	pseudoalcaligenes AD6]	1	-	1	1
	aconitate hydratase [<i>Pseudomonas</i>				
782989084	pseudoalcaligenes]	1	-	1	1
	aconitate hydratase [<i>Pseudomonas</i>				
747150739	balearica DSM 6083]	-	1	1	1
	30S ribosomal protein S20 [<i>Pseudomonas</i>				
379064149	stutzeri ATCC 14405 = CCUG 16156]	1	-	-	1
	hypothetical protein AU05_15970				
610714577	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	-	1
	putative transcriptional regulator MerR				
575877778	[<i>Pseudomonas aeruginosa</i> PA38182]	1	1	1	1
	exodeoxyribonuclease V subunit alpha				
667954277	[<i>Pseudomonas mendocina</i> S5.2]	1	-	-	1
	glutaredoxin-like protein [<i>Pseudomonas</i>				
511100478	plecoglossida NB2011]	1	1	-	1
	cell division protein FtsA [<i>Pseudomonas</i>				
747152089	balearica DSM 6083]	-	-	-	1

	phosphate acetyltransferase				
564892703	[Pseudomonas aeruginosa VRFPA06]	-	-	1	1
	DNA repair protein [Pseudomonas putida				
551049746	SJ3]	-	1	1	1
	hypothetical protein AU05_06955				
610714954	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
787853032	thioredoxin [Pseudomonas chlororaphis]	-	-	-	1
	thioredoxin [Pseudomonas				
782984794	pseudoalcaligenes]	-	-	-	1
	tRNA (guanine-N7)-methyltransferase				
610706973	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
	type II secretion system protein E				
667951395	[Pseudomonas mendocina S5.2]	-	-	-	1
	tryptophan synthase subunit alpha				
610710278	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
	glycine cleavage system protein H				
610706815	[Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
	hypothetical protein AU05_03040				
610706952	[Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
	chemotaxis protein CheY [Pseudomonas				
667951925	mendocina S5.2]	-	-	-	1
	glutathione S-transferase [Pseudomonas				
610709428	pseudoalcaligenes AD6]	-	-	-	1
	ATPase [Pseudomonas stutzeri DSM				
395807551	10701]	-	-	-	1
	GntR family transcriptional regulator				
782986508	[Pseudomonas pseudoalcaligenes]	-	-	1	1
	SNF2 family DNA/RNA helicase				
575877066	[Pseudomonas aeruginosa PA38182]	-	-	-	1
	3-methylitaconate isomerase				
568074651	[Pseudomonas sp. M1]	1	-	1	1
	Flagellin, C-terminal:Flagellin, N-				
940127213	terminal [Pseudomonas syringae pv.	-	-	-	1
	helianthi]				
	beta-hexosaminidase [Pseudomonas				
782985901	pseudoalcaligenes]	-	1	1	1
	3-demethylubiquinone-9 3-				
	methyltransferase [Pseudomonas				
691226663	cremoricolorata]	-	1	-	1
	hypothetical protein AU05_12855				
610711165	[Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
	alpha/beta hydrolase [Pseudomonas				
782984056	pseudoalcaligenes]	1	1	1	1
	metal-binding protein [Pseudomonas				
667952689	mendocina S5.2]	1	1	1	1

544277583	metal-binding protein [Pseudomonas putida LF54]	-	1	1	1
699965765	transcriptional regulator NrdR [Pseudomonas sp. MT-1]	-	-	-	1
568071565	sarcosine oxidase subunit delta [Pseudomonas sp. M1]	-	-	1	1
782986366	peptidase [Pseudomonas pseudoalcaligenes]	1	1	1	1
667955392	octaprenyl-diphosphate synthase [Pseudomonas mendocina S5.2]	-	-	1	1
610708962	heptose kinase [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
856796627	ribosomal RNA small subunit methyltransferase A [Pseudomonas weihenstephanensis]	-	-	-	1
692345481	haloacid dehalogenase [Pseudomonas rhizosphaerae]	-	-	-	1
782984621	haloacid dehalogenase [Pseudomonas pseudoalcaligenes]	-	-	-	1
126192994	hypothetical protein PA2G_00233 [Pseudomonas aeruginosa 2192]	-	-	-	1
610713618	transcriptional regulator [Pseudomonas pseudoalcaligenes AD6]	1	-	1	1
667952098	3-octaprenyl-4-hydroxybenzoate carboxy-lyase [Pseudomonas mendocina S5.2]	-	-	-	1
856793200	DNA polymerase III subunit delta [Pseudomonas helleri]	-	-	-	1
P61626	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	1	-	1	1
782989938	hypothetical protein N619_00825 [Pseudomonas pseudoalcaligenes]	1	1	1	1
782988000	Cob(I)yrinic acid a,c-diamide adenosyltransferase [Pseudomonas pseudoalcaligenes]	1	-	-	1
71554779	flavoprotein WrbA, putative [Pseudomonas savastanoi pv. phaseolicola 1448A]	-	-	-	1
667952031	xanthine phosphoribosyltransferase [Pseudomonas mendocina S5.2]	1	1	1	1
782989619	hypothetical protein N619_05055 [Pseudomonas pseudoalcaligenes]	1	1	1	1
735692593	flagellar motor switch protein FliG [Pseudomonas tuomuerensis]	-	-	-	1
782984535	glycoside hydrolase family 43 [Pseudomonas pseudoalcaligenes]	-	1	1	1

	HlyD family secretion protein				
758832961	[Pseudomonas sp. FeS53a]	-	1	-	1
	7-carboxy-7-deazaguanine synthase				
782986074	[Pseudomonas pseudoalcaligenes]	-	1	1	1
	aldolase [Pseudomonas				
782987272	pseudoalcaligenes]	-	-	-	1
	ATP-dependent Clp protease proteolytic				
	subunit, partial [Pseudomonas amygdali				
940163390	pv. lachrymans]	1	1	1	1
	coproporphyrinogen III oxidase				
667953730	[Pseudomonas mendocina S5.2]	-	-	-	1
	50S ribosomal protein L31 [Pseudomonas				
610707717	pseudoalcaligenes AD6]	-	1	1	1
	ABC transporter ATP-binding protein				
949182359	[Pseudomonas poae]	-	-	-	1
	NUDIX hydrolase [Pseudomonas				
782984983	pseudoalcaligenes]	1	1	1	1
	universal stress protein UspA				
747150751	[Pseudomonas balearica DSM 6083]	1	-	-	1
	adenine phosphoribosyltransferase				
782987700	[Pseudomonas pseudoalcaligenes]	-	1	-	1
	GNAT family acetyltransferase				
667951881	[Pseudomonas mendocina S5.2]	-	1	-	1
	pyridoxine 5'-phosphate oxidase				
610711425	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	XRE family transcriptional regulator				
799199472	[Pseudomonas fluorescens]	-	1	1	1
	GNAT family acetyltransferase				
667955538	[Pseudomonas mendocina S5.2]	1	-	1	1
	peptidase M23 [Pseudomonas mendocina				
667955171	S5.2]	1	1	1	1
	peptidase M23 [Pseudomonas				
782986234	pseudoalcaligenes]	1	1	-	1
	cytidylate kinase [Pseudomonas				
782987549	pseudoalcaligenes]	-	1	-	1
	hypothetical protein AUQ38_18650				
970757203	[Pseudomonas aeruginosa]	1	1	-	1
	hypothetical protein N619_18560				
782986833	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	FAD-dependent oxidoreductase				
782984847	[Pseudomonas pseudoalcaligenes]	-	1	-	1
	protein-L-isoaspartate O-				
	methyltransferase [Pseudomonas				
610714861	pseudoalcaligenes AD6]	-	1	-	1
610709873	N-succinylarginine dihydrolase	1	-	-	1

	[Pseudomonas pseudoalcaligenes AD6]				
	hypothetical protein ND048 (plasmid)				
34335383	[Pseudomonas putida ND6]	-	1	-	1
	signal peptide protein [Pseudomonas				
782988144	pseudoalcaligenes]	1	-	-	1
	alpha/beta hydrolase [Pseudomonas				
782987796	pseudoalcaligenes]	-	1	-	1
	lytic transglycosylase [Pseudomonas				
610712879	pseudoalcaligenes AD6]	-	-	-	1
	soluble lytic transglycosylase, putative				
327481165	[Pseudomonas stutzeri DSM 4166]	1	-	-	1
	dihydroorotase [Pseudomonas				
610708513	pseudoalcaligenes AD6]	-	1	-	1
	pentapeptide repeat-containing protein				
782989577	[Pseudomonas pseudoalcaligenes]	1	1	-	1
	MerR family transcriptional regulator				
747150981	[Pseudomonas balearica DSM 6083]	-	-	-	1
	XRE family transcriptional regulator				
565413096	[Pseudomonas moraviensis R28-S]	-	-	-	1
	hypothetical protein N619_31845				
782985885	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	23S rRNA methyltransferase				
782984876	[Pseudomonas pseudoalcaligenes]	1	-	1	1
	4-hydroxybenzoyl-CoA thioesterase				
782987573	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	Cro/C1 family transcriptional regulator				
667955182	[Pseudomonas mendocina S5.2]	-	1	1	1
	hypothetical protein AU05_16830				
610710021	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	putative DNA helicases, SNF2 family				
95110104	[Pseudomonas entomophila L48]	-	-	1	1
745844789	transposase [Pseudomonas aeruginosa]	-	-	-	1
	hypothetical protein N619_22950				
782984294	[Pseudomonas pseudoalcaligenes]	1	-	-	1
	GNAT family acetyltransferase				
782987815	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	DNA polymerase III subunit chi				
782986194	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	allantoate amidohydrolase [Pseudomonas				
787855952	chlororaphis]	-	1	1	1
	chemotaxis protein CheW [Pseudomonas				
610712881	pseudoalcaligenes AD6]	-	1	1	1
667953303	pirin [Pseudomonas mendocina S5.2]	-	-	-	1
	S-adenosylmethionine tRNA				
667955202	ribosyltransferase [Pseudomonas	1	-	-	1

	mendocina S5.2]				
	CRISPR-associated Cse4 family protein				
	[Pseudomonas stutzeri ATCC 14405 =				
379066589	CCUG 16156]	1	1	1	1
	cold-shock protein [Pseudomonas				
610711397	pseudoalcaligenes AD6]	1	1	1	1
	septum formation protein Maf				
667952661	[Pseudomonas mendocina S5.2]	-	1	-	1
	carbon-phosphorus lyase [Pseudomonas				
610706569	pseudoalcaligenes AD6]	1	1	1	1
	peptidase M24 [Pseudomonas stutzeri				
395810272	DSM 10701]	1	1	1	1
	Xaa-Pro aminopeptidase [Pseudomonas				
667952111	mendocina S5.2]	1	1	1	1
	tRNA (uracil-5-)-methyltransferase				
610714172	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
936619223	oxidoreductase [Pseudomonas putida]	-	-	-	1
	2-nitropropane dioxygenase				
782984799	[Pseudomonas pseudoalcaligenes]	1	1	-	1
	proline iminopeptidase [Pseudomonas				
856779054	psychrophila]	-	-	-	1
	chemotaxis protein [Pseudomonas				
782984638	pseudoalcaligenes]	1	-	-	1
	FAD-dependent oxidoreductase				
782984435	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	(p)ppGpp synthetase [Pseudomonas				
667951505	mendocina S5.2]	-	-	-	1
	co-chaperone HscB [Pseudomonas				
667955189	mendocina S5.2]	1	1	1	1
	dihydropteroate synthase [Pseudomonas				
735691409	tuomuerensis]	-	-	-	1
	polyhydroxyalkanoic acid system protein				
610707704	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
	nuclease [Pseudomonas				
782984737	pseudoalcaligenes]	-	1	1	1
	glucose-6-phosphate 1-dehydrogenase				
568073538	[Pseudomonas sp. M1]	-	-	1	1
	glucose-6-phosphate dehydrogenase				
610712983	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	1
	PTS fructose transporter subunit IIA				
769334136	[Pseudomonas sp. 10B238]	-	1	1	1
	multifunctional PTS system fructose-like				
	transporter subunit IIA/phosphocarrier				
	protein HPr/phosphoenolpyruvate-protein				
459960961	phosphotransferase [Pseudomonas sp.	-	-	-	1

	Lz4W]				
	PTS fructose transporter subunit IIA				
856768326	[Pseudomonas taetrolens]	-	-	-	1
	glutathione S-transferase [Pseudomonas				
610712914	pseudoalcaligenes AD6]	-	-	-	1
	Poly(A) polymerase [Pseudomonas sp.				
758835006	FeS53a]	-	-	-	1
	transcription elongation factor GreB				
848256385	[Pseudomonas stutzeri]	-	-	-	1
	aspartyl protease [Pseudomonas				
610712415	pseudoalcaligenes AD6]	1	1	1	1
	hypothetical protein PACIG1_5985				
403244310	[Pseudomonas aeruginosa CIG1]	1	1	1	1
	potassium transporter peripheral				
	membrane component [Pseudomonas				
610710255	pseudoalcaligenes AD6]	1	-	-	1
	glycine cleavage system protein R				
782986934	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	integration host factor subunit beta				
610709975	[Pseudomonas pseudoalcaligenes AD6]	1	-	-	1
	hydroxypyruvate isomerase				
610707802	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
	chemotaxis protein CheY [Pseudomonas				
667953969	mendocina S5.2]	-	-	-	1
	acetoacetyl-CoA synthetase				
782988769	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	electron transporter RnfC [Pseudomonas				
610711391	pseudoalcaligenes AD6]	1	1	1	1
	RnfABCDGE type electron transport				
	complexsubunit C [Pseudomonas sp. MT-				
699968247	1]	-	-	1	1
	electron transporter RnfC [Pseudomonas				
667953130	mendocina S5.2]	1	1	1	1
	thioesterase [Pseudomonas				
782987758	pseudoalcaligenes]	1	1	1	1
	glycosyltransferase [Pseudomonas				
667955282	mendocina S5.2]	-	-	-	1
	hypothetical protein PstZobell_04581				
	[Pseudomonas stutzeri ATCC 14405 =				
379063955	CCUG 16156]	-	1	1	1
	twitching motility protein PilT				
610706959	[Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
	ribonuclease III [Pseudomonas				
667953204	mendocina S5.2]	-	-	-	1
610713370	GTPase Era [Pseudomonas	1	1	1	1

	pseudoalcaligenes AD6]				
763479821	GTPase Era [Pseudomonas oryzihabitans]	-	1	-	1
	glycosyl transferase [Pseudomonas				
403244302	aeruginosa CIG1]	1	1	1	1
	acireductone dioxygenase [Pseudomonas				
782987132	pseudoalcaligenes]	-	1	1	1
	lactate dehydrogenase [Pseudomonas				
667955350	mendocina S5.2]	1	-	-	1
	Orotidine 5'-phosphate decarboxylase				
940061810	[Pseudomonas congelans]	-	1	1	1
	hypothetical protein PABE177_0620				
404541687	[Pseudomonas aeruginosa ATCC 700888]	1	1	1	1
	hypothetical protein DW68_08045				
667952484	[Pseudomonas mendocina S5.2]	1	1	1	1
	GNAT family acetyltransferase				
610713900	[Pseudomonas pseudoalcaligenes AD6]	1	-	1	1
	GTPase HflX [Pseudomonas				
782984867	pseudoalcaligenes]	1	1	1	1
	hypothetical protein DW68_19880				
667954746	[Pseudomonas mendocina S5.2]	1	1	1	1
	hypothetical protein AU05_00605				
610715140	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	1
	sterol-binding protein [Pseudomonas				
782984721	pseudoalcaligenes]	-	-	-	1
	magnesium transporter [Pseudomonas				
610715093	pseudoalcaligenes AD6]	1	1	-	1
	ornithine carbamoyltransferase				
782986343	[Pseudomonas pseudoalcaligenes]	-	-	1	1
	DEAD/DEAH box helicase				
667955453	[Pseudomonas mendocina S5.2]	1	-	-	1
	guanine deaminase [Pseudomonas				
782987111	pseudoalcaligenes]	-	-	-	1
	PasA protein [Pseudomonas				
610712870	pseudoalcaligenes AD6]	1	1	1	1
	Lactotransferrin OS=Homo sapiens				
P02788	GN=LTF PE=1 SV=6	1	-	-	1
	carbon-nitrogen hydrolase [Pseudomonas				
610712462	pseudoalcaligenes AD6]	-	-	-	1
	methionine aminopeptidase				
667954731	[Pseudomonas mendocina S5.2]	1	1	-	1
	sulfatase [Pseudomonas				
782984258	pseudoalcaligenes]	1	1	1	1
568072388	recombinase [Pseudomonas sp. M1]	-	-	-	1
	ferrochelatase [Pseudomonas				
782985341	pseudoalcaligenes]	1	1	-	1

667954361	dehydrogenase [Pseudomonas mendocina S5.2]	1	1	1	1
610707554	molybdenum cofactor biosynthesis protein MoaD [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
782984862	carbohydrate kinase [Pseudomonas pseudoalcaligenes]	-	-	-	1
940292376	RelA/SpoT domain protein [Pseudomonas syringae pv. spinaceae]	-	-	-	1
667952358	lactate dehydrogenase [Pseudomonas mendocina S5.2]	-	-	1	1
782984097	flavin reductase [Pseudomonas pseudoalcaligenes]	1	1	1	1
667955151	NGG1p interacting factor 3 protein, NIF3 [Pseudomonas mendocina S5.2]	-	-	-	1
610713342	phosphoribosylglycinamide formyltransferase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	1
610714593	hypothetical protein AU05_16055 [Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
782988957	glyoxalase [Pseudomonas pseudoalcaligenes]	1	-	1	1
610713672	transcriptional regulator [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
610706940	sarcosine oxidase subunit beta [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
91981632	ribosomal protein, partial [Pseudomonas protegens]	1	1	-	1
667955315	hypothetical protein DW68_22840 [Pseudomonas mendocina S5.2]	1	1	1	1
610707660	DEAD/DEAH box helicase [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
667951823	hypothetical protein DW68_04675 [Pseudomonas mendocina S5.2]	1	1	1	1
667952117	glycine cleavage system protein T [Pseudomonas mendocina S5.2]	-	-	-	1
799205893	ABC transporter substrate-binding protein [Pseudomonas fluorescens]	-	-	-	1
610714028	LysR family transcriptional regulator [Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
610714369	signal peptide protein [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
782987226	dehydrogenase [Pseudomonas pseudoalcaligenes]	1	1	-	1
111036198	putative partitioning protein (plasmid)	-	-	-	1

	[<i>Pseudomonas putida</i>]				
	glycolate oxidase subunit GlcD				
949214661	[<i>Pseudomonas veronii</i>]	1	-	1	1
	succinyl-diaminopimelate				
	aminotransferase [<i>Pseudomonas</i>				
610714894	pseudoalcaligenes AD6]	-	-	1	1
	8-amino-7-oxononanoate synthase				
667951192	[<i>Pseudomonas mendocina</i> S5.2]	-	-	-	1
	8-amino-7-oxononanoate synthase				
748440015	[<i>Pseudomonas batumici</i>]	-	-	-	1
	lipid A 3-O-deacylase [<i>Pseudomonas</i>				
610714246	pseudoalcaligenes AD6]	1	-	1	1
	hypothetical protein PA2G_02127				
126194810	[<i>Pseudomonas aeruginosa</i> 2192]	-	-	-	1
	imidazole glycerol phosphate synthase				
667951368	[<i>Pseudomonas mendocina</i> S5.2]	1	1	-	1
	alpha/beta hydrolase [<i>Pseudomonas</i>				
610709459	pseudoalcaligenes AD6]	1	1	1	1
	UTP--glucose-1-phosphate				
	uridylyltransferase [<i>Pseudomonas</i> sp.				
912966801	250J]	-	-	-	1
	UTP--glucose-1-phosphate				
	uridylyltransferase [<i>Pseudomonas putida</i>				
512382864	NBRC 14164]	1	1	1	1
	precorrin isomerase [<i>Pseudomonas</i>				
667951671	mendocina S5.2]	1	1	-	1
	CoA-transferase [<i>Pseudomonas</i>				
782986624	pseudoalcaligenes]	1	1	-	1
	spermidine/putrescine ABC transporter				
	ATP-binding protein [<i>Pseudomonas</i>				
782985610	pseudoalcaligenes]	-	-	-	1
	phosphopantetheine adenylyltransferase				
610706992	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	1
	glutathione peroxidase [<i>Pseudomonas</i>				
610710078	pseudoalcaligenes AD6]	1	1	1	1
	hypothetical protein (plasmid)				
26106206	[<i>Pseudomonas resinovorans</i>]	-	-	-	1
	transcriptional regulator-like				
218771320	[<i>Pseudomonas aeruginosa</i> LESB58]	1	1	1	1
	MarR family transcriptional regulator				
782987629	[<i>Pseudomonas pseudoalcaligenes</i>]	-	1	-	1
	succinyl-diaminopimelate transaminase				
452008970	[<i>Pseudomonas stutzeri</i> NF13]	1	-	1	1
	GTPase RsgA [<i>Pseudomonas stutzeri</i>				
379066635	ATCC 14405 = CCUG 16156]	-	-	-	1

	putative tellurite resistant protein				
26106136	(plasmid) [Pseudomonas resinovorans]	-	-	-	1
667952771	laccase [Pseudomonas mendocina S5.2]	1	1	-	1
	hypothetical protein PFLCHA0_c14750				
500241106	[Pseudomonas protegens CHA0]	1	-	1	1
	hypothetical protein DW68_02785				
667951462	[Pseudomonas mendocina S5.2]	1	-	1	1
	cell division protein [Pseudomonas				
667952308	mendocina S5.2]	1	-	-	1
	ABC transporter ATP-binding protein				
	[Pseudomonas coronafaciens pv. oryzae				
331023186	str. 1_6]	-	1	-	1
	allantoinase [Pseudomonas mendocina				
667954414	S5.2]	-	-	-	1
	peptidase [Pseudomonas				
610706493	pseudoalcaligenes AD6]	-	-	1	1
	integration host factor subunit alpha				
610714946	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
	flagellin domain-containing protein				
511102329	[Pseudomonas plecoglossicida NB2011]	-	1	1	1
	Cytoplasmic axial filament protein CafA				
	and Ribonuclease G [Pseudomonas sp.				
758827399	FeS53a]	-	-	-	1
	TetR family transcriptional regulator				
556074464	[Pseudomonas sp. VLB120]	1	1	-	1
	membrane protein [Pseudomonas				
667952234	mendocina S5.2]	1	-	1	1
	hypothetical protein SZ55_1034				
758835402	[Pseudomonas sp. FeS53a]	-	-	-	1
	sulfurtransferase [Pseudomonas				
610713088	pseudoalcaligenes AD6]	-	-	-	1
	serine/threonine protein kinase				
610709267	[Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
	ATP-NAD kinase [Pseudomonas sp.				
758834138	FeS53a]	-	-	-	1
	UTP--glucose-1-phosphate				
	uridylyltransferase [Pseudomonas				
896772421	syringae KCTC 12500]	-	-	-	1
	tRNA-dihydrouridine synthase A				
667954343	[Pseudomonas mendocina S5.2]	-	-	-	1
	coproporphyrinogen III oxidase				
699964984	[Pseudomonas sp. MT-1]	1	1	1	1
	ATP-dependent DNA helicase RecQ				
699967512	[Pseudomonas sp. MT-1]	-	-	-	1
799218195	serine/threonine protein phosphatase	-	-	-	1

	[<i>Pseudomonas fluorescens</i>]				
	hypothetical protein NCGM1179_5194				
346060449	[<i>Pseudomonas aeruginosa</i> NCMG1179]	-	-	-	1
	universal stress protein UspA				
782984792	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	-	1
	RNA-binding protein [<i>Pseudomonas</i>				
667955332	mendocina S5.2]	1	1	-	1
	hypothetical protein N619_28030				
782985213	[<i>Pseudomonas pseudoalcaligenes</i>]	-	1	-	1
	ATP--cobalamin adenosyltransferase				
782985214	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	gamma-glutamyl phosphate reductase				
395810095	[<i>Pseudomonas stutzeri</i> DSM 10701]	1	1	1	1
	16S ribosomal RNA methyltransferase				
471350311	RsmE [<i>Pseudomonas putida</i> LS46]	-	-	-	1
	hypothetical protein AU05_04120				
610713644	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	1	1
936608227	transposase [<i>Pseudomonas putida</i>]	-	-	-	1
	sarcosine oxidase, gamma subunit family				
576706995	[<i>Pseudomonas</i> sp. GM41(2012)]	-	-	-	1
	nitrogen regulatory protein P-II				
782984009	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	glutathione S-transferase [<i>Pseudomonas</i>				
667955231	mendocina S5.2]	-	1	1	1
	GTP-binding protein [<i>Pseudomonas</i>				
610710507	pseudoalcaligenes AD6]	-	1	1	1
	LOG family protein [<i>Pseudomonas</i>				
610706355	pseudoalcaligenes AD6]	-	-	-	1
	homoserine kinase [<i>Pseudomonas stutzeri</i>				
390985376	CCUG 29243]	-	-	-	1
	phosphoserine phosphatase				
928539639	[<i>Pseudomonas aeruginosa</i>]	-	1	-	1
	UTP--glucose-1-phosphate				
	uridylyltransferase [<i>Pseudomonas</i>				
735690715	tuomuerensis]	-	-	1	1
	TetR family transcriptional regulator				
782984555	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
	UDP-N-acetylenolpyruvoylglucosamine				
	reductase [<i>Pseudomonas</i>				
782985931	pseudoalcaligenes]	1	1	1	1
	hypothetical protein B723_09190				
	[<i>Pseudomonas fluorescens</i> NCIMB				
913661014	11764]	-	-	-	1
	fatty acid methyltransferase				
782984079	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1

782987733	glutamate-pyruvate aminotransferase [Pseudomonas pseudoalcaligenes]	-	1	-	1
543438099	aspartate aminotransferase [Pseudomonas alcaligenes NBRC 14159]	1	-	1	1
610706475	sporulation protein [Pseudomonas pseudoalcaligenes AD6]	1	-	-	1
852198301	cobyrinic acid a,c-diamide synthase [Pseudomonas aeruginosa]	1	-	-	1
115584620	flagellar synthesis regulator FleN [Pseudomonas aeruginosa UCBPP-PA14]	-	-	-	1
782984128	ATP synthase F0F1 subunit delta [Pseudomonas pseudoalcaligenes]	1	1	-	1
610708371	twitching motility protein PilT [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
610709584	flagellar biosynthesis protein FlgN [Pseudomonas pseudoalcaligenes AD6]	1	-	-	1
564838699	hypothetical protein X778_19805 [Pseudomonas aeruginosa VRFP07]	-	-	-	1
667955355	peptidylprolyl isomerase [Pseudomonas mendocina S5.2]	-	1	-	1
953671874	RNA polymerase subunit sigma [Pseudomonas sp. TTU2014-080ASC]	-	-	-	1
703405721	Site-specific DNA-methyltransferase (Adenine-specific) (fragment) [Pseudomonas xanthomarina]	1	-	-	1
543439226	putative LysR family transcriptional regulator [Pseudomonas alcaligenes NBRC 14159]	-	-	-	1
748440488	Periplasmic protein TonB, links inner and outer membranes [Pseudomonas batumici]	-	-	-	1
610712154	preprotein translocase subunit TatD [Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
757242685	Arsenate reductase [Pseudomonas fluorescens]	-	-	-	1
667952139	N-acetylglutamate synthase [Pseudomonas mendocina S5.2]	-	-	-	1
452007593	DNA-binding transcriptional dual regulator Crp [Pseudomonas stutzeri NF13]	-	-	-	1
610712812	hypothetical protein AU05_07845 [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
395809091	glyceraldehyde-3-phosphate dehydrogenase [Pseudomonas stutzeri DSM 10701]	-	-	-	1

	subtype I-E CRISPR-associated endonuclease Cas1 [Pseudomonas aeruginosa]	-	-	-	1
929386433	7-cyano-7-deazaguanine reductase [Pseudomonas stutzeri DSM 4166]	-	-	-	1
327480275	thymidylate synthase [Pseudomonas aeruginosa PAO1]	-	-	-	1
9946191	cell division protein ZipA homolog [Pseudomonas alcaligenes NBRC 14159]	1	-	-	1
543436004	XRE family transcriptional regulator [Pseudomonas pseudoalcaligenes]	-	-	-	1
782984443	hypothetical protein AU05_07015 [Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
610714966	aspartate ammonia-lyase [Pseudomonas alcaligenes NBRC 14159]	-	-	-	1
543436511	endonuclease III [Pseudomonas sp. 250J]	-	-	-	1
912969576	3-methyladenine DNA glycosylase [Pseudomonas pseudoalcaligenes]	-	-	-	1
782984156	tRNA-guanine transglycosylase [Pseudomonas fuscovaginae]	-	-	-	1
928208273	hypothetical protein UM91_14215 [Pseudomonas oryzae]	-	-	-	1
763479547	serine peptidase [Pseudomonas mendocina S5.2]	1	-	1	1
667953200	iron transporter [Pseudomonas mendocina S5.2]	-	-	1	1
667951376	hypothetical protein B479_16950 [Pseudomonas putida HB3267]	-	-	-	1
430794087	3-deoxy-manno-octulosonate cytidyltransferase [Pseudomonas alcaligenes NBRC 14159]	1	1	1	1
543438185	Fatty acid oxidation complex subunit alpha [Pseudomonas fluorescens]	-	-	-	1
757242550	magnesium transporter ApaG [Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
610713086	hypothetical protein PK34_01930 [Pseudomonas stutzeri]	-	1	1	1
816240299	short-chain dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
610714357	hypothetical protein DW68_15770 [Pseudomonas mendocina S5.2]	-	-	1	1
667953963	trypsin-like serine protease [Pseudomonas pseudoalcaligenes]	-	-	1	1
782986663	4-chlorobenzoate--CoA ligase [Pseudomonas fluorescens NCIMB]	-	-	-	1
913662951					

	11764]				
	acyl-CoA dehydrogenase [Pseudomonas				
610713471	pseudoalcaligenes AD6]	-	1	-	1
	D-alanine--D-alanine ligase				
667952724	[Pseudomonas mendocina S5.2]	-	1	1	1
	peptidylprolyl isomerase [Pseudomonas				
764072432	putida S13.1.2]	-	-	-	1
	glycerol acyltransferase [Pseudomonas				
782989474	pseudoalcaligenes]	1	1	1	1
	LysR family transcriptional regulator				
799188543	[Pseudomonas fluorescens]	-	-	-	1
	carbamate kinase [Pseudomonas				
782985365	pseudoalcaligenes]	-	-	-	1
	ABC transporter [Pseudomonas				
782985919	pseudoalcaligenes]	1	-	-	1
	gamma-glutamyltransferase				
610706994	[Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
	phosphodiesterase [Pseudomonas				
610712849	pseudoalcaligenes AD6]	-	-	-	1
	50S ribosomal protein L31 [Pseudomonas				
782986432	pseudoalcaligenes]	1	1	1	1
	chromosome segregation protein SMC				
782986179	[Pseudomonas pseudoalcaligenes]	1	-	-	1
	ribonuclease D [Pseudomonas				
610710067	pseudoalcaligenes AD6]	1	1	-	1
	Inner membrane protein yebE				
782986305	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	hypothetical protein SZ55_1474				
758834858	[Pseudomonas sp. FeS53a]	1	1	1	1
	transcriptional regulator [Pseudomonas				
782986092	pseudoalcaligenes]	1	1	1	1
452009523	porin [Pseudomonas stutzeri NF13]	1	1	-	1
	pilus assembly protein PilC				
861575723	[Pseudomonas sp. BICA1-14]	-	-	-	1
	tRNA pseudouridine synthase A				
610708094	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	1
	ribosomal protein S6 modification protein				
782984593	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	serine/threonine protein kinase				
667952968	[Pseudomonas mendocina S5.2]	1	-	-	1
	DNA transporter [Pseudomonas				
610708053	pseudoalcaligenes AD6]	-	1	1	1
	5'-nucleotidase [Pseudomonas				
610708312	pseudoalcaligenes AD6]	-	-	-	1
667955513	nicotinate-nucleotide adenylyltransferase	-	-	-	1

