

The Global Transcription Response of *Acinetobacter baumannii* in the Presence of
Gallium Protoporphyrin IX

By

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Abstract

Acinetobacter baumannii is a bacterium identified as a serious threat to human health by the U.S. Centers for Disease Control and Prevention (CDC). *A. baumannii* has this designation because of its prevalence in hospitals and increased frequency of drug resistance worldwide. The CDC estimates 12,000 infections and 500 deaths are caused by *A. baumannii* every year in the United States.

Exacerbating the lack of pharmaceutical options, the crucial mechanisms by which *A. baumannii* copes and interacts with human systems is uncertain, making drug development difficult. However, *A. baumannii*, like practically all other organisms, requires iron for critical enzymes involved in energy production, DNA synthesis, and detoxification. Many other human pathogens have elaborate systems to acquire heme or free iron from the host and environment. While ferric iron uptake systems have been described for *A. baumannii*, a heme utilization system has not been identified in this organism. However, studies have suggested a possible role of heme acquisition for *A. baumannii*. The first example describes the lysis of red blood cells by *A. baumannii* and the second reported the ability of gallium protoporphyrin IX (GaPPIX), a molecule that is similar to the oxygen carrying heme found in our red blood cells, to kill multidrug-resistant *A. baumannii*.

In spite of the ability of *A. baumannii* to produce heme endogenously, the susceptibility of *A. baumannii* to GaPPIX supports utilization of exogenous heme. Therefore, we hypothesized *A. baumannii* incorporates GaPPIX in a manner similar to the normal iron porphyrin ring leading to enzyme dysfunctions and cell death. In silico analyses performed on >2500 *A. baumannii* genomes from NCBI GenBank resulted in a

subset of genes from the open pangenome of *A. baumannii*. Subsequent chokepoint analysis suggested points along the heme synthesis pathway as potential drug targets. Also, we studied the effects of GaPPIX usage on total metal concentrations and catalase activity.

This work supports GaPPIX as an effective anti-*A. baumannii* compound that kills multidrug-resistant isolates. Additionally, the toxicity of GaPPIX is likely partially due to incorporation of GaPPIX into the catalase of *A. baumannii*. Overall, this work supports future investigations into the heme metabolism of *A. baumannii* for antimicrobial target identification.

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INTRODUCTION

Brief History of Germ Theory

The conception of unseen causes of disease may be traced back to Hippocrates' description of "unwholesome" air around 400 BCE. However in 30 BCE, Marcus Terentius Varro described a more direct conception of infectious agents in *Rerum Rusticarum Libri Tres* (Three Books on Agriculture) "Precautions must also be taken in the neighborhood of swamps ... because there bred certain animaculae which cannot be seen by the eyes, which float in the air and enter the body through the mouth and nose and there cause serious diseases (1)." Girolamo Fracastoro described the beginning of the germ theory of disease and named syphilis in his rhyme "Syphilis sive morbus Gallicus" (1530; "Syphilis or the French Disease) (2) that describes the disease presentation. Fracastoro outlined his concept of epidemic diseases in *De contagione et contagiosis morbis* (1546; "On Contagion and Contagious Diseases"), stating that each is caused by a different type of rapidly multiplying minute body and that these bodies are transferred from the infector to the infected in three ways: by direct contact; by carriers such as soiled clothing and linen; and through the air (3). Proof supporting the idea that unseen animaculae exist had to wait for the development of microscopes capable of visualizing these small organisms. These scopes allowed the development of the discipline of microbiology. Two of the earliest adopters of microscopes were Athanasius Kircher and Antonie van Leeuwenhoek.

Leeuwenhoek described the appearance of bacteria and protozoa in water in a letter published in the *Philosophical Transactions of the Royal Society* in 1677 (4). Kircher is likely the first to have described proof for the Germ Theory of Disease in 1658 in

“Scrutinium Physico-medicum” (5), in which, Kircher can be attributed with the first description of the plague being caused by vermiculi, microscopic worms, in victims’ blood. Kircher may have been visualizing human cells because the likely power of his microscope was only 32x magnification (6).

In spite of these writings, the widespread understanding that bacteria were transmissible, and the etiology of disease was still unappreciated into the 19th century. In spite of not understanding the cause of the diseases, correlative data aided Ignaz Semmelwies and John Snow to make major breakthroughs in medicine and public health describing the transmission of two diseases. In 1847 CE, Semmelwies reported the analysis of two obstetric wards from which he deduced hand washing would reduce “cadaveric contamination and puerperal fever.” Even though he was unaware of the bacteria that caused the disease, *Streptococcus pyogenes*, his intervention was successful (7). Likewise, John Snow used statistical modeling to track a London cholera outbreak in 1854 CE, described in Medical Hygiene 1849 CE essay, “On the Mode of Communication of Cholera” (8). This was followed by a more detailed treatise in 1855 CE that incorporated the results of his investigation on the role of the water supply in the Soho epidemic of 1854 CE (8, 9). Snow was also unaware of the bacterial agent that caused the disease.

Semmelwies’ and Snow’s contemporary Friedrich Gustav Jakob Henle wrote “Von den Miasmen und Kontagien” (‘On Miasma and Contagia’) in 1840 CE as an early argument for the germ theory of disease and was the mentor of Robert Koch. Koch’s postulates are a cornerstone of modern microbiology and concept of infectious disease. Koch discovered and described the bacterial etiological agents of tuberculosis, cholera, and anthrax. Since this development, the germ theory of disease has become universal in

modern healthcare and its acceptance has spurred research on identification of infectious organisms. Also, the acceptance of infectious agents causing disease supports the need and target for discovering drugs to treat these infections (10).

Following the direct evidence of microbes causing disease, diagnostic tools were required for the identification of infecting organisms. In addition to microscopes, Koch's staining method allowed him to identify the tuberculosis pathogen. However, following an 1882 CE lecture describing this staining method, Koch was approached by Paul Ehrlich with suggested improvements. Koch and Erlich were collaborators from then onward. Through this relationship, Erlich began work at Institute of Infectious Diseases, now the Robert Koch Institute, in Berlin, Germany. This position afforded Ehrlich with opportunities for research into vaccines.

The culmination of Ehrlich's experience with *in vivo* staining led him to hypothesize that stains and more broadly chemicals could be used to target physiology and would have a therapeutic effect. He endeavored to find chemicals to kill all pathogens. He successfully killed trypanosomes that caused Guinea Pig Trypanosoma, with trypan red (11). This buoyed him to continue with a greater screening of atoxyl, an arsenic containing compound, which had been previously shown to be effective against African Sleeping Sickness which is cause by *Trypanosoma brucei*. It was likely effective because As (III) has been shown to inhibit pyruvate oxidation pathway and tricarboxylic acid cycle and As (V) may substitute for phosphorus by binding thiols and replacing phosphate in ATP leading to uncoupled mitochondrial respiration (12, 13). Atoxyl had, however, been proven to exhibit neurotoxicity that can lead to blindness. Confident that chemical changes

to atoxyl could reduce the side effects, Ehrlich turned his focus to developing therapeutics to treat syphilis based on arsenic containing compounds (14, 15).

Ehrlich's research beginning in 1904 CE is considered the founding of chemotherapy and the start of the modern antibiotic era. This is because the first large scale screening programs began to identify "magic bullets" against syphilis (15). These chemicals would be "magic" because they were expected to exhibit therapeutic differential toxicity, meaning the chemical would be toxic toward the *Treponema pallidum* spirochetes, subgroups of which cause yaws, bejel, and syphilis, with few toxic side effects for the host. These compounds would result in a great improvement over the standard of treatment at the time. The standard of treatment at the time being inorganic mercury salts, which is another heavy metal. This treatment resulted in heavy metal toxicity and had poor efficacy. The clinical symptoms vary depending on the form or route of exposure. The neurological and neuromuscular effects are common symptoms of mercury poisoning and may be lethal. The discovery of the arsenic containing Compound 606 lead to the clinical testing and development of Salvarsan, which became the most prescribed drug in the world. Additional refinements of Salvarsan lead to the development of Neosalvarsan to improve solubility and reduce toxicity. Neosalvarsan was the most effective treatment for syphilis until penicillin was introduced in 1942 CE.

Historically in China and Egypt, mold therapy had been used to improve wound healing prior to 1700 CE. In fact, Joseph Lister used *Penicillium glaucum* lysate to cure an infection as early as 1871 CE. However, it wasn't until 1928 CE when Alexander Fleming decided to study the lysis of bacteria caused by a fungal contaminant that the first antibiotic, penicillin, would be discovered. Identifying natural products to be used as

antibiotics has proven successful since the majority of antibiotics used in human medicine are products of bacteria and fungi, the majority of these antibiotics being derived from *Streptomyces*. The genus *Streptomyces* consists of approximately five hundred and fifty species of Gram-positive soil organisms with genomes that have high GC content. These bacteria produce antimicrobial secondary metabolites while in competition with other microbes. The identification of new antibiotics using this method and chemical manipulation, shown to be effective by Ehrlich, has led to the antibiotic armamentarium that we have today.

Anti-infective Medications

This armamentarium consists of mainly 13 classes of antibiotics based on chemical structures, whose discovery covers approximately 70 years: β -lactams, sulfonamides, aminoglycosides, tetracyclines, chloramphenicol, macrolides, glycopeptides, ansamycins, quinolones, streptogramins, oxazolidinones, lipopeptides, and lincosamides. The timeline is presented in Figure 1. Additional classification methods divide the known antibiotic compounds by other characteristics or treatment strategies. For example, those based on a classification set forth in the Uniform System of Classification developed by IQVIA America and the Pharmaceutical Marketing Research Group.

β -lactams

The primary classes of β -lactams affect bacteria by inhibiting cell wall biosynthesis. This is a structure that is not shared by humans, so it is a selective drug target. All members of the β -lactam class include a four-member lactam ring that is a cyclic amide. β -lactams can be divided into groups based on five ring systems. First, penams contain 6-

DIFFERENT CLASSES OF ANTIBIOTICS - AN OVERVIEW

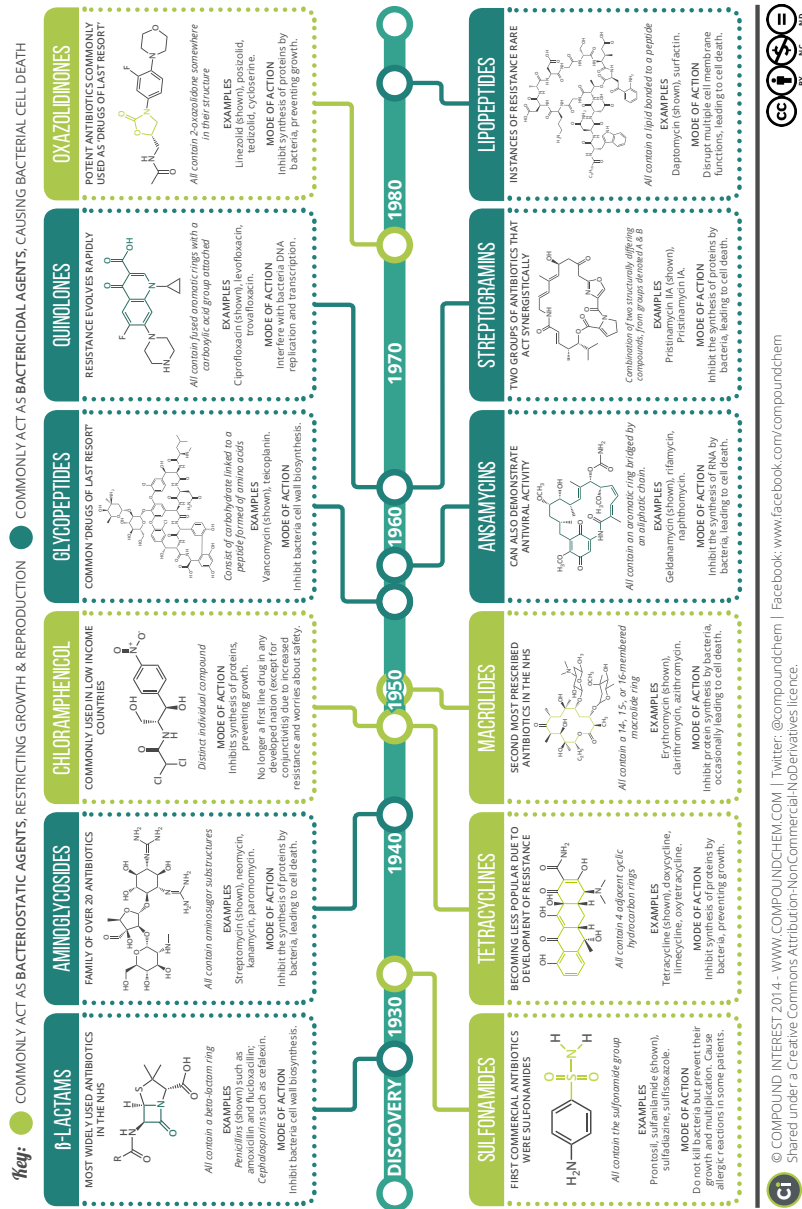


Figure 1. Timeline of the discovery of different antibiotic classes. The antibiotic era began with the discovery of penicillin and has led to the discovery of multiple classes of antibiotics.

aminopenicillanic acid such as penicillins. Second and third are unsaturated penems and carbapenems that are structurally related with the exception that penems contain sulfur in the rings, while carbapenems have carbon at the cognate position of penems. Both contain double bonds in the ring system that differentiates them from the saturated penicillins. Examples of these β -lactams can be seen in Figure 2. Fourth, cephem consist of a β -lactam ring fused to a six-member sulfur-containing dihydrothiazine ring in contrast to penicillin that contains a five-member thiazolidine ring. The central moiety for the cephem cephalosporin is 7-aminocephalosporanic acid. Examples of cephalosporins may be seen in Figure 3. Lastly, monobactam consist of a β -lactam that is not fused to another ring (17).

Sulfonamides and Trimethoprim

Sulfonamides and Trimethoprim inhibit folic acid synthesis with distinct modes of action. Sulfonamides, such as sulfanilamide or sulfisoxazole, stop para-aminobenzoic acid, PABA, from incorporating into folic acid by inhibition of dihydropterate synthase. Sulfonamides are bacteriostatic because they slow the replication of treated bacteria without killing the bacteria. Trimethoprim reduces a down-stream reaction in folic acid synthesis by inhibiting dihydrofolate reductase (18). Bactrim, the combination of a sulfonamide, sulfamethoxazole, and trimethoprim, is used to synergistically reduce folic acid synthesis. Humans do not share the targets of these drugs with bacteria, making these useful for the treatment of bronchitis, shigellosis, ear infections, and urinary tract infections (18).

Aminoglycosides

The aminoglycosides, as seen in Figure 4, are broad-spectrum, meaning they kill diverse genera of bacteria, bactericidal antibiotics that include gentamicin, amikacin,

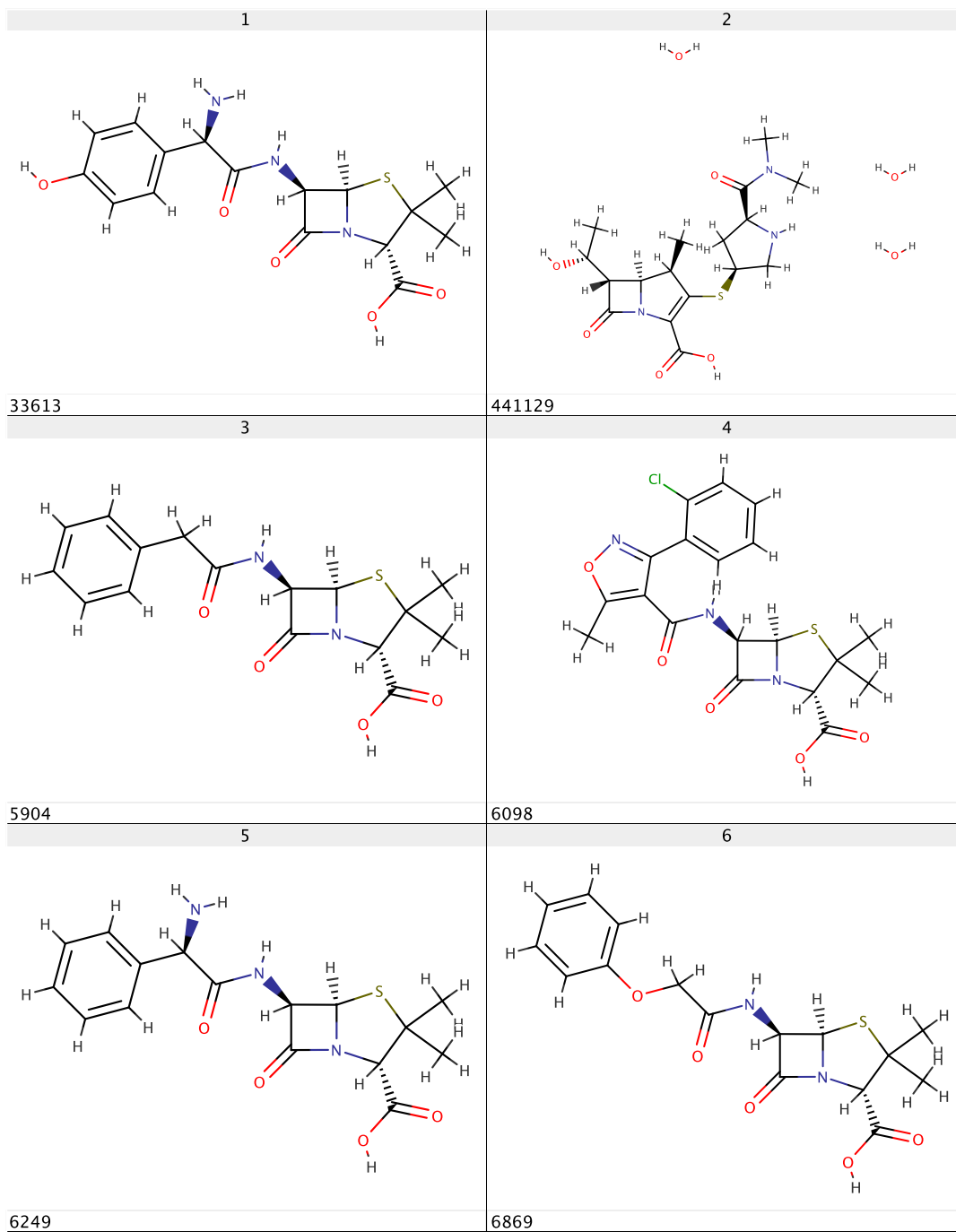


Figure 2. World Health Organization list of essential medications anti-infective β

- Lactams. 1) Amoxicillin 2) Meropenem 3) Benzylpenicillin 4) Cloxacillin 5)

Ampicillin 6) Penicillin V. Compiled from ChemBank using MarvinSketch v.16.2.29.

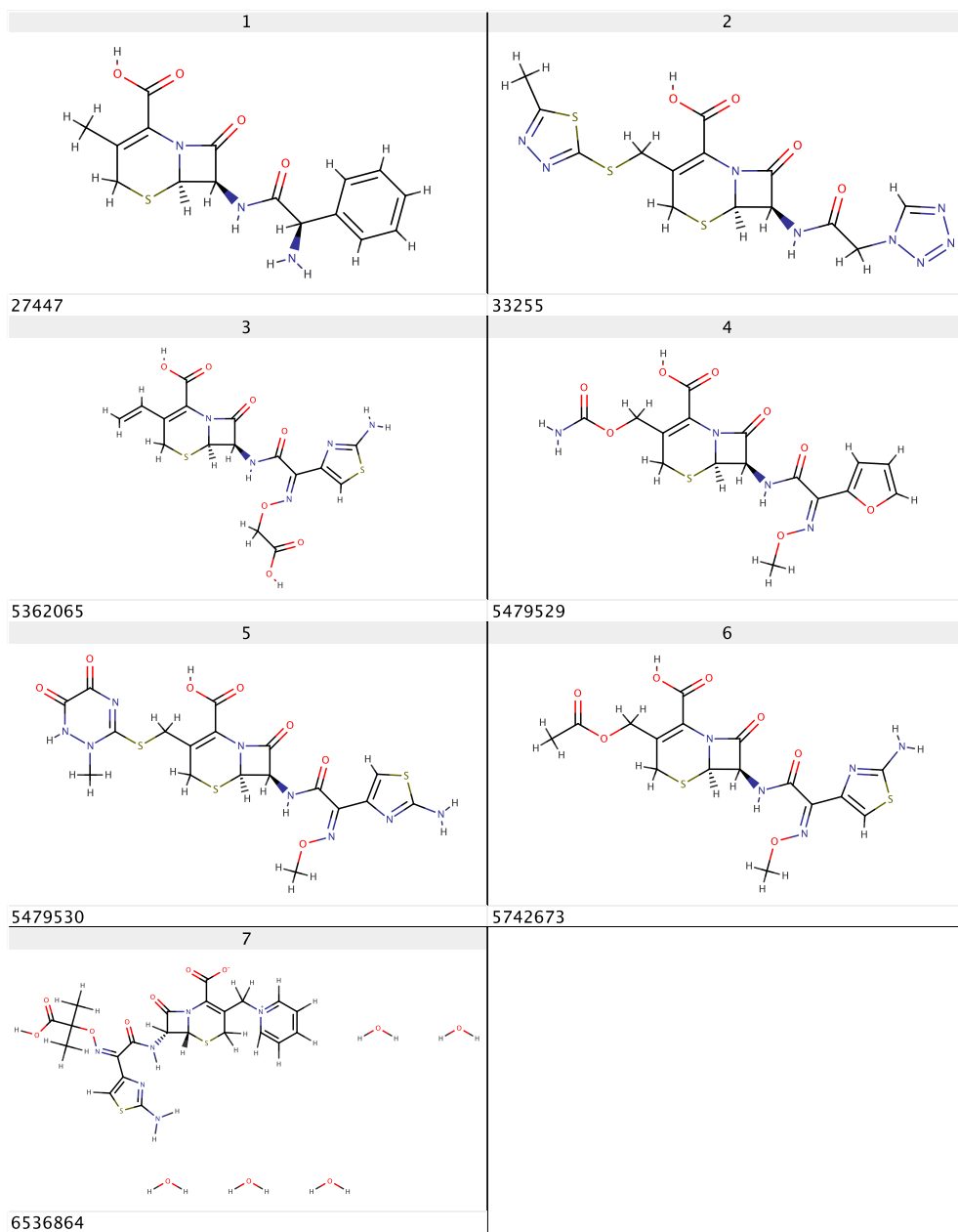


Figure 3. World Health Organization list of essential medications anti-infective cephalosporins. 1) Cefalexin 2) Cefazolin 3) Cefixime 4) Cefuroxime 5) Ceftriaxone 6) Cefotaxime 7) Ceftazidime. Compiled from ChemBank using MarvinSketch v.16.2.29.

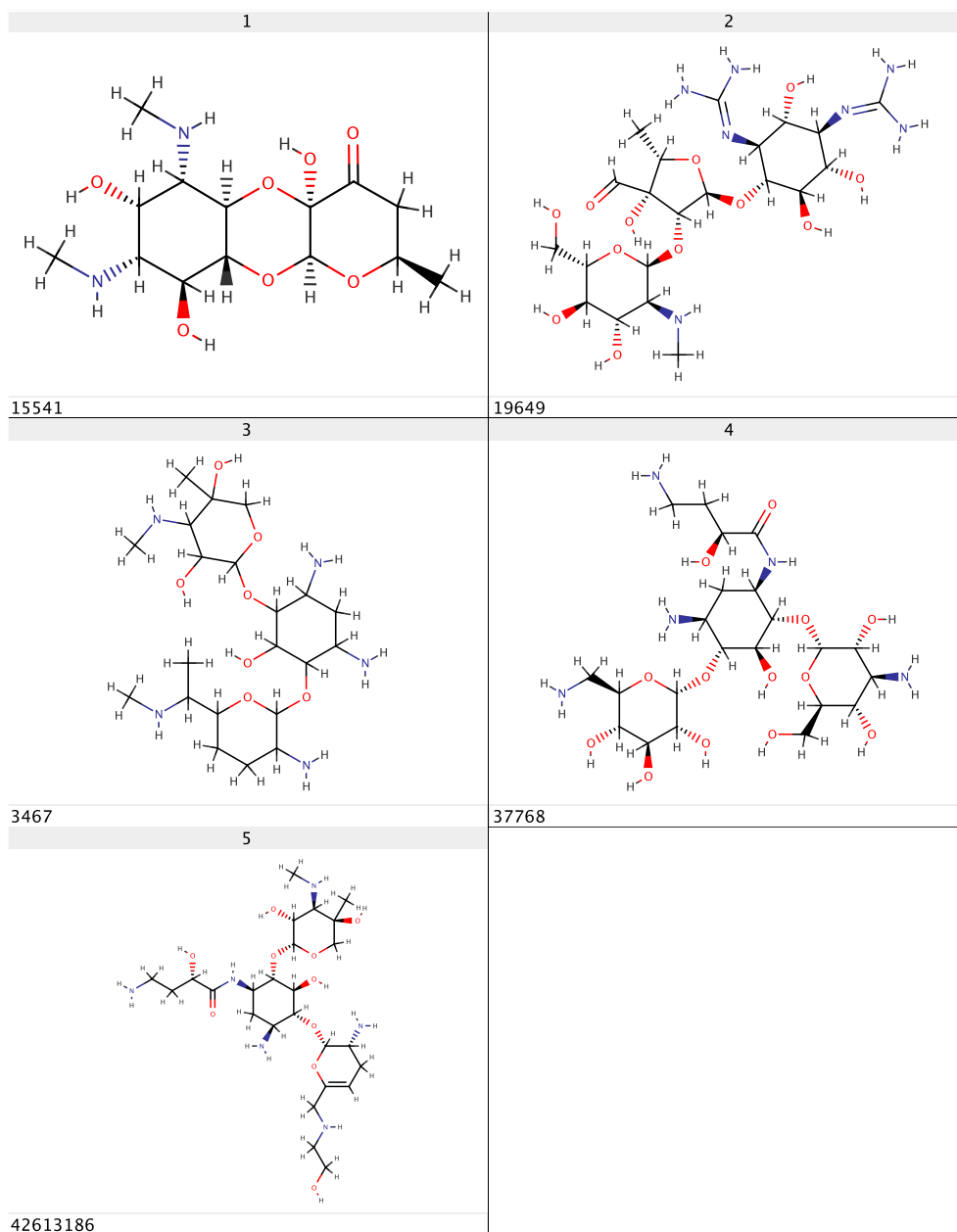


Figure 4. World Health Organization list of essential medications anti-infective aminoglycosides. 1) Spectinomycin 2) Streptomycin 3) Gentamicin 4) Amikacin 5) Plazomicin. Compiled from ChemBank using MarvinSketch v.16.2.29.

kanamycin, neomycin, streptomycin, and tobramycin. These drugs inhibit protein synthesis by binding the 30S ribosomal subunit. This subunit is distinct when compared to eukaryotic 40S ribosomal subunit. Aminoglycosides are concentration-dependent antibiotics because the peak concentrations generally have a narrow therapeutic index as the peak serum levels and their use is indicated for serious Gram-negative bacillary infections. This class may be used for empirical treatment plans due to the broad-spectrum effectiveness of this class for Gram-negative bacteria (19).

Tetracyclines

Aureomycin, the first tetracycline, was first described in 1948. Resistance to Aureomycin was reported within the first year of use, prompting an increased effort to change the structure of the drug. These compounds are characterized by the naphthacene ring system. Tetracyclines were one of the first class of drugs to be developed by semisynthetic derivatization. Conover derivatized the C7 chlorine to augment the activity of this drug. The C7 deschloro derivative of Aureomycin had more favorable solubility and pharmacological activity. This compound became Tetracycline. Aureomycin, Terramycin, and Tetracycline were in use by the mid-1950s and are believed to have saved thousands of lives by this time. This success supported the development of second-generation semisynthetic tetracyclines, including methacycline. Methacycline became the building block for the widely used doxycycline. The third-generation tetracyclines were developed in the late 1980s based on minocycline. This led to the FDA approval of tigecycline in 2006. Tetracyclines are used for treatment of many bacterial and microbial infections, such as *Haemophilis ducreyi*, *Yersinia pestis*, *Bacillus anthracis*, and *Vibrio cholerae*. The primary mode of action for tetracyclines is inhibition of protein synthesis

by binding to the 16S RNA in the 30S ribosomal subunit by H-bonds and metal bridge with magnesium and RNA in the A-region (20).

Chloramphenicol

Chloramphenicol was the first commercial antibiotic to be produced entirely by chemical synthesis based on a natural products structure. The drug was first discovered by isolation from *Streptomyces venezuelae* in 1947 and has been included on the List of Essential Medicines of the World Health Organization. Chloramphenicol is a bacteriostatic broad-spectrum antibiotic that inhibits protein synthesis by binding A2451 and A2452 in the 23S rRNA. This binding inhibits peptidyl transferase activity and disrupts substrate binding. Chloramphenicol is not currently in wide use in the United States but is highly prescribed in other countries. It is the most prescribed ophthalmic drug in Ireland and is used prophylactically in Mexico for neonates (21).

Macrolide

Pikromycin was isolated from *Streptomyces* spp. in 1950 and was found to contain the characteristic macrocyclic lactone ring present in all macrolide antibiotics (examples in Figure 5). The ring structures include 12-, 14-, 15-, and 16-membered rings (22). The most significant of these being the 14-member ring containing erythromycin, which is the progenitor of the second-generation 14-membered ring containing clarithromycin and 15-membered ring containing azithromycin. Miokamycin, rokitamycin, and tilmicosin are 16-membered ring containing second-generation macrolides. The third-generation are ketolides including the 16-membered ring compounds telithromycin, cethromycin, and solithromycin. All generations are protein synthesis inhibitors that bind the nucleobase of A2058 of the 23S rRNA leading to inhibition of protein synthesis.

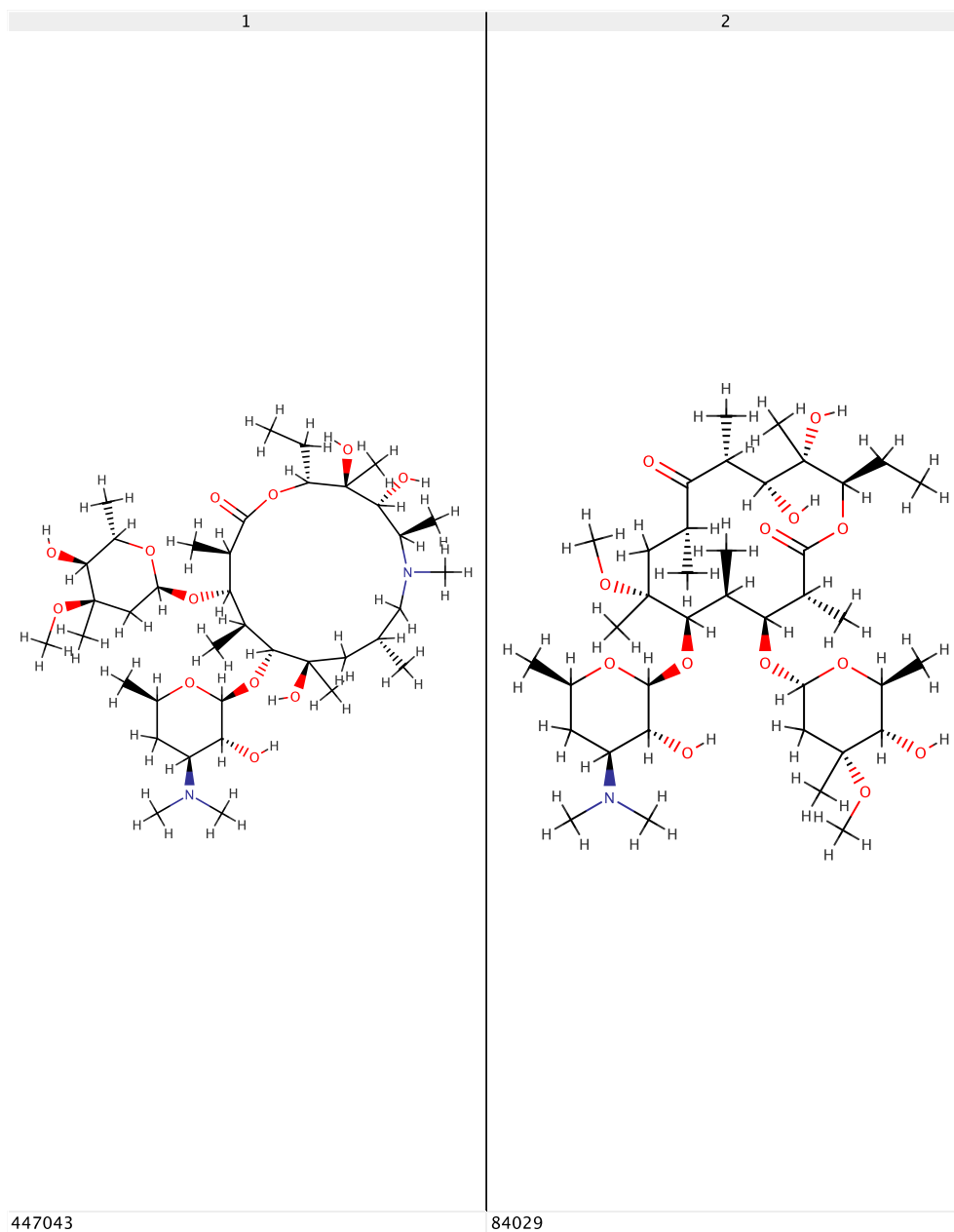


Figure 5. World Health Organization list of essential medications anti-infective macrolides 1) Azithromycin 2) Clarithromycin. Compiled from ChemBank using MarvinSketch v.16.2.29.

Glycopeptides

Glycopeptides are often considered antibiotics of last resort. This in part is due to the efficacy these drugs exhibit toward drug-resistant *Staphylococcus aureus*, *Enterococcus* spp., and *Clostridium difficile* (23). These drugs are also a last resort because of poor pharmacokinetic properties and toxicity. Glycopeptides have a core heptapeptide aromatic amino acid motif. This core can be covalently linked with sugar, chlorine, and lipid chain moieties. The first-generation of glycopeptides were natural products of actinomycetes and included vancomycin (Figure 6) and teicoplanin reported in 1958 and 1978, respectively. Vancomycin contains three aromatic amino acids, while teicoplanin contains four aromatic amino acids that are responsible for imparting the conformation to target the binding pocket for D-Ala-D-Ala. Glycopeptide resistance is present and may be encoded in the chromosome and on plasmids. These genes modify the peptidoglycan precursors leading to 1000-fold decrease in binding by the drug. The resistance and poor pharmacodynamics of these drugs has led to the development of second-generation glycopeptides, including telavancin, dalbavancin, and oritavancin (24).

Ansamycins

Ansamycins were first isolated from *Amycolatopsis mediterranei* in 1959 and possess an aromatic moiety and an aliphatic chain. The aromatic portion may be naphthalene, naphthoquinone, benzene, and benzoquinone. Rifamycin, a naphthalene-containing compound, has high potency against mycobacteria and the precursor of rifampicin. These drugs are DNA-dependent RNA synthesis inhibitors because of the high affinity against RNA-polymerase of prokaryotes. Rifampicin in combination with

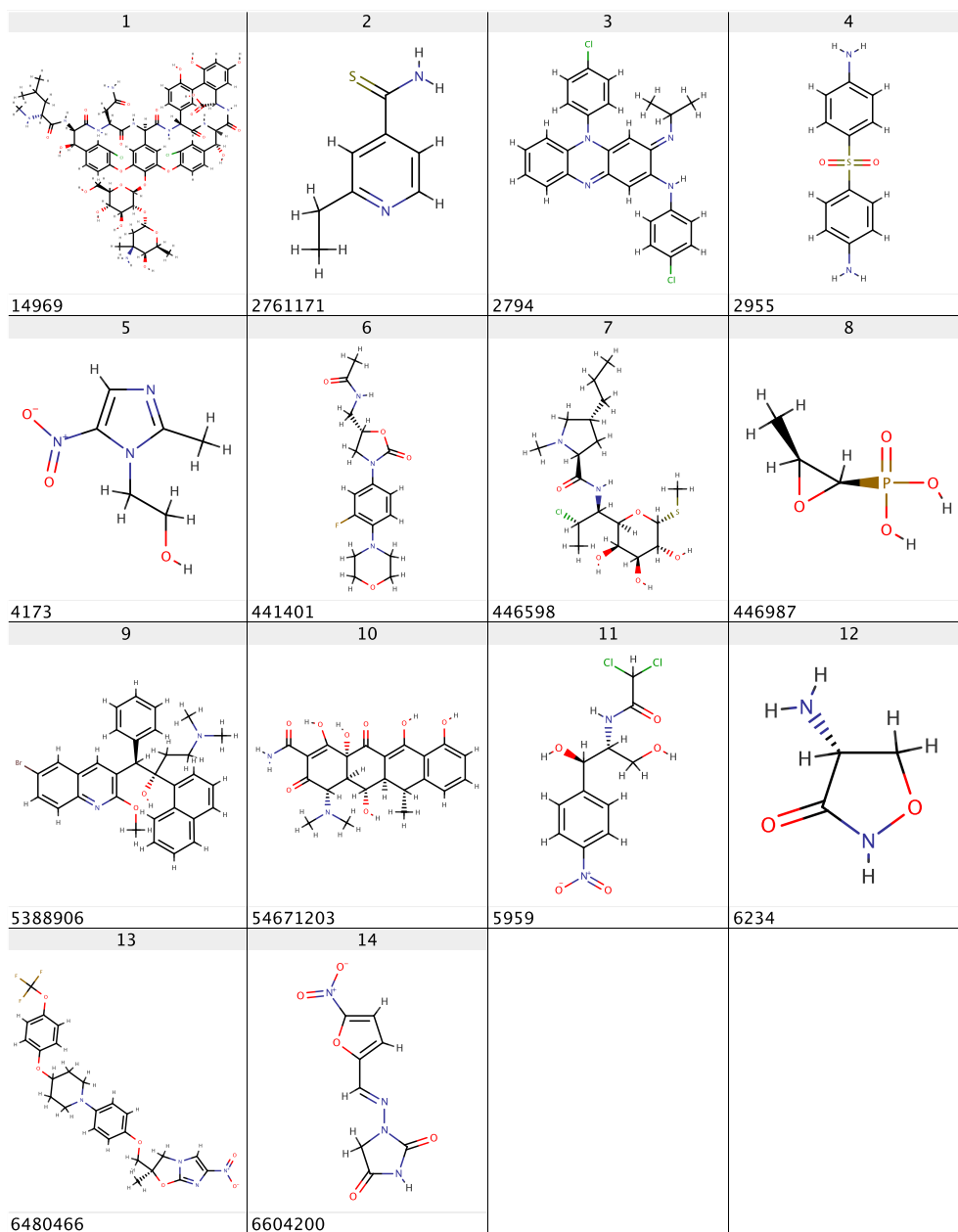


Figure 6. World Health Organization list of essential medications anti-infectives 1) Vancomycin 2) Ethionamide 3) Clofazime 4) Dapsone 5) Metronidazole 6) Linezolid 7) Clindamycin 8) Fosfomicin 9) Bedaquiline 10) Doxycycline 11) Chloramphenicol 12) Cycloserine 13) Delamanid 14) Nitrofurantoin. Compiled from ChemBank using MarvinSketch v.16.2.29.

isoniazid for treatment of tuberculosis and is included on WHO's list of essential medications (25).

Quinolones

Quinolones possess a bicyclic core, 4-quinolone, and were discovered in the early 1960s, although there is some dispute as nalidixic acid may have been discovered years earlier in the late 1950s (26). The development of the second-generation quinolones in the 1970-1980 led to broader activity and better pharmacokinetics of this class. The notable fluoroquinolones included ciprofloxacin and ofloxacin improved treatment to Gram-positive and Gram-negative pathogens. The quinolones are topoisomerase type II inhibitors, and are deleterious to DNA synthesis, specifically inhibiting bacterial topoisomerase IV and DNA gyrase that are critical for changing the supercoil conformation of DNA for synthesis. This class has had extensive derivatization leading to the development of second- and third-generations of quinolones, including fluoroquinolones (Figure 7). Two modes of resistance have been identified, mutation of target genes and plasmid borne-resistance. Plasmid-mediated resistance may include AAC(6')-Ib-cr, a derivative of aminoglycoside acetyltransferase, DNA mimics, and efflux pumps.

Streptogramins

Streptogramins consist of at least two unrelated molecules, macrolactones and cyclic hexadepsipeptides, with synergistic binding of the 50S subunit of ribosomes to inhibit protein synthesis (27). In 1952, virginiamycin became the first identified streptogramin isolated from *Streptomyces virginiae* (28).

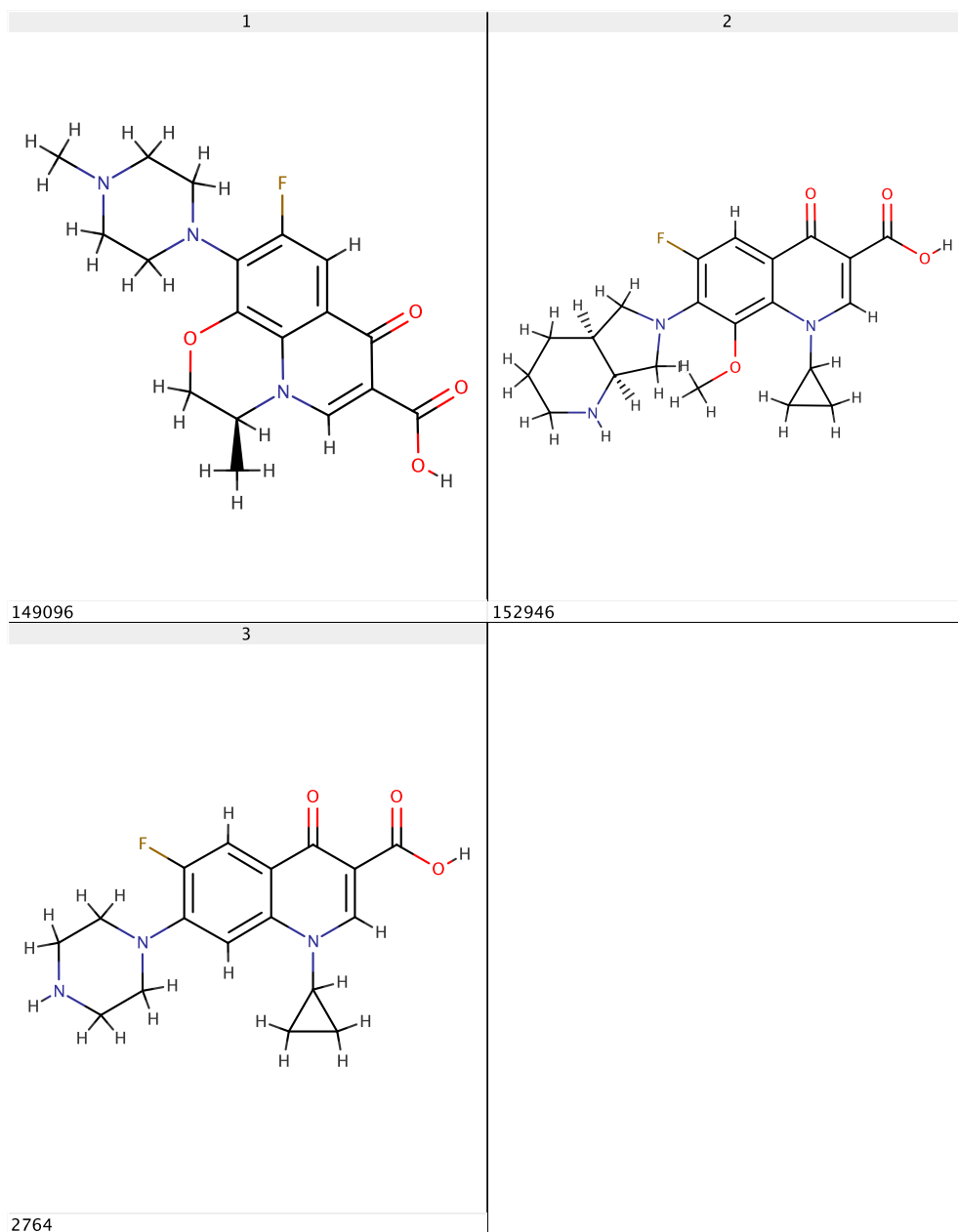


Figure 7. World Health Organization list of essential medications anti-infective fluoroquinolones 1) Levofloxacin 2) Moxifloxacin 3) Ciprofloxacin
Compiled from ChemBank using MarvinSketch v.16.2.29.