	[<i>Pseudomonas mendocina</i> S5.2]				
	murein transglycosylase [<i>Pseudomonas</i>				
782989314	pseudoalcaligenes]	-	1	1	1
	ribonuclease P [<i>Pseudomonas</i>				
782984139	pseudoalcaligenes]	-	-	-	1
	precorrin-2 C20-methyltransferase				
610714113	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	1
	Uncharacterized protein ALO44_05291				
940280813	[<i>Pseudomonas syringae</i> pv. <i>tagetis</i>]	-	-	-	1
	glycosyltransferase [<i>Pseudomonas</i> sp.				
780912405	BICA1-14]	-	-	-	1
	chromosome partitioning protein				
610714734	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	1
	XRE family transcriptional regulator				
667955298	[<i>Pseudomonas mendocina</i> S5.2]	-	-	-	1
	biotin--protein ligase [<i>Pseudomonas</i>				
610708103	pseudoalcaligenes AD6]	-	-	1	1
	AsnC family transcriptional regulator				
610715063	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	1
	formyltetrahydrofolate deformylase				
610709393	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	-	1
	aminotransferase [<i>Pseudomonas</i>				
782989566	pseudoalcaligenes]	-	1	-	1
	chemotaxis protein CheY [<i>Pseudomonas</i>				
782987188	pseudoalcaligenes]	1	1	1	1
	twitching motility protein PilT				
769336141	[<i>Pseudomonas</i> sp. 10B238]	-	-	-	1
	(p)ppGpp synthetase [<i>Pseudomonas</i>				
782989830	pseudoalcaligenes]	-	-	-	1
	hypothetical protein DW68_10640				
667952981	[<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
	putative transcription regulator				
98956471	[<i>Pseudomonas extremaustralis</i> 14-3]	-	-	-	1
	4-hydroxythreonine-4-phosphate				
	dehydrogenase [<i>Pseudomonas</i>				
610713084	pseudoalcaligenes AD6]	1	1	-	1
	methenyltetrahydrofolate cyclohydrolase				
	/5,10-methylenetetrahydrofolate				
	dehydrogenase (NADP+) [<i>Pseudomonas</i>				
928204151	fuscovaginae]	-	-	-	1
	Fur family transcriptional regulator				
747117473	[<i>Pseudomonas fluorescens</i>]	-	-	-	1
	lactate dehydrogenase [<i>Pseudomonas</i>				
782984802	pseudoalcaligenes]	1	1	1	1
568073688	hypothetical protein PM1_0210140	-	-	-	1

	[<i>Pseudomonas</i> sp. M1]				
	CDP-6-deoxy-delta-3,4-glucoseen				
667952099	reductase [<i>Pseudomonas mendocina</i> S5.2]	-	1	-	1
	histidine triad (HIT) protein				
667952990	[<i>Pseudomonas mendocina</i> S5.2]	-	1	-	1
	ABC transporter substrate-binding protein				
940724442	[<i>Pseudomonas endophytica</i>]	1	-	-	1
	30S ribosomal protein S21 [<i>Pseudomonas</i>				
9946450	aeruginosa PAO1]	1	1	1	1
	NAD-dependent dehydratase				
929887985	[<i>Pseudomonas</i> sp. RIT-PI-o]	1	-	-	1
	ABC transporter substrate-binding protein				
782989431	[<i>Pseudomonas pseudoalcaligenes</i>]	-	-	1	1
	pilus assembly protein PilZ				
568073464	[<i>Pseudomonas</i> sp. M1]	1	-	-	1
	GTP-binding protein [<i>Pseudomonas</i>				
735690184	tuomuerensis]	-	-	-	1
	ATP-binding protein [<i>Pseudomonas</i>				
949218086	veronii]	-	-	-	1
	site-specific DNA-methyltransferase				
	(adenine-specific) [<i>Pseudomonas</i>				
404541488	aeruginosa E2]	1	1	1	1
	ATPase [<i>Pseudomonas</i>				
782985173	pseudoalcaligenes]	-	1	-	1
	hypothetical protein PM1_0206505				
568072984	[<i>Pseudomonas</i> sp. M1]	-	-	-	1
	TetR family transcriptional regulator				
782985098	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	-	1
	Stringent starvation protein B				
727036231	[<i>Pseudomonas aeruginosa</i>]	-	-	-	1
	Glutamate synthase family protein, partial				
940153415	[<i>Pseudomonas amygdali</i> pv. lachrymans]	1	1	1	1
	glycosyl transferase [<i>Pseudomonas</i> sp.				
742787157	C5pp]	1	1	1	1
	Outer membrane efflux protein TolC				
	[<i>Pseudomonas savastanoi</i> pv.				
928272871	phaseolicola]	-	-	-	1
815974119	transposase [<i>Pseudomonas aeruginosa</i>]	-	-	-	1
	phosphocarrier protein HPr				
782985142	[<i>Pseudomonas pseudoalcaligenes</i>]	-	-	-	1
	16S rRNA methyltransferase				
782984187	[<i>Pseudomonas pseudoalcaligenes</i>]	-	-	-	1
	hypothetical protein LK03_14640				
691227167	[<i>Pseudomonas cremoricolorata</i>]	-	-	-	1
782986232	glutathione S-transferase [<i>Pseudomonas</i>	1	-	-	1

	pseudoalcaligenes]				
	GTP-binding protein [Pseudomonas				
610710505	pseudoalcaligenes AD6]	-	-	-	1
	hypothetical protein TX25_18405				
949230692	[Pseudomonas sp. DSM 28142]	-	-	-	1
	3-methylitaconate isomerase				
667954159	[Pseudomonas mendocina S5.2]	1	1	-	1
	tRNA modification GTPase TrmE				
	[Pseudomonas amygdali pv. mori str.				
330890255	301020]	-	-	-	1
	ligand-gated channel protein				
610714149	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	1
	conserved hypothetical protein				
126194809	[Pseudomonas aeruginosa 2192]	-	-	-	1
	hypothetical protein N619_18455				
782986812	[Pseudomonas pseudoalcaligenes]	-	-	1	1
	hydrogenase [Pseudomonas mendocina				
667955484	S5.2]	1	-	-	1
	hydroxymethylglutaryl-CoA lyase				
782988770	[Pseudomonas pseudoalcaligenes]	1	-	-	1
	ABC transporter substrate-binding protein				
713116210	[Pseudomonas mediterranea CFBP 5447]	-	-	1	1
	DNA-binding protein [Pseudomonas				
747152474	balearica DSM 6083]	-	-	-	1
	Transcriptional regulator, TetR family				
800911661	[Pseudomonas fluorescens]	-	-	-	1
	cytoplasmic axial filament protein				
390984563	[Pseudomonas stutzeri CCUG 29243]	-	-	-	1
	helix-hairpin-helix repeat-containing				
	competence protein ComEA				
395807948	[Pseudomonas stutzeri DSM 10701]	-	-	-	1
	ATP synthase B chain [Pseudomonas				
327482895	stutzeri DSM 4166]	-	1	-	1
	membrane protein [Pseudomonas				
667953734	mendocina S5.2]	-	1	-	1
	thioesterase [Pseudomonas				
782987757	pseudoalcaligenes]	-	1	-	1
	phosphohistidine phosphatase				
782987783	[Pseudomonas pseudoalcaligenes]	-	1	1	1
	23S rRNA pseudouridylate synthase				
782985933	[Pseudomonas pseudoalcaligenes]	-	-	1	1
	FAD-dependent oxidoreductase				
912966123	[Pseudomonas sp. 250J]	-	-	-	1
	iron-sulfur cluster assembly protein				
610710494	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	1

	ADP-ribose pyrophosphatase				
782984838	[<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	1
	outer membrane porin [<i>Pseudomonas</i>				
471349923	putida LS46]	-	-	-	1
	phosphopantothienoylcysteine				
	decarboxylase [<i>Pseudomonas mendocina</i>				
667951491	S5.2]	-	-	-	1
	YafB (plasmid) [<i>Pseudomonas</i>				
404306967	fluorescens R124]	1	1	-	1
	CRISPR-associated protein Cas3				
782983986	[<i>Pseudomonas pseudoalcaligenes</i>]	-	-	-	1
	phosphodiesterase [<i>Pseudomonas</i>				
610706739	pseudoalcaligenes AD6]	-	-	-	1
	precorrin isomerase, partial				
940726038	[<i>Pseudomonas endophytica</i>]	-	1	-	1
	Sua5/YciO/YrdC/YwlC family protein				
395809096	[<i>Pseudomonas stutzeri</i> DSM 10701]	-	-	-	1
	2-octaprenyl-3-methyl-6-methoxy-1,4-				
	benzoquinol hydroxylase [<i>Pseudomonas</i>				
610713579	pseudoalcaligenes AD6]	1	1	-	1
	2-octaprenyl-3-methyl-6-methoxy-1,4-				
	benzoquinol hydroxylase [<i>Pseudomonas</i>				
568071300	sp. M1]	-	-	-	1
	transposase [<i>Pseudomonas</i> sp. DSM				
949214552	29167]	-	-	-	1
	hypothetical protein DW68_13630				
667953554	[<i>Pseudomonas mendocina</i> S5.2]	-	-	-	1
	ABC transporter substrate-binding protein				
667951602	[<i>Pseudomonas mendocina</i> S5.2]	-	-	1	1
	50S ribosomal protein L27 [<i>Pseudomonas</i>				
610714335	pseudoalcaligenes AD6]	-	1	1	1
	molecular chaperone [<i>Pseudomonas</i>				
782984853	pseudoalcaligenes]	1	-	1	1
	dTDP-4-dehydrorhamnose reductase				
782988203	[<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	1
949193030	histidine kinase [<i>Pseudomonas synxantha</i>]	-	-	-	1
	ABC transporter, ATP-binding protein				
940163270	[<i>Pseudomonas amygdali</i> pv. <i>lachrymans</i>]	-	1	-	1
	3-methyladenine DNA glycosylase				
667954642	[<i>Pseudomonas mendocina</i> S5.2]	-	-	-	1
	adenosine-3'(2'),5'-bisphosphate				
	nucleotidase [<i>Pseudomonas mendocina</i>				
667952177	S5.2]	-	1	1	1
	NADP transhydrogenase subunit alpha				
756404945	[<i>Pseudomonas fluorescens</i>]	-	-	-	1

	hypothetical protein N619_28640				
782985321	[Pseudomonas pseudoalcaligenes]	1	1	1	1
	xanthine phosphoribosyltransferase				
568072250	[Pseudomonas sp. M1]	-	1	1	1
	arsenate reductase [Pseudomonas				
692343315	rhizosphaerae]	1	-	-	1
	putative transposase [Pseudomonas				
11641376	alcaligenes]	-	-	-	1
	glutathione S-transferase [Pseudomonas				
949192172	poae]	1	-	-	1
	Beta-lactamase class C [Pseudomonas				
748443794	batumici]	-	-	-	1
	chemotaxis protein CheB [Pseudomonas				
667952191	mendocina S5.2]	-	-	-	1
	Hemoglobin subunit beta OS=Homo				
P68871	sapiens GN=HBB PE=1 SV=2	-	-	1	1
	DSBA oxidoreductase [Pseudomonas				
782989939	pseudoalcaligenes]	-	1	-	1
	abortive phage infection protein				
953199535	[Pseudomonas aeruginosa]	1	-	1	1
	hypothetical protein TR67_20775				
856739991	[Pseudomonas deceptionensis]	-	-	-	1
	diguanylate cyclase [Pseudomonas				
856770609	lundensis]	-	-	-	1
	DNA polymerase II [Pseudomonas				
667955251	mendocina S5.2]	-	-	-	1
	methionine sulfoxide reductase B				
610712077	[Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
	competence protein ComEA				
667954280	[Pseudomonas mendocina S5.2]	-	-	1	1
	ATP-dependent metalloprotease				
782989533	[Pseudomonas pseudoalcaligenes]	1	-	-	1
	ABC transporter ATP-binding protein				
782986025	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	7-cyano-7-deazaguanine synthase, partial				
782990031	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	glutamine synthetase [Pseudomonas				
667953709	mendocina S5.2]	-	-	-	1
	molybdenum cofactor guanylyltransferase				
936609543	[Pseudomonas putida]	-	-	1	1
	glycine/betaine ABC transporter ATPase				
610707669	[Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
	flagellar hook-associated 2 domain-				
	containing protein [Pseudomonas stutzeri				
395809338	DSM 10701]	-	1	1	1

713119975	cytosine deaminase [<i>Pseudomonas mediterranea</i> CFBP 5447]	-	-	-	1
823571147	serine hydroxymethyltransferase, partial [<i>Pseudomonas aeruginosa</i>]	-	-	-	1
730590344	aminotransferase [<i>Pseudomonas parafulva</i>]	1	1	-	1
687287802	adenosylcobinamide kinase [<i>Pseudomonas</i> sp. YS-1p]	-	-	-	1
928535133	hypothetical protein AN920_22005 [<i>Pseudomonas aeruginosa</i>]	-	-	-	1
666089645	hypothetical protein HZ99_26475 [<i>Pseudomonas fluorescens</i>]	-	-	-	1
928204043	pyruvate dehydrogenase E1 component, homodimeric type [<i>Pseudomonas fuscovaginae</i>]	-	-	-	1
148807323	mercuric resistance operon regulatory protein [<i>Pseudomonas aeruginosa</i>]	-	-	-	1
610708271	recombination protein RecR [<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	-	1
856739987	ATPase [<i>Pseudomonas deceptionensis</i>]	-	-	-	1
667953668	enoyl-CoA hydratase [<i>Pseudomonas mendocina</i> S5.2]	-	-	-	1
667951498	exodeoxyribonuclease III [<i>Pseudomonas mendocina</i> S5.2]	-	1	-	1
782987586	N-(5'-phosphoribosyl)anthranilate isomerase [<i>Pseudomonas pseudoalcaligenes</i>]	-	-	1	1
667953659	membrane protein [<i>Pseudomonas mendocina</i> S5.2]	1	-	1	1
758833325	Integrase [<i>Pseudomonas</i> sp. FeS53a]	-	-	-	1
749473700	hypothetical protein SRM1_01789 [<i>Pseudomonas fluorescens</i>]	-	-	-	1
902689073	N-acetyl-anhydromuranmyl-L-alanine amidase [<i>Pseudomonas trivialis</i>]	-	-	-	1
782984310	cytochrome C [<i>Pseudomonas pseudoalcaligenes</i>]	-	-	-	1
782986500	2-hydroxy-3-oxopropionate reductase [<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	1
881082674	ATPase [<i>Pseudomonas aeruginosa</i>]	-	-	-	1
856776109	cell division topological specificity factor [<i>Pseudomonas lini</i>]	-	-	-	1
537449689	transcriptional regulator [<i>Pseudomonas aeruginosa</i> HB13]	-	-	-	1
610713640	diaminopimelate epimerase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	-	1

	toluene tolerance ABC efflux transporter,ATP-binding protein				
426265913	[Pseudomonas sp. UW4]	-	-	-	1
	mutant NtrC-like activator [Pseudomonas				
327479027	stutzeri DSM 4166]	-	-	-	1
	GTP cyclohydrolase [Pseudomonas				
667955005	mendocina S5.2]	-	-	-	1
	DNA mismatch repair protein MutT				
667955148	[Pseudomonas mendocina S5.2]	-	-	-	1
	XRE family transcriptional regulator				
782986426	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	2,5-dioxovalerate dehydrogenase				
940722598	[Pseudomonas endophytica]	-	-	-	1
	glucose-6-phosphate dehydrogenase				
667951600	[Pseudomonas mendocina S5.2]	-	-	-	1
	arsenical pump-driving ATPase				
953165533	[Pseudomonas aeruginosa]	-	-	-	1
	hypothetical protein TU85_22350				
856803284	[Pseudomonas helleri]	-	-	-	1
	GntR family transcriptional regulator				
925647909	[Pseudomonas psychrophila]	-	1	1	1
	hypothetical protein PU99_03870				
820917171	[Pseudomonas putida]	-	-	-	1
	ureidoglycolate hydrolase [Pseudomonas				
856799117	sp. DSM 28140]	-	-	-	1
	uroporphyrin-III methyltransferase				
769334441	[Pseudomonas sp. 10B238]	-	-	-	1
	hypothetical protein LT40_07735				
692343683	[Pseudomonas rhizosphaerae]	-	-	-	1
	Phosphonate C-P lyase [Pseudomonas				
940057110	cannabina]	-	-	-	1
	DNA-dependent helicase II				
782984041	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	ABC transporter ATP-binding protein				
703403557	[Pseudomonas xanthomarina]	-	-	-	1
	sugar ABC transporter ATPase				
667955167	[Pseudomonas mendocina S5.2]	-	-	-	1
	arylesterase [Pseudomonas protegens Pf-				
68345928	5]	-	-	-	1
928536473	nitroreductase [Pseudomonas aeruginosa]	-	-	-	1
	cobalamin biosynthesis protein CobN				
782984108	[Pseudomonas pseudoalcaligenes]	-	-	-	1
	cobalamin biosynthesis protein CobN				
763479998	[Pseudomonas oryzihabitans]	1	-	-	1
610708078	GntR family transcriptional regulator	-	-	-	1

	[<i>Pseudomonas pseudoalcaligenes</i> AD6]				
	3-octaprenyl-4-hydroxybenzoate carboxy-				
	lyase [<i>Pseudomonas pseudoalcaligenes</i>				
610713594	AD6]	1	-	1	1
	sarcosine oxidase subunit gamma				
927285564	[<i>Pseudomonas syringae</i> UMAF0158]	-	1	-	1
667954952	helicase [<i>Pseudomonas mendocina</i> S5.2]	-	-	-	1
	peptidase, M23/M37 family				
	[<i>Pseudomonas syringae</i> pv. tomato str.				
28855840	DC3000]	-	-	1	1
	iron--sulfur cluster insertion protein ErpA				
667951087	[<i>Pseudomonas mendocina</i> S5.2]	1	1	1	1
	carbon-nitrogen hydrolase [<i>Pseudomonas</i>				
799189331	fluorescens]	-	-	-	1
	DNA primase [<i>Pseudomonas</i>				
782988540	pseudoalcaligenes]	-	-	-	1
	pseudouridine synthase [<i>Pseudomonas</i>				
610714863	pseudoalcaligenes AD6]	1	-	-	1
	DNA mismatch repair protein MutS				
759599499	[<i>Pseudomonas</i> sp. PI1]	-	-	-	1
	Deoxyuridine 5'-triphosphate				
	nucleotidohydrolase [<i>Pseudomonas</i>				
631782489	knackmussii B13]	1	1	1	1
	hypothetical protein A458_11195				
390983483	[<i>Pseudomonas stutzeri</i> CCUG 29243]	-	-	-	1
	50S ribosomal protein L25 [<i>Pseudomonas</i>				
940722565	endophytica]	-	1	-	1
	hypothetical protein AU05_15475				
610710333	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	-	1
	ParA (plasmid) [<i>Pseudomonas putida</i>				
34335341	ND6]	1	-	-	1
	Elongation factor Tu, partial				
940067226	[<i>Pseudomonas syringae</i> pv. castaneae]	1	1	1	1
	recombinase RecX [<i>Pseudomonas</i>				
667954693	mendocina S5.2]	1	-	-	1
	sorbosone dehydrogenase [<i>Pseudomonas</i>				
949193325	poae]	-	-	-	1
	PTS fructose transporter subunit IIA				
759599806	[<i>Pseudomonas</i> sp. PI1]	-	1	-	1
	serine/threonine protein phosphatase				
856773541	[<i>Pseudomonas lundensis</i>]	-	-	-	1
	terpene utilization protein AtuA				
610713468	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	-	1
	dihydrofolate reductase [<i>Pseudomonas</i>				
934024356	viridiflava]	-	-	-	1

610708133	alkylhydroperoxidase [Pseudomonas pseudoalcaligenes AD6]	1	1	-	1
684198590	penicillin amidase [Pseudomonas mosselii SJ10]	-	-	1	1
747115316	DNA-binding protein [Pseudomonas fluorescens]	-	-	1	1
763478665	cold-shock protein [Pseudomonas oryzae]	-	-	1	1
801166457	hypothetical protein VP02_20580 [Pseudomonas kilonensis]	-	-	-	1
757246751	cAMP receptor protein [Pseudomonas fluorescens]	-	-	-	1
856740388	Lateral flagellin [Pseudomonas deceptionensis]	-	-	-	1
782986720	ribosomal subunit interface protein [Pseudomonas pseudoalcaligenes]	-	-	-	1
939990111	Uncharacterized protein ALO83_02103 [Pseudomonas syringae pv. alisalensis]	-	-	-	1
2393910	arginine regulatory protein [Pseudomonas aeruginosa PAO1]	-	-	-	1
782988695	LysR family transcriptional regulator [Pseudomonas pseudoalcaligenes]	-	-	-	1
254666976	effector AvrPto1 [Pseudomonas amygdali pv. mori]	-	-	-	1
780896957	acyl-CoA dehydrogenase [Pseudomonas sp. BICA1-14]	-	1	-	1
390985563	F0F1 ATP synthase subunit delta [Pseudomonas stutzeri CCUG 29243]	-	-	-	1
610715106	lipoprotein [Pseudomonas pseudoalcaligenes AD6]	-	1	-	1
782984717	preprotein translocase subunit TatA [Pseudomonas pseudoalcaligenes]	-	1	-	1
610712492	cytochrome D ubiquinol oxidase subunit III [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
667955091	TetR family transcriptional regulator [Pseudomonas mendocina S5.2]	-	-	-	1
95111719	conserved hypothetical protein [Pseudomonas entomophila L48]	-	-	-	1
771842688	FMN reductase, NADPH-dependent [Pseudomonas sp. Os17]	-	-	-	1
925645141	hypothetical protein AA303_14980 [Pseudomonas psychrophila]	-	-	-	1
610708620	peptidase inhibitor I42 [Pseudomonas pseudoalcaligenes AD6]	-	-	1	1

940258680	Rhs family protein [Pseudomonas syringae pv. syringae]	-	-	-	1
949186349	1-deoxy-D-xylulose-5-phosphate synthase [Pseudomonas synxantha]	-	1	-	1
928398125	2,4-dienoyl-CoA reductase FadH [Pseudomonas amygdali pv. morsprunorum]	1	-	-	1
543437989	hypothetical protein PA6_013_00560 [Pseudomonas alcaligenes NBRC 14159]	-	-	-	1
452009675	oxidoreductase [Pseudomonas stutzeri NF13]	-	-	-	1
667953804	NADH pyrophosphatase [Pseudomonas mendocina S5.2]	-	-	-	1
782986817	D-alanyl-D-alanine carboxypeptidase [Pseudomonas pseudoalcaligenes]	-	-	-	1
610711757	esterase [Pseudomonas pseudoalcaligenes AD6]	-	-	-	1
763480138	peptidylprolyl isomerase [Pseudomonas oryzihabitans]	1	-	-	1
610709105	cytochrome C oxidase subunit II [Pseudomonas pseudoalcaligenes AD6]	1	1	1	1
782987616	amino acid ABC transporter substrate-binding protein [Pseudomonas pseudoalcaligenes]	1	-	-	1
667951301	histidine kinase [Pseudomonas mendocina S5.2]	-	-	-	1
666694294	phosphoribosylaminoimidazole carboxylase, partial [Pseudomonas amygdali pv. tabaci str. 6605]	-	-	-	1
692344882	transcriptional initiation protein Tat [Pseudomonas rhizosphaerae]	-	-	-	1
937311325	ATP-dependent chaperone ClpB [Pseudomonas fluorescens]	1	-	1	-
568070377	ATP-dependent Clp protease ClpC [Pseudomonas sp. M1]	-	-	1	-
543438360	chaperone protein DnaK [Pseudomonas alcaligenes NBRC 14159]	1	-	1	-
395809747	molecular chaperone DnaK [Pseudomonas stutzeri DSM 10701]	1	-	1	-
689664865	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase [Pseudomonas fluorescens LMG 5329]	1	-	1	-
543439157	aconitase B [Pseudomonas alcaligenes NBRC 14159]	1	1	1	-
543438305	60 kDa chaperonin [Pseudomonas	1	-	1	-

	alcaligenes NBRC 14159]				
	NAD-glutamate dehydrogenase				
949184170	[Pseudomonas libanensis]	-	-	1	-
	NAD-glutamate dehydrogenase				
452009510	[Pseudomonas stutzeri NF13]	-	1	1	-
	NAD-dependent glutamate				
	dehydrogenase [Pseudomonas aeruginosa				
126167971	C3719]	1	1	1	-
	30S ribosomal protein S1 [Pseudomonas				
667953600	mendocina S5.2]	1	-	1	-
	DNA-directed RNA polymerase subunit				
327479318	beta' [Pseudomonas stutzeri DSM 4166]	-	1	1	-
	Dimodular nonribosomal peptide synthase				
757249530	[Pseudomonas fluorescens]	-	-	1	-
	polynucleotide				
	phosphorylase/polyadenylase				
747149972	[Pseudomonas balearica DSM 6083]	-	-	1	-
	elongation factor Tu [Pseudomonas				
747152420	balearica DSM 6083]	-	-	1	-
	elongation factor Tu [Pseudomonas				
763481882	oryzihabitans]	1	-	1	-
	elongation factor Tu, partial				
761890014	[Pseudomonas sp. 10-1B]	-	1	1	-
	Aconitate hydratase 1 [Pseudomonas				
940320112	viridiflava]	-	-	1	-
	aconitate hydratase [Pseudomonas				
856750949	deceptionensis]	-	1	1	-
	aconitate hydratase [Pseudomonas				
763479401	oryzihabitans]	-	-	1	-
	lipoamide dehydrogenase-glc				
126166619	[Pseudomonas aeruginosa C3719]	-	-	1	-
	50S ribosomal protein L14 [Pseudomonas				
940214957	syringae pv. papulans]	-	-	1	-
	Isocitrate dehydrogenase, NADP-				
	dependent [Pseudomonas syringae pv.				
940028695	berberidis]	-	-	1	-
	pyruvate dehydrogenase [Pseudomonas				
610708968	pseudoalcaligenes AD6]	1	-	1	-
	pyruvate dehydrogenase [Pseudomonas				
568071974	sp. M1]	1	-	1	-
	glycine dehydrogenase [Pseudomonas				
782985630	pseudoalcaligenes]	1	1	1	-
	glycine dehydrogenase [Pseudomonas sp.				
568075229	M1]	-	-	1	-
229364150	glycine dehydrogenase [decarboxylating]	-	-	1	-

	[<i>Pseudomonas fluorescens</i> SBW25]				
799189748	glycine dehydrogenase [<i>Pseudomonas fluorescens</i>]	-	-	1	-
610714963	aldehyde dehydrogenase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	1	-
928206879	NAD-dependent aldehyde dehydrogenase [<i>Pseudomonas fuscovaginae</i>]	1	1	1	-
713115543	aldehyde dehydrogenase [<i>Pseudomonas mediterranea</i> CFBP 5447]	-	-	1	-
543436776	putative aldehyde dehydrogenase [<i>Pseudomonas alcaligenes</i> NBRC 14159]	-	-	1	-
610708295	aldehyde dehydrogenase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	1	-
768547926	flagellin [<i>Pseudomonas stutzeri</i>]	1	-	1	-
692342690	branched-chain alpha-keto acid dehydrogenase subunit E2 [<i>Pseudomonas rhizosphaerae</i>]	-	-	1	-
631777198	4-aminobutyrate aminotransferase GabT [<i>Pseudomonas knackmussii</i> B13]	-	-	1	-
568072381	carbamoyl phosphate synthase large subunit [<i>Pseudomonas</i> sp. M1]	-	-	1	-
856781911	carbamoyl phosphate synthase large subunit [<i>Pseudomonas helleri</i>]	-	1	1	-
692344671	carbamoyl phosphate synthase large subunit [<i>Pseudomonas rhizosphaerae</i>]	-	-	1	-
735690022	isocitrate dehydrogenase [<i>Pseudomonas tuomuerensis</i>]	1	-	1	-
667954157	phosphoenolpyruvate synthase [<i>Pseudomonas mendocina</i> S5.2]	-	1	1	-
28851255	phosphonate ABC transporter, periplasmic phosphonate-binding protein, putative [<i>Pseudomonas syringae</i> pv. tomato str. DC3000]	-	1	1	-
782984125	ATP synthase F0F1 subunit beta [<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	-
734576353	ATP synthase F0F1 subunit beta [<i>Pseudomonas putida</i> S12]	-	-	1	-
575877525	putative major facilitator superfamily transporter [<i>Pseudomonas aeruginosa</i> PA38182]	-	-	1	-
873532628	ABC transporter substrate-binding protein [<i>Pseudomonas</i> sp. KG01]	-	-	1	-
735689821	50S ribosomal protein L1 [<i>Pseudomonas tuomuerensis</i>]	-	-	1	-
782987051	flagellar hook-length control protein	-	1	1	-

	[<i>Pseudomonas pseudoalcaligenes</i>] flagellar hook-length control protein				
390983973	[<i>Pseudomonas stutzeri</i> CCUG 29243] transketolase [<i>Pseudomonas putida</i> 26991643 KT2440]	-	-	1	-
	aminotransferase class I and II family protein [<i>Pseudomonas</i> sp. P482]	-	-	1	-
641461595	malate synthase [<i>Pseudomonas</i> 610707379 pseudoalcaligenes AD6]	1	-	1	-
	malate synthase [<i>Pseudomonas</i> 610707950 pseudoalcaligenes AD6]	1	1	1	-
	trigger factor [<i>Pseudomonas</i> 856797284 weihenstephanensis]	1	1	1	-
	isoleucine--tRNA ligase [<i>Pseudomonas</i> 692345893 rhizosphaerae]	-	-	1	-
	Alcohol dehydrogenase 2 [<i>Pseudomonas</i> 757251311 fluorescens]	1	1	1	-
	TRAP-type transport system, periplasmic protein [<i>Pseudomonas stutzeri</i> DSM 395810319 10701]	-	-	1	-
	C4-dicarboxylate ABC transporter [<i>Pseudomonas</i> sp. PI1]	-	-	1	-
759595871 P00761	Trypsin OS= <i>Sus scrofa</i> PE=1 SV=1 ketol-acid reductoisomerase	-	1	1	-
568072324	[<i>Pseudomonas</i> sp. M1] secretion protein SecA [<i>Pseudomonas</i> 126170865 aeruginosa C3719]	-	-	1	-
	lysyl-tRNA synthetase [<i>Pseudomonas</i> 949199626 trivialis]	1	1	1	-
	lysyl-tRNA synthetase [<i>Pseudomonas</i> 379065725 stutzeri ATCC 14405 = CCUG 16156]	-	-	1	-
	glutamate synthase subunit alpha [<i>Pseudomonas stutzeri</i> ATCC 14405 = 379065476 CCUG 16156]	-	-	1	-
	glutamate synthase subunit alpha [<i>Pseudomonas stutzeri</i> DSM 10701]	-	-	1	-
	ribonuclease E [<i>Pseudomonas</i> 713119617 mediterranea CFBP 5447]	-	-	1	-
	Ribonucleoside-diphosphate reductase [<i>Pseudomonas amygdali</i> pv. <i>erobotryae</i>]	-	-	1	-
	isocitrate lyase [<i>Pseudomonas mendocina</i> 667953937 S5.2]	-	-	1	-
	molecular chaperone SurA [<i>Pseudomonas</i> 758538591 putida]	-	-	1	-
758833082	Survival protein SurA precursor	1	-	1	-