Oxazolidinones

Oxazolidinones are azoles, such as linezolid (Figure 6), and are totally synthetic with activity against Gram-positive *S. aureus*, *Staphylococcus epidermidis*, and *Streptococcus pneumoniae* (29). The mode of action for oxazolidinones is inhibition of protein synthesis by binding to the P site of the 50S ribosomal subunit and resistance is rare (30).

Lipopeptides

Lipopeptides have two main classes either with a cyclic peptide headgroup and linear lipopeptides with one or more lipid chains and are amphiphilic. Bacillomycin, Daptomycin, Echinocandins, and Polymyxins are examples of lipopeptides. As seen in Figure 8, Polymyxin B and Colistin have very similar structures. Some maybe antibiotics and others are toll-like receptor agonists (31). These drugs may have significant toxicity due to their mode of action which is cell membrane interaction and perturbation (32).

World Health Organization Essential Medication List

The World Health Organization has compiled a model essential medications list (WHO_EML) that has been updated every two years since 1977. The last update was completed in June of 2019 (33). Fifty-three new medications and 19 new formulations were considered for addition to the list. The expert committee recommended the deletion of 9 medications, the addition of 16 new formulations, the addition of 28 new medications for EML, and 23 for EMLc.

A subset of this list includes essential anti-infectives with some being antibiotics that have efficacy toward bacteria (Table 1) including Antimycobacteria and Antituberculoïd drugs (Figure 9) (33). The expert committee highlighted the adoption and

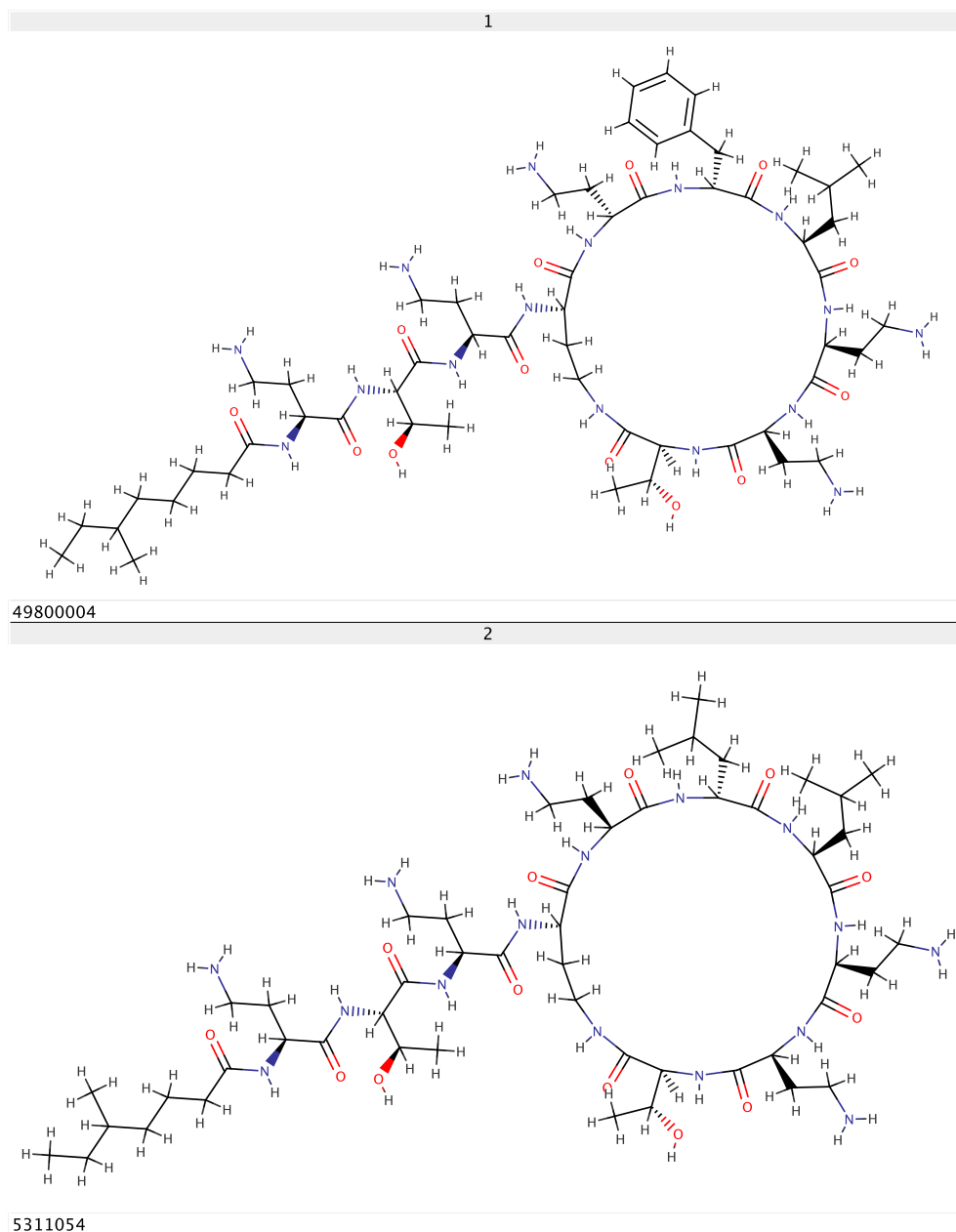


Figure 8. World Health Organization list of essential medications anti-infective polymyxins. 1) Polymyxin B 2) Colistin. Compiled from ChemBank using MarvinSketch v.16.2.29.

Table 1. WHO essential medicine list

Name	Compound ID	Molec. Form.	Mol. Wt.	Solubility	MP ^{&}	Kow ^s	Group
Amikacin	37768	C ₂₂ H ₄₃ N ₅ O ₁₃	585.6	50,000	214	-8.78	aminoglycoside
Amoxicillin	33613	C ₁₆ H ₁₉ N ₃ O ₅ S	365.4	3430	194	0.87	beta-lactam aminopenicillin
Amoxicillin clavulanic acid	23665637	C ₂₄ H ₂₈ N ₄ O ₁₀ S	564.6	ND	ND	ND	combination
Ampicillin	6249	C ₁₆ H ₁₉ N ₃ O ₄ S	349.4	1000-10000 at 70°F	388-392	1.35	beta-lactam penicillin
Azithromycin	447043	C ₃₈ H ₇₂ N ₂ O ₁₂	749	2.37	126	3.03	macrolide
Bedaquiline	5388906	C ₃₂ H ₃₁ BrN ₂ O ₂	555.5	Insoluble	118	7.74	diarylquinoline
Benzathine benzylpenicillin	25137901	C ₄₈ H ₅₆ N ₆ O ₈ S ₂	909.1	ND	ND	ND	combination
Benzylpenicillin	5904	C ₁₆ H ₁₈ N ₂ O ₄ S	334.4	210	214-217	1.83	beta-lactam penicillin
Cefalexin	27447	C ₁₆ H ₁₇ N ₃ O ₄ S	347.4	10000	326.8	0.65	beta-lactam 1st-gen cephalosporin
Cefazolin	33255	C ₁₄ H ₁₄ N ₈ O ₄ S ₃	454.5	210	198-200	-0.58	beta-lactam 1st-gen cephalosporin
Cefixime	5362065	C ₁₆ H ₁₅ N ₅ O ₇ S ₂	453.5	55.11	218-225	-0.4	beta-lactam 3rd- gen cephalosporin
Cefotaxime	5742673	C ₁₆ H ₁₇ N ₅ O ₇ S ₂	455.5	146	ND	-0.5	beta-lactam 3rd- gen cephalosporin
Ceftazidime	6536864	C ₂₂ H ₃₂ N ₆ O ₁₂ S ₂	636.7	ND	ND	ND	beta-lactam 3rd- gen cephalosporin

Table 1 1 of 4

Name	Compound ID	Molec. Form.	Mol. Wt.	Solubility	MP ^{&}	Kow ^s	Group
Ceftazidime avibactam	77050660	C ₂₉ H ₃₃ N ₉ O ₁₃ S ₃	811.8	ND	ND	ND	combination
Ceftriaxone	5479530	C ₁₈ H ₁₈ N ₈ O ₇ S ₃	554.6	105	>155	-1.7	beta-lactam 3rd- gen cephalosporin
Cefuroxime	5479529	C ₁₆ H ₁₆ N ₄ O ₈ S	424.4	145	218-225	-0.16	beta-lactam 2nd- gen cephalosporin
Chloramphenicol	5959	C ₁₁ H ₁₂ Cl ₂ N ₂ O ₅	323.13	2500	171	1.14	
Ciprofloxacin	2764	C ₁₇ H ₁₈ FN ₃ O ₃	331.34	<1	255-257	0.28	fluoroquinolone
Clarithromycin	84029	C ₃₈ H ₆₉ NO ₁₃	748	0.33	220	3.16	macrolide
Clindamycin	446598	C ₁₈ H ₃₃ ClN ₂ O ₅ S	425	30.61	ND	2.16	lincosamide
Clofazimine	2794	C ₂₇ H ₂₂ Cl ₂ N ₄	473.4	0.225	210-212	7.66	phenazine dye
Cloxacillin	6098	C ₁₉ H ₁₈ ClN ₃ O ₅ S	435.9	13.9	ND	2.48	beta-lactam
Colistin	5311054	C ₅₂ H ₉₈ N ₁₆ O ₁₃	1155.4	238	200-220	-2.4	polymyxin
Cycloserine	6234	C ₃ H ₆ N ₂ O ₂	102.09	877000	155.5	-0.9	isoxazolines
Dapsone	2955	C ₁₂ H ₁₂ N ₁ O ₂ S	248.3	380 @37c	347-349	0.97	sulfones
Delamanid	6480466	C ₂₅ H ₂₅ F ₃ N ₄ O ₆	534.5	ND	ND	ND	nitro-dihydro- imidazooxazole
Doxycycline	54671203	C ₂₂ H ₂₄ N ₂ O ₈	444.4	50000	ND	0.63	tetracycline
Ethambutol	14052	C ₁₀ H ₂₄ N ₂ O ₂	204.31	ND	171.5-174.5	-0.3	antimycobacterial
Ethambutol isoniazid pyrazinamide rifampicin	136170967	C ₆₄ H ₉₄ N ₁₂ O ₁₆	1287.5	ND	ND	ND	combination

Table 1 2 of 4

Name	Compound ID	Molec. Form.	Mol. Wt.	Solubility	MP ^κ	Kow [§]	Group
Ethambutol isoniazid rifampicin	135483893	C ₅₉ H ₈₉ N ₉ O ₁₅	1164.4	ND	ND	ND	combination
Ethionamide	2761171	C ₈ H ₁₀ N ₂ S	166.25	<1000 @70f	327-331	0.5	thioamides
Fosfomycin	446987	C ₃ H ₇ O ₄ P	138.06	50000	94	-1.6	novel
Gentamicin	3467	C ₂₁ H ₄₃ N ₅ O ₇	477.6	100000	105	-3.1	aminoglycoside
Isoniazid	3767	C ₆ H ₇ N ₃ O	137.14	>100000 @77f	340.5	-0.7	antituberculosis
Isoniazid pyrazinamide rifampicin	135483901	C ₅₄ H ₇₀ N ₁₀ O ₁₄	1083.2	ND	ND	ND	combination
Isoniazid rifampicin	135483892	C ₄₉ H ₆₅ N ₇ O ₁₃	960.1	ND	ND	ND	combination
Levofloxacin	149096	C ₁₈ H ₂₀ FN ₃ O ₄	361.4	Insoluble	225-227	2.1	fluoroquinolones
Linezolid	441401	C ₁₆ H ₂₀ FN ₃ O ₄	337.35	3000	181.5-182.5	0.9	oxazolidinone
Meropenem	441129	C ₁₇ H ₃₁ N ₃ O ₈ S	437.5	ND	ND	ND	beta-lactam carbapenem
Meropenem vaborbactam	86298703	C ₂₉ H ₄₁ BN ₄ O ₁₀ S ₂	680.6	ND	ND	ND	combination
Metronidazole X	4173	C ₆ H ₉ N ₃ O ₃	171.15	<1 @68f	316-320	-0.02	nitroimidazoles
Moxifloxacin	152946	C ₂₁ H ₂₄ FN ₃ O ₄	401.4	1146	238-242	2.9	fluoroquinolones
Nitrofurantoin	6604200	C ₈ H ₆ N ₄ O ₅	238.16	<100 @66F	514	-0.47	nitrofuran
p-aminosalicylic acid	4649	C ₇ H ₇ NO ₃	153.14	1690	150.5	0.89	antituberculosis
Phenoxyethylpeni cillin penicillin V	6869	C ₁₆ H ₁₈ N ₂ O ₅ S	350.4	<1000 @55f	248-262	2.09	beta-lactam

Table 1 3 of 4

Name	Compound ID	Molec. Form.	Mol. Wt.	Solubility	MP ^{&}	Kow [§]	Group
Piperacillin tazobactam	9918881	C ₃₃ H ₃₉ N ₉ O ₁₂ S ₂	817.9	ND	ND	ND	combination
Plazomicin	42613186	C ₂₅ H ₄₈ N ₆ O ₁₀	592.7	ND	ND	ND	aminoglycoside
Polymyxin B	49800004	C ₅₆ H ₉₈ N ₁₆ O ₁₃	1203.5	soluble	>203	ND	polymyxin
Procaine benzylpenicillin	5903	C ₂₉ H ₃₈ N ₄ O ₆ S	570.7	slightly soluble	ND	ND	combination
Pyrazinamide	1046	C ₅ H ₅ N ₃ O	123.11	15000	376-379	-0.6	Antimycobacterial
Rifabutin	135398743	C ₄₆ H ₆₂ N ₄ O ₁₁	847	190	ND	4.1	Antimycobacterial
Rifampicin	135398735	C ₄₃ H ₅₈ N ₄ O ₁₂	822.9	1400	183	2.7	Antimycobacterial
Rifapentine	135403821	C ₄₇ H ₆₄ N ₄ O ₁₂	877	ND	ND	4	Antimycobacterial
Spectinomycin	15541	C ₁₄ H ₂₄ N ₂ O ₇	332.35	150000	ND	-2.3	aminocyclitol/aminoglycoside
Streptomycin	19649	C ₂₁ H ₃₉ N ₇ O ₁₂	581.6	1000000	ND	-6.4	aminoglycoside
Trimethoprim sulfamethoxazole	358641	C ₂₄ H ₂₉ N ₇ O ₆ S	543.6	ND	ND	ND	combination
Vancomycin	14969	C ₆₆ H ₇₅ Cl ₂ N ₉ O ₂₄	1449.2	225	ND	-3.1	glycopeptide

Molecular Weight (g/mol)

*(mg/L)

& Melting Point(°C)

§ Octanol/Water Participation

Table 1 4 of 4

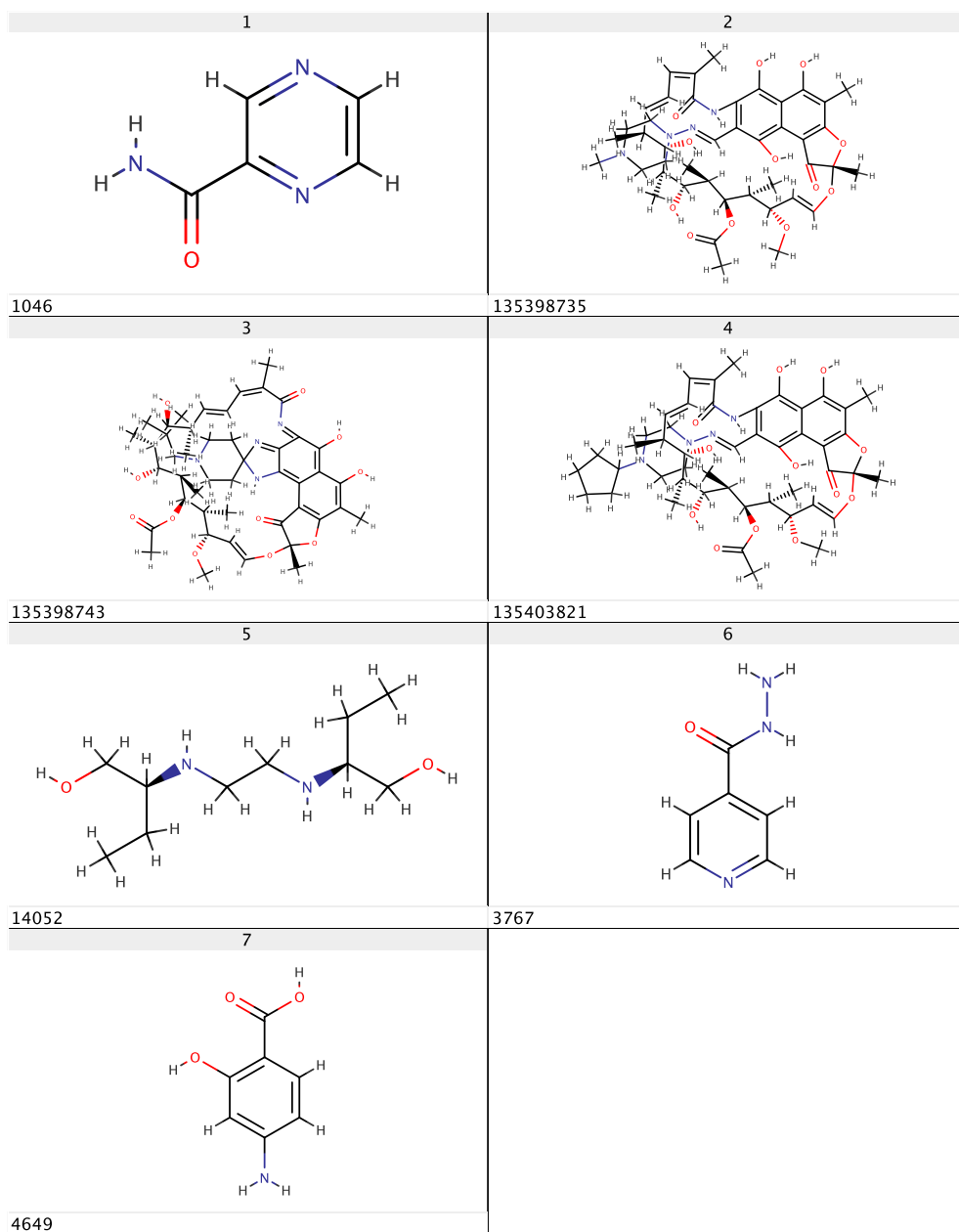


Figure 9. World Health Organization list of essential medications anti-infective antimycobacteria and antituberculoid. 1) Pyrazinamide 2) Rifampicin 3) Rifabutin 4) Rifapentine 5) Ethambutol 6) Isoniazid 7) *p*-Aminosalicylic Acid. Compiled from ChemBank using MarvinSketch.

use of Access, Watch, and Reserve (AWaRe) classification of antibiotics by the G20 Health Ministers in October 2018.

Access Group

The WHO describes an Access group of antibiotics as those that target a wide range of pathogens but have lower resistance potential when compared to drugs on Watch and Reserve groups. The Access group includes 19 drugs: Amikacin, Amoxicillin, Amoxicillin and clavulanic acid, Ampicillin, Benzathine benzylpenicillin, Benzylpenicillin, Cefalexin, Cefazolin, Chloramphenicol, Clindamycin, Cloxacillin, Doxycycline, Gentamicin, Metronidazole, Nitrofurantoin, Phenoxymethylpenicillin, Procain benzylpenicillin, Spectinomycin, and Sulfamethoxazole+trimethoprim. This list is in support of the stated goal of improving global “access to Access” antibiotics.

Watch Group

The Watch group includes drugs critical for human health but have greater resistance potential than the Access group. This group contains the highest priority antimicrobial that are considered critically important antimicrobials for human medicine. The 11 antibiotics were included because they are considered essential for first and second choice of empiric therapy for certain infectious syndromes: Azithromycin, Cefixime, Cefotaxime, Ceftazidime, Ceftriaxone, Cefuroxime, Ciprofloxacin, Clarithromycin, Meropenem, Piperacillin with tazobactam, and Vancomycin.

Reserve Group

Lastly the Reserve group drugs are only considered suitable for suspected or confirmed infections due to multi-drug-resistant organisms. These are the “last resort” medications. These seven drugs have favorable risk-benefit profiles with proven activity

against “Critical or High Priority” pathogens, examples include carbapenem-resistant *Enterobacteriaceae* (CRE)and *Acinetobacter baumannii* (CRAB)(34). The WHO maintains that drugs included in the Reserve group should be globally accessible but used strategically when other interventions are insufficient. These drugs should be prioritized as key targets of stewardship and use should be monitored and reported. Ceftazidim with avibactam, Colistin, intravenous Fosfomycin, Linezolid, Meropenem with vaborbactam, Plazomicin, and Polymyxin B are the WHO_EML Reserve group.

World Health Organization High and Critical Priority Pathogens

The first clinical use of an antibiotic, a compound that is derived from natural sources with anti-infective action against infecting bacteria or protozoa, was a tremendous advancement to human medicine. The use of antibiotics has led to a significant increase in healthspan and lifespan of people. However, before the first dose was given, it was known that resistance to the penicillin was present in nature. This recognition made many people worry that the antibiotic era would be a brief chapter in the story of human health. This would spur some discoveries and developments, but most classes of drugs were discovered before 1960 CE. The identification of resistant isolates would quickly be reported. During the intervening 90 years, drug resistance to antibiotics has begun to threaten the healthcare system. In 2019, Robert R. Redfield, M.D., the director for the United States Centers for Drug Control and Prevention (CDC) proclaimed that we are now in the post-antibiotic era (35). This is due in part to a number of species that are frequently found to be multi-drug resistant.