	(Peptidyl-prolyl cis-trans isomerase SurA)				
	[Pseudomonas sp. FeS53a]				
	molecular chaperone SurA [Pseudomonas				
856768742	lundensis]	-	-	1	-
	molecular chaperone SurA [Pseudomonas				
691225839	cremoricolorata]	-	-	1	-
	dihydrolipoamide succinyltransferase				
782988853	[Pseudomonas pseudoalcaligenes]	-	-	1	-
	2-oxoglutarate dehydrogenase E1				
	componentSucA [Pseudomonas protegens				
500241386	CHA0]	-	-	1	-
	2-oxoglutarate dehydrogenase (E1				
126193311	subunit) [Pseudomonas aeruginosa 2192]	1	1	1	-
	translation initiation factor IF-2				
610711172	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	-
	initiation factor 2 [Pseudomonas sp.				
576705331	GM41(2012)]	-	-	1	-
	translation initiation factor IF-2				
691224910	[Pseudomonas cremoricolorata]	1	1	1	-
	periplasmic nitrate reductase protein				
126192920	NapA [Pseudomonas aeruginosa 2192]	-	-	1	-
	50S ribosomal protein L25/general stress				
	protein Ctc [Pseudomonas stutzeri ATCC				
379066374	14405 = CCUG 16156]	-	-	1	-
	transcriptional regulator [Pseudomonas				
692345558	rhizosphaerae]	-	-	1	-
	Trifunctional transcriptional				
	regulator/proline				
	dehydrogenase/pyrroline-5-carboxylate				
	dehydrogenase [Pseudomonas syringae				
940090784	pv. cunninghamiae]	-	-	1	-
	hypothetical protein RL74_15905				
756406168	[Pseudomonas fluorescens]	-	-	1	-
	hypothetical protein [Pseudomonas sp.				
759596473	PI1]	-	-	1	-
	hypothetical protein HZ99_04735				
666085589	[Pseudomonas fluorescens]	-	-	1	-
	glutamine synthetase [Pseudomonas				
610706951	pseudoalcaligenes AD6]	-	-	1	-
	Glutamine synthetase type I				
758833353	[Pseudomonas sp. FeS53a]	-	1	1	-
	adenosylhomocysteinase [Pseudomonas				
782984648	pseudoalcaligenes]	-	1	1	-
	S-adenosyl-L-homocysteine hydrolase				
390981590	[Pseudomonas stutzeri CCUG 29243]	1	1	1	-

	glyceraldehyde-3-phosphate dehydrogenase, type I [Pseudomonas fluorescens R124]	-	-	1	-
404305228	2-isopropylmalate synthase [Pseudomonas mosselii SJ10]	-	1	1	-
684197829	aldehyde dismutase [Pseudomonas putida]	-	-	1	-
763167321	sulfite reductase [Pseudomonas stutzeri DSM 10701]	-	-	1	-
395808447	Sulfite reductase, beta subunit (hemoprotein) [Pseudomonas syringae pv. syringae str. B301D-R]	-	-	1	-
590456698	fructose-1,6-bisphosphate aldolase [Pseudomonas stutzeri NF13]	1	1	1	-
452007185	50S ribosomal protein L24 [Pseudomonas mendocina]	1	1	1	-
310941829	50S ribosomal protein L24 [Pseudomonas mosselii SJ10]	-	-	1	-
684199424	50S ribosomal protein L24 [Pseudomonas tuomuerensis]	-	-	1	-
735689901	beta-lactamase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
610707227	peptidylprolyl isomerase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
610712026	acyl carrier protein [Pseudomonas putida NBRC 14164]	-	-	1	-
512384876	DNA topoisomerase I [Pseudomonas oryzihabitans]	-	-	1	-
763478809	pyruvate ferredoxin/ferredoxin oxidoreductase family protein [Pseudomonas savastanoi pv. savastanoi NCPPB 3335]	-	-	1	-
298158635	dihydroxy-acid dehydratase [Pseudomonas cremoricolorata]	-	1	1	-
691225283	Dihydroxy-acid dehydratase [Pseudomonas entomophila L48]	-	1	1	-
95108551	F0F1 ATP synthase subunit alpha [Pseudomonas stutzeri CCUG 29243]	-	-	1	-
390985562	GMP synthase [Pseudomonas lundensis]	-	-	1	-
856778061	GMP synthase [Pseudomonas mediterranea CFBP 5447]	-	-	1	-
713117460	phosphoribosylformylglycinamide synthase [Pseudomonas fluorescens]	-	-	1	-
756404922	phosphoribosylformylglycinamide synthase [Pseudomonas sp. MT-1]	1	1	1	-
699968280					

	phosphoribosylaminoimidazolecarboxami de formyltransferase [Pseudomonas pseudoalcaligenes]	1	1	1	-
782984971	purine biosynthesis protein purH [Pseudomonas sp. M1]	-	-	1	-
568072540	phosphoribosylaminoimidazolecarboxami de formyltransferase [Pseudomonas rhizosphaerae]	-	1	1	-
692344765	valyl-tRNA synthetase [Pseudomonas mosselii SJ10]	-	-	1	-
684197869	valyl-tRNA ligase [Pseudomonas stutzeri NF13]	-	-	1	-
452009750	UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Pseudomonas stutzeri DSM 4166]	-	1	1	-
327479607	alanyl-tRNA synthetase [Pseudomonas coronafaciens pv. oryzae str. 1_6]	-	1	1	-
331021969	alanyl-tRNA synthetase [Pseudomonas moraviensis R28-S]	1	-	1	-
565414141	succinate-semialdehyde dehydrogenase I, NADP-dependent [Pseudomonas xanthomarina]	-	-	1	-
703404290	B12-dependent methionine synthase [Pseudomonas plecoglossicida NB2011]	1	-	1	-
511102357	methionine synthase [Pseudomonas protegens Pf-5]	-	-	1	-
68345322	phenylalanine 4-monooxygenase [Pseudomonas cremoricolorata]	-	-	1	-
691226723	Oligopeptidase A [Pseudomonas fluorescens]	-	1	1	-
757249574	oligopeptidase A [Pseudomonas oryzihabitans]	-	-	1	-
763481561	acetyl/propionyl-CoA carboxylase, alpha subunit [Pseudomonas fuscovaginae]	-	-	1	-
928205794	cysteine desulfurase IscS [Pseudomonas alcaligenes NBRC 14159]	-	1	1	-
543438276	cysteine desulfurase [Pseudomonas mendocina S5.2]	-	1	1	-
667955192	NADH dehydrogenase subunit G [Pseudomonas putida KT2440]	-	-	1	-
26990818	ornithine decarboxylase [Pseudomonas oryzihabitans]	-	-	1	-
763477995	peptidase S41 [Pseudomonas viridiflava]	-	-	1	-
934023441	C4-dicarboxylate ABC transporter [Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
610714094					

	GTP-binding protein TypA				
610706949	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
	2-keto-4-pentenoate hydratase				
610706547	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
	30S ribosomal protein S2 [Pseudomonas				
782986694	pseudoalcaligenes]	1	-	1	-
	30S ribosomal protein S2 [Pseudomonas				
500240830	protegens CHA0]	1	1	1	-
	flagellar hook-associated protein FlgK				
452007551	[Pseudomonas stutzeri NF13]	-	-	1	-
	uridylate kinase [Pseudomonas				
610714889	pseudoalcaligenes AD6]	1	1	1	-
	aldehyde dehydrogenase [Pseudomonas				
610713671	pseudoalcaligenes AD6]	-	-	1	-
	Aldehyde dehydrogenase [Pseudomonas				
758836104	sp. FeS53a]	-	-	1	-
	aldehyde dehydrogenase [Pseudomonas				
713116316	mediterranea CFBP 5447]	-	-	1	-
	gamma-glutamyl-gamma-				
	aminobutyraldehyde dehydrogenase				
928205223	[Pseudomonas fuscovaginae]	1	1	1	-
	Aldehyde dehydrogenase [Pseudomonas				
748441393	batumici]	-	-	1	-
	cytochrome C [Pseudomonas				
610713658	pseudoalcaligenes AD6]	-	-	1	-
	lysine decarboxylase [Pseudomonas sp.				
568073890	M1]	-	1	1	-
	H-NS histone [Pseudomonas mendocina				
667955052	S5.2]	-	-	1	-
	electron transfer flavoprotein alpha				
	subunit [Pseudomonas alcaligenes NBRC				
543439193	14159]	-	1	1	-
	argininosuccinate lyase [Pseudomonas				
610713626	pseudoalcaligenes AD6]	-	-	1	-
	argininosuccinate lyase [Pseudomonas sp.				
641463964	P482]	-	1	1	-
	dipicolinate synthase [Pseudomonas				
667953696	mendocina S5.2]	-	-	1	-
	acetyl-CoA synthetase [Pseudomonas				
667955311	mendocina S5.2]	1	-	1	-
	acetyl-CoA synthetase [Pseudomonas				
949209062	veronii]	-	-	1	-
	acetyl-coenzyme A synthetase				
229364493	[Pseudomonas fluorescens SBW25]	1	-	1	-
758828696	L-proline glycine betaine binding ABC	-	-	1	-

	transporter protein ProX [Pseudomonas sp. FeS53a]				
	methylmalonate-semialdehyde dehydrogenase [Pseudomonas pseudocaligenes]	-	-	1	-
782989443	methylmalonate-semialdehyde dehydrogenase [Pseudomonas pseudocaligenes AD6]	-	-	1	-
610714350	methylmalonate-semialdehyde dehydrogenase [Pseudomonas sp. CCOS 191]	-	-	1	-
821532273	methylmalonate-semialdehyde dehydrogenase [Pseudomonas sp. C5pp]	-	-	1	-
742791035	3-methylcrotonyl-CoA carboxylase [Pseudomonas putida]	-	-	1	-
758537405	RNA polymerase-associated protein HepA [Pseudomonas entomophila L48]	-	-	1	-
95109483	50S ribosomal protein L15 [Pseudomonas aeruginosa C3719]	-	-	1	-
126169039	LSU ribosomal protein L17p [Pseudomonas savastanoi pv. savastanoi NCPPB 3335]	-	-	1	-
298156382	threonine synthase [Pseudomonas frederiksborgensis]	-	-	1	-
733394114	glycyl-tRNA ligase subunit beta [Pseudomonas sp. Lz4W]	-	-	1	-
459963161	histidinol-phosphate aminotransferase [Pseudomonas alcaligenes NBRC 14159]	-	-	1	-
543437306	histidinol-phosphate aminotransferase [Pseudomonas fluorescens]	-	-	1	-
666086993	lipopolysaccharide transport periplasmic protein LptA [Pseudomonas fuscovaginae]	-	1	1	-
928208728	glucosamine--fructose-6-phosphate aminotransferase [Pseudomonas stutzeri DSM 4166]	-	-	1	-
327482886	glucosamine--fructose-6-phosphate aminotransferase [Pseudomonas tuomuerensis]	-	-	1	-
735690096	phenylalanyl-tRNA synthetase [Pseudomonas sp. ES3-33]	-	-	1	-
768456831	phenylalanyl-tRNA synthetase beta subunit [Pseudomonas fuscovaginae]	-	-	1	-
928203038	cystine transporter subunit [Pseudomonas oryzihabitans]	-	-	1	-
763480313					

	hypothetical protein SZ55_3262				
758829286	[Pseudomonas sp. FeS53a]	1	1	1	-
	branched-chain amino acid aminotransferase [Pseudomonas				
667952368	mendocina S5.2]	1	-	1	-
	Chaperone protein HscA [Pseudomonas				
749476537	fluorescens]	-	-	1	-
	heat shock protein HscA [Pseudomonas				
95109220	entomophila L48]	-	-	1	-
	molecular chaperone [Pseudomonas sp.				
556077556	VLB120]	-	-	1	-
	heat shock protein Hsp20 [Pseudomonas				
404531148	aeruginosa CI27]	-	-	1	-
	3-oxoacyl-[acyl-carrier-protein] reductase				
126195054	[Pseudomonas aeruginosa 2192]	-	-	1	-
	adenylosuccinate synthetase				
782984872	[Pseudomonas pseudoalcaligenes]	-	-	1	-
	carbonate dehydratase [Pseudomonas				
387163554	fluorescens A506]	-	-	1	-
	ATP-dependent protease ATP-binding subunit HslU [Pseudomonas				
782984731	pseudoalcaligenes]	-	-	1	-
	excinuclease ABC subunit A				
610713818	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
	excinuclease ABC subunit A				
667951037	[Pseudomonas mendocina S5.2]	-	1	1	-
	dihydrodipicolinate reductase				
459962373	[Pseudomonas sp. Lz4W]	-	-	1	-
	dihydrodipicolinate reductase				
229364516	[Pseudomonas fluorescens SBW25]	-	-	1	-
	beta-D-glucoside glucohydrolase				
610709306	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	-
	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B				
928208751	[Pseudomonas fuscovaginae]	-	1	1	-
	pyridoxine 5'-phosphate synthase				
667953207	[Pseudomonas mendocina S5.2]	-	1	1	-
	acyl-CoA carboxyltransferase beta chain				
685840547	[Pseudomonas aeruginosa]	-	-	1	-
	DNA gyrase subunit B [Pseudomonas				
758545805	putida]	-	-	1	-
	alcohol dehydrogenase [Pseudomonas				
543436521	alcaligenes NBRC 14159]	-	-	1	-
	DNA polymerase I [Pseudomonas				
229359523	fluorescens SBW25]	1	-	1	-

543437758	DNA polymerase I [Pseudomonas alcaligenes NBRC 14159]	-	1	1	-
913664725	flagellar basal body rod protein FlgB [Pseudomonas fluorescens NCIMB 11764]	-	-	1	-
641465168	dihydrodipicolinate synthase [Pseudomonas sp. P482]	-	-	1	-
610712092	succinate dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
335389965	major outer membrane lipoprotein I, partial [Pseudomonas corrugata]	-	-	1	-
610707994	phospholipid-binding protein [Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
667954971	fumarate hydratase [Pseudomonas mendocina S5.2]	-	-	1	-
320322841	fumarate hydratase, class I, putative [Pseudomonas savastanoi pv. glycinea str. B076]	-	-	1	-
667952048	diaminopimelate decarboxylase [Pseudomonas mendocina S5.2]	-	-	1	-
771845876	diaminopimelate decarboxylase [Pseudomonas sp. Os17]	-	-	1	-
782986943	phosphoribosylaminoimidazole- succinocarboxamide synthase [Pseudomonas pseudoalcaligenes]	-	-	1	-
771840851	phosphate acetyltransferase [Pseudomonas sp. Os17]	-	-	1	-
404302613	phosphate acetyltransferase [Pseudomonas fluorescens R124]	-	-	1	-
667952129	aminotransferase [Pseudomonas mendocina S5.2]	-	-	1	-
667953793	hypothetical protein DW68_14910 [Pseudomonas mendocina S5.2]	-	-	1	-
902687581	ABC transporter substrate-binding protein [Pseudomonas trivialis]	-	-	1	-
568076291	catalase/hydroperoxidase HPI(I) [Pseudomonas sp. M1]	-	-	1	-
610708895	imidazolonepropionase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
500245249	sarcosine oxidase subunit alpha [Pseudomonas protegens CHA0]	-	1	1	-
543438086	acetylornithine aminotransferase [Pseudomonas alcaligenes NBRC 14159]	-	1	1	-
928202379	acetylornithine/succinylornithine aminotransferase [Pseudomonas]	-	-	1	-

	fuscovaginae]				
	GbcA Glycine betaine demethylase				
	subunit A [Pseudomonas				
442901466	pseudoalcaligenes KF707]	-	-	1	-
	UDP-N-acetylmuramoylalanyl-D-				
	glutamate--2,6-diaminopimelate ligase				
610708003	[Pseudomonas pseudoalcaligenes AD6]	1	-	1	-
	UTP--glucose-1-phosphate				
	uridylyltransferase [Pseudomonas				
667953992	mendocina S5.2]	1	-	1	-
	beta-lactamase domain-containing protein				
575877764	[Pseudomonas aeruginosa PA38182]	-	1	1	-
	xylulose 5-phosphate 3-epimerase				
751374277	[Pseudomonas aeruginosa]	-	-	1	-
	acyl-CoA dehydrogenase [Pseudomonas				
667951184	mendocina S5.2]	1	1	1	-
	acyl-CoA dehydrogenase [Pseudomonas				
768544513	stutzeri]	-	-	1	-
	acyl-CoA dehydrogenase [Pseudomonas				
667952356	mendocina S5.2]	1	1	1	-
	acyl-CoA dehydrogenase [Pseudomonas				
856795324	weihenstephanensis]	-	-	1	-
	phosphoenolpyruvate-protein				
	phosphotransferase [Pseudomonas				
667951333	mendocina S5.2]	-	-	1	-
	chemotaxis protein CheA [Pseudomonas				
568073639	sp. M1]	-	-	1	-
	phosphoribosylglycinamide				
936610133	formyltransferase [Pseudomonas putida]	-	-	1	-
	hypothetical protein DW68_03795				
667951652	[Pseudomonas mendocina S5.2]	-	1	1	-
	pyruvate kinase [Pseudomonas putida				
388562397	ND6]	-	-	1	-
	chromosome partitioning protein ParA				
782986113	[Pseudomonas pseudoalcaligenes]	1	-	1	-
	chromosome partitioning protein ParA				
610714733	[Pseudomonas pseudoalcaligenes AD6]	1	-	1	-
	beta-ketothiolase [Pseudomonas				
98956473	extremaustralis 14-3]	-	-	1	-
	acetyl-CoA acetyltransferase				
768456408	[Pseudomonas sp. ES3-33]	-	-	1	-
	Clp protease ATP-binding protein				
610712041	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
	molybdenum cofactor biosynthesis				
953172586	protein B [Pseudomonas aeruginosa]	-	-	1	-

	phosphate transport regulator				
782984576	[Pseudomonas pseudoalcaligenes]	1	-	1	-
	phosphate transport regulator				
699965246	[Pseudomonas sp. MT-1]	-	-	1	-
	O-succinylhomoserine sulfhydrylase				
768546793	[Pseudomonas stutzeri]	-	1	1	-
	porphobilinogen deaminase				
229365167	[Pseudomonas fluorescens SBW25]	-	-	1	-
	Phosphoenolpyruvate carboxylase				
757241695	[Pseudomonas fluorescens]	-	-	1	-
	phosphoenolpyruvate carboxylase				
799200486	[Pseudomonas fluorescens]	-	-	1	-
	phosphoenolpyruvate carboxylase				
799192998	[Pseudomonas fluorescens]	-	-	1	-
	methionine--tRNA ligase [Pseudomonas				
782986083	pseudoalcaligenes]	1	1	1	-
	enolase-phosphatase [Pseudomonas				
15596882	aeruginosa PAO1]	-	-	1	-
	polyphosphate kinase [Pseudomonas				
896768340	syringae KCTC 12500]	-	-	1	-
	hypothetical protein IIA_003730				
404305427	[Pseudomonas fluorescens R124]	-	-	1	-
	Peptidyl-prolyl cis-trans isomerase				
940170464	[Pseudomonas amygdali pv. mellea]	1	1	1	-
	peptide chain release factor 3				
610714146	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
	peptide chain release factor 3				
327479556	[Pseudomonas stutzeri DSM 4166]	1	1	1	-
	membrane protein [Pseudomonas				
610713917	pseudoalcaligenes AD6]	1	1	1	-
	DNA ligase, partial [Pseudomonas				
940079052	syringae pv. castaneae]	-	-	1	-
	glutamate dehydrogenase [Pseudomonas				
782987441	pseudoalcaligenes]	-	-	1	-
	glutamate dehydrogenase [Pseudomonas				
749421815	fluorescens]	-	-	1	-
	Pyruvate carboxylase [Pseudomonas sp.				
576706557	GM41(2012)]	-	-	1	-
	homoserine dehydrogenase				
735691961	[Pseudomonas tuomuerensis]	-	-	1	-
	translocation protein TolB [Pseudomonas				
756408358	fluorescens]	-	-	1	-
	thioredoxin [Pseudomonas				
610710591	pseudoalcaligenes AD6]	-	-	1	-
768547321	cysteinyl-tRNA synthetase [Pseudomonas	-	-	1	-

	stutzeri]				
	arginyl-tRNA synthetase [Pseudomonas				
692344918	rhizosphaerae]	-	-	1	-
	gamma-glutamyl phosphate reductase				
610715113	[Pseudomonas pseudoalcaligenes AD6]	-	1	1	-
	gamma-glutamyl phosphate reductase				
667955514	[Pseudomonas mendocina S5.2]	-	-	1	-
	aldo/keto reductase [Pseudomonas				
610707986	pseudoalcaligenes AD6]	-	-	1	-
	Cold-shock protein [Pseudomonas				
940098305	amygdali pv. dendropanacis]	-	-	1	-
	Cold shock protein CspA [Pseudomonas				
758823140	sp. FeS53a]	-	-	1	-
	gamma-glutamyl-gamma-aminobutyrate				
	hydrolase [Pseudomonas				
782985344	pseudoalcaligenes]	1	1	1	-
	RNA polymerase subunit sigma-70				
856740643	[Pseudomonas deceptionensis]	-	-	1	-
	fructose 1,6-bisphosphatase				
782984707	[Pseudomonas pseudoalcaligenes]	1	1	1	-
	bifunctional N-acetylglucosamine-1-				
	phosphate uridyltransferase/glucosamine-				
	1-phosphate acetyltransferase				
820908622	[Pseudomonas putida]	-	-	1	-
	bifunctional N-acetylglucosamine-1-				
	phosphate uridyltransferase/glucosamine-				
	1-phosphate acetyltransferase				
747152951	[Pseudomonas balearica DSM 6083]	1	-	1	-
	hemin degrading factor [Pseudomonas				
610711146	pseudoalcaligenes AD6]	1	-	1	-
	transcription-repair coupling factor				
610712861	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
	transcription-repair coupling factor				
771841884	[Pseudomonas sp. Os17]	-	-	1	-
	S-adenosylmethionine synthetase				
782984655	[Pseudomonas pseudoalcaligenes]	1	1	1	-
	S-adenosylmethionine synthetase				
699965505	[Pseudomonas sp. MT-1]	-	-	1	-
	exoribonuclease R [Pseudomonas				
747115864	fluorescens]	-	-	1	-
	exoribonuclease R [Pseudomonas				
768548444	stutzeri]	-	-	1	-
	putative FAD-linked oxidoreductase				
757250847	[Pseudomonas fluorescens]	-	-	1	-
684198288	DNA topoisomerase IV subunit A	1	-	1	-

	[<i>Pseudomonas mosselii</i> SJ10]				
	DNA topoisomerase IV subunit A				
912965664	[<i>Pseudomonas</i> sp. 250J]	-	-	1	-
	alginate biosynthesis protein AlgC				
699969078	[<i>Pseudomonas</i> sp. MT-1]	-	-	1	-
	phosphomannomutase [<i>Pseudomonas</i>				
327479133	stutzeri DSM 4166]	-	1	1	-
	phosphoglucomutase [<i>Pseudomonas</i> sp.				
926556459	655]	1	-	1	-
	GTP-binding protein LepA [<i>Pseudomonas</i>				
699968232	sp. MT-1]	-	-	1	-
	heat shock protein HslV [<i>Pseudomonas</i>				
407987271	avellanae BPIC 631]	-	-	1	-
	Homoserine kinase [<i>Pseudomonas</i> sp.				
758835594	FeS53a]	-	1	1	-
	phosphoserine phosphatase/homoserine				
	phosphotransferase bifunctional protein				
387162246	[<i>Pseudomonas fluorescens</i> A506]	-	1	1	-
	CysB family transcriptional regulator				
934023128	[<i>Pseudomonas viridiflava</i>]	-	-	1	-
	1-deoxyxylulose-5-phosphate synthase				
126168864	[<i>Pseudomonas aeruginosa</i> C3719]	1	-	1	-
	1-deoxy-D-xylulose-5-phosphate synthase				
576707181	[<i>Pseudomonas</i> sp. GM41(2012)]	-	-	1	-
	Long-chain fatty acid--CoA ligase				
940056868	[<i>Pseudomonas syringae</i> pv. coriandricola]	-	-	1	-
	long-chain fatty acid--CoA ligase				
856746133	[<i>Pseudomonas deceptionensis</i>]	-	-	1	-
	long-chain fatty acid--CoA ligase				
768452999	[<i>Pseudomonas</i> sp. ES3-33]	-	-	1	-
	long-chain-fatty-acid--CoA ligase				
	[<i>Pseudomonas savastanoi</i> pv. glycinea str.				
320325470	B076]	-	-	1	-
	2,3,4,5-tetrahydropyridine-2,6-				
	carboxylate N-succinyltransferase				
733475185	[<i>Pseudomonas putida</i>]	-	-	1	-
	ribonuclease PH [<i>Pseudomonas</i>				
610714583	pseudoalcaligenes AD6]	1	1	1	-
	ribosome-binding factor A [<i>Pseudomonas</i>				
782989541	pseudoalcaligenes]	-	-	1	-
	30S ribosomal protein S18 [<i>Pseudomonas</i>				
26991556	putida KT2440]	1	-	1	-
	threonine aldolase [<i>Pseudomonas</i>				
856746092	deceptionensis]	1	1	1	-
949208277	threonine aldolase [<i>Pseudomonas</i> sp.	-	-	1	-

	DSM 29164]				
	flagellar rod assembly protein FlgJ				
684197388	[Pseudomonas mosselii SJ10]	-	1	1	-
	indole-3-glycerol-phosphate synthase				
667951101	[Pseudomonas mendocina S5.2]	1	-	1	-
	50S ribosomal protein L20 [Pseudomonas				
426268503	sp. UW4]	1	-	1	-
	MarR family transcriptional regulator				
782987506	[Pseudomonas pseudoalcaligenes]	1	1	1	-
	exodeoxyribonuclease V subunit gamma				
667954279	[Pseudomonas mendocina S5.2]	1	1	1	-
	tryptophanyl-tRNA synthetase				
543437313	[Pseudomonas alcaligenes NBRC 14159]	1	-	1	-
	NfuA Fe-S protein maturation				
758835663	[Pseudomonas sp. FeS53a]	-	-	1	-
	hypothetical protein TX23_02575				
949214027	[Pseudomonas sp. DSM 29164]	-	-	1	-
	hypothetical protein TR67_02670				
856750942	[Pseudomonas deceptionensis]	1	-	1	-
	hypothetical protein AU05_02290				
610707177	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
	catabolic dehydroquinase [Pseudomonas				
2599341	aeruginosa PAO1]	-	-	1	-
	ATP-dependent protease La Type II				
758826804	[Pseudomonas sp. FeS53a]	-	1	1	-
	NADPH:quinone reductase				
856804355	[Pseudomonas helleri]	-	-	1	-
	50S ribosomal protein L33 [Pseudomonas				
699965161	sp. MT-1]	-	-	1	-
	conserved hypothetical protein				
115588329	[Pseudomonas aeruginosa UCBPP-PA14]	1	-	1	-
	Fumarate and nitrate reduction regulatory				
758836309	protein [Pseudomonas sp. FeS53a]	-	-	1	-
	17 kDa surface antigen [Pseudomonas				
331027614	coronafaciens pv. oryzae str. 1_6]	-	-	1	-
	BNR/Asp-box repeat-containing protein				
782986900	[Pseudomonas pseudoalcaligenes]	-	-	1	-
	50S ribosomal protein L29 [Pseudomonas				
610713839	pseudoalcaligenes AD6]	-	-	1	-
	general secretion pathway protein GspE				
782985038	[Pseudomonas pseudoalcaligenes]	1	-	1	-
	DNA-binding transcriptional regulator				
	HexR [Pseudomonas syringae pv.				
940092398	cunninghamiae]	-	-	1	-
489554115	RNA-binding transcriptional accessory	-	-	1	-

	protein [<i>Pseudomonas pseudoalcaligenes</i>]				
	putative RNA-binding protein				
512381267	[<i>Pseudomonas putida</i> NBRC 14164]	-	-	1	-
	RNA-binding transcriptional accessory				
639919520	protein [<i>Pseudomonas nitroreducens</i>]	-	1	1	-
	histidyl-tRNA synthetase [<i>Pseudomonas</i>				
675290909	aeruginosa]	-	-	1	-
	histidyl-tRNA synthetase [<i>Pseudomonas</i>				
631777937	knackmussii B13]	1	-	1	-
	D-alanyl-D-alanine carboxypeptidase				
610715105	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	1	-
	C4-dicarboxylate ABC transporter				
782988581	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	-
	cysteine synthase B [<i>Pseudomonas</i>				
327481362	stutzeri DSM 4166]	-	1	1	-
	peptidase S41 [<i>Pseudomonas</i>				
763479585	oryzihabitans]	-	1	1	-
	peptidase S41 [<i>Pseudomonas</i>				
713119050	mediterranea CFBP 5447]	-	1	1	-
856775706	histidine kinase [<i>Pseudomonas lini</i>]	-	-	1	-
	histidine kinase [<i>Pseudomonas</i>				
856746183	deceptionensis]	-	-	1	-
	ATP-phosphoribosyltransferase				
126170820	[<i>Pseudomonas aeruginosa</i> C3719]	-	-	1	-
	Ribonucleoside-diphosphate reductase				
	subunit beta [<i>Pseudomonas knackmussii</i>				
631778634	B13]	-	-	1	-
	ribonucleotide-diphosphate reductase				
949186464	subunit beta [<i>Pseudomonas poae</i>]	-	1	1	-
	glycine/betaine ABC transporter				
	substrate-binding protein [<i>Pseudomonas</i>				
610710266	pseudoalcaligenes AD6]	1	1	1	-
	ATP-dependent RNA helicase HrpB				
749473322	[<i>Pseudomonas fluorescens</i>]	-	-	1	-
	hypothetical protein PpSQ1_13220,				
733473203	partial [<i>Pseudomonas putida</i>]	-	-	1	-
848254625	thioredoxin [<i>Pseudomonas stutzeri</i>]	-	1	1	-
	alcohol dehydrogenase [<i>Pseudomonas</i>				
667955472	mendocina S5.2]	-	-	1	-
	conserved hypothetical protein				
327478693	[<i>Pseudomonas stutzeri</i> DSM 4166]	1	1	1	-
	50S ribosomal protein L28 [<i>Pseudomonas</i>				
327478739	stutzeri DSM 4166]	-	-	1	-
	phosphate regulon transcriptional				
641463263	regulatory protein PhoB [<i>Pseudomonas</i>	-	-	1	-

	sp. P482]				
	endoribonuclease [Pseudomonas				
610714578	pseudoalcaligenes AD6]	1	1	1	-
	D-3-phosphoglycerate dehydrogenase				
327479061	[Pseudomonas stutzeri DSM 4166]	1	1	1	-
	malonyl CoA-ACP transacylase				
782985940	[Pseudomonas pseudoalcaligenes]	-	1	1	-
	3-methyl-2-oxobutanoate				
	hydroxymethyltransferase [Pseudomonas				
782989558	pseudoalcaligenes]	-	-	1	-
	transcription elongation factor GreA				
667955334	[Pseudomonas mendocina S5.2]	-	-	1	-
	Transcription elongation factor GreA				
940047801	[Pseudomonas syringae pv. coriandricola]	-	-	1	-
	glutamate-1-semialdehyde 2,1-				
	aminomutase [Pseudomonas				
782989331	pseudoalcaligenes]	1	-	1	-
	peptide chain release factor 1				
782985323	[Pseudomonas pseudoalcaligenes]	1	-	1	-
	phospho-2-dehydro-3-deoxyheptonate				
949204746	aldolase [Pseudomonas orientalis]	-	-	1	-
	50S rRNA methyltransferase				
763479240	[Pseudomonas oryzihabitans]	-	-	1	-
	flavodoxin [Pseudomonas				
782986417	pseudoalcaligenes]	-	-	1	-
	fumarate hydratase [Pseudomonas				
610706559	pseudoalcaligenes AD6]	1	-	1	-
	transferase, hexapeptide repeat-containing				
	protein [Pseudomonas coronafaciens pv.				
331022931	oryzae str. 1_6]	-	-	1	-
	phosphoribosylaminoimidazole				
	synthetase [Pseudomonas mendocina				
667954675	S5.2]	-	-	1	-
	GntR family transcriptional regulator				
692342938	[Pseudomonas rhizosphaerae]	-	-	1	-
	putative phosphoribosyltransferase				
95110331	[Pseudomonas entomophila L48]	-	-	1	-
	30S ribosomal protein S17 [Pseudomonas				
610713838	pseudoalcaligenes AD6]	-	1	1	-
	nucleoprotein/polynucleotide-associated				
	enzyme [Pseudomonas				
782989820	pseudoalcaligenes]	-	-	1	-
	hypothetical protein PstZobell_07652				
	[Pseudomonas stutzeri ATCC 14405 =				
379064554	CCUG 16156]	1	-	1	-

	putative M18 family aminopeptidase 2				
940059733	[<i>Pseudomonas congelans</i>]	-	-	1	-
	alanine racemase [<i>Pseudomonas</i>				
782984882	pseudoalcaligenes]	-	-	1	-
	thymidylate kinase [<i>Pseudomonas</i>				
667953364	mendocina S5.2]	1	-	1	-
	Helicase/SNF2 family domain protein				
940136590	[<i>Pseudomonas amygdali</i> pv. <i>hibisci</i>]	-	-	1	-
	coproporphyrinogen III oxidase				
782984194	[<i>Pseudomonas pseudoalcaligenes</i>]	-	-	1	-
	coproporphyrinogen oxidase				
928205019	[<i>Pseudomonas fuscovaginae</i>]	-	1	1	-
	nucleoid-associated protein				
610714777	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	1	-
	nucleoid-associated protein				
564838862	[<i>Pseudomonas aeruginosa</i> VRFPA07]	-	-	1	-
	quinone oxidoreductase [<i>Pseudomonas</i>				
667953812	mendocina S5.2]	-	1	1	-
	ubiquinone biosynthesis				
	methyltransferase UbiE [<i>Pseudomonas</i>				
667952283	mendocina S5.2]	-	-	1	-
	Ferric iron ABC transporter, iron-binding				
800912938	protein [<i>Pseudomonas fluorescens</i>]	1	-	1	-
	5-hydroxyisourate hydrolase				
610709478	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	1	-
	carbamoyltransferase [<i>Pseudomonas</i>				
782984818	pseudoalcaligenes]	-	-	1	-
	glycine zipper 2TM domain protein				
641464774	[<i>Pseudomonas</i> sp. P482]	-	-	1	-
	NADH:ubiquinone oxidoreductase				
610713892	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	1	-
	riboflavin synthase subunit alpha				
782989174	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	-
	Peptide chain release factor 2				
631778040	[<i>Pseudomonas knackmussii</i> B13]	-	-	1	-
	peptide chain release factor 2				
735692073	[<i>Pseudomonas tuomuerensis</i>]	-	-	1	-
	ribonuclease G [<i>Pseudomonas</i>				
610712460	pseudoalcaligenes AD6]	-	-	1	-
	cytoplasmic axial filament protein				
327479584	[<i>Pseudomonas stutzeri</i> DSM 4166]	1	-	1	-
	D-hydantoinase/dihydropyrimidinase Dht				
500242224	[<i>Pseudomonas protegens</i> CHA0]	-	-	1	-
	dihydropyrimidinase [<i>Pseudomonas</i> sp.				
641462103	P482]	-	-	1	-