This has led the WHO to compile a list of organisms that are considered extremely important in human health and for which new antibiotics should be developed. The

organisms of highest concern are in the critical group: carbapenem-resistant *A. baumannii*, carbapenem-resistant *Pseudomonas aeruginosa*, and 3rd generation-cephalosporin-resistant, Extended-Spectrum- β -Lactamase producing (ESBL) *Enterobacteriaceae*. Next is the High priority group that includes vancomycin-resistant *Enterococcus faecium*, methicillin-resistant and vancomycin-intermediate and resistant *S. aureus*, clarithromycin-resistant *Helicobacter pylori*, fluoroquinolone-resistant *Campylobacter*, fluoroquinolone-resistant *Salmonella* spp., and fluoroquinolone-resistant and 3rd generation-cephalosporin-resistant *Neisseria gonorrhoeae*. The Medium priority group includes penicillin-non-susceptible *Streptococcus pneumoniae*, ampicillin-resistant *Haemophilus influenzae*, and fluoroquinolone-resistant *Shigella* spp. (36).

The CDC has released correspondence in 2013 and 2019 that report on bacteria that are of concern in the community and healthcare system in the United States. In its “Antibiotic Resistance Threats in the United States, 2019” report, the CDC delineated four pathogen groups. While this report does not include viruses or parasites, it does list eighteen organisms as Urgent Threats, Serious Threats, or Concerning Threats. These organisms and groups were determined based on seven criteria: clinical impact, economic impact, incidence, 10-year projection of incidence, transmissibility, availability of effective antibiotics, and barriers to prevention.

Urgent threats are carbapenem-resistant *Acinetobacter* (including *A. baumannii*), *Candida auris*, *Clostridioides difficile*, carbapenem-resistant *Enterobacteriaceae*, drug-resistant *Neisseria gonorrhoeae*. The Serious Threats are considered drug-resistant *Campylobacter*, drug-resistant *Candida*, ESBL-producing *Enterobacteriaceae*, vancomycin-resistant *Enterococci*, multidrug-resistant *P. aeruginosa*, drug-resistant

nontyphoidal *Salmonella*, drug-resistant nontyphoidal *Salmonella*, drug-resistant *Shigella*, methicillin-resistant *S. aureus* (MRSA), drug-resistant *Streptococcus pneumoniae*, and drug-resistant tuberculosis. Lastly, erythromycin-resistant group A *Streptococcus* and clindamycin-resistant group B *Streptococcus*. Additional organisms included on the Watch List are considered threats with potential of spread or becoming more challenging in the United States are Azole-resistant *Aspergillus fumigatus*, drug-resistant *Mycoplasma genitalium*, and drug-resistant *Bordetella pertussis* (35, 37).

In this work particular attention was paid to organisms deemed of importance by the WHO and CDC and addresses the Gram-negative pathogens *P. aeruginosa*, and *E. coli*. *A. baumannii* and its susceptibility to Gallium Protoporphyrin IX (GaPPIX), which is analogous to heme-b with gallium being substituted for iron, are dealt with in much greater detail. This is due in part to the susceptibilities of *E. coli* and *P. aeruginosa* being more variable than the susceptibility of *A. baumannii*.

Escherichia coli

ESBL-producing *Enterobacteriaceae* are estimated to cause 197,400 infections with 9,100 deaths in hospital, not counting non-hospitalized infections. *E. coli* is a member of this family and contributes to a portion of these infections and deaths each year and is also a Gram-negative bacillus that is a component of the normal bacterial flora of the human colonic tract (38-40). *E. coli* within the intestinal tract is typically nonpathogenic unless the intestinal tract barriers have been violated or the host has been immunocompromised; however, there are also several highly adapted *E. coli* clones that have evolved to cause human diseases including meningitis, diarrhea, sepsis, and urinary tract infections (40). In fact, *E. coli* is the most common Gram-negative pathogen

associated with nosocomial infections, and isolates with the ability to produce extended-spectrum β -lactamase continue to increase in frequency and severity (41, 42). Genomes of six ESBL-producing isolates obtained from wounded soldiers at the Walter Reed Army Medical Center (WRAMC) were sequenced using next-generation sequencing methods for future analyses to elucidate their virulence mechanisms.

Pseudomonas aeruginosa

P. aeruginosa is a common environmental Gram-negative bacillus bacterium often associated with nosocomial infections including chronic lung infections in cystic fibrosis patients and bacteremia in burn victims. Human infections with *P. aeruginosa* can likely be traced back to 1862 when Luke observed rod-shaped particles in the blue-green pus of infections allowing this bacterium the time to develop into a formidable human pathogen (43). Nosocomial pathogens, such as *P. aeruginosa*, have developed sophisticated resistance mechanisms since the introduction of antibiotics into the clinical setting (44). *P. aeruginosa* is currently the second most prevalent Gram-negative nosocomial pathogen preceded by *E. coli* with as many as 2% of *P. aeruginosa* isolates specifically presenting with carbapenem-resistance (42). *P. aeruginosa* is referred to as an ESKAPE (*Enterococcus faecium*, *S. aureus*, *Klebsiella pneumoniae*, *A. baumannii*, *P. aeruginosa*, and *Enterobacter* species) pathogen due to its ability to escape the lethal action of antibiotics (45). In order to develop a broader understanding of the mechanisms by which nosocomial *P. aeruginosa* strains escape death by antibiotics, the genome sequences of five *P. aeruginosa* strains isolated from wounded soldiers at the Walter Reed Army Medical Center (WRAMC) were determined using next-generation sequencing methods for future bioinformatic analyses.

Acinetobacter baumannii

The Gram-negative coccobacillus *A. baumannii* is an opportunistic human pathogen causing myriad of human diseases, including pneumonia, bacteremia, urinary tract infections, meningitis, and wound infections. *A. baumannii* is the fifth most common Gram-negative pathogen associated with nosocomial infections (42, 46). Of concern is the increasing multidrug resistance of *A. baumannii* isolates, which has caused this bacterium to be included as an ESKAPE pathogen, underscoring its ability to “escape” antimicrobials (45). In fact, *A. baumannii* strains resistant to all known antibiotics have been encountered, demonstrating the paramount impact of this pathogen on public health (46). To gain a better appreciation for the genomic plasticity, genomes of 24 *A. baumannii* strains isolated from wounded warriors at Walter Reed Army Medical Center (WRAMC) and San Antonio Military Medical Center (SAMMC), Fort Sam Houston, San Antonio, TX, were sequenced using next-generation sequencing for future analyses to investigate the resistance and virulence mechanisms of this emerging pathogen.

The CDC stated that we are now in the post-antibiotic era due in part to the urgent threat of carbapenem-resistant *Acinetobacter* (47) and the World Health Organization has also recognized carbapenem-resistant *A. baumannii* should be a critical focus for research and drug development (36). Additional focus on this Gram-negative opportunistic nosocomial pathogen that is often multi- or pan-drug resistant and the etiologic cause of pneumonia, meningitis, soft tissue infections and sepsis is warranted (48). This is underscored by isolates that are shown to cause uncommon pathologies. For example, *A. baumannii* has rarely been isolated as the causative agent of necrotizing fasciitis (49); however, Charnot-Katsikas et al., described the isolation of *A. baumannii* prior to antibiotic

therapy in two separate patients with necrotizing fasciitis. These *A. baumannii* exhibited extensive drug resistance including carbapenem resistance (49). The carbapenem resistance, unusual clinical appearance, and time of isolation of *A. baumannii* specimens such as these beg investigation. To that end, two isolates obtained from the male patient described in the report by Charnot-Katsikas et al. were investigated. These were isolated before antibiotic treatment from a blood specimen (NFAb1) and three days later from post-mortem tissue following antibiotic treatment (NFAb2) in order to investigate the properties of drug-resistant *A. baumannii* leading to severe infection and mortality over the course of an infection.

***Acinetobacter baumannii* and Gallium Protoporphyrin IX**

Since the introduction of antibiotics, the threat of antimicrobial resistance has followed, leading to new challenges in patient treatment. Resistant bacterial strains are selected with immediacy and regularity after antibiotics are introduced as therapeutic agents (50-53). This continued battle with resistance has led to the initial emergence of pathogens displaying multi-drug resistance (MDR) phenotypes, which was followed by the isolation of clinical isolates extremely drug-resistant (XDR) or totally drug-resistant (TDR) to antibiotics used in human medicine, an outcome that has recreated the pre-antibiotic era (54, 55). This crisis has involved major Gram-positive and Gram-negative pathogens including *Enterococcus* spp., *S. aureus*, *Enterobacteriaceae*, *Neisseria gonorrhoeae*, *P. aeruginosa* and *Acinetobacter* spp. (55). The emergence of all of these multiple drug-resistant organisms (MDROs) has led to extensive patient treatment and hospital stays, while incurring great cost, morbidity and mortality, outcomes that resulted in a call to action from the Infectious Diseases Society of America (56). The problems have been

further compounded by the decreased effort of pharmaceutical companies to develop new classes of antimicrobials (54, 55). All these issues highlight the critical need for alternative therapeutic options that could be used alone or in combination with standard antimicrobials for the treatment of MDROs.

Iron acquisition has been considered one of the bacterial functions that could be used as an alternative target because of the critical role this metal plays in the physiology of bacteria, including pathogens that cause severe human infections (57, 58). Siderophore-mediated iron acquisition processes have been used for the development of sideromycins, derivatives in which siderophores have been covalently linked to antibiotics as is in the case of albomycin and salmycin (59). This “Trojan Horse” strategy has also included the use of the semi-metal Gallium (III) as an anti-infective agent. Ga binds to virtually all biological complexes that normally contain Fe (III) but is not reduced to Ga (II) under physiological conditions thus disrupting critical redox-driven biological processes (60). Accordingly, Ga has been used as simple salts or complexed with organic compounds such as bacterial siderophores and porphyrins including protoporphyrin IX (61, 62). Gallium nitrate and gallium desferrioxamine showed antimicrobial activity against *P. aeruginosa* by killing free-living bacteria, blocking biofilm formation and targeting iron metabolism (63, 64). Non-iron metalloporphyrins have also been tested as antibacterial with Ga-protoporphyrin IX (GaPPIX), seen in Figure 10, effecting the most potent action against Gram-positive and Gram-negative bacteria involving high-affinity pathways, which depend on the expression of heme/hemoglobin receptors, or low-affinity processes, whose mechanism of action are unknown (65). Furthermore, GaPPIX showed antimicrobial

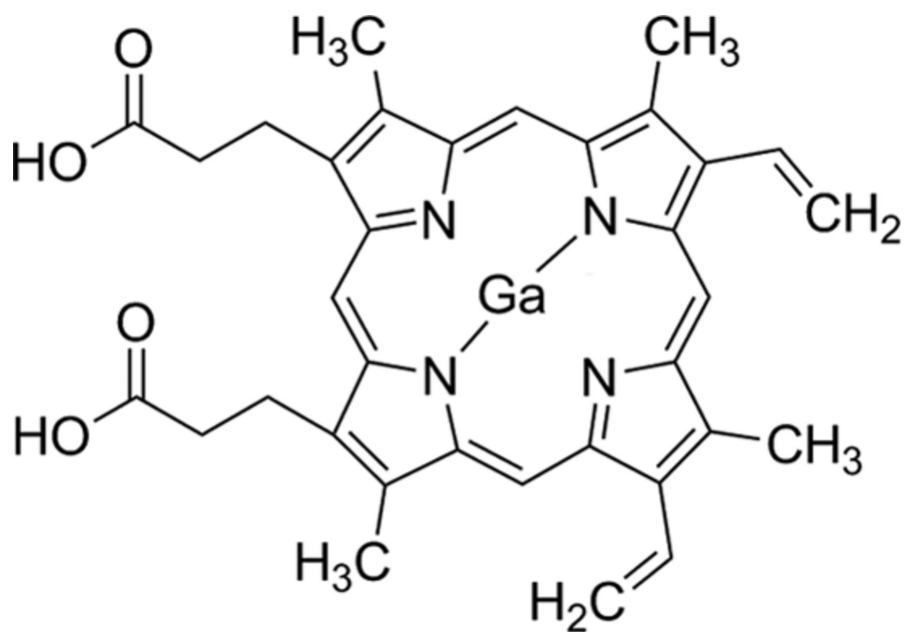


Figure 10. Gallium Protoporphyrin IX (GaPPIX). GaPPIX is a non-ferrous porphyrin analogous to heme B. Ga has taken the place of Fe in the porphyrin ring.

activity against *N. gonorrhoeae* when used topically in a murine vaginal infection model (66).

The Gram-negative obligate aerobe *A. baumannii* is an opportunistic pathogen capable of causing a wide range of serious disease in humans, particularly in those with impaired immune systems (46, 67). The inherent and acquired resistance of clinical isolates of this pathogen complicates the severity of *A. baumannii* infections (52, 68). This necessitates the investigation into novel chemotherapeutics needed for the treatment of infections particularly those caused by MDR *A. baumannii* isolates obtained from nosocomial and wounded patients. In spite of the increased occurrence of these infections, little is known about the pathobiology of this relevant pathogen. One of the best-understood interactions of this pathogen with the human host is its ability to acquire iron during the infection process. The genetic and functional analysis of *A. baumannii* ATCC 19606^T showed that this strain acquires iron via the acinetobactin-mediated siderophore system, which proved to be critical for the infection of human alveolar epithelial cells, *Galleria mellonella* caterpillars and mice (53). Furthermore, preliminary experimental data (69) and genomic *in silico* studies (70) indicate that *A. baumannii* expresses hemin-acquisition systems that remain to be characterized experimentally. These observations suggest that Ga-containing derivatives could be effective microbiocides that could be used against MDR strains involved in human infections.

Therefore, this study investigates the effect of GaPPIX as antimicrobial agents against a collection of *A. baumannii* clinical isolates that include strains obtained from military personnel wound infections. Our results show that GaPPIX is an effective

antimicrobial agent when tested under *in vitro*, *ex vivo*, and *in vivo* conditions independent of the antimicrobial resistance phenotype of the tested strains.

It should be noted that *A. baumannii* has been shown to regulate expression based on host factors that are common during primary and secondary pneumonia. These factors include mucin, which is a secretion in the lumen of the alveoli and interstitial fluid that would be present in damaged alveoli or after the bacterium has breached the epithelial layer. The study of these host factors that alter *A. baumannii* gene expression show an organism that is capable of adapting its physiology based on the niche to which it has access (71).

The human body keeps free metal concentrations at a low level by binding to metal-binding proteins to prevent pathogens from easily utilizing the free metals, such as iron, to aid in their growth. Particularly, the majority of iron in the body is stored in heme in red blood cells, which is the oxygen-carrying component of hemoglobin. However, several bacterial pathogens, including *A. baumannii*, can lyse red blood cells in the host, and proteases degrade proteins freeing heme from the host cell. This liberated heme can then be acquired by bacteria (72, 73).

This iron and heme are critical for certain processes, including neutralizing toxic free radicals. Catalase is an enzyme that requires heme and is commonly found in aerobic cells; it is responsible for detoxifying oxygen radicals like hydrogen peroxide. It catalyzes the breakdown of hydrogen peroxide into water and oxygen ($\text{H}_2\text{O}_2 \rightarrow 2\text{H}_2\text{O} + \text{O}_2$) (15). The structure of catalase is made up of four subunits each with an iron protoporphyrin IX ring (heme group) at the center of the active sites (73).

The crucial role of heme in *A. baumannii* physiology supported the study of how *A. baumannii* responds to the heme analog GaPPIX. The hypothesis being many responses

to this molecule will be similar when compared to response of the organism to exogenous heme. The subsequent incorporation of GaPPIX directly into heme-sites or substitution of Ga in Fe containing centers of critical enzymes was examined. RNASeq was used to assess global gene expression. Additionally, the effects GaPPIX has on the catalase activity of *A. baumannii* was investigated. These efforts were aided by computational analyses of heme and GaPPIX binding to *A. baumannii* catalase. This was further studied in protein lysate and enriched samples. Investigation efforts to determine the mode of action for the lethal effects of GaPPIX on *A. baumannii* suggest GaPPIX and a dose-dependent reduction in catalase activity may contribute to decreased viability of the bacteria. Purification of natively expressed enzymes with catalase activity showed a diminished amount of putative catalase protein in GaPPIX-treated sample. Inductively Coupled Plasma Mass Spectrometry (ICP-MS) analysis did not support large disruption of metal homeostasis. The reduction of putative catalase in the catalase fraction may be the result of transcriptional regulation because of the presence of GaPPIX. Global transcriptional analysis supports metal acquisition regulation and may indicate mechanisms that are more numerous than only lethal oxidative stress. These studies support future work on the physiological response of *A. baumannii* to GaPPIX and heme B.

MATERIALS AND METHODS

Bacterial strains and growth conditions

All strains used in this work were stored at -80°C as Luria-Bertani (LB) glycerol stocks. All strains were routinely cultured in LB agar or broth at 37°C. For antimicrobial susceptibility determinations, strains were passaged on 5% sheep blood agar prior to growth in cation-adjusted Mueller-Hinton broth (CAMH; Oxoid, Basingstoke, Hampshire, England) as previously described (74). Iron-rich and iron-chelated conditions were achieved by adding 100 µM FeCl₃ and the synthetic iron chelator 2,2'-dipyridyl (DIP), respectively, to the culture media. The identity of the *A. baumannii* isolates used were confirmed by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) using a Bruker microflex analyzer. The MALDI Biotyper v3.1 software package (Bruker Daltonic, Billerica, MA) was used to characterize MS fingerprints comprised of the means of 240 mass spectra profiles for each isolate analyzed. Score values greater than 2.000 were considered acceptable for species-level identification. All *A. baumannii* strains provided by Dr. D. Zurawski (Walter Reed Army Institute of Research [WRAIR]) were described previously (75). A 10 mg/ml stock solution of GaPPIX (Frontier Scientific, Logan, UT), for use whenever GaPPIX was required, was prepared using cell-culture grade dimethyl sulfoxide (DMSO) (Sigma-Aldrich, St. Louis, MO) and then sterilized using 0.2-µm nylon membrane filters (Pall Corp., Port Washington, NY).

Antimicrobial susceptibility testing

Strains were subjected to automated and manual antimicrobial susceptibility testing (AST) of standard antimicrobials and the experimental GaPPIX. Minimal inhibitory concentration (MIC) breakpoints and categorical interpretations for conventional antibiotics were mainly based on Clinical and Laboratory Standards Institute (CLSI) breakpoints (76). However, the European Committee on Antimicrobial Susceptibility Testing (EUCAST) breakpoints (http://www.eucast.org/fileadmin/src/media/PDFs/EUCAST_files/Breakpoint_Tables/Breakpoint_Table_v_3.1.pdf) were used to interpret the MIC of gentamicin for *A. baumannii* 19606^T. Currently, there are no breakpoints for tigecycline or GaPPIX.

Epsilon meter (Etest)-based MIC tests (BioMérieux, Durham, NC) were performed and interpreted according to the manufacturer's instructions. Briefly, suspensions of the strains equivalent to a 0.5 McFarland standard were used to inoculate Mueller-Hinton agar plates (Remel, Lenexa, KS) prior to strip placement. Plates were incubated for 22 h in ambient air at 35°C prior to MIC interpretation. The MIC was interpreted by observing the concentration of the drug on the strip where the growth of the organism intersected.

Isolate AST of GaPPIX and doxycycline was carried out by the Kirby-Bauer disk-diffusion method according to standard procedures (77). GaPPIX stock solution was added to sterile 6-mm paper disks to deliver 50 µg or 100 µg of GaPPIX per disk and allowed to dry. GaPPIX paper disks and HardyDisk (Hardy Diagnostics, Franklin, OH) containing 30 µg doxycycline were applied to the surface of Mueller Hinton agar plates inoculated with bacteria. Zones of inhibition (ZOI) were measured after incubation in ambient

atmosphere at 37°C for 24 h. ZOI of doxycycline were classified as resistant, intermediate, or susceptible based on CLSI standards.

For automated AST determinations, the VITEK 2 XL (BioMérieux) and the BD Phoenix (BD Diagnostic Systems, Sparks, MD) were used according to the manufacturer's instructions. The bioMérieux susceptibility card AST-GN73 and Phoenix NMIC/ID-130 panels were used for each platform, respectively. Interpretive criteria were based on CLSI breakpoints (76).

Broth microdilution MICs

The MIC of GaPPIX was determined using the antimicrobial broth microdilution technique in the absence or presence of 10% heat inactivated normal serum according to standard procedures (74). Briefly, broth microdilution plates were inoculated with 10^5 colony forming units (CFU)/ml of each test organism in CAMHB and incubated for 24 h at 37°C in ambient air. Two-fold dilutions of GaPPIX were performed ranging from 5 µg/ml to 166 µg/ml including a sample with no added antibiotic as a growth control on each plate. A more defined GaPPIX MIC was determined with 1 µg/ml resolution covering a range of 10 µg/ml to 20 µg/ml for selected strains. Plates were read for turbidity at OD₅₉₅. The MIC was determined as the well of the microtiter plate with the lowest drug concentration at which there was no detectable growth. The MICs were determined at least 3 times in triplicate (n=9) using fresh biological samples each time.

GaPPIX resistance frequency

CAMH broth samples were inoculated with a 1:100 dilution of 24-h cultures of ATCC 19606^T or ACICU and then incubated for 6 h at 37°C. Bacteria were plated onto

CAMH agar plates containing 2x (40 µg/ml) and 4x (80 µg/ml) MIC of GaPPIX. The number of bacteria in the inoculum was confirmed by plate count. Colonies were observed after 24 h and used to determine mutation frequency. The assay was performed twice in triplicate.

Time-kill assays

Time-kill kinetics assays were performed to determine the rapidity of bactericidal activity of GaPPIX. These assays were performed basically as described previously (78). Briefly, after routine growth, 10^6 CFUs/ml of *A. baumannii* ATCC 19606^T or ACICU were inoculated into CAMH broth. Cultures were then treated with 0, 10, 20 or 40 µg/ml GaPPIX, concentrations that corresponded to 0, 0.5, 1 or 2 times the MIC, respectively. CFUs were determined at 0, 2, 4, 6 and 24 h post-inoculation by plate count. Assays were performed twice in triplicate (n=6) using fresh biological samples each time.

A549 *ex vivo* assays

To test the cytotoxicity of GaPPIX, an opaque white 96-well plate was seeded with 10^4 A549 human pulmonary adenocarcinoma cells and incubated for 24 h in Dulbecco's Modified Eagle's Medium (DMEM; Mediatech, Inc., Manassas, VA) supplemented with 10% heat-inactivated fetal bovine serum (HyClone, Logan, UT), penicillin and streptomycin at 37°C with 5% CO₂ atmosphere as previously described (53). Following incubation, the medium was exchanged for DMEM containing 10% heat-inactivated fetal bovine serum without antibiotics and supplemented with 2-fold dilutions ranging from 10 µg/ml to 640 µg/ml GaPPIX. The samples were incubated for 24 h and cell viability was assayed using the Celltiter-Glo luminescent cell viability assay (Promega, Madison, WI).

Luminescence was measured for 10 ms with a FilterMax F5 instrument. Experiments were performed twice in octuplet (n=16). Groups were compared by analysis of variance (ANOVA) with Tukey's multiple comparisons.

To test the antimicrobial effect of GaPPIX on the infection of submerged A549 cells monolayers, 24-well tissue culture plates were seeded with approximately 10^4 cells per well and then incubated for 16 h, as described previously (53). Bacteria were cultured for 24 h in CAMH broth at 37°C with shaking at 200 rpm, collected by centrifugation at 21,000 x g for 10 min, washed, resuspended, and diluted in DMEM with 10% heat-inactivated fetal bovine serum without antibiotics or supplemented with 20 or 40 µg/ml GaPPIX. The A549 monolayers were infected with 10^4 CFU of the *A. baumannii* ATCC 19606^T or ACICU strains. Inocula were estimated spectrophotometrically at OD₆₀₀ and then confirmed by plate count. Infected monolayers were incubated for 24 h at 37°C in 5% CO₂. The tissue culture supernatants were collected, the A549 monolayers were lysed with sterile distilled H₂O, and the lysates were added to the cognate tissue culture supernatants. Combined lysate samples were serially diluted and then plated on nutrient agar. After overnight incubation at 37°C, CFUs were counted, and the viable plate count for each sample was calculated and recorded. Experiments were performed twice in octuplet (n=16) using fresh biological samples each time and compared by ANOVA with Tukey's multiple comparisons.

Galleria mellonella in vivo assays

Toxicity and ability of GaPPIX to treat experimental infections were tested using final instar larvae of the Greater Wax moth, *G. mellonella* (Grubco Inc., Fairfield, OH) as described previously (53). Briefly, larvae weighing between 0.25 g and 0.35 g were

randomly assigned to groups of 10 for each trial and then injected into the last-left proleg using a syringe pump (New Era Pump Systems Inc., Farmingdale, NY) and 26½ gauge needles. Larvae were inspected for survival every 24 h for 5 days. Dead larvae were removed at times of inspection. If greater than 2 larvae died in any control group, the results of the cognate trial were excluded from analysis and the trial was repeated. Trials were performed in triplicate (n=30).

GaPPIX *in vivo* toxicity was tested by using mass-matched *G. mellonella* larvae (i.e., mean mass of each group was statistically indistinguishable by ANOVA from any other group). Larvae were injected with 5 µl of 2-fold dilutions ranging from 0.2 mM to 25 mM GaPPIX solubilized in 0.5 N NaOH, 1.5% DMSO. Control groups were either injected or not injected with carrier solution. Pro-bit analysis was performed using R 3.0 (www.r-project.org). To test antimicrobial activity, larvae were injected with a 5 µl bolus of 10⁵ CFUs of *A. baumannii* ATCC 19606^T or *A. baumannii* ACICU suspended in phosphate-buffered saline solution (PBS) containing 2% DMSO (carrier) or carrier supplemented with either 20 µg/ml or 40 µg/ml GaPPIX. Uninjected larvae and larvae injected with the same volume of sterile carrier were used as controls. Kaplan-Meier survival analysis and odds ratios were determined using Prism 6.0 (GraphPad Software, Inc., La Jolla, CA).

Whole genome sequencing and pangenome analysis

P. aeruginosa, *E. coli*, and *A. baumannii* isolates, routinely stored at -80°C in 10% glycerol (79), were used to isolate total DNA from overnight LB cultures grown with agitation at 37°C using the DNeasy blood and tissue kit (Qiagen, Valencia, CA, USA). Absorption at 260 nm and 280 nm were measured for each sample to determine quantity

and quality of DNA using the Nanodrop 2000 spectrophotometer (Thermo Scientific, Wilmington, DE, USA). DNA concentrations for library preparation were determined by the SYBR green (Life Technologies, Grand Island, NY, USA) standard curve method in black 96-well plates (Corning, Tewksbury, MA, USA) using a FilterMax F5 spectrophotometer with Multi-Mode Analysis software version 3.4.0.25 (Molecular Devices, Sunnyvale, CA, USA). Whole DNA was sheared to approximately 500 bp in microTUBE-50 using M220 Focused-ultrasonicator (Covaris, Woburn, MA, USA). Fragmentation of resultant libraries was examined with a Bioanalyzer 2100 High Sensitivity DNA analysis kit (Agilent Technologies, Santa Clara, CA, USA) using version B.02.08.SI648 software. Individual libraries were normalized, pooled, and then sequenced using MiSeq v3 600-cycle kit (Illumina, San Diego, CA, USA) to perform 300-bp paired-end sequencing on a MiSeq instrument (Illumina) per manufacturer's instructions. De novo assembly was performed using Genomics Workbench 8.0 with the bacterial genome finishing module (CLC bio, Boston, MA, USA) on a workstation with an AMD Opteron 2.10 GHz 16-core processor with 128 GB DDR3 ECC RAM. Genomes were annotated with Prokka version 1.10 on a quadcore i7 workstation with 32 GB DDR3 running Ubuntu 14.04 LTS (80). Additional genomes of the CDC & FDA Antibiotic Resistance Isolate Bank *A. baumannii* isolates were assembled from sequences deposited into the National Center for Biotechnology Information (NCBI) Short Read Archive (SRA).

Pangenomic analysis was performed on greater than 2,581 *A. baumannii* whole genomes that were deposited into NCBI GenBank using Roary and Bacterial Pan Genome Analysis (BPGA) genome analysis software to better understand the possible gene constitution of *A. baumannii*.

Quantification of metals with inductively coupled plasma-mass spectrometry

Cells grown in 10 mL of CAMH without or with 5, 10, or 15 $\mu\text{g/ml}$ GaPPIX were collected by centrifugation at 10,000 x g for 20 min at 4°C in 15-ml metal-free plastic conical tubes (VWR). Supernatant was collected into fresh metal-free conical tube and stored at -80°C. The cell pellet was resuspended in metal analysis grade H₂O and centrifuged 3 times at 10,000 x g for 20 min at 4°C and stored at -80°C. The frozen pellets and supernatants were lyophilized. Each dried sample was suspended in 0.25 ml of metal-analysis grade water and 1 ml metal-trace HNO₃ was added into each tube. The samples were incubated at 60°C for 24 h and then *qs* to 10 ml with metal-analysis grade H₂O. The samples were analyzed with an Elan 9000 ICP-MS system running TotalQuant procedure with 1% HNO₃ as blank. The assay was performed in sextuplet.

Transcriptomic analyses

Growth Conditions

Twenty-five ml of CAMH broth or CAMH broth with 10 $\mu\text{g/ml}$ GaPPIX were inoculated with 0.25 ml of overnight CAMH cultures in 125-ml flasks, which were incubated at 37°C with shaking at 200 rpm for 18 h.

Library preparation and nucleotide sequencing

RNA was extracted from cells as described previously (81). Briefly, 25 ml of acid phenol (pH 4.3 \pm 0.2) and 0.1% SDS at 90°C was directly added to an equal volume of cell culture for 10 min at 90°C with agitation every 2 min. The aqueous fraction was then extracted using Maxwell 16 LEV Total RNA Purification kit per manufacturer's instruction.

RNA quantity was routinely estimated using a Nanodrop ND-2000 spectrophotometer and quality was assessed with an Agilent Bioanalyzer 2100 using the RNA 6000 Pico LabChip Kit (Agilent). Zymo-Seq RiboFree Total RNA Library Kit was used to create sequencing libraries of DNA-free total RNA as per manufacture instructions. Amazon Web Services was utilized to perform library mapping to *A. baumannii* ACICU genome. Briefly, FastQC was used to assess quality of the sequencing reads (82). Trimmomatic was used to remove 14bp of low diversity regions from the 5' end (83). HISAT2 was used for sequence alignment and count features (84). Then DESeq2 and edgeR were used to determine the differentially expressed genes (85, 86). The nucleotide sequences of differentially transcribed genes were further analyzed using Blast2GO 4.0.7 and the KEGG metabolic pathway mapping system (87, 88).

Protein determination and enzyme assays for catalase activity

Using bovine serum albumin as a standard, the Bradford method was used to determine protein concentrations of the samples. SDS-PAGE was used to determine protein purity. Enzyme assays for catalase activity were measured using a microtiter assay. Aliquots of enzyme preparation were added to the reaction mixture, and the decrease in absorbance at 240 nm was tested.

Enzyme purification

Catalase enrichment was purified as described previously (89). Cells from both *A. baumannii* ATCC 19606^T and ACICU strains were collected from 100 ml broth by centrifugation at 35,000 rpm for an hour, washed twice with 50 mM potassium phosphate buffer (pH 7.0), and then suspended in the buffer with protease inhibitor. The suspended cells were passed through a French press (Thermo Electron Corporation, Needham Heights,

Massachusetts) twice to ensure complete lysis. The lysate was centrifuged at 10,000 x g for 15 min. Once centrifugation was completed, the supernatant underwent ethanol fractionation using absolute ethanol (Pharmco Products, Brookfield, Connecticut). First, the samples precipitated at 30% ethanol overnight at 4°C, subjected to centrifugation for 20 min at 13,000 rpm; the supernatant was collected. The supernatant then underwent 80% ethanol fractionation for 24 h at -80°C followed by centrifugation at 13,000 rpm for 20 min; the cell pellet was then collected.

Each collected pellet fraction was applied to a DEAE Sepharose Fast Flow ion exchange chromatography column (GE Healthcare, Uppsala, Sweden) that was equilibrated with 50 mM Tris-HCl buffer (pH 7.5) at a flow rate of 3 ml/min. Then, 50 mM Tris-HCl buffer (pH 7.5) was used to wash the protein (120 ml) and then eluted with an increasing step gradient of 15 % and 30 % (v/v) 1 M NaCl in 50 mM Tris-HCl buffer (pH 7.5). After the completed run, fractions were screened for high catalase activity. Those fractions with high activity eluted at 30% (v/v) 1 M NaCl were collected, concentrated by ultrafiltration and centrifugation at 4,000 rpm for 15 min. The purified fractions were then applied to Superdex 200 gel filtration chromatography column (GE Healthcare, Uppsala, Sweden) that was equilibrated with 1 M NaCl in 50 mM potassium phosphate buffer (pH 7.0).

Characterization of catalase activity

Catalase activity was visually measured in a test tube by adding 100 µl of 1% Triton-X 100 (Sigma-Aldrich, USA), 100 µl of 30% hydrogen peroxide (Sigma-Aldrich), and 100 µl of sample containing catalase activity. After the reaction occurred, the bubble column that formed in the tube was measured with a ruler (90).

Peptide Mass Fingerprint analysis was performed at the Proteomics and Mass Spectrometry Core Facility, University of Georgia (Athens, Georgia). Briefly, protein concentration was estimated by interpolation of a BSA standard curve of a Pierce™ BCA Protein Assay kit as per instruction. Approximately 1 µg of pooled SEC-enriched proteins were size-fractionated via SDS-PAGE. Bands were visualized with (gel code blue) and extracted with new razorblades.

Model preparation and molecular dynamics equilibration

All simulation trajectories were generated using the Gromacs (91-98) set of molecular dynamics (MD) packages. The crystal structure of catalase HPII from *E. coli* was first obtained from the RCSB Protein Data Bank (PDB ID: 3P9Q) (99). In order to develop an apoenzyme model suitable for docking, the resolved ligands were removed, and their coordinates saved for later analysis. The resulting structure was used to generate the Gromacs compatible structure file (gro) and build the system topology via pdb2gmx. The gro structure was solvated in a rhombic dodecahedron with TIP3P water in 100 mM sodium chloride plus neutralizing ions. The system was energy minimized and equilibrated at a constant volume (NVT) for 100 ps using a modified Berendsen coupling method to ensure a temperature of 310 K was achieved. Additional equilibration at a constant pressure (NPT) was then performed for another 100 ps using a Berendsen barostat to bring the system to 1.0 bar. The final structure was then extracted to PDB format for use in docking studies.

Gallium Protoporphyrin IX docking to catalase

All docking procedures utilized a crystal structure of catalase HPII from *E. coli*, PDB ID: 3P9Q. Structures were energy minimized and equilibrated in Gromacs (91-98) (see Molecular Dynamics Equilibration methods) and prepared as a docking receptor for

Autodock Vina (100) in UCSF Chimera (100). All hydrogens were added and charges merged to allow for the subsequent removal of non-polar hydrogens. Docked ligands include heme and gallium protoporphyrin IX, both of which were designed in Avogadro (101). The exported PDB files were prepared in Chimera for docking in Autodock Vina following the same steps as the receptor. Two phases of docking were performed for each ligand, including to the receptor surface as well as to the known active site.

RESULTS

Whole genome sequencing

In an effort to better understand the genetic constituents that may be playing a role in the resistance and pathogenic phenotypes exhibited by clinical strains of several species of the so-called ESKAPE group. *P. aeruginosa*, *A. baumannii*, and *E. coli* isolates were subjected to whole genome shotgun sequencing (103-105). The resulting sequences were assembled into contigs and open reading frames (ORFs) were annotated based on similarity to gene sequences that already exist in public databases.

A total of 37 isolates had draft genomes deposited into NCBI database. The *P. aeruginosa* group includes 5 draft genomes (Table 2). A total of 6 *E. coli* draft genomes were completed and deposited into the NCBI database as seen in Table 3. A more substantial effort was dedicated to genomic sequencing and annotation of *A. baumannii*. Twenty-six genomes were sequenced, annotated, and deposited into the NCBI database. These included 24 WRAIR isolates (Table 4) and 2 isolates from a lethal case of necrotizing fasciitis.

Table 2. Assembly metrics and accession numbers of *Pseudomonas aeruginosa* genomes

Strain ID	No. of contigs	N50 contigs (bp)	Total size (bp)	Coverage (X)	%G+C	No. of		Accession no.
						ORFs ^a	RNA	
105777	105	179475	7408561	30	65.33	7012	67	LODH000000000
105819	63	302533	7208927	26	65.65	6703	68	LOHH000000000
105880	86	215191	6914271	17	65.98	6490	60	LOHI000000000
105857	93	304460	6933765	27	65.99	6563	67	LOHJ000000000
105738	137	102664	6783146	39	66.06	6269	67	LOHK000000000

^a Open Reading Frames

Table 3. Assembly metrics and accession numbers of *Escherichia coli* genomes

Strain ID	No. of contigs	N50 contigs (bp)	Total size (bp)	Coverage (X)	%G+ C	No. of ORFs ^a	No. of RNA	Accession no.
105454	101	191011	5335253	16	50.68	5121	70	LOJL000000000
105547	93	127705	4858207	18	50.68	4649	74	LOJM000000000
109497	99	222697	5221557	34	50.78	5050	74	LORD000000000
108191	98	115521	4727016	28	50.81	4518	73	LORE000000000
105433	89	138092	4820700	33	50.74	4556	73	LORF000000000
105438	81	204373	5226940	34	50.68	4996	60	LORC000000000

^a Open Reading Frames

Table 4. Assembly metrics and accession numbers of *A. baumannii* genomes

Strain ID	No. of contigs	N50 contigs (bp)	Total size (bp)	Coverage (X)	%G+C	No. of ORFs ^a	No. of RNA	Accession no.
AB2828	107	124070	4426896	30	39.21	4274	53	LRDT0000000000
AB3340	76	132604	4010248	28	38.86	3864	49	LRDU0000000000
AB3560	58	247914	4012126	30	38.92	3894	59	LRDV0000000000
AB967	27	401652	3795032	29	38.84	3633	62	LRDS0000000000
AB3785	70	134647	3894584	29	39.01	3745	58	LRDX0000000000
AB3638	78	108414	4294582	31	38.72	4113	62	LRDW0000000000
AB3806	86	96852	4295294	33	38.75	4117	59	LRDY0000000000
AB3927	45	227995	4113781	30	38.82	3978	58	LRDZ0000000000
AB4026	67	160728	3905198	30	38.99	3749	50	LRER0000000000
AB4027	72	152887	3903961	32	39.00	3749	54	LREC0000000000
AB4025	69	152887	3902672	29	39.00	3741	55	LREA0000000000
AB4456	58	182799	4001807	27	38.92	3857	47	LREF0000000000
AB4052	43	262160	3921338	33	39.00	3739	51	LRED0000000000
AB4448	43	369360	3992257	28	38.92	3854	58	LREE0000000000
AB4490	98	84980	3947403	31	38.99	3786	60	LREG0000000000
AB4498	76	128212	3905177	32	39.00	3753	57	LRER0000000000
AB4795	78	113293	3882341	33	39.03	3727	62	LREI0000000000
AB4878	45	223470	3862567	26	38.98	3685	50	LREJ0000000000
AB4957	50	223470	3882040	33	38.97	3722	60	LREL0000000000
AB4932	39	237199	3865974	33	38.99	3703	60	LRER0000000000
AB5001	33	223470	3789469	30	38.99	3586	52	LREN0000000000
AB4991	52	310788	3877107	28	39.09	3686	58	LRER0000000000
AB5674	34	419504	3869253	29	39.03	3679	52	LREP0000000000
AB5197	58	184472	3959484	33	39.04	3799	58	LREO0000000000

^a Open Reading Frames

The CDC FDA AR Isolate collection of *A. baumannii* strains had previously been sequenced and antibiograms determined as part of an initiative of the CDC to improve drug development. These raw sequence reads were made available from NCBI SRA. These sequences were retrieved from the SRA database and used to assemble and annotate 40 of the 41 *A. baumannii* isolates contained in the panel. The assembly and annotation statistics may be seen in Tables 5 and 6, respectively. The full annotation of AR_0274 is provided in APPENDIX E as a representative example of the other isolates. The drug resistance phenotypes of these isolates are of particular interest. Therefore, additional efforts in annotation were undertaken with the 40 assembled genomes. The NCBI, Resfinder, CARD, and ARG-ANNOT databases were used to determine putative resistance genes. Table 7 provides a description of genes in AR isolates as an example. An explanation of the gene products for these annotations may be found in APPENDIX F which was compiled from the CDC AR isolate bank glossary (106). These data can support phenotypic analyses or be used to identify phenotypic and genomic incongruities.