576708647	dihydropyrimidinase [Pseudomonas sp. GM41(2012)]	-	-	1	-
782989169	zinc-binding protein [Pseudomonas pseudoalcaligenes]	-	1	1	-
26988861	3-ketoacyl-CoA thiolase [Pseudomonas putida KT2440]	-	-	1	-
691227598	saccharopine dehydrogenase [Pseudomonas cremoricolorata]	-	1	1	-
298159494	Ferredoxin, 2Fe-2S [Pseudomonas savastanoi pv. savastanoi NCPPB 3335]	-	-	1	-
667955176	aminotransferase [Pseudomonas mendocina S5.2]	-	-	1	-
782985249	1,2-oxophytodienoate reductase [Pseudomonas pseudoalcaligenes]	1	-	1	-
703407316	Flagellar hook protein FlgE [Pseudomonas xanthomarina]	-	-	1	-
610708095	peptidoglycan-binding protein LysM [Pseudomonas pseudoalcaligenes AD6]	1	-	1	-
610711019	diguanylate cyclase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
667951256	twitching motility protein PilT [Pseudomonas mendocina S5.2]	-	1	1	-
763480180	twitching motility protein PilT [Pseudomonas oryzae]	-	-	1	-
543437072	putative oxidoreductase [Pseudomonas alcaligenes NBRC 14159]	-	1	1	-
782988613	glycine cleavage system protein R [Pseudomonas pseudoalcaligenes]	-	1	1	-
610712463	protease TldD [Pseudomonas pseudoalcaligenes AD6]	1	-	1	-
782986723	S-formylglutathione hydrolase [Pseudomonas pseudoalcaligenes]	-	-	1	-
610714865	S-formylglutathione hydrolase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
543438352	ATP-dependent zinc metalloprotease FtsH [Pseudomonas alcaligenes NBRC 14159]	-	-	1	-
782987048	anti-anti-sigma factor [Pseudomonas pseudoalcaligenes]	-	1	1	-
782987117	chromosome segregation protein SMC [Pseudomonas pseudoalcaligenes]	1	-	1	-
619867824	methionyl-tRNA formyltransferase [Pseudomonas aeruginosa RB]	-	-	1	-
568071667	methionyl-tRNA formyltransferase [Pseudomonas sp. M1]	-	1	1	-

782984839	thiamine biosynthesis protein ThiC [Pseudomonas pseudoalcaligenes]	1	-	1	-
610709475	guanine deaminase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
667953045	NAD(P)H-quinone oxidoreductase [Pseudomonas mendocina S5.2]	1	1	1	-
667953587	pseudouridine synthase [Pseudomonas mendocina S5.2]	1	1	1	-
610708041	peptidylprolyl isomerase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
667954097	peptidylprolyl isomerase [Pseudomonas mendocina S5.2]	-	1	1	-
459960336	threonine aldolase [Pseudomonas sp. Lz4W]	1	-	1	-
610708944	heptose 1-phosphate adenylyltransferase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
543436572	DNA-directed RNA polymerase subunit omega [Pseudomonas alcaligenes NBRC 14159]	-	-	1	-
940042138	Flavodoxin/nitric oxide synthase [Pseudomonas cannabina]	-	-	1	-
758821734	Flavoprotein WrbA [Pseudomonas sp. FeS53a]	-	-	1	-
816870985	3-deoxy-D-manno-octulosonate 8- phosphate phosphatase [Pseudomonas putida KG-4]	-	1	1	-
782989467	CreA [Pseudomonas pseudoalcaligenes]	1	1	1	-
782989427	signal peptide protein [Pseudomonas pseudoalcaligenes]	-	-	1	-
610708054	ribosomal large subunit pseudouridine synthase D [Pseudomonas pseudoalcaligenes AD6]	1	-	1	-
610710097	hypothetical protein AU05_17220 [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
768547160	crotonase [Pseudomonas stutzeri]	-	-	1	-
782988660	NADPH-dependent FMN reductase [Pseudomonas pseudoalcaligenes]	-	1	1	-
782984641	adenosylmethionine-8-amino-7- oxononanoate aminotransferase [Pseudomonas pseudoalcaligenes]	-	-	1	-
610712863	5'-methylthioadenosine phosphorylase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
213924270	glutamate--cysteine ligase [Pseudomonas syringae pv. tomato T1]	-	-	1	-
667951005	GTP cyclohydrolase [Pseudomonas]	-	1	1	-

	mendocina S5.2]				
	aromatic acid decarboxylase				
395809807	[Pseudomonas stutzeri DSM 10701]	-	-	1	-
	3,4-dihydroxy-2-butanone 4-phosphate				
691225938	synthase [Pseudomonas cremoricolorata]	-	-	1	-
	hypothetical protein PAE2_4690				
404541484	[Pseudomonas aeruginosa E2]	-	-	1	-
687281913	helicase [Pseudomonas sp. YS-1p]	-	-	1	-
	protein involved in RimO-mediated beta-methylthiolation of ribosomal protein S12				
873531767	YcaO [Pseudomonas sp. KG01]	-	1	1	-
	YcaO domain protein [Pseudomonas				
928206547	fuscovaginae]	-	-	1	-
	Glutamine synthetase [Pseudomonas				
940029552	caricapapayae]	-	-	1	-
	flagellar biosynthesis protein FlgN				
782987004	[Pseudomonas pseudoalcaligenes]	-	-	1	-
	FAD-dependent oxidoreductase				
610713666	[Pseudomonas pseudoalcaligenes AD6]	1	-	1	-
	phospho-2-dehydro-3-deoxyheptonate				
949198972	aldolase [Pseudomonas trivialis]	1	-	1	-
	ABC transporter substrate-binding protein				
856751721	[Pseudomonas deceptionensis]	-	-	1	-
	30S ribosomal protein S12 [Pseudomonas				
9950486	aeruginosa PAO1]	1	1	1	-
	phosphate ABC transporter ATP-binding				
	protein [Pseudomonas pseudoalcaligenes				
610711000	AD6]	-	-	1	-
	hypothetical protein AU05_15995				
610714582	[Pseudomonas pseudoalcaligenes AD6]	1	-	1	-
	hypothetical protein RY26_03440				
749426630	[Pseudomonas fluorescens]	-	-	1	-
	recombination and repair protein				
782989514	[Pseudomonas pseudoalcaligenes]	1	-	1	-
	metal-binding protein [Pseudomonas				
820916407	putida]	-	1	1	-
	hypothetical protein N619_04885				
782989548	[Pseudomonas pseudoalcaligenes]	1	-	1	-
	16S rRNA methyltransferase				
733473453	[Pseudomonas putida]	1	-	1	-
	carbon-phosphorus lyase complex subunit				
	PhnJ [Pseudomonas syringae				
927283786	UMAF0158]	1	1	1	-
	hypothetical protein AU05_03085				
610706961	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	-

	DgcA, Dimethylglycine catabolism				
9951723	[<i>Pseudomonas aeruginosa</i> PAO1] putative FMN oxidoreductase	-	-	1	-
575876826	[<i>Pseudomonas aeruginosa</i> PA38182] PEP synthetase regulatory protein	-	-	1	-
610714055	[<i>Pseudomonas pseudoalcaligenes</i> AD6] coproporphyrinogen III oxidase	-	1	1	-
610713494	[<i>Pseudomonas pseudoalcaligenes</i> AD6] flagellar motor switch protein	1	1	1	-
511102202	[<i>Pseudomonas plecoglossicida</i> NB2011] pseudouridine synthase [Pseudomonas	-	-	1	-
667955321	mendocina S5.2] uroporphyrinogen decarboxylase	1	1	1	-
610712652	[<i>Pseudomonas pseudoalcaligenes</i> AD6] uroporphyrinogen decarboxylase	-	-	1	-
747149633	[<i>Pseudomonas balearica</i> DSM 6083] uroporphyrinogen decarboxylase	-	-	1	-
404302170	[<i>Pseudomonas fluorescens</i> R124] sirohydrochlorin ferrochelatase	-	-	1	-
667953961	[<i>Pseudomonas mendocina</i> S5.2] UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase	-	1	1	-
735692121	[<i>Pseudomonas tuomuerensis</i>] phosphoserine phosphatase SerB	-	-	1	-
26991587	[<i>Pseudomonas putida</i> KT2440] phosphoserine phosphatase	-	-	1	-
667952413	[<i>Pseudomonas mendocina</i> S5.2] Ribosomal protein L11 methyltransferase	-	-	1	-
758826346	[<i>Pseudomonas</i> sp. FeS53a] ATP-dependent RNA helicase RhIE	-	-	1	-
748440126	[<i>Pseudomonas batumici</i>] DEAD/DEAH box helicase	-	-	1	-
667952198	[<i>Pseudomonas mendocina</i> S5.2] DEAD/DEAH box helicase	-	1	1	-
452007165	[<i>Pseudomonas stutzeri</i> NF13] DEAD/DEAH box helicase	-	-	1	-
749424051	[<i>Pseudomonas fluorescens</i>] FAD-dependent oxidoreductase	-	-	1	-
769336286	[<i>Pseudomonas</i> sp. 10B238] FAD dependent oxidoreductase	-	-	1	-
387162407	[<i>Pseudomonas fluorescens</i> A506] 3-octaprenyl-4-hydroxybenzoate carboxy- lyase [Pseudomonas stutzeri CCUG	-	-	1	-
390984962	29243]	1	-	1	-
610714354	TetR family transcriptional regulator	1	-	1	-

	[Pseudomonas pseudoalcaligenes AD6]				
	phosphoribosyl-ATP pyrophosphatase				
543439707	[Pseudomonas alcaligenes NBRC 14159]	-	1	1	-
	sulfurtransferase [Pseudomonas				
610713513	pseudoalcaligenes AD6]	-	-	1	-
	tyrosine--tRNA ligase [Pseudomonas				
610713045	pseudoalcaligenes AD6]	-	-	1	-
	tyrosine--tRNA ligase [Pseudomonas				
689664261	fluorescens LMG 5329]	1	1	1	-
	hypothetical protein N619_23250				
782984352	[Pseudomonas pseudoalcaligenes]	-	1	1	-
	cell division protein ZipA [Pseudomonas				
782987121	pseudoalcaligenes]	-	1	1	-
	tRNA uridine 5-				
	carboxymethylaminomethyl modification				
667951719	protein [Pseudomonas mendocina S5.2]	-	1	1	-
	tricarboxylate transport protein TctC				
390981488	[Pseudomonas stutzeri CCUG 29243]	-	-	1	-
	hypothetical protein TU80_07905				
949220288	[Pseudomonas veronii]	1	1	1	-
	aspartate carbamoyltransferase catalytic				
735691164	subunit [Pseudomonas tuomuerensis]	-	-	1	-
	ABC transporter substrate-binding protein				
610711233	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
	glutamine amidotransferase				
610710056	[Pseudomonas pseudoalcaligenes AD6]	1	-	1	-
	polyhydroxybutyrate synthase, partial				
54306501	[Pseudomonas oleovorans]	1	-	1	-
	membrane protein [Pseudomonas				
610709138	pseudoalcaligenes AD6]	1	1	1	-
	ornithine carbamoyltransferase				
667955080	[Pseudomonas mendocina S5.2]	-	1	1	-
	conserved hypothetical protein				
126170812	[Pseudomonas aeruginosa C3719]	1	1	1	-
	hypothetical protein PACG_02560				
126168492	[Pseudomonas aeruginosa C3719]	-	-	1	-
	phosphogluconate dehydratase Edd				
500244290	[Pseudomonas protegens CHA0]	-	-	1	-
	SAM-dependent methyltransferase				
856776268	[Pseudomonas lundensis]	-	-	1	-
	lipoprotein [Pseudomonas				
782987599	pseudoalcaligenes]	1	1	1	-
	glycosyltransferase [Pseudomonas				
610711133	pseudoalcaligenes AD6]	1	-	1	-
610713334	arsenate reductase [Pseudomonas	-	-	1	-

	pseudoalcaligenes AD6]				
	folylpolyglutamate synthase				
782987588	[Pseudomonas pseudoalcaligenes]	1	-	1	-
	NADH dehydrogenase [Pseudomonas				
667953930	mendocina S5.2]	1	1	1	-
	two-component response regulator				
	[Pseudomonas stutzeri ATCC 14405 =				
379067026	CCUG 16156]	-	-	1	-
	channel protein TolC [Pseudomonas				
610708928	pseudoalcaligenes AD6]	-	1	1	-
	ribosomal RNA small subunit				
	methyltransferase A [Pseudomonas				
856740628	deceptionensis]	-	-	1	-
	UDP-N-acetylglucosamine				
	acyltransferase [Pseudomonas				
610714879	pseudoalcaligenes AD6]	-	-	1	-
	ATP-binding protein [Pseudomonas				
751084233	stutzeri]	-	1	1	-
	XRE family transcriptional regulator				
610709272	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
	ADP compounds hydrolase NudE				
543438651	[Pseudomonas alcaligenes NBRC 14159]	-	-	1	-
	hydroxypyruvate isomerase				
782986501	[Pseudomonas pseudoalcaligenes]	-	-	1	-
801168101	dehydrogenase [Pseudomonas kilonensis]	-	-	1	-
	Oxidoreductase [Pseudomonas amygdali				
928348245	pv. lachrymans]	-	-	1	-
	sulfurtransferase [Pseudomonas				
782988524	pseudoalcaligenes]	-	1	1	-
	hypothetical protein TU75_24145				
949181418	[Pseudomonas poae]	-	-	1	-
733475705	frataxin [Pseudomonas putida]	-	-	1	-
	choline dehydrogenase [Pseudomonas				
782984683	pseudoalcaligenes]	1	-	1	-
	choline dehydrogenase [Pseudomonas				
856762155	taetrolens]	-	-	1	-
	hypothetical protein AU05_18750, partial				
610709367	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
6715615	FtsZ [Pseudomonas aeruginosa PAO1]	-	-	1	-
	LysR family transcriptional regulator				
610707215	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
	hypothetical protein N619_17685				
782986681	[Pseudomonas pseudoalcaligenes]	-	1	1	-
	lipoprotein [Pseudomonas mendocina				
667955507	S5.2]	-	-	1	-

610707718	nuclease [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
747151424	chemotaxis protein CheY [Pseudomonas balearica DSM 6083]	-	-	1	-
782985879	pirin [Pseudomonas pseudoalcaligenes]	-	1	1	-
787855095	pirin [Pseudomonas chlororaphis]	-	-	1	-
928538041	hypothetical protein AN920_08910 [Pseudomonas aeruginosa]	-	1	1	-
641465530	hopJ type III effector family protein [Pseudomonas sp. P482]	-	-	1	-
685840988	putative lipoprotein [Pseudomonas aeruginosa]	-	-	1	-
610711136	penicillin-binding protein [Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
902690736	penicillin-binding protein [Pseudomonas trivialis]	-	-	1	-
459962415	penicillin-binding protein 1B [Pseudomonas sp. Lz4W]	-	-	1	-
667952179	dihydroorotase [Pseudomonas mendocina S5.2]	1	-	1	-
327482765	aminopeptidase P [Pseudomonas stutzeri DSM 4166]	-	-	1	-
782986412	dihydrofolate reductase [Pseudomonas pseudoalcaligenes]	1	1	1	-
323714630	Chain A, Crystal Structure Of A Serine Dehydrogenase From Pseudomonas Aeruginosa Pao1 In Complex With Nad	-	-	1	-
610709090	NGG1p interacting factor 3 protein, NIF3 [Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
667953013	hypothetical protein DW68_10810 [Pseudomonas mendocina S5.2]	1	-	1	-
667954348	pilus assembly protein [Pseudomonas mendocina S5.2]	-	-	1	-
610707665	BetI family transcriptional regulator [Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
543439155	hypothetical protein PA6_006_02010 [Pseudomonas alcaligenes NBRC 14159]	-	-	1	-
610708956	glycosyl transferase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
610713065	anthranilate synthase component I [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
782984222	aldose epimerase [Pseudomonas pseudoalcaligenes]	-	1	1	-
768548633	ATPase AAA [Pseudomonas stutzeri]	-	-	1	-
667953736	cytochrome Cbb3 [Pseudomonas]	-	-	1	-

	mendocina S5.2]				
	glycine cleavage system protein T				
610707849	[Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
	glutamine synthetase [Pseudomonas				
782986027	pseudoalcaligenes]	-	-	1	-
	glycine cleavage system protein H				
556077377	[Pseudomonas sp. VLB120]	-	-	1	-
	phosphoglycolate phosphatase				
782988498	[Pseudomonas pseudoalcaligenes]	1	-	1	-
	Polyhydroxyalkanoate granule-associated				
758832316	protein PhaF [Pseudomonas sp. FeS53a]	-	-	1	-
	iojap family protein [Pseudomonas				
610715111	pseudoalcaligenes AD6]	-	-	1	-
	iojap family protein [Pseudomonas sp.				
568072666	M1]	-	-	1	-
	integration host factor subunit beta				
667953601	[Pseudomonas mendocina S5.2]	-	1	1	-
	Fis family transcriptional regulator				
407991779	[Pseudomonas avellanae BPIC 631]	-	-	1	-
	lipocalin family protein [Pseudomonas				
511103329	plecoglossica NB2011]	-	1	1	-
	outer membrane lipoprotein Blc				
	[Pseudomonas stutzeri ATCC 14405 =				
379063830	CCUG 16156]	-	-	1	-
	GTPase HflX [Pseudomonas				
787857809	chlororaphis]	-	-	1	-
	D-amino acid oxidase [Pseudomonas				
667952765	mendocina S5.2]	1	1	1	-
	membrane protein [Pseudomonas				
610707282	pseudoalcaligenes AD6]	-	1	1	-
	Succinylarginine dihydrolase				
758824090	[Pseudomonas sp. FeS53a]	-	-	1	-
	succinylarginine dihydrolase				
	[Pseudomonas coronafaciens pv. oryzae				
331021962	str. 1_6]	-	1	1	-
	NADPH quinone reductase MdaB				
610707776	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
	hypothetical protein (plasmid)				
111036205	[Pseudomonas putida]	1	1	1	-
	hypothetical protein PP_4836				
26991516	[Pseudomonas putida KT2440]	1	-	1	-
	GntR family transcriptional regulator,				
759597925	partial [Pseudomonas sp. PI1]	-	1	1	-
	homoserine acetyltransferase				
782988061	[Pseudomonas pseudoalcaligenes]	-	-	1	-

	homoserine acetyltransferase				
610706968	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
	methionine sulfoxide reductase A				
703403298	[Pseudomonas xanthomarina]	-	1	1	-
	glutamate-pyruvate aminotransferase				
929905281	[Pseudomonas sp. RIT-PI-q]	-	-	1	-
	ATP-binding protein [Pseudomonas				
667955049	mendocina S5.2]	-	-	1	-
	quinolinate synthetase complex, A				
387161897	subunit [Pseudomonas fluorescens A506]	-	-	1	-
	quinolinate synthetase [Pseudomonas				
928210868	fuscovaginae]	-	-	1	-
	lipoprotein [Pseudomonas				
782985124	pseudoalcaligenes]	1	1	1	-
	D-alanyl-D-alanine carboxypeptidase				
667954687	[Pseudomonas mendocina S5.2]	1	1	1	-
	succinylglutamate desuccinylase				
782989905	[Pseudomonas pseudoalcaligenes]	-	1	1	-
	DNA repair protein [Pseudomonas				
782987848	pseudoalcaligenes]	-	-	1	-
	putative metallo-beta-lactamase family				
	protein [Pseudomonas fluorescens				
229360339	SBW25]	-	-	1	-
	molybdopterin-synthase				
	adenylyltransferase [Pseudomonas				
667952832	mendocina S5.2]	-	-	1	-
	molybdopterin-synthase				
	adenylyltransferase [Pseudomonas sp.				
768455433	ES3-33]	1	1	1	-
	molybdopterin-synthase				
	adenylyltransferase [Pseudomonas				
856767290	taetrolens]	-	-	1	-
	type 4 pilus biogenesis protein PilZ				
543438166	[Pseudomonas alcaligenes NBRC 14159]	-	-	1	-
	ATPase AAA [Pseudomonas				
610709430	pseudoalcaligenes AD6]	1	-	1	-
	3-hydroxyacyl-CoA dehydrogenase				
568075856	[Pseudomonas sp. M1]	-	-	1	-
	Fatty acid oxidation complex subunit				
749473734	alpha [Pseudomonas fluorescens]	-	-	1	-
	hypothetical protein AU05_12710				
610711138	[Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
820917281	thioredoxin [Pseudomonas putida]	-	1	1	-
	glycolate oxidase subunit GlcD				
799198064	[Pseudomonas fluorescens]	-	-	1	-

	molybdenum cofactor biosynthesis				
	protein MoaD [Pseudomonas				
782985286	pseudoalcaligenes]	1	1	1	-
	amidase, hydantoinase/carbamoylase				
641462100	family protein [Pseudomonas sp. P482]	-	1	1	-
	allantoate amidohydrolase [Pseudomonas				
752310060	plecoglossicida]	-	-	1	-
	methylglyoxal synthase [Pseudomonas				
782985589	pseudoalcaligenes]	-	-	1	-
	membrane protein [Pseudomonas				
782984680	pseudoalcaligenes]	-	-	1	-
	conjugal transfer protein TraR				
610710934	[Pseudomonas pseudoalcaligenes AD6]	1	-	1	-
	hypothetical protein N619_11515				
782987527	[Pseudomonas pseudoalcaligenes]	-	-	1	-
	lactate dehydrogenase [Pseudomonas				
768548527	stutzeri]	-	-	1	-
	Neisseria PilC domain protein				
703405248	[Pseudomonas xanthomarina]	1	-	1	-
	methionine aminopeptidase				
782986693	[Pseudomonas pseudoalcaligenes]	-	-	1	-
	3-isopropylmalate dehydratase small				
568073601	subunit [Pseudomonas sp. M1]	-	1	1	-
471347360	porin [Pseudomonas putida LS46]	-	1	1	-
	ribonuclease D [Pseudomonas				
782987444	pseudoalcaligenes]	-	-	1	-
	DNA polymerase III subunit epsilon				
667953800	[Pseudomonas mendocina S5.2]	1	-	1	-
	hypothetical protein N619_29300				
782985443	[Pseudomonas pseudoalcaligenes]	1	-	1	-
	DnaA initiator-associating protein DiaA				
735691531	[Pseudomonas tuomuerensis]	1	1	1	-
	peptidylprolyl isomerase [Pseudomonas				
691224867	cremoricolorata]	1	1	1	-
	helix-hairpin-helix repeat-containing				
	competence protein ComEA				
	[Pseudomonas stutzeri ATCC 14405 =				
379063110	CCUG 16156]	-	-	1	-
	cytochrome D ubiquinol oxidase subunit				
782985170	III [Pseudomonas pseudoalcaligenes]	-	1	1	-
	5,10-methylenetetrahydrofolate reductase				
747114451	[Pseudomonas fluorescens]	-	-	1	-
799197595	integrase [Pseudomonas fluorescens]	-	-	1	-
	lysophospholipase L2 [Pseudomonas				
757245813	fluorescens]	1	-	1	-

610714253	membrane protein [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
667955179	GTP-binding protein [Pseudomonas mendocina S5.2]	-	-	1	-
557561695	adenosylcobinamide kinase [Pseudomonas aeruginosa VRFP05]	-	-	1	-
610714850	dihydroorotate dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	1	1	1	-
782987169	glutathione S-transferase [Pseudomonas pseudoalcaligenes]	1	1	1	-
782987578	LysR family transcriptional regulator [Pseudomonas pseudoalcaligenes]	-	-	1	-
782988204	Fis family transcriptional regulator [Pseudomonas pseudoalcaligenes]	-	-	1	-
610711181	RNA-binding protein [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
610707553	molybdenum cofactor biosynthesis protein MoaE [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
610706955	nitrogen regulation protein NR(I) [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
782988094	phosphopantetheine adenylyltransferase [Pseudomonas pseudoalcaligenes]	-	1	1	-
9947770	hypothetical protein PA1789 [Pseudomonas aeruginosa PAO1]	-	-	1	-
856740898	hypothetical protein TR67_18285 [Pseudomonas deceptionensis]	-	-	1	-
799188735	cytochrome C [Pseudomonas fluorescens]	-	-	1	-
610708933	ADP-ribose pyrophosphatase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
758828366	ATPase AAA_5 [Pseudomonas sp. FeS53a]	-	-	1	-
95113201	glycine cleavage complex protein T, aminomethyltransferase, tetrahydrofolate-dependent [Pseudomonas entomophila L48]	-	-	1	-
564836747	flagellar hook-length control protein [Pseudomonas aeruginosa VRFP07]	-	-	1	-
756408778	excinuclease ABC subunit B [Pseudomonas fluorescens]	-	-	1	-
1545864	UvrB, partial [Pseudomonas aeruginosa PAO1]	-	-	1	-
782990045	nucleotidyltransferase, partial [Pseudomonas pseudoalcaligenes]	1	1	1	-
327479831	HlyD family secretion protein	-	-	1	-

	[<i>Pseudomonas stutzeri</i> DSM 4166]				
	30S ribosomal protein S20 [<i>Pseudomonas</i>				
861575390	sp. BICA1-14]	-	1	1	-
	isopropylmalate isomerase large subunit				
395808063	[<i>Pseudomonas stutzeri</i> DSM 10701]	-	-	1	-
	hypothetical protein MT1_3040				
699967753	[<i>Pseudomonas</i> sp. MT-1]	-	1	1	-
	flagellar motor switch protein FliM				
782987053	[<i>Pseudomonas pseudoalcaligenes</i>]	-	-	1	-
	hypothetical protein DW68_13775				
667953582	[<i>Pseudomonas mendocina</i> S5.2]	-	1	1	-
	hypothetical protein N619_20875				
782987236	[<i>Pseudomonas pseudoalcaligenes</i>]	-	-	1	-
	diguanylate cyclase [<i>Pseudomonas</i>				
782985543	<i>pseudoalcaligenes</i>]	-	-	1	-
758545503	sulfurtransferase [<i>Pseudomonas putida</i>]	-	-	1	-
	methionine sulfoxide reductase B				
782988828	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	-
	dehydrogenase [<i>Pseudomonas balearica</i>				
747150895	DSM 6083]	-	-	1	-
	asparaginase [<i>Pseudomonas mendocina</i>				
667951880	S5.2]	-	1	1	-
	serine/threonine protein phosphatase				
937311101	[<i>Pseudomonas fluorescens</i>]	-	-	1	-
	isovaleryl-CoA dehydrogenase				
747150046	[<i>Pseudomonas balearica</i> DSM 6083]	-	-	1	-
	hypothetical protein N619_22735				
782984260	[<i>Pseudomonas pseudoalcaligenes</i>]	-	-	1	-
	type II secretion system protein E				
666087751	[<i>Pseudomonas fluorescens</i>]	-	-	1	-
	hypothetical protein PACIG1_5965				
403244290	[<i>Pseudomonas aeruginosa</i> CIG1]	-	-	1	-
	ATP synthase subunit B [<i>Pseudomonas</i>				
699965022	sp. MT-1]	-	-	1	-
	flagellin [<i>Pseudomonas syringae</i> pv.				
66046695	<i>syringae</i> B728a]	-	-	1	-
	3-methylitaconate isomerase				
610714056	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	1	-
	iron ABC transporter substrate-binding				
730590720	protein [<i>Pseudomonas parafulva</i>]	1	1	1	-
	lipoprotein [<i>Pseudomonas</i>				
782984246	<i>pseudoalcaligenes</i>]	-	-	1	-
	aminopeptidase [<i>Pseudomonas</i>				
610708035	<i>pseudoalcaligenes</i> AD6]	-	-	1	-
631781426	hypothetical protein PKB_4580	1	1	1	-

	[<i>Pseudomonas knackmussii</i> B13]				
	thioredoxin [<i>Pseudomonas</i>				
610712692	pseudoalcaligenes AD6]	1	1	1	-
	hypothetical protein PT85_15030				
735690182	[<i>Pseudomonas tuomuerensis</i>]	-	-	1	-
745838823	transposase [<i>Pseudomonas aeruginosa</i>]	-	1	1	-
	Thioredoxin OS= <i>Homo sapiens</i>				
P10599	GN=TXN PE=1 SV=3	1	1	1	-
	(dimethylallyl)adenosine tRNA				
	methylthiotransferase [<i>Pseudomonas</i>				
949196577	trivialis]	1	1	1	-
	phosphoribosyl-AMP cyclohydrolase				
667952280	[<i>Pseudomonas mendocina</i> S5.2]	1	-	1	-
	GTP cyclohydrolase [<i>Pseudomonas</i>				
856746052	deceptionensis]	1	1	1	-
	hypothetical protein PSJM300_08915				
395808446	[<i>Pseudomonas stutzeri</i> DSM 10701]	1	1	1	-
	serine/threonine protein kinase				
667954990	[<i>Pseudomonas mendocina</i> S5.2]	-	-	1	-
	queuine tRNA-ribosyltransferase				
641464770	[<i>Pseudomonas</i> sp. P482]	-	1	1	-
	cell envelope biogenesis protein TolA				
610708675	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	1	-
	RNA polymerase sigma-H factor AlgU				
934025088	[<i>Pseudomonas viridiflava</i>]	-	1	1	-
	4-hydroxy-3-methylbut-2-en-1-yl				
	diphosphate synthase [<i>Pseudomonas</i>				
763480521	oryzihabitans]	-	-	1	-
	membrane protein [<i>Pseudomonas</i>				
799193036	fluorescens]	-	-	1	-
	dihydroneopterin aldolase [<i>Pseudomonas</i>				
684199351	mosselii SJ10]	-	-	1	-
	hypothetical protein V527_16755				
564883369	[<i>Pseudomonas aeruginosa</i> VRFP06]	1	-	1	-
	agmatine deiminase [<i>Pseudomonas</i>				
735690279	tuomuerensis]	1	1	1	-
	sulfurtransferase TusE [<i>Pseudomonas</i>				
610713924	pseudoalcaligenes AD6]	-	-	1	-
	transcription elongation factor GreB				
758540235	[<i>Pseudomonas putida</i>]	-	1	1	-
	LacI family transcriptional regulator				
610714010	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	1	-
	imidazole glycerol phosphate synthase				
	subunit HisH [<i>Pseudomonas stutzeri</i>				
327482786	DSM 4166]	-	-	1	-