Pangenome study of *Acinetobacter baumannii*

The concept of a pangenome is that through vertical mutations, duplication, deletion, and horizontal gene transfer the total gene pool of bacterial species may increase. This can be seen by the diversity of drug-resistance phenotypes or unusual clinical presentation such as necrotizing fasciitis. The pangenome of *A. baumannii* was assembled based on 2582 genomes that could be obtained from NCBI as listed in APPENDIX G. All genomes were annotated with PROKKA (80) to improve comparisons between genomes. Those genomes that were annotated through the same pipeline were used in parallel analyses using ROARY and BPGA pangenome analysis softwares (107, 108). The profiles

Table 5. CDC FDA *Acinetobacter baumannii* MARSUCA assembly

Isolate	Size	Contig
AR_0273	4180739	81
AR_0274	4156779	86
AR_0275	4381637	75
AR_0276	4326301	138
AR_0277	4222099	88
AR_0278	4258762	81
AR_0279	4262058	86
AR_0280	4034138	68
AR_0281	3894062	75
AR_0282	4146258	85
AR_0283	4270070	67
AR_0284	4122084	86
AR_0285	4183463	81
AR_0286	4199597	74
AR_0287	3889271	105
AR_0288	4025821	68
AR_0289	3993438	105
AR_0290	4247516	65
AR_0291	4183797	80
AR_0292	3604505	426
AR_0293	3740193	347
AR_0294	3836458	227
AR_0295	4127351	
AR_0296	3990638	236
AR_0297	4061495	238
AR_0298	4152347	170
AR_0299	4525241	111
AR_0300	4101026	80
AR_0301	4068023	81
AR_0302	4056979	132
AR_0303	4204727	105
AR_0304	3998867	136
AR_0305	4167632	99
AR_0306	4282382	78
AR_0307	4132089	102
AR_0308	4092701	87
AR_0309	4066741	121
AR_0310	4078628	121
AR_0311	3969640	86

Isolate	Size	Contig
AR_0312	4029316	89
AR_0313	4014093	79

Table 6. CDC FDA *Acinetobacter baumannii* PROKKA annotation

Isolate	contig	size	cds	rRNA	tmRNA	tRNA	repeat region
AR_0273	81	4013648	3812	8	1	61	
AR_0274	86	4053606	3795	15	1	68	
AR_0275	75	4182042	3983	13	1	63	
AR_0276	136	4050411	3814	13	1	65	
AR_0277	88	4221623	4011	10	1	62	
AR_0278	81	4160717	3929	12	1	71	
AR_0279	86	4251847	4041	19	1	63	
AR_0280	68	4009974	3758	10	1	66	
AR_0281	75	3886508	3617	10	1	62	
AR_0282	85	4130149	3916	14	1	69	
AR_0283	67	4137335	3896	12	1	66	
AR_0284	86	4089187	3864	7	1	63	
AR_0285	81	4388265	4150	20	1	76	
AR_0286	74	4161253	3943	12	1	66	
AR_0287	105	3916460	3718	10	1	63	
AR_0288	68	4005043	3778	11	1	63	
AR_0289	105	3987330	3788	14	1	66	
AR_0290	65	4114054	3881	10	1	62	
AR_0291	80	4120752	3913	15	1	61	
AR_0292	426	3437769	3126	8	1	62	
AR_0293	347	3603246	3318	9	1	62	
AR_0294	227	3734811	3443	11	1	61	
AR_0296	236	3909080	3721	9	1	65	
AR_0297	238	3972023	3737	7	1	61	
AR_0298	170	4079987	3831	18	1	70	
AR_0299	111	5027305	4746	9	1	83	
AR_0300	80	4051300	3805	9	1	64	
AR_0301	81	4012325	3770	15	1	65	
AR_0302	132	4068217	3868	18	1	72	
AR_0303	105	4153646	3922	22	1	74	
AR_0304	136	3968520	3716	15	1	61	
AR_0305	99	4158050	3839	18	1	75	
AR_0306	78	4240571	4065	14	1	71	2
AR_0307	102	4100756	3872	13	1	66	
AR_0308	87	4099663	3794	12	1	68	
AR_0309	121	4053605	3880	15	1	64	
AR_0310	121	4047308	3869	18	1	65	
AR_0311	86	3931182	3674	15	1	67	
AR_0312	89	4051235	3846	15	1	63	

Isolate	contig	size	cds	rRNA	tmRNA	tRNA	repeat region
AR_0313	79	4025256	3783	17	1	70	

Table 7. NCBI resistance gene annotation

	AR_0273	AR_0274	AR_0275	AR_0276	AR_0277	AR_0278	AR_0279	AR_0280	AR_0281	AR_0282
#_FOUND	10	14	13	1	10	19	19	13	14	12
A7J11_02581	42.39	42.39	.	.	.
aac(3)-I	.	100	100	100	.
	100.00;10									
aac(3)-IIa	0.00	.	.	.	100
aac(6')-Ian
aac(6')-Ipb
aadA1	.	100	.	.	.	100	100	100	100	.
aadA2
ant(2'')-Ia	.	28.27	.	.	.	28.4	28.4	28.27	28.27	.
ant(3'')-IIa	100	100	100	.	100	100	100	100	100	100
aph(3'')-Ib	89.55	89.55	89.55	.	91.86	89.55	89.55	89.55	89.55	89.55
aph(3')-Ia	100	0.00	100	.	.	100.00	100	100	100	100
		100.00;10				69.49;30.				
		0.00				39;30.39;				

	AR 0273	AR 0274	AR 0275	AR 0276	AR 0277	AR 0278	AR 0279	AR 0280	AR 0281	AR 0282
aph(3')-VIa	100	100	.	.	.
aph(6)-IId	100	100	100	.	100	100	100	100	100	100
armA	.	.	100	.	.	100	100	.	.	100
arr-2
blaADC-10
blaADC-11
blaADC-152	100
blaADC-162	.	.	100	.	.	100	100	.	.	100
blaADC-170
blaADC-25	100
blaADC-26
blaADC-30	.	100	100	100	.
blaADC-33
blaADC-5
blaADC-56
blaADC-79
blaADC-87	100
blaOXA-104
blaOXA-115	100	.
blaOXA-139
blaOXA-160

	AR 0273	AR 0274	AR 0275	AR 0276	AR 0277	AR 0278	AR 0279	AR 0280	AR 0281	AR 0282
blaOXA-223
blaOXA-23	100	.	100
blaOXA-237	100.00;83
blaOXA-2445
blaOXA-65	100
blaOXA-66	100	100	100	.	.	100	100	100	.	100
blaOXA-69
blaOXA-71
blaOXA-72
blaPER-7
blaTEM-1	100
blaTEM-12	.	100	100	.	.	100.00;10	100	100	100.00;10	100
catA1	0.00	100	100	0.00	.
catB8	100	100	.	.	.
cmIA5
cmIB1	100
mph(E)	.	.	100	.	.	100	100	.	.	100
msr(E)	.	.	100	.	.	100	100	.	.	100

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	AR 0273	AR 0274	AR 0275	AR 0276	AR 0277	AR 0278	AR 0279	AR 0280	AR 0281	AR 0282
qacEdelta1	.	100	.	.	.	100	100	100	100	.
sul1	.	100	.	.	.	100	100	100	100	.
sul2	86.83	86.83	86.83	.	87.67	86.83	86.83	.	86.83	86.83
tet(A)
tet(B)	99.51	99.51	99.51	.	.	99.51	99.51	99.51	99.51	99.51

Table 7. NCBI

	AR_0283	AR_0284	AR_0285	AR_0286	AR_0287	AR_0288	AR_0289	AR_0290	AR_0291	AR_0292
#_FOUND	18	10	10	17	13	15	11	18	18	9
A7J11_02581	42.39	.	.	42.39	.	42.39	.	42.39	42.39	.
aac(3)-I	100	.	.	100
aac(3)-IIa	.	100	42.04
aac(6')-Ian	.	100
aac(6')-Ipb	100	.	100	.	.	.
aadA1	100	.	.	100	45.33	100	45.33	100	100	.
aadA2
ant(2'')-Ia	28.4	.	.	28.4	28.4	28.4	9.87	28.4	28.4	28.27;8.5 3
ant(3'')-IIa	100	100	100	100	100	100	100	100	100	100
aph(3'')-Ib	89.55	91.86	91.86	89.55	89.55	89.55	89.55	89.55	89.55	89.55
aph(3')-Ia	100.00;10 0.00;100. 00;100.00	.	.	100	.	.	.	100	100	.

	AR 0283	AR 0284	AR 0285	AR 0286	AR 0287	AR 0288	AR 0289	AR 0290	AR 0291	AR 0292
aph(3')-VIa	100	100	100	.
aph(6)-IId	100	100	95.74	100	100	100	100	100	100	100
armA	100	.	.	100	.	100	.	100	100	.
arr-2
blaADC-10
blaADC-11
blaADC-152	.	100
blaADC-162	100	100	100	.
blaADC-170	.	.	100
blaADC-25
blaADC-26
blaADC-30	.	.	.	100	100	100	100	.	.	84.81
blaADC-33
blaADC-5
blaADC-56
blaADC-79
blaADC-87
blaOXA-104
blaOXA-115
blaOXA-139	.	.	27.05	.	11.47
					34.42;53.					
blaOXA-160	.	.	33.82	.	62

	AR 0283	AR 0284	AR 0285	AR 0286	AR 0287	AR 0288	AR 0289	AR 0290	AR 0291	AR 0292
blaOXA-223
blaOXA-23
blaOXA-237
blaOXA-24	.	.	100	100
blaOXA-65	.	100	100
blaOXA-66	100	.	.	100	100	100	100	100	100	100
blaOXA-69
blaOXA-71
blaOXA-72	79.83	33.45;100
blaPER-700
blaTEM-1	.	100
blaTEM-12	100.00;10	100	100	.
catA1	0.00	100	100	.
catB8	100	.	.	100	.	100	.	100	100	.
cmIA5
cmIB1	.	100
mph(E)	100	.	.	100	.	100	.	100	100	.
msr(E)	100	.	.	100	.	100	.	100	100	.

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	AR 0283	AR 0284	AR 0285	AR 0286	AR 0287	AR 0288	AR 0289	AR 0290	AR 0291	AR 0292
qacEdelta1	100	.	.	100	.	100	.	100	100	.
sul1	100	.	.	100	.	100	.	100	100	.
sul2	.	87.67	65.07;87.67	.	86.83	.	86.83	.	.	.
tet(A)
tet(B)	99.51	.	.	99.51	99.51	99.51	99.51	99.51	99.51	99.51

Table 7. NCBI

	AR_0293	AR_0294	AR_0295	AR_0296	AR_0297	AR_0298	AR_0299	AR_0300	AR_0301	AR_0302
#_FOUND	10	11	0	8	10	19	17	17	13	15
A7J11_02581	42.39	.	42.39	.	.
aac(3)-I	100
aac(3)-IIa	.	100
aac(6')-Ian	.	100
aac(6')-I_p	100	100	.
										91.16;100
aadA1	45.33	100	.	100	45.33	0
aadA2	.	.	.	10000;100.0
ant(2'')-Ia	28.4	.	.	100	.	28.4	28.8	28.4	28.4	28.27
ant(3'')-IIa	100	100	.	100	100	100	100	100	100	36.50;64.
aph(3'')-Ib	89.55	91.86	.	.	89.55	89.55	89.55	89.55	89.55	89.55
						30.39;30.				
						39;30.39;				
						30.39;30.				
						39;100.00				
aph(3')-Ia	.	.	.	100	.	;30.39	.	100	.	.

	AR 0293	AR 0294	AR 0295	AR 0296	AR 0297	AR 0298	AR 0299	AR 0300	AR 0301	AR 0302
aph(3')-VIa	.	100	100	.	.	.
aph(6)-IId	100	100	.	100	100	100	100	100	100	100
armA	100	100	100	.	100
arr-2	100	.	.	.
blaADC-10
blaADC-11
blaADC-152
blaADC-162	.	.	.	100
blaADC-170
blaADC-25
blaADC-26	100	.	.	.
blaADC-30	84.2	.	.	100	.	100	.	100	100	.
blaADC-33	100.00;10 0.00
blaADC-5	.	50.95;100 .00
blaADC-56
blaADC-79
blaADC-87
blaOXA-104	100	.	.	.
blaOXA-115	100
blaOXA-139
blaOXA-160

	AR 0293	AR 0294	AR 0295	AR 0296	AR 0297	AR 0298	AR 0299	AR 0300	AR 0301	AR 0302
blaOXA-223	.	.	.	100
blaOXA-23	.	.	.	100
blaOXA-237	100
blaOXA-24
blaOXA-65	.	100
blaOXA-66	100	.	.	100	100	100	.	100	100	.
blaOXA-69
blaOXA-71
	100.00;10								26.45;100	
blaOXA-72	0.0000	.
blaPER-7	100	.	.	.
blaTEM-1	.	100
blaTEM-12	100
catA1
catB8	100	.	100	.	85.62
cmIA5	100	.	.	.
cmIB1	.	100
mph(E)	.	.	.	100	100	100	100	100	100	100
msr(E)	.	.	.	100	100	100	100	100	100	100

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	AR 0293	AR 0294	AR 0295	AR 0296	AR 0297	AR 0298	AR 0299	AR 0300	AR 0301	AR 0302
qacEdelta1	.	.	.	100	.	100	65.80;65.80;65.80;100.00	100	.	100.00;100.00;100.00
sul1	.	.	.	100	.	100	100.00;100.00;100.00	100	.	100.00;100.00;85.4
sul2	.	87.67	.	.	86.83	86.83	86.83	04	86.83	.
tet(A)
tet(B)	99.51	.	.	.	99.51	99.51	100	99.51	99.51	99.51

Table 7. NCBI

	AR_0303	AR_0304	AR_0305	AR_0306	AR_0307	AR_0308	AR_0309	AR_0310	AR_0311	AR_0312
#_FOUND	17	12	6	9	18	16	15	15	16	8
A7J11_02581	42.39	.	.	.	42.39	42.39	.	.	42.39	.
aac(3)-I	.	100	100	100	.	.
aac(3)-IIa	.	.	100	100
aac(6')-Ian	.	.	100
aac(6')-Ipb	.	100
aadA1	100	45.33	.	.	100	100	68.06;100	91.16;91.	100	.
aadA2
ant(2'')-Ia	28.4	53	.	.	28.4	28.4	28.27	28.27	28.4	.
ant(3'')-IIa	100	100	100	100	100	100	64.51;36.	64.51;36.	100	100
aph(3'')-Ib	89.55	89.55	.	91.86	89.55	89.55	89.55	89.55	89.55	.
aph(3')-Ia	100	.	.	.	100	.	.	.	100	100.00;10
									100	0.00

	AR 0303	AR 0304	AR 0305	AR 0306	AR 0307	AR 0308	AR 0309	AR 0310	AR 0311	AR 0312
aph(3')-VIa
aph(6)-Id	100	100	.	100	100	100	100	100	100	.
armA	100	.	.	.	100	100	100	100	100	.
arr-2
blaADC-10
blaADC-11
blaADC-152	.	.	100	100
blaADC-162	100
blaADC-170
blaADC-25
blaADC-26
blaADC-30	.	100	.	.	100	100
blaADC-33	100	100	.	.
blaADC-5
blaADC-56	100	.
blaADC-79	100
blaADC-87
blaOXA-104
blaOXA-115	100	100	100	.
blaOXA-139
blaOXA-160	.	68.6

	AR 0303	AR 0304	AR 0305	AR 0306	AR 0307	AR 0308	AR 0309	AR 0310	AR 0311	AR 0312
blaOXA-223
blaOXA-23
blaOXA-237	.	.	.	100
blaOXA-24
blaOXA-65	.	.	100	100
blaOXA-66	100	100	.	.	100
blaOXA-69	100
blaOXA-71	100.00;10 0.00
blaOXA-72
blaPER-7
blaTEM-1	.	.	100	100
blaTEM-12	100
catA1	100
catB8	100	.	.	.	100	100	85.62	85.62	100	.
cmIA5
cmIB1	.	.	.	100	84.60;21. 88;13.82; 93.76
mph(E)	100	.	.	.	100	100	100	100	100	.
msr(E)	100	.	.	.	100	100	100	100	100	.

	AR 0303	AR 0304	AR 0305	AR 0306	AR 0307	AR 0308	AR 0309	AR 0310	AR 0311	AR 0312
qacEdelta1	100	.	.	.	100	100	100	100	100	.
sul1	100	.	.	.	100	100	54.52;100	82.98;100	100	.
sul2	86.83	86.83	.	87.67	86.83	86.83
tet(A)
tet(B)	99.51	99.51	.	.	99.51	99.51	99.51	99.51	99.51	100

Table 7. NCBI

#_FOUND	AR_0313	Resistance gene count:	Average identity of gene found:
	14		
A7J11_02581	.	13.0	42.4
aac(3)-I	100	10.0	100.0
aac(3)-IIa	.	6.0	90.3
aac(6')-Ian	.	3.0	100.0
aac(6')-Ip	.	5.0	100.0
aadA1	100	22.0	87.6
aadA2	.	1.0	100.0
ant(2'')-Ia	28.13	25.0	31.2
ant(3'')-IIa	100	36.0	100.0
aph(3'')-Ib	.	35.0	89.9
aph(3')-Ia	100	15.0	100.0

	AR_0313	Resistance gene count:	Average identity of gene found:
aph(3')-VIa	.	7.0	100.0
aph(6)-Id	.	35.0	99.9
armA	.	19.0	100.0
arr-2	.	1.0	100.0
blaADC-10	100	1.0	100.0
blaADC-11	100	1.0	100.0
blaADC-152	.	4.0	100.0
blaADC-162	.	9.0	100.0
blaADC-170	.	1.0	100.0
blaADC-25	.	1.0	100.0
blaADC-26	.	1.0	100.0
blaADC-30	.	16.0	98.1
blaADC-33	.	2.0	100.0
blaADC-5	.	0.0	ND
blaADC-56	.	1.0	100.0
blaADC-79	.	1.0	100.0
blaADC-87	.	1.0	100.0
blaOXA-104	.	1.0	100.0
blaOXA-115	.	5.0	100.0
blaOXA-139	.	2.0	19.3
blaOXA-160	.	2.0	51.2

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	AR_0313	Resistance gene count:	Average identity of gene found:
blaOXA-223	.	1.0	100.0
blaOXA-23	100	4.0	100.0
blaOXA-237	.	2.0	100.0
blaOXA-24	.	2.0	100.0
blaOXA-65	.	6.0	100.0
blaOXA-66	.	23.0	100.0
blaOXA-69	100	2.0	100.0
blaOXA-71	.	0.0	ND
blaOXA-72	.	1.0	79.8
blaPER-7	.	1.0	100.0
blaTEM-1	.	5.0	100.0
blaTEM-12	100	10.0	100.0
catA1	100	2.0	100.0
catB8	.	16.0	97.3
cmlA5	.	1.0	100.0
cmlB1	.	4.0	100.0
mph(E)	.	21.0	100.0
msr(E)	.	21.0	100.0

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	Resistance gene	Average identity
AR_0313	count:	of gene found:
qacEdelta1	18.97;100 .00	19.0 100.0
sul1	100.00;88 .21;17.86	17.0 100.0
sul2	.	21.0 87.0
tet(A)	100	1.0 100.0
tet(B)	.	31.0 99.5

as seen in panels A and B of Figure 11 show the number of new genes increases with the addition of new genomes. This also shows that with the current genomes genes present in the pangenome have not reached a plateau. The same analysis was performed on the *A. baumannii* AR Isolate bank separately to determine if a similar result would be obtained. This is important as the AR Isolates are considered to sample the diversity of *A. baumannii*, so as to be suitable for drug development.

Additional analyses on the pangenome were performed on the AR Isolate bank (Figures 12 and 13). Broadly effective treatments would be targeted to core genes, genes found in greater than 99% of isolates. There are a large number of poorly characterized genes (inset Figure 12). KEGG identification of core, accessory, and unique shows the percentage of processes that are performed by enzymes of the pangenome (Figure 13).

The chokepoint analysis performed on the *A. baumannii* ACICU provides numerous targets for drug development and those related to the heme are seen in Figure 14. Chokepoint pathways, compounds, and enzymes are in Tables 8, 9, and 10. Dead-end metabolites are listed in Table 11.

Source and antibiotic susceptibility profiles of *Acinetobacter baumannii* strains used in this study

GaPPIX proved to be an effective antimicrobial when tested against Gram-negative bacteria *Yersinia enterocolitica*, Gram-positive bacteria *S. aureus* and acid-fast bacilli *Mycobacterium smegmatis* (65). In spite of initial promising results, the application of GaPPIX to other pathogens has not been systematically tested. Thus, we used an approach similar to that described in the aforementioned publication to test the GaPPIX susceptibility of an *A. baumannii* strain collection that included 30 *A. baumannii* strains isolated from

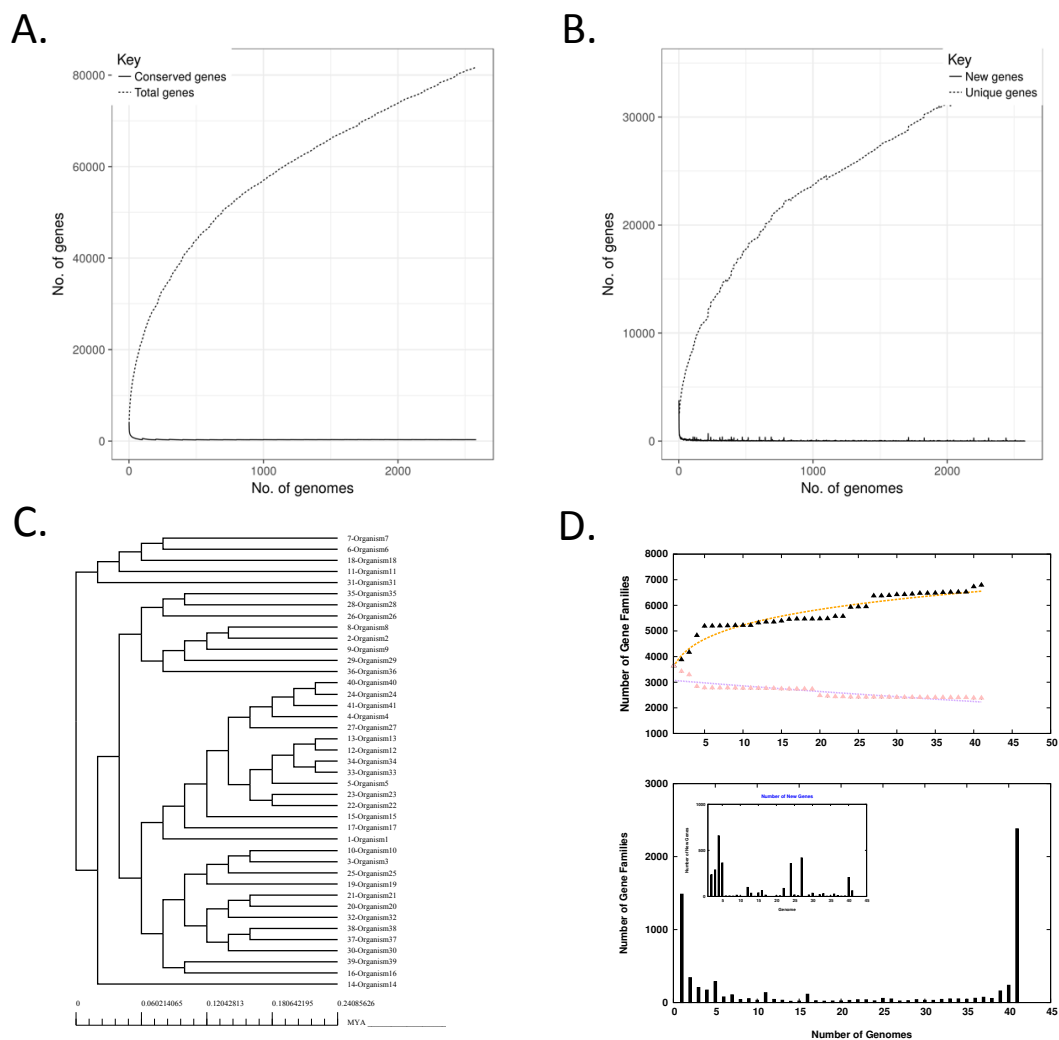


Figure 11. *A. baumannii* pangenome analysis. A combination of Roary and BPGA pan genome analysis software were used. Roary was utilized to prepare a pangenome of all GenBank *A. baumannii* isolate genomes (2581). These data are shown in panels A and B. BPGA was utilized to prepare the pangenome of 41 isolates of the FDA-CDC Antibiotic Resistance Isolate Bank (C and D).

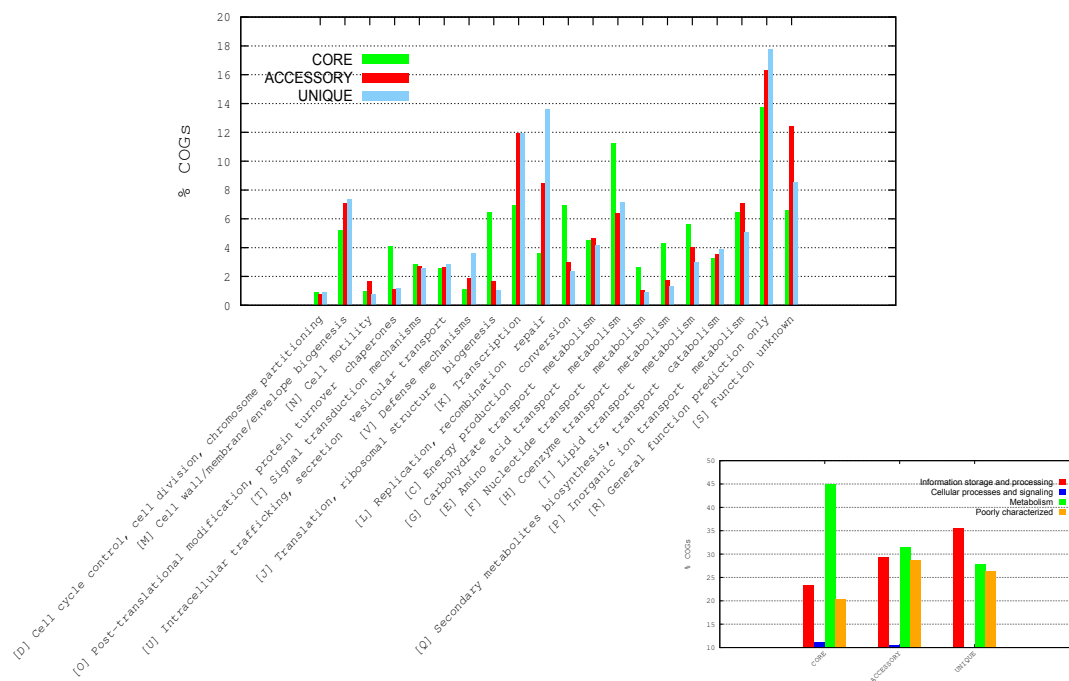


Figure 12. *A. baumannii* BPGA pangenome COG analysis. 41 *A. baumannii* isolates from CDC-FDA Antibiotic Resistance Bank were subjected to pangenome analysis with BPGA. The resulting Clusters of Orthologous Groups of proteins are shown.

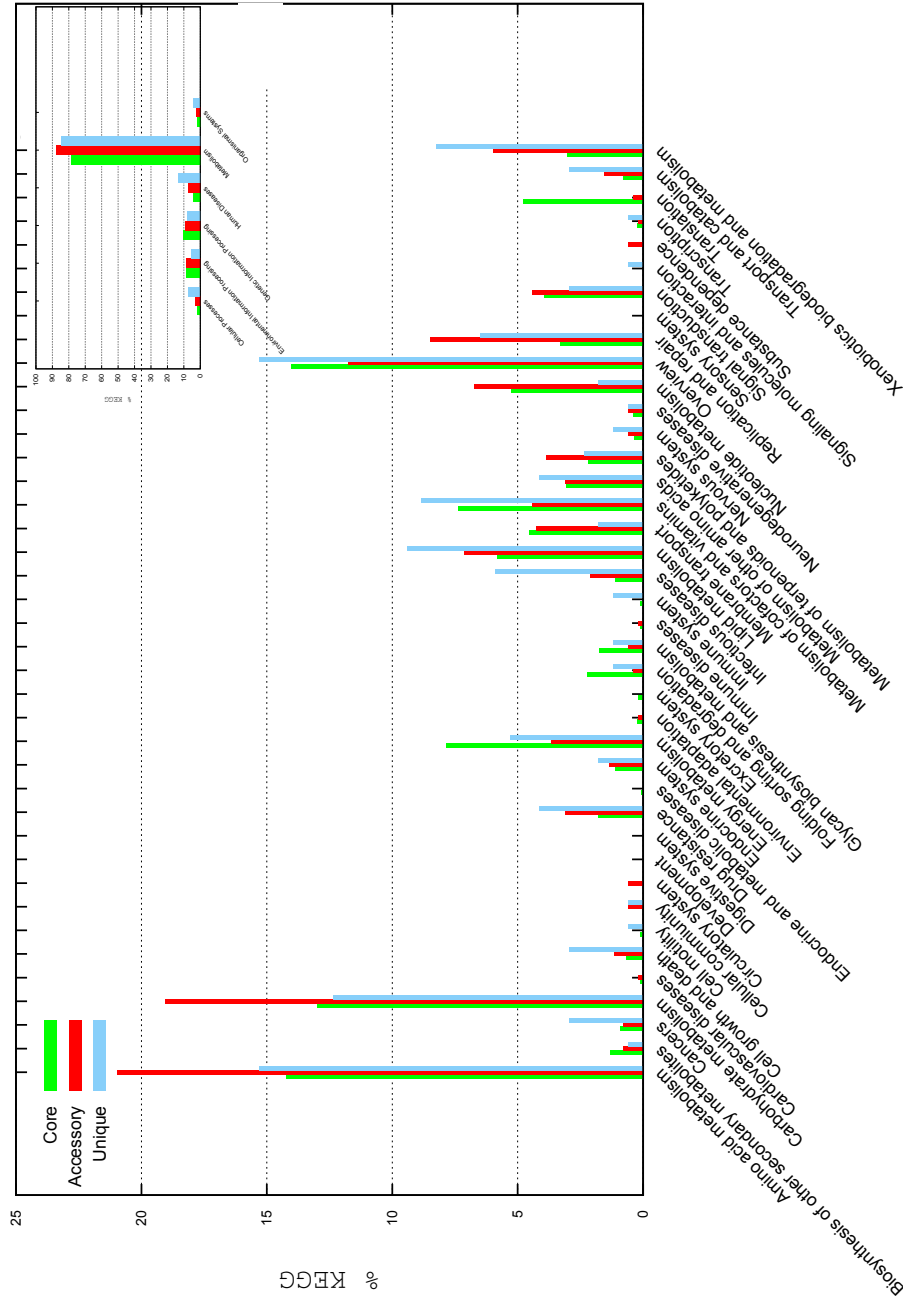


Figure 13. *A. baumannii* pangenome KEGG analysis. 41 *A. baumannii* isolates

from CDC-FDA Antibiotic Resistance Bank were subjected to pangenome analysis

with BPGA. The resulting KEGG identifications are shown.

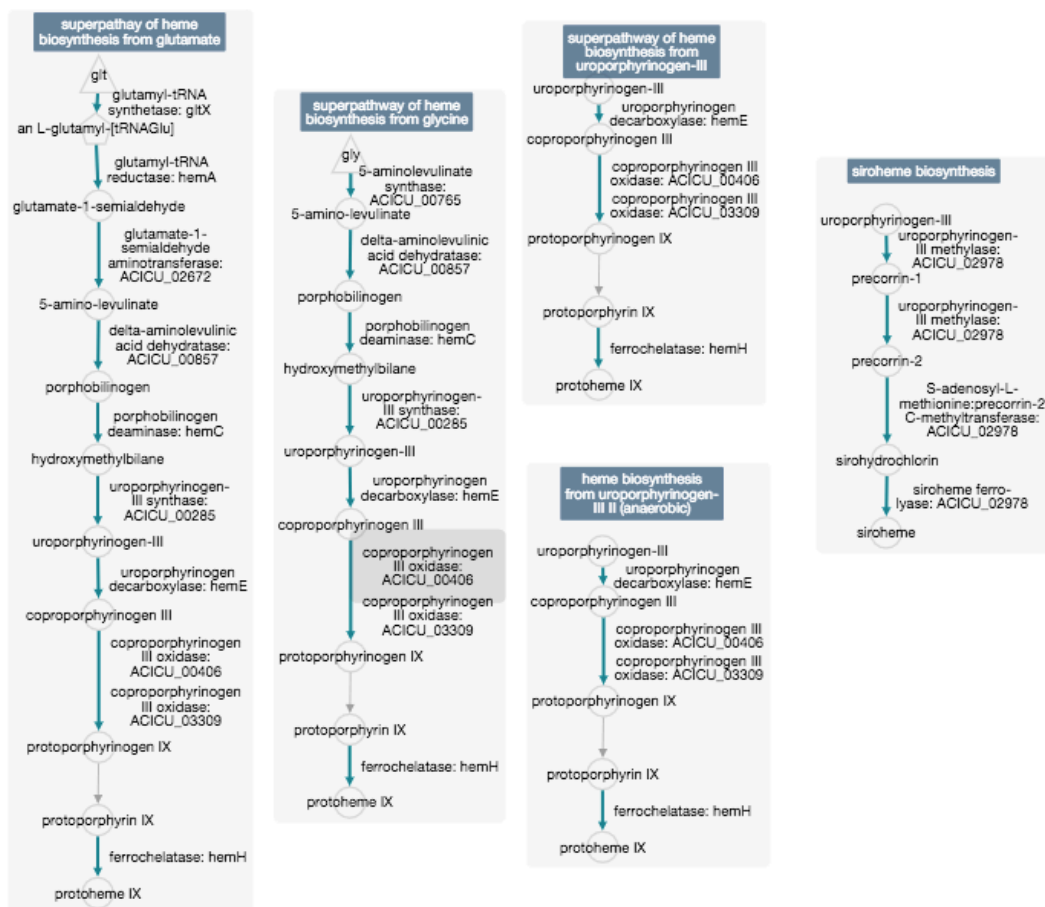


Figure 14. Chokepoint analysis related to heme metabolism of *A. baumannii*

ACICU. BioCyc Pathway Tool 14.5 Chokepoint analysis of *A. baumannii* ACICU was performed excluding human reactions, isozymes, and enzymes present in only one pathway. Those relating to heme metabolism are shown.

Table 8. Chokepoint pathways in *Acinetobacter baumannii* ACICU

	Reactions Chokepoints	Chokepoint Pathway(s)
Producing Side	PANTOTHENATE-KIN-RXN	COA-PWY-1 // PANTO-PWY // PANTOSYN-PWY
	THIAZOLSYN2-RXN	PWY-6891 // PWY-6895 // PWY-6892 // THISYN-PWY
	PORPHOBILSYNTH-RXN	PWY-5188 // PWY-5918 // PWY-5189 // PWY-5920
	R343-RXN	PWY-5508 // PWY-5509
	2.8.1.6-RXN	PWY-7380 // PWY0-1507
	OHMETHYLBILANESY N-RXN	PWY-5188 // PWY-5918 // PWY-5189 // PWY-5920
	PANTEPADENYLYLTR AN-RXN	COA-PWY-1 // COA-PWY // PANTOSYN-PWY
	PYRIMSYN3-RXN	PWY-6890 // THISYN-PWY // PWY-6895 // PWY-6910 // PWY-6897
	UROCANATE-HYDRATASE-RXN	HISDEG-PWY // PWY-5028
	IMIDAZOLONEPROPIONASE-RXN	HISDEG-PWY // PWY-5028
	AICARTRANSFORM-RXN	PWY-6124 // PWY-841 // PWY-6123 // DENOVOPURINE2-PWY
	GLYRIBONUCSYN-RXN	PWY-6122 // DENOVOPURINE2-PWY // PWY-6121 // PWY-841 // PWY-6277
	RXN-9655	PWY0-862 // PWY-6284 // PWY-5971
	RXN-9789	PWY-6891 // PWY-6895 // PWY-6892 // THISYN-PWY
	GLURS-RXN	PWY-5188 // PWY-5918 // TRNA-CHARGING-PWY
	RXN-11924	PWY-6675 // DISSULFRED-PWY

Reactions	Chokepoints	Chokepoint Pathway(s)
PHOSACETYLTRANS- RXN		PWY-5482 // P41-PWY // P163-PWY // FERMENTATION-PWY // PWY0-1312 // PWY-5676 // PWY-5485
COBINPGUANYLYLTR ANS-RXN		PWY-5508 // PWY-5509 // COBALSYN-PWY
R345-RXN		PWY-5508 // PWY-5509
COBALAMIN5PSYN- RXN		PWY-5509 // COBALSYN- PWY
AIRS-RXN		PWY-6122 // DENOVO PURINE2-PWY // PWY-6121 // PWY-841 // PWY-6277
THIAZOLSYN3-RXN		PWY-6897 // PWY-7353
SAICARSYN-RXN		PWY-6124 // PWY-841 // PWY-6123 // DENOVO PURINE2-PWY
DTMPKI-RXN		PWY-7197 // PWY-7187 // PWY-7184 // PWY0-166 // PWY-7211
FGAMSYN-RXN		PWY-6122 // DENOVO PURINE2-PWY // PWY-6121 // PWY-841 // PWY-6277
DMBPPRIBOSYLTRAN S-RXN		PWY-5508 // PWY-5509 // COBALSYN-PWY
NICONUCADENYLYLT RAN-RXN		PYRIDNUCSAL-PWY // PYRIDNUCSYN-PWY // PWY0-781 // PWY-5653 // NADSYN-PWY
DETHIOBIOTIN-SYN- RXN		PWY-7380 // PWY0-1507
R344-RXN		PWY-5508 // PWY-5509
CDPDIGLYSYN-RXN		PWY-5667 // PWY4FS-8 // PWY0-1319 // PHOSLIPSYN- PWY // PWY4FS-7

Reactions	Chokepoints	Chokepoint Pathway(s)
5.4.2.10-RXN		UDPNAGSYN-PWY // PWY0-1261
2.3.1.157-RXN		UDPNAGSYN-PWY // PWY0-1261
THYMIDYLATESYN-RXN		1CMET2-PWY // PWY-7187 // PWY-7184 // PWY0-166 // PWY-7211
R601-RXN		PWY0-1336 // ANARESP1-PWY // REDCITCYC // FERMENTATION-PWY
UROGENIIISYN-RXN		PWY-5188 // PWY-5918 // PWY-5189 // PWY-5920
ASPARTATEKIN-RXN		HOMOSERSYN-PWY // MET-SAM-PWY // PWY-5345 // THRESYN-PWY // PWY-3001 // METSYN-PWY // PWY-5347 // DAPLYSINESYN-PWY // P4-PWY // PWY0-781
ARGSUCCINSYN-RXN		PWY-4984 // ARGSYN-PWY // ARGSYNBSUB-PWY // PWY-7400
GLUTKIN-RXN		ARGININE-SYN4-PWY // CITRULBIO-PWY // PROSYN-PWY
RXN-8665		TRPCAT-PWY // PWY-5651 // NADSYN-PWY
ACETYLGLUTKIN-RXN		ARGSYNBSUB-PWY // GLUTORN-PWY // ARGSYN-PWY
N-ACETYLGLUTPREDUC T-RXN		ARGSYNBSUB-PWY // GLUTORN-PWY // ARGSYN-PWY
ARYLFORMAMIDASE-RXN		TRPCAT-PWY // PWY-5651 // NADSYN-PWY
DIMETHUROPORDEHYDROG-RXN		PWY-5194 // PWY-7377

	Reactions Chokepoints	Chokepoint Pathway(s)
	UROPORIIIMETHYLTR ANSA-RXN	PWY-5194 // PWY-7377
	UROGENDECARBOX- RXN	HEME-BIOSYNTHESIS-II // PWY-5920 // PWY-5918 // HEMESYN2-PWY // PWY0- 1415
	Reactions that are chokepoints on the consuming side	in pathways
Consuming Side	PANTOTHENATE-KIN- RXN	COA-PWY-1 // PANTO- PWY // PANTOSYN-PWY
	PGPPHOSPHA-RXN	PWY-5668 // PWY4FS-8 // PWY4FS-7 // PWY0-1545 // PHOSLIPSYN-PWY // PWY- 5269
	THIAZOLSYN2-RXN	PWY-6891 // PWY-6895 // PWY-6892 // THISYN-PWY
	PORPHOBILSYNTH- RXN	PWY-5188 // PWY-5918 // PWY-5189 // PWY-5920
	R343-RXN	PWY-5508 // PWY-5509
	2.8.1.6-RXN	PWY-7380 // PWY0-1507
	3-OXOADIPATE-ENOL- LACTONASE-RXN	PROTocatechuate- ortho-cleavage-PWY // catechol-ortho- cleavage-PWY
	OHMETHYLBILANESY N-RXN	PWY-5188 // PWY-5918 // PWY-5189 // PWY-5920
	PANTEPADENYLYLTR AN-RXN	COA-PWY-1 // COA-PWY // PANTOSYN-PWY
	PYRIMSYN3-RXN	PWY-6890 // THISYN-PWY // PWY-6895 // PWY-6910 // PWY-6897
	UROCANATE- HYDRATASE-RXN	HISDEG-PWY // PWY-5028
	AICARTRANSFORM- RXN	PWY-6124 // PWY-841 // PWY-6123 // DENOVOPURINE2-PWY

Table 8 4 of 7

Reactions Choquepoints	Choquepoint Pathway(s)
GLYRIBONUCSYN-RXN	PWY-6122 // DENOVO PURINE2-PWY // PWY-6121 // PWY-841 // PWY-6277
RXN-9789	PWY-6891 // PWY-6895 // PWY-6892 // THISYN-PWY
GLURS-RXN	PWY-5188 // PWY-5918 // TRNA-CHARGING-PWY
RXN-11924	PWY-6675 // DISSULFRED-PWY
R345-RXN	PWY-5508 // PWY-5509
RXN-8770	PWY-5509 // COBALSYN-PWY
RXN-6261	PWY-5508 // PWY-5509
AIRS-RXN	PWY-6122 // DENOVO PURINE2-PWY // PWY-6121 // PWY-841 // PWY-6277
THIAZOLSYN3-RXN	PWY-6897 // PWY-7353
SAICARSYN-RXN	PWY-6124 // PWY-841 // PWY-6123 // DENOVO PURINE2-PWY
ACETATEKIN-RXN	PWY-5482 // P41-PWY // P163-PWY // FERMENTATION-PWY // PWY0-1312 // PWY-5676 // PWY-5485
DTMPKI-RXN	PWY-7197 // PWY-7187 // PWY-7184 // PWY0-166 // PWY-7211
OHMETPYRKIN-RXN	PWY-6910 // PWY-6897 // PWY-7356
FGAMSYN-RXN	PWY-6122 // DENOVO PURINE2-PWY // PWY-6121 // PWY-841 // PWY-6277
DMBPPRIBOSYLTRAN S-RXN	PWY-5508 // PWY-5509 // COBALSYN-PWY

Table 8 5 of 7

Reactions	Chokepoints	Chokepoint Pathway(s)
QUINOPRIBOTRANS- RXN		PYRIDNUCSYN-PWY // PWY0-781 // PWY-5653 // NADSYN-PWY
BUTYRYL-COA- DEHYDROGENASE- RXN		CENTFERM-PWY // GLUDEG-II-PWY // PWY- 5676 // P163-PWY
R344-RXN		PWY-5508 // PWY-5509
2.3.1.157-RXN		UDPNAGSYN-PWY // PWY0-1261
DCDPKIN-RXN		PWY-7197 // PWY-7184 // PWY0-166 // PWY-7211
DGDPKIN-RXN		PWY-7222 // PWY-6125 // DENOPOPURINE2-PWY // PWY-7226 // PWY-841 // PWY-7228 // PWY-7224
DTDPKIN-RXN		PWY-7197 // PWY-7187 // PWY-7184 // PWY0-166 // PWY-7211
DUDPKIN-RXN		PWY-7184 // PWY0-166 // PWY-7211
THYMIDYLATESYN- RXN		1CMET2-PWY // PWY-7187 // PWY-7184 // PWY0-166 // PWY-7211
R601-RXN		PWY0-1336 // ANARESP1- PWY // REDCITCYC // FERMENTATION-PWY
IMPCYCLOHYDROLAS E-RXN		PWY-6124 // PWY-841 // PWY-6123 // DENOPOPURINE2-PWY
ARGSUCCINLYA-RXN		PWY-4984 // ARGSYN-PWY // ARGSYNBSUB-PWY // PWY-7400

Reactions	Chokepoints	Chokepoint Pathway(s)
ASPARTATE- SEMIALDEHYDE- DEHYDROGENASE- RXN		HOMOSERSYN-PWY // MET-SAM-PWY // PWY- 5345 // THRESYN-PWY // PWY-3001 // METSYN-PWY // PWY-5347 // DAPLYSINESYN-PWY // P4- PWY // PWY0-781
GLUTSEMIALDEHYDR OG-RXN		ARGININE-SYN4-PWY // CITRULBIO-PWY // PROSYN-PWY
NAG1P-URIDYLTRANS- RXN		UDPNAGSYN-PWY // PWY0-1261
ACETYLGLUTKIN-RXN		ARGSYNBSUB-PWY // GLUTORN-PWY // ARGSYN-PWY
N- ACETYLGLUTPREDUC T-RXN		ARGSYNBSUB-PWY // GLUTORN-PWY // ARGSYN-PWY
ARYLFORMAMIDASE- RXN		TRPCAT-PWY // PWY-5651 // NADSYN-PWY
DIMETHUROPORDEHY DROG-RXN		PWY-5194 // PWY-7377
PROTOHEMEFERROCH ELAT-RXN		HEME-BIOSYNTHESIS-II // PWY-5920 // PWY-5918 // HEMESYN2-PWY // PWY0- 1415
PNPOXI-RXN		PLPSAL-PWY // PYRIDOXSYN-PWY // PWY0-845
P-PANTOCYSDECARB- RXN RXN-8675		COA-PWY-1 // COA-PWY // PANTOSYN-PWY PWY-5194 // PWY-7377
XANTHOSINEPHOSPH ORY-RXN		SALVPURINE2-PWY // PWY-5695 // PWY-6353