	GTPase CgtA [<i>Pseudomonas mendocina</i>				
667955389	S5.2]	1	-	1	-
	Amino acid ABC transporter permease				
	[<i>Pseudomonas syringae</i> pv.				
940032607	broussonetiae]	-	-	1	-
	glucose-6-phosphate dehydrogenase				
735691193	[<i>Pseudomonas tuomuerensis</i>]	-	-	1	-
	transcriptional regulator PdhR				
782989507	[<i>Pseudomonas pseudoalcaligenes</i>]	1	-	1	-
	lipoprotein [<i>Pseudomonas</i>				
782986447	pseudoalcaligenes]	1	-	1	-
320594367	SpoT [<i>Pseudomonas brassicacearum</i>]	-	-	1	-
	thioesterase superfamily protein				
641464984	[<i>Pseudomonas</i> sp. P482]	1	1	1	-
	allantoinase [<i>Pseudomonas</i>				
782987107	pseudoalcaligenes]	-	1	1	-
	poly(A) polymerase [<i>Pseudomonas</i>				
928534659	aeruginosa]	-	-	1	-
	periplasmic protein [<i>Pseudomonas</i>				
782987501	pseudoalcaligenes]	-	-	1	-
	amino acid ABC transporter substrate-				
	binding protein [<i>Pseudomonas mendocina</i>				
667954742	S5.2]	1	1	1	-
	globin [<i>Pseudomonas pseudoalcaligenes</i>				
610715065	AD6]	-	1	1	-
	hypothetical protein N619_16370				
782986448	[<i>Pseudomonas pseudoalcaligenes</i>]	-	-	1	-
	extracellular solute-binding protein				
556074186	[<i>Pseudomonas</i> sp. VLB120]	-	-	1	-
	diguanylate phosphodiesterase				
782986630	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	1	-
	glutathione S-transferase [<i>Pseudomonas</i>				
667952231	mendocina S5.2]	1	-	1	-
	S-adenosylmethionine:tRNA				
	ribosyltransferase-isomerase				
940260035	[<i>Pseudomonas savastanoi</i> pv. savastanoi]	-	-	1	-
	S-adenosylmethionine tRNA				
	ribosyltransferase [<i>Pseudomonas</i> sp.				
769334974	10B238]	-	-	1	-
	S-adenosylmethionine tRNA				
	ribosyltransferase [<i>Pseudomonas mosselii</i>				
684197949	SJ10]	-	-	1	-
	peptidase M16 [<i>Pseudomonas</i>				
735690212	tuomuerensis]	-	-	1	-
388558656	TetR family transcriptional regulator	-	-	1	-

	[Pseudomonas putida ND6]				
943826955	helicase [Pseudomonas aeruginosa]	-	1	1	-
	cytochrome C [Pseudomonas mendocina				
667951901	S5.2]	-	-	1	-
	Alpha-lactalbumin OS=Bos taurus				
P00711	GN=LALBA PE=1 SV=2	1	1	1	-
	GTP-binding protein Der [Pseudomonas				
568074841	sp. M1]	-	-	1	-
	cell division topological specificity factor				
544279597	[Pseudomonas putida LF54]	1	-	1	-
	Regulatory protein merR [Pseudomonas				
346059310	aeruginosa NCMG1179]	-	-	1	-
	Putative DNA helicase [Pseudomonas				
631779403	knackmussii B13]	1	-	1	-
	hypothetical protein RT21_07630				
769335368	[Pseudomonas sp. 10B238]	-	-	1	-
404304302	ATPase [Pseudomonas fluorescens R124]	1	1	1	-
	sarcosine oxidase subunit gamma				
733395397	[Pseudomonas frederiksbergensis]	-	-	1	-
	spermidine/putrescine ABC transporter				
	ATP-binding protein [Pseudomonas sp.				
751049975	W15Feb9B]	-	-	1	-
	proteophosphoglycan precursor				
856784202	[Pseudomonas psychrophila]	-	-	1	-
	tRNA modification GTPase TrmE				
848258389	[Pseudomonas stutzeri]	-	-	1	-
	mutant NtrC activator [Pseudomonas				
768550207	stutzeri]	1	1	1	-
	1-(5-phosphoribosyl)-5-[(5-				
	phosphoribosylamino)methylideneamino]				
	imidazole-4-carboxamide isomerase				
667952291	[Pseudomonas mendocina S5.2]	-	-	1	-
	diguanylate cyclase [Pseudomonas				
782988245	pseudoalcaligenes]	1	1	1	-
	adenylate cyclase [Pseudomonas				
782984575	pseudoalcaligenes]	1	-	1	-
	histidine kinase [Pseudomonas mendocina				
667955000	S5.2]	-	-	1	-
	hypothetical protein DW68_20970				
667954955	[Pseudomonas mendocina S5.2]	1	-	1	-
	FAD dependent oxidoreductase				
631779061	[Pseudomonas knackmussii B13]	-	-	1	-
247720643	BEL-3 [Pseudomonas aeruginosa]	-	-	1	-
	precorrin-4 C11-methyltransferase				
928539114	[Pseudomonas aeruginosa]	-	-	1	-

780899570	RelE toxin [Pseudomonas sp. BICA1-14]	-	-	1	-
	MarR family transcriptional regulator				
749427552	[Pseudomonas fluorescens]	-	-	1	-
	thiol:disulfide interchange protein DsbA				
	[Pseudomonas amygdali pv. lachrymans				
330986812	str. M301315]	-	-	1	-
	acyl-CoA dehydrogenase [Pseudomonas				
751051506	sp. W15Feb9B]	-	-	1	-
856792980	ATPase [Pseudomonas helleri]	-	-	1	-
	septum formation protein Maf				
782985131	[Pseudomonas pseudoalcaligenes]	-	-	1	-
	thymidylate synthase [Pseudomonas				
782988142	pseudoalcaligenes]	-	-	1	-
	Rhs family protein [Pseudomonas				
939982134	syringae pv. atrofaciens]	-	-	1	-
	cytochrome c5 [Pseudomonas stutzeri				
379065399	ATCC 14405 = CCUG 16156]	-	-	1	-
	NADPH-dependent 7-cyano-7-				
	deazaguanine reductase [Pseudomonas				
667954353	mendocina S5.2]	-	1	1	-
	TetR family transcriptional regulator				
691224610	[Pseudomonas cremoricolorata]	1	-	1	-
	ATP-dependent DNA helicase RecQ				
782984599	[Pseudomonas pseudoalcaligenes]	-	-	1	-
856772596	histidine kinase [Pseudomonas lini]	-	-	1	-
	uracil phosphoribosyltransferase				
568074543	[Pseudomonas sp. M1]	-	-	1	-
	CRISPR-associated protein, Cas1 family				
346056902	[Pseudomonas aeruginosa NCMG1179]	-	-	1	-
	hypothetical protein HZ99_01640				
666085020	[Pseudomonas fluorescens]	-	-	1	-
	putative outer membrane lipoprotein				
928208269	[Pseudomonas fuscovaginae]	-	-	1	-
	membrane protein [Pseudomonas				
610713498	pseudoalcaligenes AD6]	-	-	1	-
	cytochrome B559 subunit alpha				
782984295	[Pseudomonas pseudoalcaligenes]	-	-	1	-
	magnesium transporter [Pseudomonas sp.				
568072694	M1]	-	-	1	-
	exodeoxyribonuclease V subunit alpha				
782987256	[Pseudomonas pseudoalcaligenes]	1	-	1	-
	hypothetical protein QX25_02355				
751086325	[Pseudomonas stutzeri]	1	-	1	-
	hypothetical protein NCGM1179_1603				
346056897	[Pseudomonas aeruginosa NCMG1179]	-	-	1	-

667953694	plastocyanin [<i>Pseudomonas mendocina</i> S5.2]	1	-	1	-
610707658	amino acid ABC transporter substrate- binding protein [<i>Pseudomonas</i> <i>pseudoalcaligenes</i> AD6]	-	-	1	-
610707869	N-acetylmuramoyl-L-alanine amidase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	1	-
610708278	glutamine synthetase [<i>Pseudomonas</i> <i>pseudoalcaligenes</i> AD6]	-	-	1	-
751050249	transporter, partial [<i>Pseudomonas</i> sp. W15Feb9B]	-	-	1	-
768548547	dihydropteroate synthase [<i>Pseudomonas</i> <i>stutzeri</i>]	-	-	1	-
387161777	transcriptional regulator, MerR family [<i>Pseudomonas fluorescens</i> A506]	-	-	1	-
856771559	MerR family transcriptional regulator [<i>Pseudomonas lini</i>]	-	-	1	-
404303862	Aerobic-type carbon monoxide dehydrogenase, large subunit [<i>Pseudomonas fluorescens</i> R124]	-	-	1	-
9949728	NalD [<i>Pseudomonas aeruginosa</i> PAO1]	-	-	1	-
782986698	farnesyl-diphosphate synthase [<i>Pseudomonas pseudoalcaligenes</i>]	1	-	1	-
667953224	3-hydroxybutyryl-CoA dehydratase [<i>Pseudomonas mendocina</i> S5.2]	-	1	1	-
763481530	cold-shock protein [<i>Pseudomonas</i> <i>oryzihabitans</i>]	-	-	1	-
782986114	chromosome partitioning protein [<i>Pseudomonas pseudoalcaligenes</i>]	-	-	1	-
856745037	flagellar hook-length control protein [<i>Pseudomonas deceptionensis</i>]	-	-	1	-
610709304	helicase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	-	1	-
747149152	potassium transporter peripheral membrane component [<i>Pseudomonas</i> <i>balearica</i> DSM 6083]	-	-	1	-
713115471	AraC family transcriptional regulator [<i>Pseudomonas mediterranea</i> CFBP 5447]	-	-	1	-
949218252	XRE family transcriptional regulator [<i>Pseudomonas</i> sp. DSM 29167]	-	-	1	-
667953727	adenine phosphoribosyltransferase [<i>Pseudomonas mendocina</i> S5.2]	1	-	1	-
751053711	type 4 fimbriae expression regulatory protein PilR [<i>Pseudomonas</i> sp. W15Feb9B]	-	-	1	-

	ribosomal protein S6 modification protein				
568071409	[Pseudomonas sp. M1]	-	-	1	-
	flagellar basal body protein FliL				
782984532	[Pseudomonas pseudoalcaligenes]	-	1	1	-
	glyceraldehyde 3-phosphate				
	dehydrogenase [Pseudomonas aeruginosa				
430853	PAO1]	-	-	1	-
	long-chain fatty acid--CoA ligase				
761895406	[Pseudomonas sp. 10-1B]	-	-	1	-
	NADH dehydrogenase subunit I				
675289511	[Pseudomonas aeruginosa]	-	1	1	-
	hypothetical protein N619_06610				
782988919	[Pseudomonas pseudoalcaligenes]	-	-	1	-
	Sarcosine oxidase subunit gamma				
940080406	[Pseudomonas syringae pv. coryli]	-	-	1	-
	GntR family transcriptional regulator				
756404648	[Pseudomonas fluorescens]	-	-	1	-
949195450	DoxX [Pseudomonas synxantha]	-	-	1	-
	Cro/C1 family transcriptional regulator				
568070717	[Pseudomonas sp. M1]	1	1	1	-
	aminotransferase [Pseudomonas				
667951624	mendocina S5.2]	1	-	1	-
	ABC transporter substrate-binding protein				
940722301	[Pseudomonas endophytica]	-	-	1	-
	putative VirB3 [Pseudomonas savastanoi				
940266555	pv. savastanoi]	-	-	1	-
	lipoprotein [Pseudomonas mendocina				
667951571	S5.2]	-	-	1	-
	protein-export protein SecB				
543438616	[Pseudomonas alcaligenes NBRC 14159]	1	1	1	-
	ferredoxin-NADP reductase				
856793094	[Pseudomonas helleri]	-	1	1	-
	ABC transporter ATP-binding protein				
856766944	[Pseudomonas taetrolens]	-	-	1	-
856804623	membrane protein [Pseudomonas helleri]	-	-	1	-
	polyketide cyclase [Pseudomonas				
749419707	fluorescens]	-	-	1	-
	hypothetical protein DW68_02175				
667951342	[Pseudomonas mendocina S5.2]	-	-	1	-
	transcriptional regulator [Pseudomonas				
953176104	aeruginosa]	-	-	1	-
	hypothetical protein TU78_01485				
856768177	[Pseudomonas taetrolens]	-	-	1	-
	histidine kinase [Pseudomonas mendocina				
667955360	S5.2]	-	-	1	-

787857804	chemotaxis protein [Pseudomonas chlororaphis]	-	-	1	-
928206566	lactate dehydrogenase-like oxidoreductase [Pseudomonas fuscovaginae]	-	-	1	-
782984135	16S rRNA methyltransferase [Pseudomonas pseudoalcaligenes]	-	-	1	-
768454345	recombination protein RecR [Pseudomonas sp. ES3-33]	-	-	1	-
610709153	TetR family transcriptional regulator [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
631780795	two-component response regulator [Pseudomonas knackmussii B13]	-	-	1	-
940225570	Preprotein translocase, subunit YajC [Pseudomonas savastanoi pv. retacarpa]	-	-	1	-
543439590	amino-acid acetyltransferase [Pseudomonas alcaligenes NBRC 14159]	-	-	1	-
782988244	chemotaxis protein CheY [Pseudomonas pseudoalcaligenes]	-	-	1	-
756407155	S-formylglutathione hydrolase [Pseudomonas fluorescens]	-	-	1	-
610714567	integration host factor [Pseudomonas pseudoalcaligenes AD6]	-	1	1	-
126171223	hypothetical protein PACG_05486 [Pseudomonas aeruginosa C3719]	-	-	1	-
940128430	Cysteine synthase [Pseudomonas syringae pv. helianthi]	-	-	1	-
95109378	putative ATP-dependent DNA helicase Lhr [Pseudomonas entomophila L48]	-	-	1	-
346055813	probable metallo-oxidoreductase [Pseudomonas aeruginosa NCMG1179]	-	-	1	-
940724550	azurin [Pseudomonas endophytica]	-	-	1	-
667953932	NADH dehydrogenase [Pseudomonas mendocina S5.2]	1	1	1	-
940309410	hypothetical protein ALO41_02922 [Pseudomonas amygdali pv. ulmi]	-	-	1	-
374081525	Type IVA conjugal transfer protein virB7 (plasmid) [Pseudomonas savastanoi]	-	-	1	-
610706570	phosphonate metabolism PhnG [Pseudomonas pseudoalcaligenes AD6]	1	-	1	-
500243825	ATP-dependent helicase [Pseudomonas protegens CHA0]	-	-	1	-
568070961	membrane protein [Pseudomonas sp. M1]	-	-	1	-
660509991	cardiolipin synthetase [Pseudomonas aeruginosa PAO1H2O]	-	-	1	-

	water stress/hypersensitive response domain-containing protein [Pseudomonas aeruginosa]	-	-	1	-
928535720	Branched-chain amino acid ABC transporter, periplasmic amino acid-binding protein [Pseudomonas syringae pv. atrofaciens]	-	-	1	-
939987533	transcriptional xre family [Pseudomonas sp. Os17]	-	-	1	-
771844501	flagellar protein FlaG protein [Pseudomonas plecoglossicida NB2011]	-	-	1	-
511102221	general secretion pathway protein GspE [Pseudomonas mediterranea CFBP 5447]	-	-	1	-
713118311	thiol:disulfide interchange protein precursor [Pseudomonas stutzeri ATCC 14405 = CCUG 16156]	-	-	1	-
379063226	cytoplasmic protein [Pseudomonas syringae pv. syringae B728a]	-	-	1	-
66047267	hypothetical protein VC34_14370 [Pseudomonas fluorescens]	-	-	1	-
799198253	2-nitropropane dioxygenase [Pseudomonas pseudoalcaligenes AD6]	-	-	1	-
610708426	Glyceraldehyde-3-phosphate dehydrogenase 3 [Pseudomonas fluorescens]	-	-	1	-
757244124	hypothetical protein PstZobell_03211 [Pseudomonas stutzeri ATCC 14405 = CCUG 16156]	-	-	1	-
379063691	hypothetical protein N619_24525 [Pseudomonas pseudoalcaligenes]	1	-	1	-
782984588	hypothetical protein PSA5_05160 [Pseudomonas syringae pv. actinidiae]	-	-	1	-
913050000	hypothetical protein PF66_03169 [Pseudomonas fuscovaginae]	-	-	1	-
928205630	hypothetical protein PP_3411 [Pseudomonas putida KT2440]	-	-	1	-
26990124	DNA primase [Pseudomonas alcaligenes NBRC 14159]	-	-	1	-
543436157	Glycerophosphoryl diester phosphodiesterase [Pseudomonas syringae pv. alisalensis]	-	-	1	-
939992149	membrane protein [Pseudomonas pseudoalcaligenes]	-	-	1	-
782986828	putative transposase [Pseudomonas stutzeri ATCC 14405 = CCUG 16156]	-	-	1	-
379064634		-	-	1	-

	hypothetical protein AA957_27165				
902692278	[Pseudomonas trivialis]	-	-	1	-
	chemotaxis protein CheY [Pseudomonas				
751083447	stutzeri]	-	-	1	-
	AraC family transcriptional regulator				
327482266	[Pseudomonas stutzeri DSM 4166]	-	-	1	-
	RNA polymerase sigma factor SigX				
26988813	[Pseudomonas putida KT2440]	-	-	1	-
	hypothetical protein AN459_27330				
953199534	[Pseudomonas aeruginosa]	-	-	1	-
	arginine succinyltransferase				
928202380	[Pseudomonas fuscovaginae]	-	-	1	-
	hypothetical protein DA83_23045				
912968066	[Pseudomonas sp. 250J]	-	-	1	-
	Gluconolactonase [Pseudomonas				
940101697	amygdali pv. erioobotryae]	-	-	1	-
	biofilm formation protein PelB				
771849181	[Pseudomonas sp. St29]	-	-	1	-
	ribosomal protein S6 modification protein				
782984594	[Pseudomonas pseudoalcaligenes]	1	1	1	-
	Hemoglobin subunit alpha OS=Homo				
P69905	sapiens GN=HBA1 PE=1 SV=2	1	-	1	-
	DNA mismatch repair protein MutT				
610709093	[Pseudomonas pseudoalcaligenes AD6]	1	-	1	-
	oxidoreductase [Pseudomonas				
733394902	frederiksbergensis]	-	-	1	-
	putative FkbP-type peptidyl-prolyl cis-				
848256913	trans isomerase [Pseudomonas stutzeri]	-	-	1	-
	hydroxydechloroatrazine				
	ethylaminohydrolase [Pseudomonas				
752311602	plecoglossicida]	-	-	1	-
	hypothetical protein TU74_05735				
856775235	[Pseudomonas lundensis]	-	-	1	-
	competence/damage-inducible protein				
	CinA-likeprotein [Pseudomonas sp. MT-				
699967183	1]	-	-	1	-
	hydrogenase [Pseudomonas				
610715084	pseudoalcaligenes AD6]	-	1	1	-
	putative chemotaxis protein CheW				
699965486	[Pseudomonas sp. MT-1]	-	-	1	-
	50S ribosomal protein L34 [Pseudomonas				
9951911	aeruginosa PAO1]	-	-	1	-
799217506	porin [Pseudomonas fluorescens]	-	-	1	-
	hypothetical protein AA303_03865				
925647298	[Pseudomonas psychrophila]	-	-	1	-

	hypothetical protein ACR52_16045				
873533680	[Pseudomonas sp. KG01]	-	-	1	-
	phosphoesterase [Pseudomonas				
564833263	aeruginosa VRFP07]	-	-	1	-
	hypothetical protein VC34_26650				
799191782	[Pseudomonas fluorescens]	-	-	1	-
	uncharacterized protein POS17_0640				
771840547	[Pseudomonas sp. Os17]	-	-	1	-
	Homoserine/homoserine lactone efflux				
749476366	protein [Pseudomonas fluorescens]	-	-	1	-
949201598	hemagglutinin [Pseudomonas orientalis]	1	-	1	-
	peptide synthetase [Pseudomonas sp.				
929888625	RIT-PI-o]	-	-	1	-
	elongation factor G [Pseudomonas sp.				
556075566	VLB120]	1	1	-	-
	hypothetical protein ACS96_31000,				
861344790	partial [Pseudomonas aeruginosa]	1	1	-	-
	protein disaggregation chaperone, partial				
733473544	[Pseudomonas putida]	-	1	-	-
	Aconitate hydratase 2, 2-methylisocitrate				
748444887	dehydratase [Pseudomonas batumici]	-	1	-	-
	chaperonin GroEL [Pseudomonas stutzeri				
395809569	DSM 10701]	-	1	-	-
	elongation factor Tu [Pseudomonas				
667951068	mendocina S5.2]	-	1	-	-
	translation elongation factor Tu				
576707100	[Pseudomonas sp. GM41(2012)]	-	1	-	-
	elongation factor Tu [Pseudomonas				
331018158	amygdali pv. lachrymans str. M302278]	-	1	-	-
	succinyl-CoA synthetase subunit beta				
747150682	[Pseudomonas balearica DSM 6083]	-	1	-	-
	polynucleotide				
	phosphorylase/polyadenylase				
756408424	[Pseudomonas fluorescens]	-	1	-	-
	DNA-directed RNA polymerase subunit				
763481886	beta' [Pseudomonas oryzihabitans]	-	1	-	-
	hypothetical protein PstZobell_00472,				
	partial [Pseudomonas stutzeri ATCC				
379063152	14405 = CCUG 16156]	1	1	-	-
	NAD-specific glutamate dehydrogenase				
631780690	[Pseudomonas knackmussii B13]	-	1	-	-
	flagellar basal body rod protein FlgF				
782987014	[Pseudomonas pseudoalcaligenes]	1	1	-	-
	flagellar rod assembly protein FlgJ				
751049064	[Pseudomonas sp. W15Feb9B]	-	1	-	-

856797097	glycine dehydrogenase [<i>Pseudomonas weihenstephanensis</i>]	-	1	-	-
331022078	flagellin [<i>Pseudomonas coronafaciens</i> pv. <i>oryzae</i> str. 1_6]	1	1	-	-
26987205	50S ribosomal protein L14 [<i>Pseudomonas putida</i> KT2440]	-	1	-	-
452009094	isocitrate dehydrogenase [<i>Pseudomonas stutzeri</i> NF13]	1	1	-	-
667952824	50S ribosomal protein L25 [<i>Pseudomonas mendocina</i> S5.2]	-	1	-	-
229360807	probable alcohol dehydrogenase [<i>Pseudomonas fluorescens</i> SBW25]	-	1	-	-
699968415	carbamoylphosphate synthetase large subunit [<i>Pseudomonas</i> sp. MT-1]	-	1	-	-
684199428	50S ribosomal protein L6 [<i>Pseudomonas mosselii</i> SJ10]	-	1	-	-
26987340	isoleucyl-tRNA synthetase [<i>Pseudomonas putida</i> KT2440]	-	1	-	-
404306144	isoleucyl-tRNA synthetase [<i>Pseudomonas fluorescens</i> R124]	-	1	-	-
799223384	ABC transporter substrate-binding protein [<i>Pseudomonas fluorescens</i>]	-	1	-	-
161378146	30S ribosomal protein S3 [<i>Pseudomonas putida</i> KT2440]	1	1	-	-
747150679	2-oxoglutarate dehydrogenase [<i>Pseudomonas balearica</i> DSM 6083]	-	1	-	-
735692048	ferritin [<i>Pseudomonas tuomuerensis</i>]	-	1	-	-
568072010	transketolase [<i>Pseudomonas</i> sp. M1]	-	1	-	-
949203443	dihydrolipoamide acetyltransferase [<i>Pseudomonas orientalis</i>]	-	1	-	-
747152569	dihydrolipoamide acetyltransferase [<i>Pseudomonas balearica</i> DSM 6083]	-	1	-	-
631780982	hypothetical protein PKB_4131 [<i>Pseudomonas knackmussii</i> B13]	-	1	-	-
763482577	flagellar basal body rod protein FlgG [<i>Pseudomonas oryzae</i> habitans]	-	1	-	-
543437460	lysine--tRNA ligase [<i>Pseudomonas alcaligenes</i> NBRC 14159]	1	1	-	-
928204263	DNA gyrase, A subunit [<i>Pseudomonas fuscovaginae</i>]	1	1	-	-
568073549	DNA gyrase subunit A [<i>Pseudomonas</i> sp. M1]	1	1	-	-
395809590	preprotein translocase subunit SecA [<i>Pseudomonas stutzeri</i> DSM 10701]	1	1	-	-
568075961	isocitrate dehydrogenase [<i>Pseudomonas</i> sp.]	-	1	-	-

	sp. M1]				
	3-oxoacyl-ACP synthase [Pseudomonas				
684197226	mosselii SJ10]	-	1	-	-
	S-adenosyl-L-homocysteine hydrolase				
126169267	[Pseudomonas aeruginosa C3719]	-	1	-	-
	conserved hypothetical protein				
126168746	[Pseudomonas aeruginosa C3719]	-	1	-	-
	glyceraldehyde-3-phosphate				
	dehydrogenase [Pseudomonas putida				
471350719	LS46]	1	1	-	-
	formaldehyde dehydrogenase,				
	glutathione-independent [Pseudomonas				
510314399	sp. G5(2012)]	-	1	-	-
	isocitrate lyase [Pseudomonas stutzeri				
327480917	DSM 4166]	-	1	-	-
	isocitrate lyase [Pseudomonas balearica				
747151052	DSM 6083]	1	1	-	-
	proline--tRNA ligase [Pseudomonas				
782985537	pseudoalcaligenes]	1	1	-	-
	pyruvate carboxylase subunit B				
459962932	[Pseudomonas sp. Lz4W]	1	1	-	-
	Pyruvate carboxylase subunit B				
	[Pseudomonas savastanoi pv.				
928279327	phaseolicola]	-	1	-	-
	inosine-5-monophosphate dehydrogenase				
782986244	[Pseudomonas pseudoalcaligenes]	1	1	-	-
	Inosine-5'-monophosphate dehydrogenase				
757243180	[Pseudomonas fluorescens]	1	1	-	-
	inosine-5-monophosphate dehydrogenase				
763480578	[Pseudomonas oryzihabitans]	1	1	-	-
	GMP synthase [Pseudomonas				
763480579	oryzihabitans]	-	1	-	-
	Acetyl-CoA carboxylase biotin				
	carboxylase subunit [Pseudomonas				
940188183	amygdali pv. mori]	1	1	-	-
	acetyl-CoA carboxylase [Pseudomonas				
929903958	sp. RIT-PI-q]	-	1	-	-
	transcription elongation factor NusA				
735691608	[Pseudomonas tuomuerensis]	-	1	-	-
	urocanate hydratase [Pseudomonas				
820918799	putida]	-	1	-	-
	heat shock protein 90 [Pseudomonas				
66045257	syringae pv. syringae B728a]	-	1	-	-
	Oligopeptidase A [Pseudomonas				
631776986	knackmussii B13]	-	1	-	-

543435665	50S ribosomal protein L21 [Pseudomonas alcaligenes NBRC 14159]	1	1	-	-
928534389	50S ribosomal protein L21 [Pseudomonas aeruginosa]	-	1	-	-
928539718	sulfite reductase [Pseudomonas aeruginosa]	1	1	-	-
928485731	alanyl-tRNA synthetase [Pseudomonas psychrophila]	-	1	-	-
929896344	3-phosphoshikimate 1- carboxyvinyltransferase [Pseudomonas sp. RIT-PI-q]	-	1	-	-
443284491	Electron transfer flavoprotein, alpha subunit [Pseudomonas syringae pv. syringae B64]	-	1	-	-
735691579	glutamyl-tRNA amidotransferase [Pseudomonas tuomuerensis]	-	1	-	-
327479577	aspartyl/glutamyl-tRNA amidotransferase subunit A [Pseudomonas stutzeri DSM 4166]	-	1	-	-
667955211	valyl-tRNA synthetase [Pseudomonas mendocina S5.2]	-	1	-	-
782984424	succinate-semialdehyde dehydrogenase [Pseudomonas pseudoalcaligenes]	1	1	-	-
820906775	succinate-semialdehyde dehydrogenase [Pseudomonas putida]	-	1	-	-
940040381	Succinate-semialdehyde dehydrogenase [Pseudomonas cannabina]	-	1	-	-
799189025	3-oxoacyl-ACP reductase [Pseudomonas fluorescens]	-	1	-	-
556072865	GTP-binding protein TypA [Pseudomonas sp. VLB120]	1	1	-	-
543435907	50S ribosomal protein L2 [Pseudomonas alcaligenes NBRC 14159]	-	1	-	-
667953543	cysteine synthase [Pseudomonas mendocina S5.2]	1	1	-	-
763480531	2-isopropylmalate synthase [Pseudomonas oryzae]	-	1	-	-
953170253	carbon-nitrogen hydrolase [Pseudomonas aeruginosa]	-	1	-	-
610712027	glutamate--tRNA ligase [Pseudomonas pseudoalcaligenes AD6]	1	1	-	-
684199356	serine/threonine protein kinase [Pseudomonas mosselii SJ10]	-	1	-	-
379065498	PrkA family serine protein kinase [Pseudomonas stutzeri ATCC 14405 =	-	1	-	-

	CCUG 16156]				
	phosphoribosylamine--glycine ligase				
327481995	[Pseudomonas stutzeri DSM 4166]	-	1	-	-
	dihydroxy-acid dehydratase				
667951319	[Pseudomonas mendocina S5.2]	1	1	-	-
	argininosuccinate synthase [Pseudomonas				
667953123	mendocina S5.2]	1	1	-	-
	Bifunctional purine biosynthesis protein				
631782007	PurH [Pseudomonas knackmussii B13]	-	1	-	-
	50S ribosomal protein L17 [Pseudomonas				
229364743	fluorescens SBW25]	1	1	-	-
	histidine ammonia-lyase [Pseudomonas				
667951178	mendocina S5.2]	-	1	-	-
	putative enoyl-CoA hydratase				
757242554	[Pseudomonas fluorescens]	-	1	-	-
	DNA-binding protein [Pseudomonas				
692342644	rhizosphaerae]	-	1	-	-
	flagellar hook protein FlgE [Pseudomonas				
395807940	stutzeri DSM 10701]	1	1	-	-
	50S ribosomal protein L3 [Pseudomonas				
735689912	tuomuerensis]	-	1	-	-
	argininosuccinate lyase [Pseudomonas				
543438726	alcaligenes NBRC 14159]	-	1	-	-
	30S ribosomal protein S19 [Pseudomonas				
610713843	pseudoalcaligenes AD6]	-	1	-	-
	heat shock protein Hsp20 [Pseudomonas				
565412902	moraviensis R28-S]	1	1	-	-
	translation initiation factor IF-3				
763478717	[Pseudomonas oryzihabitans]	-	1	-	-
	seryl-tRNA synthetase [Pseudomonas				
667953960	mendocina S5.2]	-	1	-	-
	exonuclease SbcC [Pseudomonas stutzeri				
395809927	DSM 10701]	-	1	-	-
	histidinol dehydrogenase [Pseudomonas				
782985162	pseudoalcaligenes]	1	1	-	-
	histidinol-phosphate aminotransferase				
934021397	[Pseudomonas viridiflava]	-	1	-	-
	aldehyde dehydrogenase [Pseudomonas				
692345349	rhizosphaerae]	1	1	-	-
	polyphosphate kinase [Pseudomonas				
660509839	aeruginosa PAO1H2O]	1	1	-	-
	polyphosphate kinase [Pseudomonas				
648454655	thermotolerans]	-	1	-	-
	serine hydroxymethyltransferase				
667953066	[Pseudomonas mendocina S5.2]	1	1	-	-

	hypothetical protein CL52_08915				
747150796	[<i>Pseudomonas balearica</i> DSM 6083]	-	1	-	-
	recombination associated protein				
556073713	[<i>Pseudomonas</i> sp. VLB120]	1	1	-	-
	chaperone protein HscA [<i>Pseudomonas</i>				
610710496	<i>pseudoalcaligenes</i> AD6]	-	1	-	-
	chaperone protein HscA [<i>Pseudomonas</i>				
459960804	sp. Lz4W]	-	1	-	-
	spermidine/putrescine ABC transporter				
	substrate-binding protein [<i>Pseudomonas</i>				
568071573	sp. M1]	-	1	-	-
	hypothetical protein ALO53_200180				
940160871	[<i>Pseudomonas amygdali</i> pv. <i>photiniae</i>]	-	1	-	-
	arginine deiminase [<i>Pseudomonas</i>				
564892050	<i>aeruginosa</i> VRFP06]	-	1	-	-
	arginine deiminase [<i>Pseudomonas</i> sp.				
641464898	P482]	-	1	-	-
	heat shock protein GrpE [<i>Pseudomonas</i>				
610711189	<i>pseudoalcaligenes</i> AD6]	-	1	-	-
	diaminopimelate decarboxylase				
610713639	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	-
	diaminopimelate decarboxylase				
327479175	[<i>Pseudomonas stutzeri</i> DSM 4166]	1	1	-	-
	major outer membrane lipoprotein I,				
335389923	partial [<i>Pseudomonas argentinensis</i>]	-	1	-	-
	Peptidyl-prolyl cis-trans isomerase				
939990767	[<i>Pseudomonas syringae</i> pv. <i>aceris</i>]	-	1	-	-
	phosphoglyceromutase [<i>Pseudomonas</i>				
927288104	<i>syringae</i> UMAF0158]	-	1	-	-
	dihydrodipicolinate synthase				
763481301	[<i>Pseudomonas oryzihabitans</i>]	1	1	-	-
	alkyl hydroperoxide reductase subunit F,				
	partial [<i>Pseudomonas stutzeri</i> ATCC				
379063791	14405 = CCUG 16156]	-	1	-	-
	alkyl hydroperoxide reductase				
735691137	[<i>Pseudomonas tuomuerensis</i>]	-	1	-	-
	putative Zinc-dependent peptidase, M48				
95109114	family [<i>Pseudomonas entomophila</i> L48]	-	1	-	-
	DNA ligase [<i>Pseudomonas syringae</i> pv.				
939983271	<i>aceris</i>]	-	1	-	-
	acetylglutamate kinase [<i>Pseudomonas</i> sp.				
568072273	M1]	1	1	-	-
	glycyl-tRNA synthetase subunit beta				
26986805	[<i>Pseudomonas putida</i> KT2440]	-	1	-	-
949183519	glycine-tRNA synthetase subunit beta	-	1	-	-

	[<i>Pseudomonas poae</i>]				
	phosphoribosylaminoimidazole- succinocarboxamide synthase				
667954593	[<i>Pseudomonas mendocina</i> S5.2]	1	1	-	-
	PTS fructose transporter subunit IIA				
667952615	[<i>Pseudomonas mendocina</i> S5.2]	-	1	-	-
	MaoC domain-containing protein				
327482419	[<i>Pseudomonas stutzeri</i> DSM 4166]	-	1	-	-
	3-methylcrotonyl-CoA carboxylase				
751084600	[<i>Pseudomonas stutzeri</i>]	-	1	-	-
	3-methylcrotonyl-CoA carboxylase				
610711736	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	-
	inorganic pyrophosphatase [<i>Pseudomonas</i>				
213925990	<i>syringae</i> pv. <i>tomato</i> T1]	-	1	-	-
	acetyl-CoA acetyltransferase				
780910519	[<i>Pseudomonas</i> sp. BICA1-14]	-	1	-	-
	acetyl-CoA acetyltransferase				
799188176	[<i>Pseudomonas fluorescens</i>]	-	1	-	-
	acyl-CoA dehydrogenase [<i>Pseudomonas</i>				
689664327	<i>fluorescens</i> LMG 5329]	-	1	-	-
	acyl-CoA dehydrogenase [<i>Pseudomonas</i>				
953170983	<i>aeruginosa</i>]	-	1	-	-
	30S ribosomal protein S15 [<i>Pseudomonas</i>				
565415531	<i>moraviensis</i> R28-S]	-	1	-	-
	hypothetical protein DA83_11575				
912970078	[<i>Pseudomonas</i> sp. 250J]	-	1	-	-
	acetolactate synthase 3 regulatory subunit				
782989582	[<i>Pseudomonas pseudoalcaligenes</i>]	1	1	-	-
	thiosulfate transporter subunit				
667951411	[<i>Pseudomonas mendocina</i> S5.2]	1	1	-	-
	toluene tolerance protein [<i>Pseudomonas</i>				
782985157	<i>pseudoalcaligenes</i>]	-	1	-	-
	Phosphate regulon transcriptional regulatory protein PhoB (SphR)				
758835766	[<i>Pseudomonas</i> sp. FeS53a]	-	1	-	-
	acetylornithine aminotransferase				
551052983	[<i>Pseudomonas putida</i> SJ3]	-	1	-	-
	betaine aldehyde dehydrogenase BADH				
213927561	[<i>Pseudomonas syringae</i> pv. <i>tomato</i> T1]	-	1	-	-
	threonine aldolase [<i>Pseudomonas</i>				
782989906	<i>pseudoalcaligenes</i>]	-	1	-	-
	threonine aldolase, low-specificity				
771844480	[<i>Pseudomonas</i> sp. Os17]	-	1	-	-
	RNA polymerase subunit sigma-70				
856762083	[<i>Pseudomonas taetrolens</i>]	-	1	-	-

	hypothetical protein O162_20920				
551050848	[Pseudomonas putida SJ3]	-	1	-	-
	peptide ABC transporter substrate-binding protein [Pseudomonas				
733393887	frederiksborgensis]	-	1	-	-
	2-nitropropane dioxygenase				
787852971	[Pseudomonas chlororaphis]	-	1	-	-
	DNA gyrase subunit B [Pseudomonas				
126169684	aeruginosa C3719]	1	1	-	-
	DNA gyrase, B subunit [Pseudomonas sp.				
426265136	UW4]	-	1	-	-
	protein-disulfide isomerase				
610709109	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
902690849	cupin [Pseudomonas trivialis]	-	1	-	-
	protease TldD [Pseudomonas				
782985135	pseudoalcaligenes]	-	1	-	-
	S-adenosylmethionine synthetase				
758834815	[Pseudomonas sp. FeS53a]	-	1	-	-
	aldo/keto reductase [Pseudomonas				
782985179	pseudoalcaligenes]	1	1	-	-
	cysteinyl-tRNA synthetase [Pseudomonas				
735693072	tuomuerensis]	1	1	-	-
	cysteinyl-tRNA synthetase [Pseudomonas				
816237732	stutzeri]	-	1	-	-
	indole-3-glycerol-phosphate synthase				
543436124	[Pseudomonas alcaligenes NBRC 14159]	1	1	-	-
	TetR family transcriptional regulator				
684195389	[Pseudomonas mosselii SJ10]	-	1	-	-
	carbamoyl phosphate synthase small				
	subunit [Pseudomonas pseudoalcaligenes				
610711185	AD6]	1	1	-	-
	ribose-phosphate pyrophosphokinase				
	(Phosphoribosyl pyrophosphate				
	synthetase) [Pseudomonas entomophila				
95109072	L48]	-	1	-	-
	RNA-binding transcriptional accessory				
515930042	protein [Pseudomonas mendocina]	-	1	-	-
	transcription accessory protein				
755317807	[Pseudomonas fulva]	-	1	-	-
	RNA-binding transcriptional accessory				
639538673	protein [Pseudomonas syringae]	-	1	-	-
	RNA polymerase sigma-H factor				
610711463	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
	phospho-2-dehydro-3-deoxyheptonate				
610708308	aldolase [Pseudomonas pseudoalcaligenes	-	1	-	-

	AD6]				
	chemotaxis protein CheA [Pseudomonas				
610709522	pseudoalcaligenes AD6]	1	1	-	-
	CysB family transcriptional regulator				
667954177	[Pseudomonas mendocina S5.2]	-	1	-	-
	putative ABC-type amino acid transport				
	protein, periplasmic component				
115588506	[Pseudomonas aeruginosa UCBPP-PA14]	-	1	-	-
	amino acid ABC transporter substrate-				
	binding protein [Pseudomonas mendocina				
667954095	S5.2]	-	1	-	-
	DNA polymerase III subunit beta				
543436066	[Pseudomonas alcaligenes NBRC 14159]	-	1	-	-
	elongation factor 4 [Pseudomonas putida				
512381984	NBRC 14164]	-	1	-	-
	GTP-binding protein [Pseudomonas				
610709720	pseudoalcaligenes AD6]	-	1	-	-
763481983	thioredoxin [Pseudomonas oryzihabitans]	-	1	-	-
	short-chain dehydrogenase [Pseudomonas				
610712064	pseudoalcaligenes AD6]	-	1	-	-
	fumarate and nitrate reduction regulatory				
	protein [Pseudomonas fluorescens				
229363842	SBW25]	-	1	-	-
	peptidylprolyl isomerase [Pseudomonas				
667953038	mendocina S5.2]	1	1	-	-
	phosphate ABC transporter ATP-binding				
940722383	protein [Pseudomonas endophytica]	-	1	-	-
	exoribonuclease R [Pseudomonas				
730590999	parafulva]	-	1	-	-
	exoribonuclease R [Pseudomonas				
713118193	mediterranea CFBP 5447]	-	1	-	-
641463031	ribonuclease R [Pseudomonas sp. P482]	1	1	-	-
	ATP phosphoribosyltransferase catalytic				
782985161	subunit [Pseudomonas pseudoalcaligenes]	1	1	-	-
	3,4-dihydroxy-2-butanone 4-phosphate				
	synthase [Pseudomonas balearica DSM				
747152365	6083]	-	1	-	-
	chemotaxis protein CheY [Pseudomonas				
782984590	pseudoalcaligenes]	-	1	-	-
	two-component response regulator OmpR				
126170034	[Pseudomonas aeruginosa C3719]	-	1	-	-
	imidazoleglycerol-phosphate dehydratase				
610710200	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
	RNA helicase [Pseudomonas				
610714014	pseudoalcaligenes AD6]	-	1	-	-

	RNA helicase [Pseudomonas mendocina				
667954115	S5.2]	-	1	-	-
	delta-aminolevulinic acid dehydratase				
782984506	[Pseudomonas pseudoalcaligenes]	-	1	-	-
404305467	TatD [Pseudomonas fluorescens R124]	-	1	-	-
	FAD linked oxidase domain protein				
387159720	[Pseudomonas fluorescens A506]	1	1	-	-
	DNA-directed RNA polymerase subunit				
	omega [Pseudomonas stutzeri DSM				
395810125	10701]	-	1	-	-
	CoA-transferase [Pseudomonas				
782983958	pseudoalcaligenes]	-	1	-	-
	hypothetical protein DW68_10995				
667953048	[Pseudomonas mendocina S5.2]	-	1	-	-
	3-dehydroquinate dehydratase				
426265685	[Pseudomonas sp. UW4]	-	1	-	-
	leucyl aminopeptidase [Pseudomonas				
26987716	putida KT2440]	-	1	-	-
	Tryptophanyl-tRNA synthetase				
	[Pseudomonas syringae pv. syringae str.				
590455813	B301D-R]	-	1	-	-
	transcriptional regulator [Pseudomonas				
667954877	mendocina S5.2]	-	1	-	-
	1,2-oxophytodienoate reductase				
667952773	[Pseudomonas mendocina S5.2]	-	1	-	-
	FKBP-type peptidyl-prolyl cis-trans				
	isomerase [Pseudomonas stutzeri ATCC				
379067130	14405 = CCUG 16156]	-	1	-	-
	tricarboxylic transport membrane protein				
667953186	[Pseudomonas mendocina S5.2]	1	1	-	-
	membrane protein [Pseudomonas				
782985744	pseudoalcaligenes]	-	1	-	-
	phosphoribosylaminoimidazole				
	synthetase [Pseudomonas				
610713341	pseudoalcaligenes AD6]	1	1	-	-
	phosphoribosylaminoimidazole				
735692026	synthetase [Pseudomonas tuomuerensis]	-	1	-	-
	ATP phosphoribosyltransferase				
	regulatory subunit [Pseudomonas				
667952434	mendocina S5.2]	-	1	-	-
	arabinose 5-phosphate isomerase				
	[Pseudomonas amygdali pv. aesculi str.				
330869986	0893_23]	-	1	-	-
	threonine aldolase [Pseudomonas				
667951239	mendocina S5.2]	-	1	-	-

543436495	L-threonine aldolase [Pseudomonas alcaligenes NBRC 14159]	-	1	-	-
213924484	biotin carboxylase/biotin carboxyl carrier protein [Pseudomonas syringae pv. tomato T1]	-	1	-	-
667953457	fumarate hydratase [Pseudomonas mendocina S5.2]	-	1	-	-
543439661	agmatine deiminase [Pseudomonas alcaligenes NBRC 14159]	-	1	-	-
430794317	hypothetical protein B479_18100 [Pseudomonas putida HB3267]	-	1	-	-
543438995	ribosomal RNA large subunit methyltransferase K/L [Pseudomonas alcaligenes NBRC 14159]	-	1	-	-
733471041	ribonuclease PH [Pseudomonas putida]	1	1	-	-
543437716	tryptophan synthase beta chain [Pseudomonas alcaligenes NBRC 14159]	-	1	-	-
667953802	enoyl-CoA hydratase [Pseudomonas mendocina S5.2]	1	1	-	-
856745880	enoyl-CoA hydratase [Pseudomonas deceptionensis]	-	1	-	-
610714882	Skp [Pseudomonas pseudoalcaligenes AD6]	1	1	-	-
610711176	triosephosphate isomerase [Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
949218052	cold-shock protein [Pseudomonas veronii]	-	1	-	-
28852820	ribosomal protein L20 [Pseudomonas syringae pv. tomato str. DC3000]	-	1	-	-
689663960	2-dehydro-3-deoxyphosphooctonate aldolase [Pseudomonas fluorescens LMG 5329]	-	1	-	-
430791968	oxidoreductase FAD/NAD(P)-binding subunit [Pseudomonas putida HB3267]	-	1	-	-
126168250	D-serine dehydratase [Pseudomonas aeruginosa C3719]	-	1	-	-
782987622	short-chain dehydrogenase [Pseudomonas pseudoalcaligenes]	-	1	-	-
799200525	UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase [Pseudomonas fluorescens]	-	1	-	-
543437274	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B [Pseudomonas alcaligenes NBRC 14159]	-	1	-	-
379064002	aspartyl/glutamyl-tRNA amidotransferase subunit B [Pseudomonas stutzeri ATCC	-	1	-	-

	14405 = CCUG 16156]				
	membrane protein [Pseudomonas				
610708079	pseudoalcaligenes AD6]	-	1	-	-
	lipoprotein [Pseudomonas				
782987799	pseudoalcaligenes]	-	1	-	-
	flavodoxin [Pseudomonas				
610709261	pseudoalcaligenes AD6]	-	1	-	-
	carboxynorspermidine decarboxylase				
	[Pseudomonas stutzeri ATCC 14405 =				
379064372	CCUG 16156]	-	1	-	-
	secretin [Pseudomonas				
782987842	pseudoalcaligenes]	-	1	-	-
	transcriptional regulator [Pseudomonas				
782986586	pseudoalcaligenes]	1	1	-	-
	peptidylprolyl isomerase [Pseudomonas				
610707781	pseudoalcaligenes AD6]	-	1	-	-
	chemotaxis transducer [Pseudomonas				
327480501	stutzeri DSM 4166]	-	1	-	-
	Methyl-accepting chemotaxis protein				
703406503	[Pseudomonas xanthomarina]	-	1	-	-
	aldehyde dehydrogenase [Pseudomonas				
756404093	fluorescens]	-	1	-	-
	phosphogluconate dehydratase				
787853853	[Pseudomonas chlororaphis]	-	1	-	-
	phosphogluconate dehydratase				
229364217	[Pseudomonas fluorescens SBW25]	-	1	-	-
	molybdate ABC transporter substrate-				
820906577	binding protein [Pseudomonas putida]	-	1	-	-
	ADP compounds hydrolase				
229359713	[Pseudomonas fluorescens SBW25]	-	1	-	-
	glutamate--cysteine ligase [Pseudomonas				
610708789	pseudoalcaligenes AD6]	-	1	-	-
	aminopeptidase [Pseudomonas				
610708629	pseudoalcaligenes AD6]	-	1	-	-
	membrane protein [Pseudomonas				
782984868	pseudoalcaligenes]	-	1	-	-
	choline dehydrogenase [Pseudomonas				
15600565	aeruginosa PAO1]	-	1	-	-
	hypothetical protein N619_15605				
782986303	[Pseudomonas pseudoalcaligenes]	-	1	-	-
	tyrosine--tRNA ligase, partial				
782988466	[Pseudomonas pseudoalcaligenes]	-	1	-	-
	aminomethyltransferase [Pseudomonas				
667953192	mendocina S5.2]	1	1	-	-
768547787	flagellar hook protein FlgL [Pseudomonas	1	1	-	-

	stutzeri]				
	Flagellar hook-associated protein FlgL				
758829264	[Pseudomonas sp. FeS53a]	-	1	-	-
	phosphoribosylaminoimidazole				
730590636	carboxylase [Pseudomonas parafulva]	-	1	-	-
	flagellar motor switch protein				
768455914	[Pseudomonas sp. ES3-33]	-	1	-	-
	ribonuclease activity regulator protein				
733471611	RraA [Pseudomonas putida]	-	1	-	-
	ribonuclease activity regulator protein				
691226847	RraA [Pseudomonas cremoricolorata]	-	1	-	-
	mannose-1-phosphate guanylyltransferase				
713115980	[Pseudomonas mediterranea CFBP 5447]	-	1	-	-
	N-methylproline demethylase				
953162611	[Pseudomonas aeruginosa]	1	1	-	-
	conserved hypothetical protein				
327478635	[Pseudomonas stutzeri DSM 4166]	-	1	-	-
	surface antigen protein, Rickettsia 17 kDa				
341580349	family [Pseudomonas protegens Pf-5]	1	1	-	-
	glucose-1-phosphate				
	thymidyltransferase [Pseudomonas				
667951383	mendocina S5.2]	-	1	-	-
	Imidazole glycerol phosphate synthase,				
	amidotransferase subunit [Pseudomonas				
443281711	syringae pv. syringae B64]	-	1	-	-
	50S ribosomal subunit protein L29				
95108750	[Pseudomonas entomophila L48]	-	1	-	-
	aminotransferase [Pseudomonas				
610710508	pseudoalcaligenes AD6]	1	1	-	-
	hypothetical protein TZ03_02375				
761894804	[Pseudomonas sp. 10-1B]	-	1	-	-
	TetR family transcriptional regulator				
782987614	[Pseudomonas pseudoalcaligenes]	-	1	-	-
	Outer membrane efflux protein TolC				
939996355	[Pseudomonas syringae pv. alisalensis]	-	1	-	-
	NAD(P)H-quinone oxidoreductase				
667954668	[Pseudomonas mendocina S5.2]	-	1	-	-
	RNA polymerase-associated protein				
937560378	RapA [Pseudomonas aeruginosa]	1	1	-	-
	chemotaxis protein CheY [Pseudomonas				
782987887	pseudoalcaligenes]	1	1	-	-
	3-oxoacyl-[acyl-carrier-protein] synthase				
	II [Pseudomonas alcaligenes NBRC				
543438171	14159]	1	1	-	-
610713082	LPS biosynthesis protein [Pseudomonas	-	1	-	-

	pseudoalcaligenes AD6]				
	TonB-dependent receptor [Pseudomonas				
816239875	stutzeri]	-	1	-	-
	aspartate carbamoyltransferase catalytic				
	subunit [Pseudomonas pseudoalcaligenes				
610708514	AD6]	-	1	-	-
	Scaffold protein for (4Fe-4S) cluster				
	assembly ApbC, MRP-like [Pseudomonas				
748441045	batumici]	-	1	-	-
	3-deoxy-D-manno-octulosonate 8-				
	phosphate phosphatase [Pseudomonas				
610712474	pseudoalcaligenes AD6]	-	1	-	-
	uracil phosphoribosyltransferase				
689659976	[Pseudomonas fluorescens LMG 5329]	1	1	-	-
	alanine aminotransferase AlaA				
543437002	[Pseudomonas alcaligenes NBRC 14159]	1	1	-	-
	conserved hypothetical protein				
229365223	[Pseudomonas fluorescens SBW25]	1	1	-	-
	UPF0701 protein [Pseudomonas				
631782498	knackmussii B13]	-	1	-	-
	acetolactate synthase 3 catalytic subunit				
667955281	[Pseudomonas mendocina S5.2]	1	1	-	-
	methylcitrate synthase [Pseudomonas				
782988922	pseudoalcaligenes]	-	1	-	-
	peptide chain release factor 2				
747150294	[Pseudomonas balearica DSM 6083]	-	1	-	-
	oxidative stress regulatory protein OxyR				
848254179	[Pseudomonas stutzeri]	1	1	-	-
	succinylarginine dihydrolase				
937309195	[Pseudomonas fluorescens]	-	1	-	-
	isovaleryl-CoA dehydrogenase				
782988774	[Pseudomonas pseudoalcaligenes]	-	1	-	-
799194930	cytochrome C [Pseudomonas fluorescens]	-	1	-	-
	GTP-binding protein [Pseudomonas				
782986224	pseudoalcaligenes]	-	1	-	-
	ATP F0F1 synthase subunit B				
782984129	[Pseudomonas pseudoalcaligenes]	-	1	-	-
	hypothetical protein DW68_17905				
667954364	[Pseudomonas mendocina S5.2]	-	1	-	-
	ribosomal protein L11 methyltransferase				
543437192	[Pseudomonas alcaligenes NBRC 14159]	-	1	-	-
	LuxR family transcriptional regulator				
610707221	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
	acetyltransferase [Pseudomonas				
667954184	mendocina S5.2]	-	1	-	-

782985328	lipid A 3-O-deacylase [Pseudomonas pseudoalcaligenes]	-	1	-	-
782984067	serine dehydratase [Pseudomonas pseudoalcaligenes]	-	1	-	-
782984989	hypothetical protein N619_26760 [Pseudomonas pseudoalcaligenes]	-	1	-	-
940255852	putative Lipoprotein [Pseudomonas amygdali pv. sesami]	-	1	-	-
126169301	twitching motility protein PilT [Pseudomonas aeruginosa C3719]	-	1	-	-
610709164	ornithine carbamoyltransferase [Pseudomonas pseudoalcaligenes AD6]	1	1	-	-
856781677	alcohol dehydrogenase [Pseudomonas psychrophila]	-	1	-	-
610714049	transporter [Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
782986688	cysteine sulfinatase [Pseudomonas pseudoalcaligenes]	-	1	-	-
782986691	succinyl-diaminopimelate aminotransferase [Pseudomonas pseudoalcaligenes]	1	1	-	-
782986533	NADPH quinone reductase MdaB [Pseudomonas pseudoalcaligenes]	1	1	-	-
782988145	phosphoenolpyruvate-protein phosphotransferase [Pseudomonas pseudoalcaligenes]	1	1	-	-
782984137	tRNA modification GTPase MnmE [Pseudomonas pseudoalcaligenes]	-	1	-	-
667953931	NADH:ubiquinone oxidoreductase [Pseudomonas mendocina S5.2]	1	1	-	-
782987709	cytochrome Cbb3 [Pseudomonas pseudoalcaligenes]	-	1	-	-
667954719	UDP-N-acetylglucosamine acyltransferase [Pseudomonas mendocina S5.2]	1	1	-	-
758829417	Acetyl-coenzyme A carboxyl transferase beta chain [Pseudomonas sp. FeS53a]	-	1	-	-
565414490	lytic transglycosylase [Pseudomonas moraviensis R28-S]	-	1	-	-
692344040	peptidase [Pseudomonas rhizosphaerae]	-	1	-	-
782989440	TetR family transcriptional regulator [Pseudomonas pseudoalcaligenes]	-	1	-	-
610712090	succinate dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
928214811	glutamine amidotransferase of	-	1	-	-

	anthranilate synthase or aminodeoxychorismate synthase [Pseudomonas fuscovaginae]				
	NUDIX hydrolase [Pseudomonas pseudoalcaligenes]	-	1	-	-
782987854	ABC transporter substrate-binding protein [Pseudomonas pseudoalcaligenes AD6]	1	1	-	-
610710294	dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
610710506	aspartate-semialdehyde dehydrogenase [Pseudomonas pseudoalcaligenes AD6]	1	1	-	-
610708097	GTP cyclohydrolase [Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
610709465	thiamine-phosphate pyrophosphorylase [Pseudomonas pseudoalcaligenes]	1	1	-	-
782989332	conjugal transfer protein [Pseudomonas putida]	-	1	-	-
758547084	Aromatic-amino-acid transaminase [Pseudomonas sp. GM41(2012)]	1	1	-	-
576705854	anthranilate synthase component I [Pseudomonas sp. MT-1]	-	1	-	-
699968876	anthranilate synthase component I [Pseudomonas alcaligenes NBRC 14159]	-	1	-	-
543436127	methenyltetrahydrofolate cyclohydrolase [Pseudomonas pseudoalcaligenes]	-	1	-	-
782988789	methenyltetrahydrofolate cyclohydrolase [Pseudomonas tuomuerensis]	-	1	-	-
735693105	heat shock protein HSP33 [Pseudomonas aeruginosa C3719]	-	1	-	-
126170041	DEAD/DEAH box helicase [Pseudomonas tuomuerensis]	-	1	-	-
735691225	membrane protease HflC [Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
610707863	imelysin [Pseudomonas pseudoalcaligenes]	-	1	-	-
782986403	chemotaxis protein CheY [Pseudomonas fluorescens]	-	1	-	-
749427763	16S rRNA methyltransferase [Pseudomonas mendocina S5.2]	-	1	-	-
667951718	DNA polymerase III subunit epsilon [Pseudomonas oryzihabitans]	-	1	-	-
763480466	MerR (plasmid) [Pseudomonas putida]	-	1	-	-
257070349	SpoVR family protein [Pseudomonas pseudoalcaligenes]	-	1	-	-
782988527	hypothetical protein N619_23870	-	1	-	-
782984465		-	1	-	-

	[<i>Pseudomonas pseudoalcaligenes</i>]				
	PA5285-like protein [<i>Pseudomonas</i>				
19033139	stutzeri A15]	-	1	-	-
667953941	cupin [<i>Pseudomonas mendocina</i> S5.2]	-	1	-	-
	glycine cleavage system protein T				
782984546	[<i>Pseudomonas pseudoalcaligenes</i>]	-	1	-	-
	aconitate hydratase [<i>Pseudomonas</i>				
610708331	pseudoalcaligenes AD6]	-	1	-	-
	ADP-ribose pyrophosphatase				
928485759	[<i>Pseudomonas psychrophila</i>]	-	1	-	-
	flagellar biosynthesis protein FlgN				
667954527	[<i>Pseudomonas mendocina</i> S5.2]	-	1	-	-
	nicotinate-nucleotide pyrophosphorylase				
666087085	[<i>Pseudomonas fluorescens</i>]	-	1	-	-
	membrane protein [<i>Pseudomonas</i>				
667954723	mendocina S5.2]	-	1	-	-
	GntR family transcriptional regulator				
544278987	[<i>Pseudomonas putida</i> LF54]	-	1	-	-
	hypothetical protein ADJ52_15505				
881082676	[<i>Pseudomonas aeruginosa</i>]	-	1	-	-
	ABC transporter ATP-binding protein				
667954264	[<i>Pseudomonas mendocina</i> S5.2]	-	1	-	-
	periplasmic tricarboxylate-binding				
	receptor, TTT family [<i>Pseudomonas</i>				
68343117	protegens Pf-5]	-	1	-	-
	poly(hydroxyalkanoate) granule-				
	associated protein [<i>Pseudomonas</i>				
730590881	parafulva]	-	1	-	-
	Signal recognition particle-docking				
	protein FtsY [<i>Pseudomonas syringae</i> pv.				
940279127	tagetis]	-	1	-	-
	succinylglutamate-semialdehyde				
	dehydrogenase [<i>Pseudomonas</i>				
610709872	pseudoalcaligenes AD6]	-	1	-	-
	octaprenyl-diphosphate synthase				
610714337	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	-	-
	glycerol-3-phosphate dehydrogenase				
856793394	[<i>Pseudomonas weihenstephanensis</i>]	-	1	-	-
	glycerol-3-phosphate dehydrogenase				
686656464	[<i>Pseudomonas aeruginosa</i>]	-	1	-	-
	ATP-NAD kinase [<i>Pseudomonas</i>				
610712078	pseudoalcaligenes AD6]	-	1	-	-
	dihydroorotase [<i>Pseudomonas</i>				
799221433	fluorescens]	-	1	-	-
610707205	methylglyoxal synthase [<i>Pseudomonas</i>	1	1	-	-

	pseudoalcaligenes AD6]				
	flagellar hook capping - N-terminal				
	region family protein [Pseudomonas sp.				
641464468	P482]	1	1	-	-
	proline iminopeptidase [Pseudomonas				
733470991	putida]	-	1	-	-
	50S ribosomal protein L31 [Pseudomonas				
747149618	balearica DSM 6083]	-	1	-	-
825577898	porin [Pseudomonas sp. TJI-51]	1	1	-	-
	hypothetical protein ALO88_04817				
940023220	[Pseudomonas syringae pv. antirrhini]	-	1	-	-
	cell division protein DedD [Pseudomonas				
763479137	oryzihabitans]	-	1	-	-
	Na(+)-translocating NADH-quinone				
	reductase subunit A [Pseudomonas				
667953326	mendocina S5.2]	-	1	-	-
	Tfp pilus assembly protein tip-				
	associated adhesin PilY1 [Pseudomonas				
699968708	sp. MT-1]	-	1	-	-
	phenylhydantoinase [Pseudomonas				
799220000	fluorescens]	1	1	-	-
	dinucleoside polyphosphate hydrolase				
327479072	[Pseudomonas stutzeri DSM 4166]	1	1	-	-
	recombination and repair protein				
667955341	[Pseudomonas mendocina S5.2]	-	1	-	-
	general secretion pathway protein GspE				
610712231	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
	general secretion pathway protein GspE				
733392188	[Pseudomonas frederiksbergensis]	-	1	-	-
	precorrin-8X methylmutase				
557561620	[Pseudomonas aeruginosa VRFPA05]	-	1	-	-
	ABC transporter ATPase [Pseudomonas				
610712878	pseudoalcaligenes AD6]	-	1	-	-
	serine peptidase [Pseudomonas				
782985775	pseudoalcaligenes]	-	1	-	-
	16S ribosomal RNA methyltransferase				
	KsgA/Dim1 family protein [Pseudomonas				
459960274	sp. Lz4W]	-	1	-	-
	hypothetical protein PSJM300_04310				
395807533	[Pseudomonas stutzeri DSM 10701]	-	1	-	-
	S-adenosylmethionine tRNA				
	ribosyltransferase [Pseudomonas				
782986201	pseudoalcaligenes]	-	1	-	-
	hypothetical protein PA6_007_01480				
543438918	[Pseudomonas alcaligenes NBRC 14159]	-	1	-	-

	hypothetical protein BV82_0961				
641464574	[Pseudomonas sp. P482]	-	1	-	-
	cytochrome oxidase [Pseudomonas				
610713501	pseudoalcaligenes AD6]	1	1	-	-
	cytochrome C [Pseudomonas				
782987084	pseudoalcaligenes]	1	1	-	-
	dihydropteroate synthase [Pseudomonas				
568072375	sp. M1]	1	1	-	-
	ABC transporter substrate-binding protein				
667955424	[Pseudomonas mendocina S5.2]	-	1	-	-
	16S rRNA methyltransferase				
816873894	[Pseudomonas putida KG-4]	-	1	-	-
	homoserine acetyltransferase				
820908305	[Pseudomonas putida]	-	1	-	-
	Fis family transcriptional regulator				
610713265	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
	flagellar motor switch protein G				
556075888	[Pseudomonas sp. VLB120]	-	1	-	-
	iojap family protein [Pseudomonas				
782989603	pseudoalcaligenes]	1	1	-	-
	GTPase HflX [Pseudomonas				
692344829	rhizosphaerae]	-	1	-	-
	N-6 DNA methylase [Pseudomonas				
511102648	plecoglossicida NB2011]	-	1	-	-
	protein-P II uridylyltransferase				
610714893	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
	membrane protein [Pseudomonas				
747151035	balearica DSM 6083]	-	1	-	-
	TetR family transcriptional regulator				
782985360	[Pseudomonas pseudoalcaligenes]	-	1	-	-
	glycolate oxidase subunit GlcD				
610707954	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
	glycolate oxidase subunit GlcD				
758544978	[Pseudomonas putida]	-	1	-	-
	excinuclease ABC subunit B				
949199226	[Pseudomonas trivialis]	-	1	-	-
	Flavin-binding protein [Pseudomonas sp.				
758827150	FeS53a]	-	1	-	-
	preprotein translocase [Pseudomonas				
610707697	pseudoalcaligenes AD6]	-	1	-	-
	Zinc uptake regulation protein				
757243925	[Pseudomonas fluorescens]	-	1	-	-
	flagellar hook-length control protein				
953173742	[Pseudomonas aeruginosa]	1	1	-	-
568072232	hypothetical protein PM1_0202620	-	1	-	-

	[Pseudomonas sp. M1]				
	aromatic acid decarboxylase				
848257782	[Pseudomonas stutzeri]	-	1	-	-
	diguanylate cyclase [Pseudomonas				
610708664	pseudoalcaligenes AD6]	1	1	-	-
	glycerol kinase [Pseudomonas mendocina				
667955083	S5.2]	-	1	-	-
	cell division protein FtsA [Pseudomonas				
699966024	sp. MT-1]	-	1	-	-
	hypothetical protein (plasmid)				
26106122	[Pseudomonas resinovorans]	-	1	-	-
	malate:quinone oxidoreductase				
782986662	[Pseudomonas pseudoalcaligenes]	-	1	-	-
	putative metal-binding enzyme				
800914188	[Pseudomonas fluorescens]	-	1	-	-
	molybdopterin biosynthesis protein MoeB				
	[Pseudomonas amygdali pv.				
330873305	morsprunorum str. M302280]	-	1	-	-
	sarcosine oxidase subunit gamma				
782988029	[Pseudomonas pseudoalcaligenes]	-	1	-	-
	translation initiation factor Sui1				
610709647	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
	sulfurtransferase TusD [Pseudomonas				
543438514	alcaligenes NBRC 14159]	1	1	-	-
	flagellar basal body rod modification				
	protein [Pseudomonas stutzeri DSM				
395807939	10701]	-	1	-	-
	zinc-binding protein [Pseudomonas				
667955156	mendocina S5.2]	-	1	-	-
	diguanylate cyclase [Pseudomonas				
936615556	putida]	-	1	-	-
	chromosomal replication initiation protein				
782984141	[Pseudomonas pseudoalcaligenes]	-	1	-	-
	penicillin amidase [Pseudomonas				
610711615	pseudoalcaligenes AD6]	-	1	-	-
	ribosomal protein S6 modification protein				
759596354	[Pseudomonas sp. PI1]	-	1	-	-
	hypothetical protein PA3615				
9949773	[Pseudomonas aeruginosa PAO1]	-	1	-	-
	metal ion transporter [Pseudomonas				
379066604	stutzeri ATCC 14405 = CCUG 16156]	1	1	-	-
	23S rRNA methyltransferase				
610706381	[Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
	amino acid dehydrogenase [Pseudomonas				
782984440	pseudoalcaligenes]	-	1	-	-

	universal stress protein UspA				
610713530	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	-
	GNAT family acetyltransferase				
610715138	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	-
	bifunctional glutamine-synthetase				
	adenylyltransferase/deadenyltransferase,				
733474726	partial [<i>Pseudomonas putida</i>]	-	1	-	-
	ADP-heptose--LPS heptosyltransferase				
610708965	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	-
	Long-chain-fatty-acid--CoA ligase				
758823099	[<i>Pseudomonas</i> sp. FeS53a]	-	1	-	-
	copper-binding protein [<i>Pseudomonas</i>				
667951895	mendocina S5.2]	-	1	-	-
	3-ketoacyl- reductase [<i>Pseudomonas</i>				
940008138	syringae pv. apii]	-	1	-	-
	lactate dehydrogenase [<i>Pseudomonas</i>				
610711199	pseudoalcaligenes AD6]	-	1	-	-
	farnesyl-diphosphate synthase				
610714887	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	-
	RNA polymerase sigma factor, sigma-70				
928206100	family [<i>Pseudomonas fuscovaginae</i>]	-	1	-	-
	DNA polymerase III subunit epsilon				
749425540	[<i>Pseudomonas fluorescens</i>]	-	1	-	-
	thymidylate synthase [<i>Pseudomonas</i>				
610711642	pseudoalcaligenes AD6]	-	1	-	-
	carboxylesterase [<i>Pseudomonas</i>				
610714766	pseudoalcaligenes AD6]	-	1	-	-
	nicotinate-nucleotide adenylyltransferase				
782989304	[<i>Pseudomonas pseudoalcaligenes</i>]	-	1	-	-
	Indole-3-glycerol phosphate synthase				
404306396	[<i>Pseudomonas fluorescens</i> R124]	-	1	-	-
	ATP-dependent metalloprotease				
856781915	[<i>Pseudomonas helleri</i>]	1	1	-	-
	signal transduction protein [<i>Pseudomonas</i>				
452006194	stutzeri NF13]	-	1	-	-
	class V aminotransferase [<i>Pseudomonas</i>				
610712817	pseudoalcaligenes AD6]	-	1	-	-
	UDP-N-acetylmuramoyl-L-alanyl-D-				
	glutamate synthetase [<i>Pseudomonas</i> sp.				
873534063	KG01]	-	1	-	-
	4-amino-4-deoxychorismate lyase				
667953362	[<i>Pseudomonas mendocina</i> S5.2]	-	1	-	-
	glutathione S-transferase [<i>Pseudomonas</i>				
949201084	trivialis]	-	1	-	-
782984632	pilus assembly protein PilG	1	1	-	-

	[<i>Pseudomonas pseudoalcaligenes</i>]				
	acyl-CoA dehydrogenase [<i>Pseudomonas</i>				
610715076	<i>pseudoalcaligenes</i> AD6]	-	1	-	-
	glucose-6-phosphate dehydrogenase				
856746141	[<i>Pseudomonas deceptionensis</i>]	-	1	-	-
	branched-chain amino acid ABC				
	transporter substrate-binding protein				
610706305	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	-
	Putrescine transport ATP-binding protein				
	[<i>Pseudomonas syringae</i> pv.				
940236636	<i>rhapiolepidis</i>]	-	1	-	-
	hypothetical protein (plasmid)				
111036224	[<i>Pseudomonas putida</i>]	1	1	-	-
	2OG-Fe(II) oxygenase [<i>Pseudomonas</i>				
787852597	<i>chlororaphis</i>]	-	1	-	-
	ribosomal protein S12				
	methylthiotransferase [<i>Pseudomonas</i>				
667953477	<i>mendocina</i> S5.2]	1	1	-	-
	PhoH family protein [<i>Pseudomonas</i>				
543436827	<i>alcaligenes</i> NBRC 14159]	-	1	-	-
	cell envelope biogenesis protein TolA				
782985559	[<i>Pseudomonas pseudoalcaligenes</i>]	-	1	-	-
667953879	lipase [<i>Pseudomonas mendocina</i> S5.2]	-	1	-	-
	DNA-binding protein [<i>Pseudomonas</i>				
751083778	<i>stutzeri</i>]	-	1	-	-
	4-hydroxy-3-methylbut-2-enyl				
	diphosphate reductase [<i>Pseudomonas</i>				
787853239	<i>chlororaphis</i>]	-	1	-	-
	Exodeoxyribonuclease III [<i>Pseudomonas</i>				
940277711	<i>syringae</i> pv. <i>tagetis</i>]	-	1	-	-
	succinate dehydrogenase (D subunit)				
9947545	[<i>Pseudomonas aeruginosa</i> PAO1]	-	1	-	-
	membrane protein [<i>Pseudomonas</i>				
667951088	<i>mendocina</i> S5.2]	-	1	-	-
	ATP-binding protein [<i>Pseudomonas</i>				
733394268	<i>frederiksborgensis</i>]	1	1	-	-
	energy transducer TonB [<i>Pseudomonas</i>				
782986119	<i>pseudoalcaligenes</i>]	-	1	-	-
	Universal stress family protein				
443283294	[<i>Pseudomonas syringae</i> pv. <i>syringae</i> B64]	-	1	-	-
	membrane protein [<i>Pseudomonas</i>				
667953181	<i>mendocina</i> S5.2]	-	1	-	-
	signal recognition particle protein				
426269549	[<i>Pseudomonas</i> sp. UW4]	1	1	-	-
771850325	histidine kinase [<i>Pseudomonas</i> sp. St29]	-	1	-	-

	formyltetrahydrofolate deformylase				
856762120	[<i>Pseudomonas taetrolens</i>]	-	1	-	-
	preprotein translocase subunit YajC				
944134665	[<i>Pseudomonas aeruginosa</i>]	-	1	-	-
	iron transporter [<i>Pseudomonas</i>				
610710196	pseudoalcaligenes AD6]	-	1	-	-
768544663	peptidase M16 [<i>Pseudomonas stutzeri</i>]	1	1	-	-
	sulfate ABC transporter ATP-binding				
856740811	protein [<i>Pseudomonas deceptionensis</i>]	-	1	-	-
	3-hydroxyisobutyrate dehydrogenase				
782985655	[<i>Pseudomonas pseudoalcaligenes</i>]	-	1	-	-
	hypothetical protein DW68_08760				
667952618	[<i>Pseudomonas mendocina</i> S5.2]	-	1	-	-
	cold-shock protein [<i>Pseudomonas</i>				
782985542	pseudoalcaligenes]	-	1	-	-
	peptidase M16 [<i>Pseudomonas</i>				
610706982	pseudoalcaligenes AD6]	-	1	-	-
	peptidase M16 [<i>Pseudomonas balearica</i>				
747152697	DSM 6083]	-	1	-	-
	RNA polymerase sigma factor				
565415905	[<i>Pseudomonas moraviensis</i> R28-S]	-	1	-	-
	hypothetical protein DW68_20465				
667954858	[<i>Pseudomonas mendocina</i> S5.2]	-	1	-	-
	3-octaprenyl-4-hydroxybenzoate carboxy-				
856793851	lyase [<i>Pseudomonas helleri</i>]	-	1	-	-
	ribosomal subunit interface protein				
610714868	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	-
	MerR family transcriptional regulator				
782987271	[<i>Pseudomonas pseudoalcaligenes</i>]	-	1	-	-
	adenine phosphoribosyltransferase				
768547887	[<i>Pseudomonas stutzeri</i>]	-	1	-	-
	UDP-glucose 4-epimerase [<i>Pseudomonas</i>				
940054955	amygdali pv. ciccaronei]	-	1	-	-
	oxidoreductase [<i>Pseudomonas putida</i>				
764073703	S13.1.2]	-	1	-	-
	iron ABC transporter substrate-binding				
782986005	protein [<i>Pseudomonas pseudoalcaligenes</i>]	-	1	-	-
	two-component response regulator				
395810382	[<i>Pseudomonas stutzeri</i> DSM 10701]	-	1	-	-
	acyl-CoA dehydrogenase [<i>Pseudomonas</i>				
782987811	pseudoalcaligenes]	-	1	-	-
	amino acid transporter [<i>Pseudomonas</i>				
799190668	fluorescens]	-	1	-	-
758542698	serine kinase [<i>Pseudomonas putida</i>]	-	1	-	-
937318211	GntR family transcriptional regulator	-	1	-	-

	[<i>Pseudomonas fluorescens</i>]				
	sporulation protein [<i>Pseudomonas</i>				
782989102	pseudoalcaligenes]	-	1	-	-
	peptidylprolyl isomerase [<i>Pseudomonas</i>				
610714753	pseudoalcaligenes AD6]	-	1	-	-
820908237	membrane protein [<i>Pseudomonas putida</i>]	-	1	-	-
	CmpX protein [<i>Pseudomonas syringae</i> pv.				
940053689	coriandricola]	-	1	-	-
	transmembrane protein [<i>Pseudomonas</i>				
782984708	pseudoalcaligenes]	-	1	-	-
	threonine deaminase [<i>Pseudomonas</i>				
95113139	entomophila L48]	-	1	-	-
	hypothetical protein (plasmid)				
295443595	[<i>Pseudomonas putida</i>]	-	1	-	-
	oxidoreductase, FAD-binding protein				
452009219	[<i>Pseudomonas stutzeri</i> NF13]	-	1	-	-
	hypothetical protein AU05_05270				
610706583	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	-	-
	sarcosine oxidase, gamma subunit				
	[<i>Pseudomonas syringae</i> pv. tomato str.				
28850922	DC3000]	-	1	-	-
	sarcosine oxidase subunit delta				
610709051	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	-
	organic solvent ABC transporter				
	substrate-binding protein [<i>Pseudomonas</i>				
667952680	mendocina S5.2]	-	1	-	-
	cobalamin biosynthesis protein CobW				
610706667	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	-
	hypothetical protein ALO88_101379				
940023223	[<i>Pseudomonas syringae</i> pv. antirrhini]	-	1	-	-
	GntR family transcriptional regulator				
610707794	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	-
801164442	lipase [<i>Pseudomonas kilonensis</i>]	-	1	-	-
	cell division protein FtsH [<i>Pseudomonas</i>				
861575003	sp. BICA1-14]	-	1	-	-
	Cell division topological specificity factor				
939989643	[<i>Pseudomonas syringae</i> pv. alisalensis]	-	1	-	-
	hypothetical protein AN400_28865,				
943807199	partial [<i>Pseudomonas aeruginosa</i>]	-	1	-	-
	glyceraldehyde-3-phosphate				
	dehydrogenase [<i>Pseudomonas mendocina</i>				
667953035	S5.2]	1	1	-	-
	Uncharacterized protein ALO80_02603				
940033110	[<i>Pseudomonas caricapapayae</i>]	-	1	-	-
610715085	thiamine-phosphate pyrophosphorylase	-	1	-	-

	[<i>Pseudomonas pseudoalcaligenes</i> AD6]				
	phosphoribosylglycinamide				
	formyltransferase [<i>Pseudomonas</i>				
782986831	<i>pseudoalcaligenes</i>]	-	1	-	-
568075804	thioesterase [<i>Pseudomonas</i> sp. M1]	-	1	-	-
	putative response regulator [<i>Pseudomonas</i>				
95111694	<i>entomophila</i> L48]	1	1	-	-
	putative oxidoreductase; putative D-				
	amino acid dehydrogenase [<i>Pseudomonas</i>				
95113305	<i>entomophila</i> L48]	-	1	-	-
	hypothetical protein DW68_12660				
667953374	[<i>Pseudomonas mendocina</i> S5.2]	-	1	-	-
	putative metallo-oxidoreductase				
913606780	[<i>Pseudomonas</i> sp. 593]	-	1	-	-
	N-(5'-phosphoribosyl)anthranilate				
856780552	isomerase [<i>Pseudomonas psychrophila</i>]	-	1	-	-
	serine/threonine protein phosphatase				
782986040	[<i>Pseudomonas pseudoalcaligenes</i>]	-	1	-	-
	uncharacterized protein PST29_1132				
771847235	[<i>Pseudomonas</i> sp. St29]	-	1	-	-
	branched-chain alpha-keto acid				
	dehydrogenase subunit E2, partial				
763481205	[<i>Pseudomonas oryzae</i> habitans]	-	1	-	-
	ribonuclease III [<i>Pseudomonas</i> sp.				
861575835	BICA1-14]	-	1	-	-
	transcriptional regulator, RpiR family				
327478857	[<i>Pseudomonas stutzeri</i> DSM 4166]	-	1	-	-
	hypothetical protein QV12_01665				
758546881	[<i>Pseudomonas putida</i>]	-	1	-	-
	aldose epimerase [<i>Pseudomonas</i>				
667951839	<i>mendocina</i> S5.2]	-	1	-	-
912965556	histidine kinase [<i>Pseudomonas</i> sp. 250J]	-	1	-	-
	arabinose efflux permease family protein				
928203886	[<i>Pseudomonas fuscovaginae</i>]	-	1	-	-
	uroporphyrinogen-III synthase				
856745809	[<i>Pseudomonas deceptionensis</i>]	-	1	-	-
	bacterial regulatory s, gntR family protein				
641461754	[<i>Pseudomonas</i> sp. P482]	1	1	-	-
	aspartate ammonia-lyase [<i>Pseudomonas</i>				
749426704	<i>fluorescens</i>]	-	1	-	-
	hypothetical protein PACI27_2906				
404533788	[<i>Pseudomonas aeruginosa</i> CI27]	-	1	-	-
	recombination protein RecR				
940725888	[<i>Pseudomonas endophytica</i>]	-	1	-	-
395809176	Na(+)-translocating NADH-quinone	-	1	-	-

	reductase subunit F [Pseudomonas stutzeri DSM 10701]				
	hypothetical protein AO353_04335				
937309450	[Pseudomonas fluorescens]	-	1	-	-
	acyl-CoA hydrolase [Pseudomonas fuscovaginae]	-	1	-	-
928205144	FAD-dependent oxidoreductase				
751053839	[Pseudomonas sp. W15Feb9B]	-	1	-	-
	putative inner membrane protein translocase component YidC				
327482911	[Pseudomonas stutzeri DSM 4166]	-	1	-	-
	Glyco_tran_WecB, partial [uncultured Pseudomonas sp.]	-	1	-	-
643017479	chorismate--pyruvate lyase [Pseudomonas pseudoalcaligenes]	-	1	-	-
782989706	acetyl-CoA acetyltransferase				
667955370	[Pseudomonas mendocina S5.2]	-	1	-	-
	3-oxoadipate enol-lactonase				
782985577	[Pseudomonas pseudoalcaligenes]	-	1	-	-
	arsenate reductase [Pseudomonas psychrophila]	-	1	-	-
856784430	SagB-type dehydrogenase domain protein				
782989408	[Pseudomonas pseudoalcaligenes]	-	1	-	-
	cytochrome C [Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
610711022	iron-hydroxamate ABC transporter substrate-binding protein [Pseudomonas pseudoalcaligenes AD6]	-	1	-	-
610712412	Sulfatase [Pseudomonas syringae pv. tagetis]	-	1	-	-
940277931	hypothetical protein CCBH4851_00604				
937560375	[Pseudomonas aeruginosa]	-	1	-	-
	thiol:disulfide interchange protein				
782987083	[Pseudomonas pseudoalcaligenes]	-	1	-	-
	rRNA methylase [Pseudomonas stutzeri DSM 10701]	-	1	-	-
395810153	ABC transporter ATP-binding protein				
782985154	[Pseudomonas pseudoalcaligenes]	-	1	-	-
	hypothetical protein PKB_2975				
631779844	[Pseudomonas knackmussii B13]	-	1	-	-
	penicillin amidase [Pseudomonas pseudoalcaligenes]	-	1	-	-
782988170	major facilitator transporter				
761532713	[Pseudomonas fluorescens]	-	1	-	-
568071110	2'-5' RNA ligase [Pseudomonas sp. M1]	-	1	-	-

	serine/threonine protein phosphatase, partial [<i>Pseudomonas pseudoalcaligenes</i>				
610713344	AD6]	-	1	-	-
	cytochrome c family protein				
641460972	[<i>Pseudomonas</i> sp. P482]	-	1	-	-
	diguanylate cyclase [<i>Pseudomonas</i>				
747111037	fluorescens]	-	1	-	-
	spermidine/putrescine ABC transporter				
	ATP-binding protein [<i>Pseudomonas</i> sp.				
768456628	ES3-33]	-	1	-	-
	flagellar protein FlaG [<i>Pseudomonas</i> sp.				
912966285	250J]	-	1	-	-
	hypothetical protein N619_24020				
782984494	[<i>Pseudomonas pseudoalcaligenes</i>]	-	1	-	-
	transcriptional regulator [<i>Pseudomonas</i>				
913662820	fluorescens NCIMB 11764]	-	1	-	-
	hypothetical protein TX25_21190				
949229227	[<i>Pseudomonas</i> sp. DSM 28142]	-	1	-	-
	GNAT family acetyltransferase				
610710348	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	-	-
	hypothetical protein TU86_06630				
856797180	[<i>Pseudomonas weihenstephanensis</i>]	-	1	-	-
	mannose-1-phosphate guanyltransferase				
856774906	[<i>Pseudomonas lini</i>]	1	1	-	-
856784055	glycosylase [<i>Pseudomonas psychrophila</i>]	-	1	-	-
	cytochrome c oxidase, cbb3-type, subunit				
641464609	II [<i>Pseudomonas</i> sp. P482]	-	1	-	-
	flagellar biosynthesis sigma factor				
610709525	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	1	-	-
	8-amino-7-oxononanoate synthase				
703403289	[<i>Pseudomonas xanthomarina</i>]	-	1	-	-
	thiamine biosynthesis protein ApbE				
667953331	[<i>Pseudomonas mendocina</i> S5.2]	-	1	-	-
	hypothetical protein AU05_25025				
610707690	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	-	1	-	-
	hypothetical protein A458_06805				
390982614	[<i>Pseudomonas stutzeri</i> CCUG 29243]	-	1	-	-
	o-succinylbenzoate--CoA ligase				
576708382	[<i>Pseudomonas</i> sp. GM41(2012)]	-	1	-	-
	mechanosensitive ion channel protein				
820907543	MscS [<i>Pseudomonas putida</i>]	-	1	-	-
	3-ketoacyl-CoA thiolase FadA				
500244003	[<i>Pseudomonas protegens</i> CHA0]	-	1	-	-
	ATP synthase delta chain [<i>Pseudomonas</i>				
327482894	stutzeri DSM 4166]	-	1	-	-

782985184	cytochrome C [Pseudomonas pseudoalcaligenes]	-	1	-	-
782984652	hypothetical protein N619_24895 [Pseudomonas pseudoalcaligenes]	-	1	-	-
928538017	LuxR family transcriptional regulator [Pseudomonas aeruginosa]	-	1	-	-
799196390	DNA helicase [Pseudomonas fluorescens]	-	1	-	-
782987562	competence protein ComEA [Pseudomonas pseudoalcaligenes]	1	1	-	-
667955113	hypothetical protein DW68_21785 [Pseudomonas mendocina S5.2]	-	1	-	-
733391920	murein transglycosylase [Pseudomonas frederiksbergensis]	-	1	-	-
768547426	porin [Pseudomonas stutzeri]	-	1	-	-
751378798	arsenate reductase [Pseudomonas aeruginosa]	-	1	-	-
782986386	ATP-binding protein [Pseudomonas pseudoalcaligenes]	-	1	-	-
761890531	dethiobiotin synthetase [Pseudomonas sp. 10-1B]	-	1	-	-
426269580	molybdopterin biosynthesis MoaE [Pseudomonas sp. UW4]	-	1	-	-
940028943	Endo-1,4-D-glucanase [Pseudomonas caricapapayae]	-	1	-	-
928538198	Rieske family iron-sulfur cluster-binding protein [Pseudomonas aeruginosa]	-	1	-	-
4079828	N-acetyl-anhydromuramyl-L-alanine amidase [Pseudomonas aeruginosa PAO1]	-	1	-	-
769335529	hypothetical protein RT21_07165 [Pseudomonas sp. 10B238]	-	1	-	-
631777928	co-chaperone HscB [Pseudomonas knackmussii B13]	-	1	-	-
379063737	DNA-directed RNA polymerase subunit beta [Pseudomonas stutzeri ATCC 14405 = CCUG 16156]	1	-	-	-
327479317	DNA-directed RNA polymerase subunit beta [Pseudomonas stutzeri DSM 4166]	1	-	-	-
212373997	DNA-directed RNA polymerase beta subunit, partial [Pseudomonas sp. R-35724]	1	-	-	-
26987192	elongation factor G [Pseudomonas putida KT2440]	1	-	-	-
641463602	translation elongation factor Tu [Pseudomonas sp. P482]	1	-	-	-

	translation elongation factor Tu				
213925890	[<i>Pseudomonas syringae</i> pv. tomato T1]	1	-	-	-
	unnamed protein product [<i>Pseudomonas</i>				
207008600	savastanoi pv. phaseolicola 1448A]	1	-	-	-
	aldehyde dehydrogenase, partial				
953179058	[<i>Pseudomonas aeruginosa</i>]	1	-	-	-
	multifunctional fatty acid oxidation				
	complex subunit alpha [<i>Pseudomonas</i>				
667953312	mendocina S5.2]	1	-	-	-
	multifunctional fatty acid oxidation				
	complex subunit alpha [<i>Pseudomonas</i>				
856791870	helleri]	1	-	-	-
	4-aminobutyrate aminotransferase				
568071352	[<i>Pseudomonas</i> sp. M1]	1	-	-	-
	aconitate hydratase [<i>Pseudomonas</i> sp.				
568070527	M1]	1	-	-	-
	50S ribosomal protein L14 [<i>Pseudomonas</i>				
763481870	oryzihabitans]	1	-	-	-
	dihydrolipoamide acetyltransferase				
	[<i>Pseudomonas coronafaciens</i> pv. <i>oryzae</i>				
331021070	str. 1_6]	1	-	-	-
	flagellar rod assembly				
	protein/muramidase FlgJ [<i>Pseudomonas</i>				
341579962	protegens Pf-5]	1	-	-	-
	flagellar rod assembly protein FlgJ				
733393055	[<i>Pseudomonas frederiksbergensis</i>]	1	-	-	-
	putative amino acid ABC transporter				
	substrate-binding protein [<i>Pseudomonas</i>				
543438638	alcaligenes NBRC 14159]	1	-	-	-
	ribonuclease E [<i>Pseudomonas</i>				
610712835	pseudoalcaligenes AD6]	1	-	-	-
	ribonuclease E [<i>Pseudomonas</i>				
799205707	fluorescens]	1	-	-	-
	dihydrolipoamide succinyltransferase				
902688146	[<i>Pseudomonas trivialis</i>]	1	-	-	-
	dihydrolipoamide succinyltransferase				
346057251	[<i>Pseudomonas aeruginosa</i> NCMG1179]	1	-	-	-
	2-oxoglutarate dehydrogenase				
768547938	[<i>Pseudomonas stutzeri</i>]	1	-	-	-
	cytochrome [<i>Pseudomonas mendocina</i>				
667951900	S5.2]	1	-	-	-
	malate synthase [<i>Pseudomonas</i>				
667951940	mendocina S5.2]	1	-	-	-
	Glyceraldehyde-3-phosphate				
940109631	dehydrogenase [<i>Pseudomonas</i>	1	-	-	-

	ficuserectae]				
	isoleucine--tRNA ligase [Pseudomonas				
928534381	aeruginosa]	1	-	-	-
699966805	isocitrate lyase [Pseudomonas sp. MT-1]	1	-	-	-
	aminopeptidase N [Pseudomonas stutzeri				
379063676	ATCC 14405 = CCUG 16156]	1	-	-	-
	transcriptional regulator [Pseudomonas				
751054043	sp. W15Feb9B]	1	-	-	-
	aromatic amino acid aminotransferase				
543436946	[Pseudomonas alcaligenes NBRC 14159]	1	-	-	-
	aromatic amino acid aminotransferase				
747151633	[Pseudomonas balearica DSM 6083]	1	-	-	-
	transcription elongation factor NusA				
667955324	[Pseudomonas mendocina S5.2]	1	-	-	-
	molecular chaperone SurA [Pseudomonas				
667951122	mendocina S5.2]	1	-	-	-
	flagellar basal body rod protein FlgG				
799188738	[Pseudomonas fluorescens]	1	-	-	-
	proline--tRNA ligase [Pseudomonas				
768545982	stutzeri]	1	-	-	-
	serine/threonine protein kinase				
763479546	[Pseudomonas oryzihabitans]	1	-	-	-
	3-oxoacyl-ACP synthase [Pseudomonas				
949222485	veronii]	1	-	-	-
	3-oxoacyl-ACP synthase [Pseudomonas				
692343367	rhizosphaerae]	1	-	-	-
667954711	enolase [Pseudomonas mendocina S5.2]	1	-	-	-
	ATP F0F1 synthase subunit alpha				
735690102	[Pseudomonas tuomuerensis]	1	-	-	-
	succinate-semialdehyde dehydrogenase				
452006669	[Pseudomonas stutzeri NF13]	1	-	-	-
	2-isopropylmalate synthase				
26987761	[Pseudomonas putida KT2440]	1	-	-	-
	polyphosphate kinase [Pseudomonas				
499855577	entomophila]	1	-	-	-
	dihydroxy-acid dehydratase				
511102682	[Pseudomonas plecoglossicida NB2011]	1	-	-	-
	dihydrodipicolinate reductase				
327482038	[Pseudomonas stutzeri DSM 4166]	1	-	-	-
	Valyl-tRNA synthetase [Pseudomonas sp.				
758832860	FeS53a]	1	-	-	-
	acetyl-CoA carboxylase biotin				
699966970	carboxylase [Pseudomonas sp. MT-1]	1	-	-	-
	methylmalonate-semialdehyde				
568071777	dehydrogenase [Pseudomonas sp. M1]	1	-	-	-

	methylmalonate-semialdehyde				
459962726	dehydrogenase [Pseudomonas sp. Lz4W]	1	-	-	-
	3-phosphoshikimate 1-				
	carboxyvinyltransferase [Pseudomonas				
631780754	knackmussii B13]	1	-	-	-
	Alanyl-tRNA synthetase [Pseudomonas				
298157436	savastanoi pv. savastanoi NCPPB 3335]	1	-	-	-
	oligopeptidase A [Pseudomonas				
387162163	fluorescens A506]	1	-	-	-
	oligopeptidase A [Pseudomonas				
735690151	tuomuerensis]	1	-	-	-
	oligopeptidase A [Pseudomonas				
95108350	entomophila L48]	1	-	-	-
	3-ketoacyl-ACP reductase [Pseudomonas				
856784257	psychrophila]	1	-	-	-
768548107	peptidase S41 [Pseudomonas stutzeri]	1	-	-	-
	methionine synthase, partial				
666930959	[Pseudomonas syringae pv. syringae FF5]	1	-	-	-
	ribosome-recycling factor [Pseudomonas				
747151539	balearica DSM 6083]	1	-	-	-
	phosphate uptake regulator, PhoU				
327482719	[Pseudomonas stutzeri DSM 4166]	1	-	-	-
	major outer membrane lipoprotein I,				
335389933	partial [Pseudomonas azotifigens]	1	-	-	-
	recombination associated protein				
556042270	(plasmid) [Pseudomonas sp. VLB120]	1	-	-	-
	aspartyl/glutamyl-tRNA amidotransferase				
	subunit A [Pseudomonas stutzeri DSM				
395807417	10701]	1	-	-	-
	Leucine--tRNA ligase [Pseudomonas				
939992682	syringae pv. alisalensis]	1	-	-	-
	adenylosuccinate synthetase				
713118194	[Pseudomonas mediterranea CFBP 5447]	1	-	-	-
	chaperone protein HscA [Pseudomonas				
565413155	moraviensis R28-S]	1	-	-	-
734479368	protein GbcA [Pseudomonas aeruginosa]	1	-	-	-
	Adenylosuccinate lyase [Pseudomonas				
940037098	caricapapayae]	1	-	-	-
	enoyl-CoA hydratase [Pseudomonas				
511104152	plecoglossicida NB2011]	1	-	-	-
	acyl-CoA dehydrogenase [Pseudomonas				
873535067	sp. KG01]	1	-	-	-
	Cytochrome c5 [Pseudomonas				
749477533	fluorescens]	1	-	-	-
229364985	putative sensor kinase/response regulatory	1	-	-	-

	fusion protein [Pseudomonas fluorescens SBW25]				
735690527	DNA-binding protein [Pseudomonas tuomuerensis]	1	-	-	-
856797919	recombinase RecA [Pseudomonas weihenstephanensis]	1	-	-	-
699968673	phosphonates ABC transporter substrate- binding protein [Pseudomonas sp. MT-1]	1	-	-	-
756407417	excinuclease ABC subunit A [Pseudomonas fluorescens]	1	-	-	-
310941849	30S ribosomal protein S19 [Pseudomonas straminea]	1	-	-	-
28855507	heat shock protein HslV [Pseudomonas syringae pv. tomato str. DC3000]	1	-	-	-
937310987	arginine--tRNA ligase [Pseudomonas fluorescens]	1	-	-	-
213927466	RNA polymerase sigma-70 factor [Pseudomonas syringae pv. tomato T1]	1	-	-	-
667951494	acetylglutamate kinase [Pseudomonas mendocina S5.2]	1	-	-	-
544280202	PTS fructose transporter subunit IIA [Pseudomonas putida LF54]	1	-	-	-
667952025	endoribonuclease [Pseudomonas mendocina S5.2]	1	-	-	-
115265547	peptide chain release factor [Pseudomonas syringae pv. actinidiae]	1	-	-	-
747149353	phosphoglycerate mutase [Pseudomonas balearica DSM 6083]	1	-	-	-
641462852	betaine aldehyde dehydrogenase [Pseudomonas sp. P482]	1	-	-	-
667953201	elongation factor 4 [Pseudomonas mendocina S5.2]	1	-	-	-
395807494	UDP-N-acetylmuramoylalanyl-D- glutamate--2,6-diaminopimelate ligase [Pseudomonas stutzeri DSM 10701]	1	-	-	-
610706886	acetylornithine aminotransferase [Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
758824094	Succinylornithine transaminase [Pseudomonas sp. FeS53a]	1	-	-	-
691226129	ATP-dependent protease [Pseudomonas cremoricolorata]	1	-	-	-
940099802	Quinone oxidoreductase [Pseudomonas syringae pv. delphinii]	1	-	-	-
610707233	carbonate dehydratase [Pseudomonas pseudoalcaligenes AD6]	1	-	-	-

542006874	RNA-binding protein [Pseudomonas mendocina EGD-AQ5]	1	-	-	-
667952655	glutamyl-tRNA amidotransferase [Pseudomonas mendocina S5.2]	1	-	-	-
500244417	methionyl-tRNA synthetase MetG [Pseudomonas protegens CHA0]	1	-	-	-
667953313	3-ketoacyl-CoA thiolase [Pseudomonas mendocina S5.2]	1	-	-	-
543438306	10 kDa chaperonin [Pseudomonas alcaligenes NBRC 14159]	1	-	-	-
610709196	H-NS histone [Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
610708009	UDP-N-acetylmuramate--alanine ligase [Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
327478617	alkyl hydroperoxide reductase subunit F [Pseudomonas stutzeri DSM 4166]	1	-	-	-
684197729	Skp [Pseudomonas mosselii SJ10]	1	-	-	-
610709462	isochorismatase [Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
848255664	DEAD-box ATP dependent DNA helicase [Pseudomonas stutzeri]	1	-	-	-
610713938	glutathione reductase [Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
782987741	universal stress protein UspA [Pseudomonas pseudoalcaligenes]	1	-	-	-
908350736	acetyl-CoA carboxylase [Pseudomonas syringae pv. actinidiae ICMP 18884]	1	-	-	-
667953248	ATP-dependent helicase HrpA [Pseudomonas mendocina S5.2]	1	-	-	-
26991957	50S ribosomal protein L33 [Pseudomonas putida KT2440]	1	-	-	-
610709988	3-oxoacyl-ACP reductase [Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
610714876	DNA polymerase III subunit alpha [Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
543436254	histidinol-phosphate aminotransferase [Pseudomonas alcaligenes NBRC 14159]	1	-	-	-
763482539	aspartate aminotransferase [Pseudomonas oryzae]	1	-	-	-
782988597	imidazolonepropionase [Pseudomonas pseudoalcaligenes]	1	-	-	-
213928071	ribose-phosphate pyrophosphokinase [Pseudomonas syringae pv. tomato T1]	1	-	-	-
940308658	3-deoxy-7-phosphoheptulonate synthase, s II [Pseudomonas syringae pv. viburni]	1	-	-	-

	NADH dehydrogenase I, F subunit				
213925135	[<i>Pseudomonas syringae</i> pv. tomato T1]	1	-	-	-
	chemotaxis-specific methyltransferase				
610416967	[<i>Pseudomonas aeruginosa</i> PA96]	1	-	-	-
	hypothetical protein DW68_01650				
667951238	[<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
	phosphoserine phosphatase				
568075935	[<i>Pseudomonas</i> sp. M1]	1	-	-	-
	F0F1 ATP synthase subunit epsilon				
213926748	[<i>Pseudomonas syringae</i> pv. tomato T1]	1	-	-	-
	amino acid ABC transporter substrate-				
926552707	binding protein [<i>Pseudomonas</i> sp. 655]	1	-	-	-
	DNA topoisomerase IV subunit B				
782984835	[<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	-
	DNA topoisomerase IV subunit B				
747115833	[<i>Pseudomonas fluorescens</i>]	1	-	-	-
	FMN-binding oxidoreductase				
26987052	[<i>Pseudomonas putida</i> KT2440]	1	-	-	-
	3,4-dihydroxy-2-butanone 4-phosphate				
667951012	synthase [<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
	Dehydrogenase [<i>Pseudomonas</i>				
404303865	<i>fluorescens</i> R124]	1	-	-	-
	peptidase U62 modulator of DNA gyrase				
430791724	[<i>Pseudomonas putida</i> HB3267]	1	-	-	-
	chromosome segregation SMC protein,				
	putative [<i>Pseudomonas stutzeri</i> DSM				
327480470	4166]	1	-	-	-
	chromosome segregation protein SMC				
763479343	[<i>Pseudomonas oryzae</i>]	1	-	-	-
	chromosome partitioning protein ParA				
749421507	[<i>Pseudomonas fluorescens</i>]	1	-	-	-
	Chorismate synthase [<i>Pseudomonas</i> sp.				
758837075	FeS53a]	1	-	-	-
	tryptophan--tRNA ligase [<i>Pseudomonas</i>				
610712494	<i>pseudoalcaligenes</i> AD6]	1	-	-	-
	metallo-beta-lactamase family protein				
390984462	[<i>Pseudomonas stutzeri</i> CCUG 29243]	1	-	-	-
	glutathione S-transferase [<i>Pseudomonas</i>				
667953688	<i>mendocina</i> S5.2]	1	-	-	-
	flagellar motor switch protein				
	[<i>Pseudomonas coronafaciens</i> pv. <i>oryzae</i>				
331022101	str. 1_6]	1	-	-	-
568074710	flavodoxin [<i>Pseudomonas</i> sp. M1]	1	-	-	-
	long-chain fatty acid--CoA ligase				
667953226	[<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-

	long-chain fatty acid--CoA ligase				
667953227	[Pseudomonas mendocina S5.2]	1	-	-	-
768548862	membrane protein [Pseudomonas stutzeri]	1	-	-	-
	hydrolase TatD [Pseudomonas				
782985949	pseudoalcaligenes]	1	-	-	-
	Transcriptional activator protein Anr				
757248892	[Pseudomonas fluorescens]	1	-	-	-
	oligoribonuclease [Pseudomonas				
782984861	pseudoalcaligenes]	1	-	-	-
	50S ribosomal protein L29 [Pseudomonas				
9950472	aeruginosa PAO1]	1	-	-	-
	RNA polymerase omega subunit				
9951656	[Pseudomonas aeruginosa PAO1]	1	-	-	-
	putative two-component response				
	regulator [Pseudomonas alcaligenes				
543436310	NBRC 14159]	1	-	-	-
	hex regulon repressor [Pseudomonas				
229364098	fluorescens SBW25]	1	-	-	-
	NADH-quinone oxidoreductase subunit				
	C/D [Pseudomonas alcaligenes NBRC				
543438546	14159]	1	-	-	-
	exodeoxyribonuclease V subunit beta				
713120022	[Pseudomonas mediterranea CFBP 5447]	1	-	-	-
	exodeoxyribonuclease V subunit beta				
749421639	[Pseudomonas fluorescens]	1	-	-	-
	Exodeoxyribonuclease V beta chain				
631781300	[Pseudomonas knackmussii B13]	1	-	-	-
	GntR family transcriptional regulator				
667951623	[Pseudomonas mendocina S5.2]	1	-	-	-
	conserved hypothetical protein				
115587928	[Pseudomonas aeruginosa UCBPP-PA14]	1	-	-	-
	malate:quinone oxidoreductase				
610714331	[Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
	Kappa-casein OS=Bos taurus GN=CSN3				
P02668	PE=1 SV=1	1	-	-	-
801165640	cupin [Pseudomonas kilonensis]	1	-	-	-
	N-ethylammelane chlorohydrolase				
610709985	[Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
	peptide deformylase [Pseudomonas				
610710258	pseudoalcaligenes AD6]	1	-	-	-
	cold-shock protein [Pseudomonas				
610710480	pseudoalcaligenes AD6]	1	-	-	-
	transcriptional regulator [Pseudomonas				
937645048	sp. In5]	1	-	-	-
820917069	type 4 fimbriae expression regulatory	1	-	-	-

	protein PilR [Pseudomonas putida]				
	transcriptional regulator [Pseudomonas				
929906507	sp. RIT-PI-q]	1	-	-	-
	hypothetical protein PA6_003_00110				
543439535	[Pseudomonas alcaligenes NBRC 14159]	1	-	-	-
	Biotin carboxylase/biotin carboxyl carrier				
940297504	protein [Pseudomonas tremae]	1	-	-	-
	5,10-methylenetetrahydrofolate reductase				
782984647	[Pseudomonas pseudoalcaligenes]	1	-	-	-
	glycoside hydrolase family 43				
667952104	[Pseudomonas mendocina S5.2]	1	-	-	-
	glycerol kinase [Pseudomonas				
782986340	pseudoalcaligenes]	1	-	-	-
	3-deoxy-D-manno-octulosonate 8-				
	phosphate phosphatase [Pseudomonas				
667952676	mendocina S5.2]	1	-	-	-
	Glutathione S-transferase P OS=Homo				
P09211	sapiens GN=GSTP1 PE=1 SV=2	1	-	-	-
	cysteine synthase [Pseudomonas				
782989833	pseudoalcaligenes]	1	-	-	-
	GTPase HflX [Pseudomonas				
610707865	pseudoalcaligenes AD6]	1	-	-	-
	PEP synthetase regulatory protein				
782988925	[Pseudomonas pseudoalcaligenes]	1	-	-	-
	diguanylate cyclase [Pseudomonas				
782985217	pseudoalcaligenes]	1	-	-	-
	peptide chain release factor 2				
543437459	[Pseudomonas alcaligenes NBRC 14159]	1	-	-	-
	membrane protein [Pseudomonas				
667954349	mendocina S5.2]	1	-	-	-
	phosphoserine phosphatase				
856785588	[Pseudomonas aeruginosa]	1	-	-	-
	putative outer membrane receptor				
390984582	[Pseudomonas stutzeri CCUG 29243]	1	-	-	-
	phosphoenolpyruvate-protein				
	phosphotransferase [Pseudomonas				
768550184	stutzeri]	1	-	-	-
	ATP-binding protein [Pseudomonas				
667953135	mendocina S5.2]	1	-	-	-
	sulfoxide reductase catalytic subunit				
	YedY [Pseudomonas pseudoalcaligenes				
610711127	AD6]	1	-	-	-
	putative type I secretion system outer				
	membrane protein [Pseudomonas				
543437606	alcaligenes NBRC 14159]	1	-	-	-

667953307	lytic transglycosylase [<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
949180235	thioredoxin [<i>Pseudomonas libanensis</i>]	1	-	-	-
757240028	SsrA-binding protein [<i>Pseudomonas fluorescens</i>]	1	-	-	-
631780721	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta [<i>Pseudomonas knackmussii</i> B13]	1	-	-	-
734576264	methionyl-tRNA formyltransferase [<i>Pseudomonas putida</i> S12]	1	-	-	-
758834844	Aspartate carbamoyltransferase [<i>Pseudomonas</i> sp. FeS53a]	1	-	-	-
610707000	SAM-dependent methyltransferase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	-
820911324	cytochrome C [<i>Pseudomonas putida</i>]	1	-	-	-
610709523	protein phosphatase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	-
324097711	hypothetical protein G1E_26228 [<i>Pseudomonas</i> sp. TJI-51]	1	-	-	-
684197777	RNA-binding protein [<i>Pseudomonas mosselii</i> SJ10]	1	-	-	-
610714945	MerR family transcriptional regulator [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	-
739188356	acyl-CoA thioesterase [<i>Pseudomonas oleovorans</i>]	1	-	-	-
610715137	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	-
782984460	magnesium chelatae [<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	-
856768583	50S ribosomal protein L11 [<i>Pseudomonas taetrolens</i>]	1	-	-	-
782989561	Fis family transcriptional regulator [<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	-
782989903	succinylglutamate-semialdehyde dehydrogenase [<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	-
940296770	Peptide methionine sulfoxide reductase MsrA [<i>Pseudomonas tremac</i>]	1	-	-	-
610706960	twitching motility protein PilT [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	-
556076335	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [<i>Pseudomonas</i> sp. VLB120]	1	-	-	-

	Queuine tRNA-ribosyltransferase				
940055129	[Pseudomonas cannabina]	1	-	-	-
	stringent starvation protein A				
610707992	[Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
	adenosylmethionine-8-amino-7-oxononanoate aminotransferase				
667952195	[Pseudomonas mendocina S5.2]	1	-	-	-
	flagellar motor switch protein G				
327481268	[Pseudomonas stutzeri DSM 4166]	1	-	-	-
	glucose-6-phosphate dehydrogenase				
759595069	[Pseudomonas sp. PI1]	1	-	-	-
	Nitrate reductase [Pseudomonas sp.				
576714506	GM30]	1	-	-	-
	pseudouridine synthase [Pseudomonas				
782985494	pseudoalcaligenes]	1	-	-	-
	TetR family transcriptional regulator				
568071738	[Pseudomonas sp. M1]	1	-	-	-
667952695	ATPase [Pseudomonas mendocina S5.2]	1	-	-	-
	3-isopropylmalate dehydratase small				
631780731	subunit [Pseudomonas knackmussii B13]	1	-	-	-
	cell division protein FtsY [Pseudomonas				
799221454	fluorescens]	1	-	-	-
	conserved hypothetical protein				
126197058	[Pseudomonas aeruginosa 2192]	1	-	-	-
	Catalase OS=Homo sapiens GN=CAT				
P04040	PE=1 SV=3	1	-	-	-
	membrane protein [Pseudomonas				
782986702	pseudoalcaligenes]	1	-	-	-
	ferredoxin-NADP reductase				
691226531	[Pseudomonas cremoricolorata]	1	-	-	-
	ribonuclease G [Pseudomonas alcaligenes				
543437281	NBRC 14159]	1	-	-	-
	LysR family transcriptional regulator				
395807974	[Pseudomonas stutzeri DSM 10701]	1	-	-	-
	collagen pro alpha-chain precursor				
782985724	[Pseudomonas pseudoalcaligenes]	1	-	-	-
	Trp repressor binding protein WrbA				
443282870	[Pseudomonas syringae pv. syringae B64]	1	-	-	-
	tRNA:Cm32/Um32 methyltransferase				
758832845	[Pseudomonas sp. FeS53a]	1	-	-	-
	Transcription elongation factor GreB				
748443576	[Pseudomonas batumici]	1	-	-	-
	saccharopine dehydrogenase				
610714741	[Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
324097453	isovaleryl-CoA dehydrogenase	1	-	-	-

	[<i>Pseudomonas</i> sp. TJI-51]				
	polyhydroxyalkanoic acid system protein				
667952284	[<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
	Queuosine Biosynthesis QueE Radical				
758821704	SAM [<i>Pseudomonas</i> sp. FeS53a]	1	-	-	-
	ATPase AAA [<i>Pseudomonas</i>				
782987040	pseudoalcaligenes]	1	-	-	-
	chromosome partitioning protein				
928533775	[<i>Pseudomonas aeruginosa</i>]	1	-	-	-
	RNA helicase [<i>Pseudomonas</i>				
782985585	pseudoalcaligenes]	1	-	-	-
	aromatic acid decarboxylase				
929906645	[<i>Pseudomonas</i> sp. RIT-PI-q]	1	-	-	-
	NifU-like protein [<i>Pseudomonas</i>				
631777926	knackmussii B13]	1	-	-	-
	cell envelope biogenesis protein TolA				
667953003	[<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
	excinuclease ABC subunit B				
923159854	[<i>Pseudomonas coronafaciens</i> pv. porri]	1	-	-	-
	arsenate reductase [<i>Pseudomonas putida</i>				
388558975	ND6]	1	-	-	-
	16 kDa heat shock protein B				
631780734	[<i>Pseudomonas knackmussii</i> B13]	1	-	-	-
	proline iminopeptidase [<i>Pseudomonas</i>				
763480248	oryzihabitans]	1	-	-	-
	lactate dehydrogenase [<i>Pseudomonas</i>				
691225065	cremoricolorata]	1	-	-	-
	conserved hypothetical protein				
115589371	[<i>Pseudomonas aeruginosa</i> UCBPP-PA14]	1	-	-	-
	16S ribosomal RNA methyltransferase				
26991662	RsmE [<i>Pseudomonas putida</i> KT2440]	1	-	-	-
	hypothetical protein UB23_08935				
768455801	[<i>Pseudomonas</i> sp. ES3-33]	1	-	-	-
	putative transcriptional regulator MerR				
388559501	[<i>Pseudomonas putida</i> ND6]	1	-	-	-
	nucleoside triphosphate hydrolase				
782989821	[<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	-
	SNF2 family DNA/RNA helicase				
471350575	[<i>Pseudomonas putida</i> LS46]	1	-	-	-
	ABC transporter substrate-binding protein				
610714365	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	-
	23S rRNA pseudouridine synthase RluC				
543438181	[<i>Pseudomonas alcaligenes</i> NBRC 14159]	1	-	-	-
	Fis family transcriptional regulator				
782988208	[<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	-

768551629	dipeptidase [<i>Pseudomonas fluorescens</i>]	1	-	-	-
28850579	DNA-binding protein [<i>Pseudomonas syringae</i> pv. tomato str. DC3000]	1	-	-	-
610712883	pirin [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	-
782987610	acyl-CoA dehydrogenase [<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	-
912968530	chemotaxis protein CheW [<i>Pseudomonas</i> sp. 250J]	1	-	-	-
610709157	glycerol-3-phosphate dehydrogenase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	-
667951127	sulfurtransferase [<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
610714579	(p)ppGpp synthetase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	-
782988068	tRNA (guanine-N7)-methyltransferase [<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	-
512385421	GTPase Der [<i>Pseudomonas putida</i> NBRC 14164]	1	-	-	-
395809989	tRNA (uracil-5-)-methyltransferase [<i>Pseudomonas stutzeri</i> DSM 10701]	1	-	-	-
758824158	Adenosylcobinamide-phosphate guanylyltransferase [<i>Pseudomonas</i> sp. FeS53a]	1	-	-	-
511100737	dihydroorotase [<i>Pseudomonas plecoglossicida</i> NB2011]	1	-	-	-
733393143	hypothetical protein JZ00_19580 [<i>Pseudomonas frederiksbergensis</i>]	1	-	-	-
667952797	molybdenum cofactor biosynthesis protein MoaC [<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
928533881	FAD-dependent oxidoreductase [<i>Pseudomonas aeruginosa</i>]	1	-	-	-
856777861	hypothetical protein TU76_23250 [<i>Pseudomonas psychrophila</i>]	1	-	-	-
667955470	globin [<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
68343519	putative 3-hydroxyacyl-CoA dehydrogenase [<i>Pseudomonas protegens</i> Pf-5]	1	-	-	-
758547083	hypothetical protein QV12_00915 [<i>Pseudomonas putida</i>]	1	-	-	-
379065011	GTP-binding protein YsxC [<i>Pseudomonas stutzeri</i> ATCC 14405 = CCUG 16156]	1	-	-	-
667951284	peptidase M16 [<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-

667953681	short-chain dehydrogenase [<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
940721634	ribonuclease III [<i>Pseudomonas endophytica</i>]	1	-	-	-
800914139	Hypothetical ATP-binding protein UPF0042, contains P-loop [<i>Pseudomonas fluorescens</i>]	1	-	-	-
747150174	short-chain dehydrogenase [<i>Pseudomonas balearica</i> DSM 6083]	1	-	-	-
667951125	magnesium transporter ApaG [<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
782987163	erythronate-4-phosphate dehydrogenase [<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	-
295982626	Chain A, The Crystal Structure Of A Functionally Unknown Protein Pa17 <i>Pseudomonas Aeruginosa</i> Pao1	1	-	-	-
759598655	ADP-heptose--LPS heptosyltransferase [<i>Pseudomonas</i> sp. PI1]	1	-	-	-
940104621	Bmp family protein [<i>Pseudomonas amygdali</i> pv. <i>criobotryae</i>]	1	-	-	-
557705144	carbon-phosphorus lyase complex subunit PhnI [<i>Pseudomonas aeruginosa</i> PA1]	1	-	-	-
26106142	replication initiator protein (plasmid) [<i>Pseudomonas resinovorans</i>]	1	-	-	-
667951083	biotin--protein ligase [<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
667954644	tRNA 2-thiocytidine biosynthesis protein TtcA [<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
330875529	pca operon transcriptional activator PcaQ [<i>Pseudomonas amygdali</i> pv. <i>morsprunorum</i> str. M302280]	1	-	-	-
782989181	aspartyl protease [<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	-
34335340	ParB (plasmid) [<i>Pseudomonas putida</i> ND6]	1	-	-	-
395807497	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase [<i>Pseudomonas stutzeri</i> DSM 10701]	1	-	-	-
912967068	serine/threonine protein kinase [<i>Pseudomonas</i> sp. 250J]	1	-	-	-
610708936	esterase [<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	-
782988037	ferredoxin [<i>Pseudomonas pseudoalcaligenes</i>]	1	-	-	-
940221093	Sigma E regulatory protein MucB/RseB	1	-	-	-

	[Pseudomonas syringae pv. primulae]				
	ATP F0F1 synthase subunit B				
735690104	[Pseudomonas tuomuerensis]	1	-	-	-
	phosphate acyltransferase [Pseudomonas				
610712828	pseudoalcaligenes AD6]	1	-	-	-
	transcriptional regulator [Pseudomonas				
631777112	knackmussii B13]	1	-	-	-
	murein transglycosylase [Pseudomonas				
667955502	mendocina S5.2]	1	-	-	-
	hypothetical protein VP02_01010				
801170682	[Pseudomonas kilonensis]	1	-	-	-
	isocitrate dehydrogenase [Pseudomonas				
610710043	pseudoalcaligenes AD6]	1	-	-	-
	molybdenum cofactor biosynthesis				
	protein MoaE [Pseudomonas mendocina				
667952799	S5.2]	1	-	-	-
	polyhydroxyalkanoate synthesis protein				
	PhaF [Pseudomonas aeruginosa				
575876457	PA38182]	1	-	-	-
	hypothetical protein AN454_16085				
953169346	[Pseudomonas aeruginosa]	1	-	-	-
	cell division protein FtsA [Pseudomonas				
512381854	putida NBRC 14164]	1	-	-	-
	AraC family transcriptional regulator				
953196677	[Pseudomonas aeruginosa]	1	-	-	-
	pilus assembly protein PilZ				
610712819	[Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
	Peroxiredoxin-1 OS=Homo sapiens				
Q06830	GN=PRDX1 PE=1 SV=1	1	-	-	-
	Stringent starvation protein B				
758827333	[Pseudomonas sp. FeS53a]	1	-	-	-
	DNA transporter [Pseudomonas				
782985246	pseudoalcaligenes]	1	-	-	-
	type 11 methyltransferase [Pseudomonas				
761533422	fluorescens]	1	-	-	-
	LexA repressor [Pseudomonas				
3980197	aeruginosa]	1	-	-	-
	spermidine/putrescine ABC transporter				
	ATP-binding protein [Pseudomonas				
667953051	mendocina S5.2]	1	-	-	-
	ABC transporter substrate-binding protein				
756407756	[Pseudomonas fluorescens]	1	-	-	-
	phosphoribosylglycinamide				
	formyltransferase [Pseudomonas				
763480775	oryzihabitans]	1	-	-	-

	cobalamin biosynthesis protein CobN				
667951695	[<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
	short chain dehydrogenase [<i>Pseudomonas</i>				
631780960	knackmussii B13]	1	-	-	-
	peptidylprolyl isomerase [<i>Pseudomonas</i>				
801170825	kilonensis]	1	-	-	-
	sarcosine oxidase subunit gamma				
713116049	[<i>Pseudomonas mediterranea</i> CFBP 5447]	1	-	-	-
	cell division protein MraZ [<i>Pseudomonas</i>				
610707999	pseudoalcaligenes AD6]	1	-	-	-
	short chain dehydrogenase/reductase				
	oxidoreductase [<i>Pseudomonas avellanae</i>				
407988023	BPIC 631]	1	-	-	-
	DNA mismatch repair protein				
764076832	[<i>Pseudomonas putida</i> S13.1.2]	1	-	-	-
	phosphogluconate dehydratase				
667953036	[<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
747108742	hemerythrin [<i>Pseudomonas fluorescens</i>]	1	-	-	-
	Flagellin protein FlaA [<i>Pseudomonas</i> sp.				
758837143	FeS53a]	1	-	-	-
	zinc-binding protein [<i>Pseudomonas</i>				
610709086	pseudoalcaligenes AD6]	1	-	-	-
	Sua5/YciO/YrdC/Yw1C family protein				
327481127	[<i>Pseudomonas stutzeri</i> DSM 4166]	1	-	-	-
	flagellar biosynthesis protein FliS				
735691839	[<i>Pseudomonas tuomuerensis</i>]	1	-	-	-
	MerR family transcriptional regulator				
949203967	[<i>Pseudomonas orientalis</i>]	1	-	-	-
	glutathione S-transferase [<i>Pseudomonas</i>				
771847176	sp. St29]	1	-	-	-
	cytochrome D ubiquinol oxidase subunit				
928538730	II [<i>Pseudomonas aeruginosa</i>]	1	-	-	-
	DSBA oxidoreductase [<i>Pseudomonas</i>				
66043538	syringae pv. syringae B728a]	1	-	-	-
	tRNA (5-methylaminomethyl-2-				
	thiouridylate)-methyltransferase				
404303738	[<i>Pseudomonas fluorescens</i> R124]	1	-	-	-
	urea carboxylase [<i>Pseudomonas</i>				
756404173	fluorescens]	1	-	-	-
	NADH dehydrogenase [<i>Pseudomonas</i>				
610713893	pseudoalcaligenes AD6]	1	-	-	-
	poly(A) polymerase [<i>Pseudomonas</i>				
747149982	balearica DSM 6083]	1	-	-	-
	phosphoribosylglycinamide				
703405640	formyltransferase 1 [<i>Pseudomonas</i>	1	-	-	-

	xanthomarina]				
	Fructose-bisphosphate aldolase A				
	OS=Oryctolagus cuniculus GN=ALDOA				
P00883	PE=1 SV=2	1	-	-	-
	Ribosome small subunit-stimulated				
758835970	GTPase EngC [Pseudomonas sp. FeS53a]	1	-	-	-
	orotidine 5'-phosphate decarboxylase				
759597787	[Pseudomonas sp. PI1]	1	-	-	-
	allantoate amidohydrolase [Pseudomonas				
610413751	aeruginosa PA96]	1	-	-	-
	cytochrome D ubiquinol oxidase subunit				
751086322	II [Pseudomonas stutzeri]	1	-	-	-
	Pyruvate dehydrogenase E1 component,				
939997495	partial [Pseudomonas syringae pv. aceris]	1	-	-	-
	conserved hypothetical protein				
327482068	[Pseudomonas stutzeri DSM 4166]	1	-	-	-
	trans-aconitate methyltransferase				
758536822	[Pseudomonas putida]	1	-	-	-
	multidrug transporter [Pseudomonas				
713118313	mediterranea CFBP 5447]	1	-	-	-
	Methionine aminopeptidase				
758821824	[Pseudomonas sp. FeS53a]	1	-	-	-
	hypothetical protein BN889_06423				
575877253	[Pseudomonas aeruginosa PA38182]	1	-	-	-
	hypothetical protein AU05_22225				
610708433	[Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
	aldehyde dehydrogenase [Pseudomonas				
26989210	putida KT2440]	1	-	-	-
	tRNA (guanine-N(1)-)-methyltransferase				
699968266	[Pseudomonas sp. MT-1]	1	-	-	-
	pilus assembly protein [Pseudomonas				
610712248	pseudoalcaligenes AD6]	1	-	-	-
	multidrug transporter [Pseudomonas				
787855250	chlororaphis]	1	-	-	-
	hypothetical protein AU05_22700				
610708327	[Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
	NrdR family transcriptional regulator				
667951015	[Pseudomonas mendocina S5.2]	1	-	-	-
	hypothetical protein PSPTOT1_1794				
213927941	[Pseudomonas syringae pv. tomato T1]	1	-	-	-
	sugar fermentation stimulation protein A				
426269737	[Pseudomonas sp. UW4]	1	-	-	-
	UvrABC system protein C [Pseudomonas				
940180626	meliae]	1	-	-	-
782989485	acetyl-CoA acetyltransferase	1	-	-	-

	[<i>Pseudomonas pseudoalcaligenes</i>]				
703407653	transposase [<i>Pseudomonas xanthomarina</i>]	1	-	-	-
	hypothetical protein AM274_30220				
926552931	[<i>Pseudomonas</i> sp. 655]	1	-	-	-
	urease subunit alpha [<i>Pseudomonas</i> sp.				
768454334	ES3-33]	1	-	-	-
	4-hydroxy-3-methylbut-2-enyl				
	diphosphate reductase [<i>Pseudomonas</i>				
390984617	stutzeri CCUG 29243]	1	-	-	-
	acetyl-CoA carboxylase [<i>Pseudomonas</i>				
692345832	rhizosphaerae]	1	-	-	-
	sulfurtransferase TusE [<i>Pseudomonas</i>				
782987882	pseudoalcaligenes]	1	-	-	-
	signal transduction protein [<i>Pseudomonas</i>				
379064956	stutzeri ATCC 14405 = CCUG 16156]	1	-	-	-
771844157	histidine kinase [<i>Pseudomonas</i> sp. Os17]	1	-	-	-
	LysR family transcriptional regulator				
733393164	[<i>Pseudomonas frederiksbergensis</i>]	1	-	-	-
	ATPase AAA [<i>Pseudomonas</i>				
610709189	pseudoalcaligenes AD6]	1	-	-	-
	FAD-dependent oxidoreductase				
821534776	[<i>Pseudomonas</i> sp. CCOS 191]	1	-	-	-
	hypothetical protein N005_16080				
713117381	[<i>Pseudomonas mediterranea</i> CFBP 5447]	1	-	-	-
	cytochrome B559 subunit alpha				
610710359	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	-
	NADH-quinone oxidoreductase subunit L				
667953923	[<i>Pseudomonas mendocina</i> S5.2]	1	-	-	-
	Multicopper oxidase [<i>Pseudomonas</i>				
748441850	batumici]	1	-	-	-
	hypothetical protein AU05_14435				
610710470	[<i>Pseudomonas pseudoalcaligenes</i> AD6]	1	-	-	-
	transcriptional regulator [<i>Pseudomonas</i>				
768553698	fluorescens]	1	-	-	-
	chemotaxis protein CheB [<i>Pseudomonas</i>				
782984637	pseudoalcaligenes]	1	-	-	-
	amino acid adenylation [<i>Pseudomonas</i> sp.				
926555687	655]	1	-	-	-
	precorrin-3B C17-methyltransferase,				
	partial [<i>Pseudomonas pseudoalcaligenes</i>				
610708147	AD6]	1	-	-	-
	sulfate ABC transporter periplasmic				
	sulfate-binding protein [<i>Pseudomonas</i>				
379065850	stutzeri ATCC 14405 = CCUG 16156]	1	-	-	-
459959278	hypothetical protein B195_19306	1	-	-	-

	[Pseudomonas sp. Lz4W]				
	hypothetical protein VC33_27195				
799188440	[Pseudomonas fluorescens]	1	-	-	-
	uroporphyrinogen-III synthase				
610713622	[Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
	ABC transporter ATP-binding protein				
929906083	[Pseudomonas sp. RIT-PI-q]	1	-	-	-
	hypothetical protein UM91_22925				
763477882	[Pseudomonas oryzihabitans]	1	-	-	-
	DNA-binding protein [Pseudomonas sp.				
751048836	W15Feb9B]	1	-	-	-
	Type IV pilus bioproteins protein				
	[Pseudomonas syringae pv.				
940231754	rhapiolepidis]	1	-	-	-
	LysR family transcriptional regulator				
761531258	[Pseudomonas fluorescens]	1	-	-	-
	pantoate--beta-alanine ligase				
452009581	[Pseudomonas stutzeri NF13]	1	-	-	-
257070341	TniR (plasmid) [Pseudomonas putida]	1	-	-	-
	Rieske family iron-sulfur cluster-binding				
953188777	protein [Pseudomonas aeruginosa]	1	-	-	-
	cupin [Pseudomonas aeruginosa				
564830502	VRFPA08]	1	-	-	-
	hypothetical protein HB4184_15610				
936612917	[Pseudomonas putida]	1	-	-	-
	ssDNA exonuclease RecJ [Pseudomonas				
747150290	balearica DSM 6083]	1	-	-	-
	coenzyme PQQ synthesis protein F				
95108664	[Pseudomonas entomophila L48]	1	-	-	-
	hypothetical protein AU05_22420				
610708365	[Pseudomonas pseudoalcaligenes AD6]	1	-	-	-
735692433	transporter [Pseudomonas tuomuerensis]	1	-	-	-

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