Table 9. Chokepoint compounds in *Acinetobacter baumannii* ACICU

	Reactions	Chokepoints	Chokepoint Compound(s)
Producing Side	PANTOTHENATE-KIN-RXN		4-P-PANTOTHENATE // PANTOTHENATE
	THIAZOLSYN2-RXN		CPD-13575 // Thiocarboxyadenylated-ThiS-Proteins // Thi-S
	PORPHOBILSYNTH-RXN		PORPHOBILINOGEN // 5-AMINO-LEVULINATE
	R343-RXN		CPD-694 // CPD-689
	2.8.1.6-RXN		DETHIOBIOTIN // BIOTIN
	OHMETHYLBILANESY N-RXN		HYDROXYMETHYLBILANE // PORPHOBILINOGEN
	PANTEPADENYLYLTRA N-RXN		DEPHOSPHO-COA // PANTETHEINE-P
	PYRIMSYN3-RXN		AMINO-HYDROXYMETHYL-METHYL-PYR-P // AMINO-HYDROXYMETHYL-METHYLPYRIMIDINE-PP
	UROCANATE-HYDRATASE-RXN		4-IMIDAZOLONE-5-PROPIONATE // UROCANATE
	IMIDAZOLONEPROPIONASE-RXN		N-FORMIMINO-L-GLUTAMATE
	AICARTRANSFORM-RXN		AICAR // PHOSPHORIBOSYL-FORMAMIDO-CARBOXAMIDE
	GLYRIBONUCSYN-RXN		5-PHOSPHO-RIBOSYL-GLYCINEAMIDE // 5-P-BETA-D-RIBOSYL-AMINE
	RXN-9655		Trans-D2-decenoyl-ACPs
	RXN-9789		Adenylated-ThiS-Proteins // Thi-S
	GLURS-RXN		Charged-GLT-tRNAs // GLT-tRNAs
	RXN-11924		DsrC-disulfide-form // DsrC-L-Cysteine
	PHOSACETYLTRANS-RXN		ACETYL-P
	COBINPGUANYLYLTRANS-RXN		ADENOSYLCOBINAMIDE-GDP
	R345-RXN		CPD-690 // CPD-691
	COBALAMIN5PSYN-RXN		ADENOSYLCOBALAMIN-5-P

Reactions	Chokepoints	Chokepoint Compound(s)
AIRS-RXN		5-PHOSPHORIBOSYL-N-FORMYLGLYCINEAMIDINE // 5-PHOSPHORIBOSYL-5-AMINOIMIDAZOLE
THIAZOLSYN3-RXN		THZ-P // THZ
SAICARSYN-RXN		PHOSPHORIBOSYL-CARBOXY-AMINOIMIDAZOLE // P-RIBOSYL-4-SUCCARB-AMINOIMIDAZOLE
DTMPKI-RXN		TMP // TDP
FGAMSYN-RXN		5-PHOSPHORIBOSYL-N-FORMYLGLYCINEAMIDINE // 5-P-RIBOSYL-N-FORMYLGLYCINEAMIDE
DMBPPRIBOSYLTRANS-RXN		ALPHA-RIBAZOLE-5-P // DIMETHYLBENZIMIDAZOLE
NICONUCADENYLYLT RAN-RXN		DEAMIDO-NAD
DETHIOBIOTIN-SYN-RXN		DETHIOBIOTIN
R344-RXN		CPD-694 // CPD-690
CDPDIGLYSYN-RXN		CDPDIACYLGLYCEROL
5.4.2.10-RXN		GLUCOSAMINE-1P
2.3.1.157-RXN		GLUCOSAMINE-1P // N-ACETYLD-GLUCOSAMINE-1-P
THYMIDYLATESYN-RXN		DUMP // TMP
R601-RXN		Menaquinols // Menaquinones
UROGENIIISYN-RXN		UROPORPHYRINOGEN-III
ASPARTATEKIN-RXN		L-BETA-ASPARTYL-P
ARGSUCCINSYN-RXN		L-ARGININO-SUCCINATE
GLUTKIN-RXN		L-GLUTAMATE-5-P
RXN-8665		N-FORMYLKYNURENINE
ACETYLGLUTKIN-RXN		N-ACETYL-GLUTAMYL-P // ACETYL-GLU
N-ACETYLGLUTPREDUCT-RXN		N-ACETYL-GLUTAMYL-P // CPD-469

	Reactions	Chokepoints	Chokepoint Compound(s)
Consuming Side	ARYLFORMAMIDASE-RXN		N-FORMYLKYNURENINE // CPD-14736
	DIMETHUROPORDEHYDROG-RXN		DIHYDROSIROHYDROCHLORIN // SIROHYDROCHLORIN
	UROPORIIMETHYLTRANSA-RXN		CPD-9038
	UROGENDECARBOX-RXN		COPROPORPHYRINOGEN_III
	PANTOTHENATE-KIN-RXN		4-P-PANTOTHENATE // PANTOTHENATE
	PGPPHOSPHATE-RXN		L-1-PHOSPHATIDYL-GLYCEROL-P
	THIAZOLSYN2-RXN		CPD-13575 // Thiocarboxyadenylated-ThiS-Proteins // Thi-S
	PORPHOBILSYNTH-RXN		PORPHOBILINOGEN // 5-AMINO-LEVULINATE
	R343-RXN		CPD-694 // CPD-689
	2.8.1.6-RXN		DETHIOBIOTIN // BIOTIN
	3-OXOADIPATE-ENOL-LACTONASE-RXN		3-OXOADIPATE-ENOL-LACTONE
	OHMETHYLBILANESYN-RXN		HYDROXYMETHYLBILANE // PORPHOBILINOGEN
	PANTEPADENYLYLTRANSA-RXN		DEPHOSPHO-COA // PANTETHEINE-P
	PYRIMSYN3-RXN		AMINO-HYDROXYMETHYL-METHYL-PYR-P // AMINO-HYDROXYMETHYL-METHYLPYRIMIDINE-PP
	UROCANATE-HYDRATASE-RXN		4-IMIDAZOLONE-5-PROPIONATE // UROCANATE
	AICARTRANSFORM-RXN		AICAR // PHOSPHORIBOSYL-FORMAMIDO-CARBOXAMIDE
	GLYRIBONUCSYN-RXN		5-PHOSPHO-RIBOSYL-GLYCINEAMIDE // 5-P-BETA-D-RIBOSYL-AMINE
	RXN-9789		Adenylated-ThiS-Proteins // Thi-S
	GLURS-RXN		Charged-GLT-tRNAs // GLT-tRNAs

Reactions	Chokepoints	Chokepoint Compound(s)
RXN-11924		DsrC-disulfide-form // DsrC-L-Cysteine
R345-RXN		CPD-690 // CPD-691
RXN-8770		ADENOSYLCOBALAMIN-5-P
RXN-6261		CPD-691
AIRS-RXN		5-PHOSPHORIBOSYL-N-FORMYLGLYCINEAMIDINE // 5-PHOSPHORIBOSYL-5-AMINOIMIDAZOLE
THIAZOLSYN3-RXN		THZ-P // THZ
SAICARSYN-RXN		PHOSPHORIBOSYL-CARBOXY-AMINOIMIDAZOLE // P-RIBOSYL-4-SUCCARB-AMINOIMIDAZOLE
ACETATEKIN-RXN		ACETYL-P
DTMPKI-RXN		TMP // TDP
OHMETPYRKIN-RXN		HMP
FGAMSYN-RXN		5-PHOSPHORIBOSYL-N-FORMYLGLYCINEAMIDINE // 5-P-RIBOSYL-N-FORMYLGLYCINEAMIDE
DMBPPRIBOSYLTRANS-RXN		ALPHA-RIBAZOLE-5-P // DIMETHYLBENZIMIDAZOLE
QUINOPRIBOTRANS-RXN		QUINOLINATE
BUTYRYL-COA-DEHYDROGENASE-RXN		CROTONYL-COA
R344-RXN		CPD-694 // CPD-690
2.3.1.157-RXN		GLUCOSAMINE-1P // N-ACETYLD-GLUCOSAMINE-1-P
DCDPKIN-RXN		DCDP
DGDPKIN-RXN		DGDP
DTDPKIN-RXN		TDP
DUDPKIN-RXN		DUDP
THYMIDYLATESYN-RXN		DUMP // TMP
R601-RXN		Menaquinols // Menaquinones

Reactions	Chokepoints	Chokepoint Compound(s)
IMPCYCLOHYDROLAS E-RXN		PHOSPHORIBOSYL- FORMAMIDO-CARBOXAMIDE
ARGSUCCINLYA-RXN		L-ARGININO-SUCCINATE
ASPARTATE- SEMIALDEHYDE- DEHYDROGENASE- RXN		L-BETA-ASPARTYL-P
GLUTSEMIALDEHYDR OG-RXN		L-GLUTAMATE-5-P
NAG1P-URIDYLTRANS- RXN		N-ACETYL-D-GLUCOSAMINE-1- P
ACETYLGLUTKIN-RXN		N-ACETYL-GLUTAMYL-P // ACETYL-GLU
N- ACETYLGLUTPREDUCT- RXN		N-ACETYL-GLUTAMYL-P // CPD- 469
ARYLFORMAMIDASE- RXN		N-FORMYLKYNURENINE // CPD- 14736
DIMETHUROPORDEHY DROG-RXN		DIHYDROSIROHYDROCHLORIN // SIROHYDROCHLORIN
PROTOHEMEFERROCH ELAT-RXN		PROTOPORPHYRIN_IX
PNPOXI-RXN		PYRIDOXINE-5P
P-PANTOCYSDECARB- RXN		R-4-PHOSPHOPANTOTHENOYL- L-CYSTEINE
RXN-8675		CPD-9038
XANTHOSINEPHOSPHO RY-RXN		XANTHOSINE

Table 10. Chokepoint enzymes in *Acinetobacter baumannii* ACICU

	Reactions Chokepoints	Chokepoint Enzyme(s)
Producing Side	PANTOTHENATE-KIN-RXN	EC-2.7.1.33
	THIAZOLSYN2-RXN	EC-2.8.1.10
	PORPHOBILSYNTH-RXN	EC-4.2.1.24
	R343-RXN	EC-1.16.8.1
	2.8.1.6-RXN	EC-2.8.1.6
	OHMETHYLBILANESYN-RXN	EC-2.5.1.61
	PANTEPADENYLYLTRAN-RXN	EC-2.7.7.3
	PYRIMSYN3-RXN	EC-2.7.4.7
	UROCANATE-HYDRATASE-RXN	EC-4.2.1.49
	IMIDAZOLONEPROPIONASE-RXN	EC-3.5.2.7
	AICARTRANSFORM-RXN	EC-2.1.2.3
	GLYRIBONUCSYN-RXN	EC-6.3.4.13
	RXN-9655	EC-2.3.1.86 // EC-2.3.1.85 // EC-4.2.1.59
	RXN-9789	EC-2.7.7.73
	GLURS-RXN	EC-6.1.1.17
	RXN-11924	
	PHOSACETYLTRANS-RXN	EC-2.3.1.8
	COBINPGUANYLYLTRAN-RXN	EC-2.7.7.62
	R345-RXN	EC-6.3.5.10
	COBALAMIN5PSYN-RXN	EC-2.7.8.26
AIRS-RXN	EC-6.3.3.1	
THIAZOLSYN3-RXN	EC-2.7.1.50	
SAICARSYN-RXN	EC-6.3.2.6	
DTMPKI-RXN	EC-2.7.4.12 // EC-2.7.4.13 // EC-2.7.4.9	

	Reactions Chokepoints	Chokepoint Enzyme(s)
	FGAMSYN-RXN	EC-6.3.5.3
	DMBPPRIBOSYLTRANS-RXN	EC-2.4.2.21
	NICONUCADENYLYLTRAN-RXN	EC-2.7.7.18
	DETHIOBIOTIN-SYN-RXN	EC-6.3.3.3
	R344-RXN	EC-2.5.1.17
	CDPDIGLYSYN-RXN	EC-2.7.7.41
	5.4.2.10-RXN	EC-5.4.2.10
	2.3.1.157-RXN	EC-2.3.1.157
	THYMIDYLATESYN-RXN	EC-2.1.1.45
	R601-RXN	EC-1.3.5.4
	UROGENIIISYN-RXN	EC-4.2.1.75
	ASPARTATEKIN-RXN	EC-2.7.2.4
	ARGSUCCINSYN-RXN	EC-6.3.4.5
	GLUTKIN-RXN	EC-2.7.2.11
	RXN-8665	EC-1.13.11.11 // EC-1.13.11.52
	ACETYLGLUTKIN-RXN	EC-2.7.2.8
	N-ACETYLGLUTPREDUCT-RXN	EC-1.2.1.38
	ARYLFORMAMIDASE-RXN	EC-3.5.1.9
	DIMETHUROPORDEHYDROG-RXN	EC-1.3.1.76
	UROPORIIIMETHYLTRANSA-RXN	
	UROGENDECARBOX-RXN	EC-4.1.1.37
	Reactions that are chokepoints on the consuming side	EC-Number
Consuming Side	PANTOTHENATE-KIN-RXN	EC-2.7.1.33
	PGPPHOSPHA-RXN	EC-3.1.3.27

Reactions Chokepoints	Chokepoint Enzyme(s)
THIAZOLSYN2-RXN	EC-2.8.1.10
PORPHOBILSYNTH-RXN	EC-4.2.1.24
R343-RXN	EC-1.16.8.1
2.8.1.6-RXN	EC-2.8.1.6
3-OXOADIPATE-ENOL-LACTONASE-RXN	EC-3.1.1.24
OHMETHYLBILANESYN-RXN	EC-2.5.1.61
PANTEPADENYLYLTRAN-RXN	EC-2.7.7.3
PYRIMSYN3-RXN	EC-2.7.4.7
UROCANATE-HYDRATASE-RXN	EC-4.2.1.49
AICARTRANSFORM-RXN	EC-2.1.2.3
GLYRIBONUCSYN-RXN	EC-6.3.4.13
RXN-9789	EC-2.7.7.73
GLURS-RXN	EC-6.1.1.17
RXN-11924	
R345-RXN	EC-6.3.5.10
RXN-8770	EC-3.1.3.73
RXN-6261	EC-6.3.1.10
AIRS-RXN	EC-6.3.3.1
THIAZOLSYN3-RXN	EC-2.7.1.50
SAICARSYN-RXN	EC-6.3.2.6
ACETATEKIN-RXN	EC-2.7.2.1
DTMPKI-RXN	EC-2.7.4.12 // EC-2.7.4.13 // EC-2.7.4.9
OHMETPYRKIN-RXN	EC-2.7.1.49
FGAMSYN-RXN	EC-6.3.5.3
DMBPPRIBOSYLTRANS-RXN	EC-2.4.2.21
QUINOPRIBOTRANS-RXN	EC-2.4.2.19

Reactions	Chokepoints	Chokepoint Enzyme(s)
BUTYRYL-COA- DEHYDROGENASE-RXN		EC-1.3.8.1
R344-RXN		EC-2.5.1.17
2.3.1.157-RXN		EC-2.3.1.157
DCDPKIN-RXN		EC-2.7.4.6
DGDPKIN-RXN		EC-2.7.4.6
DTDPKIN-RXN		EC-2.7.4.6
DUDPKIN-RXN		EC-2.7.4.6
THYMIDYLATESYN- RXN		EC-2.1.1.45
R601-RXN		EC-1.3.5.4
IMPCYCLOHYDROLASE- RXN		EC-3.5.4.10
ARGSUCCINLYA-RXN		EC-4.3.2.1
ASPARTATE- SEMIALDEHYDE- DEHYDROGENASE-RXN		EC-1.2.1.11
GLUTSEMIALDEHYDRO G-RXN		EC-1.2.1.41
NAG1P-URIDYLTRANS- RXN		EC-2.7.7.23
ACETYLGLUTKIN-RXN		EC-2.7.2.8
N- ACETYLGLUTPREDUCT- RXN		EC-1.2.1.38
ARYLFORMAMIDASE- RXN		EC-3.5.1.9
DIMETHUROPORDEHY DROG-RXN		EC-1.3.1.76
PROTOHEMEFERROCHE LAT-RXN		EC-4.99.1.1
PNPOXI-RXN		EC-1.4.3.5
P-PANTOCYSDECARB- RXN		EC-4.1.1.36
RXN-8675		

Reactions	Chokepoints	Chokepoint Enzyme(s)
XANTHOSINEPHOSPHO RY-RXN		EC-2.4.2.1

Table 11. Deadend metabolites in *A. baumannii* ACICU

DEM	Pathways	MetaCyc Compound	MetaCyc Rxns Consuming DEM	Pathways of compound
SIROHEME	PWY-5194	SIROHEME	RXN-15805	PWY-5194
HISTAMINE	PWY-6173	HISTAMINE	HISTAMINE-N-METHYLTRANSFERASE RXN // GAMMA- GLUTAMYLHISTAMINE-SYNTHASE- RXN // RXN-9600 // RXN-19438	PWY-6173
ACRYLATE	PWY-7308	ACRYLATE	RXN-10985	PWY-7308
CPD-13851		CPD-13851	RXN0-6957	
CPD-8890	PWY-5461	CPD-8890	RXN-15989 // RXN-9292 // 1.3.7.2- RXN // 1.3.7.5-RXN // 1.3.7.4-RXN //	PWY-5461
BILIVERDINE		BILIVERDINE	BILIVERDIN-REDUCTASE-RXN	
PHOSPHORYL- CHOLINE	LIPASYN-PWY	PHOSPHORYL-CHOLINE	RXN-5647 // 2.7.7.15-RXN	LIPASYN-PWY
CPD-13691		CPD-13691	RXN-12703 // RXN-17645	
ETHANAMINE		ETHANAMINE	RXN-12905 // RXN-13592 // R467- RXN // THEANINE-HYDROLASE-RXN	
CPD-3706		CPD-3706	RXN-14126	
ETHYLENE-CMPD		ETHYLENE-CMPD	RXN-17580	
L-ARA4N- MODIFIED-KDO2- LIPID-A	PWY0-1338	L-ARA4N-MODIFIED-KDO2-LIPID-A		PWY0-1338
3-Methyl- Adenines		3-Methyl-Adenines		
DIACETYL		DIACETYL	ACETOINDEHYDROG-A-RXN // RXN- 11036 // ACETOINDEHYDROG-RXN // RXN-11032	
CPD-11984	PWY-6385	CPD-11984	RXN-11027	PWY-6385
CPD-11592		CPD-11592	RXN-10751	

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CARBON-MONOXIDE	PWY-6890 // THISYN-PWY // PWY-6895	CARBON-MONOXIDE	1.2.2.4-RXN // RXN-17357 // 1.2.7.4-RXN // RXN-12907 // TRANS-RXN-556 // ACETYLSYNCLTH-RXN	1.2.2.4-RXN // RXN-17357 // 1.2.7.4-RXN // RXN-12907 // TRANS-RXN-556 // ACETYLSYNCLTH-RXN	PWY-6890 // THISYN-PWY // PWY-6895
CPD-13910 URIDINE	CPD-13910 URIDINE		RXN-12873 URIDINEKIN-RXN // URPHOS-RXN // URIDINE-NUCLEOSIDASE-RXN // RXN-18070 // URKI-RXN // TRANS-RXN-1081	RXN-12873 URIDINEKIN-RXN // URPHOS-RXN // URIDINE-NUCLEOSIDASE-RXN // RXN-18070 // URKI-RXN // TRANS-RXN-1081	
RIBOSE-1P	PWY-6620 // PWY-6608 // SALVPURINE2-PWY // PWY-5695 // SALVADEHYPOX-PWY // PWY-6353	RIBOSE-1P	PPENTOMUT-RXN // RXN-14456 // RXN0-1402 // RXN-17337 // XANTHOSINEPHOSPHORY-RXN // URPHOS-RXN // RXN0-5199 // PNP-RXN // ADENPHOSPHOR-RXN // INOPHOSPHOR-RXN // RXN-10763 // URATE-RIBONUCLEOTIDE-PHOSPHORYLASE-RXN	PPENTOMUT-RXN // RXN-14456 // RXN0-1402 // RXN-17337 // XANTHOSINEPHOSPHORY-RXN // URPHOS-RXN // RXN0-5199 // PNP-RXN // ADENPHOSPHOR-RXN // INOPHOSPHOR-RXN // RXN-10763 // URATE-RIBONUCLEOTIDE-PHOSPHORYLASE-RXN	PWY-6620 // PWY-6608 // SALVPURINE2-PWY // PWY-5695 // SALVADEHYPOX-PWY // PWY-6353
CPD-1137 CPD-15999	CPD-1137 CPD-15999		ITACONYL-COA-HYDRATASE-RXN	ITACONYL-COA-HYDRATASE-RXN	PWY-5508
ADENOSYLCOBALAMIN AMIN	PWY-5508 PWY-5508 // PWY-5509 // COBALSYN-PWY	ADENOSYLCOBALAMIN	COBALAMINSYN-RXN	COBALAMINSYN-RXN	PWY-5508 // PWY-5509 // COBALSYN-PWY
CYTIDINE		CYTIDINE	RXN0-361 // CYTIDEAM2-RXN // RXN-16944 // CYTIKIN-RXN // CYTIDINEKIN-RXN // TRANS-RXN-108B	RXN0-361 // CYTIDEAM2-RXN // RXN-16944 // CYTIKIN-RXN // CYTIDINEKIN-RXN // TRANS-RXN-108B	
PYRIDOXAL_PHOSPHATE	PYRIDOXSYN-PWY // PLPSAL-PWY // PWY0-845	PYRIDOXAL_PHOSPHATE	RXN0-5240 // 3.1.3.74-RXN // RXN30-3797 // RXN0-7074 // PYRDAMPTRANS-RXN	RXN0-5240 // 3.1.3.74-RXN // RXN30-3797 // RXN0-7074 // PYRDAMPTRANS-RXN	PYRIDOXSYN-PWY // PLPSAL-PWY // PWY0-845

GERANYLGERANYL-PWY-5120
PP

GERANYLGERANYL-PP

CASBENE-SYNTHASE-RXN // 2.5.1.42- PWY-5120
RXN // 4.2.3.17-RXN // 5.5.1.13-RXN
// RXN-8528 // 2.5.1.41-RXN // RXN-
10627 // RXN-10630 // RXN-10632
// RXN-11485 // RXN-11486 // RXN-
11778 // RXN-11779 // RXN-4861 //
RXN-8813 // RXN-10631 // RXN-
9456 // RXN-9457 // RXN-3701 //
RXN-10441 // RXN-14929 // RXN-
15429 // RXN-15494 // RXN-15705
// RXN-15706 // RXN-15707 // RXN-
15708 // RXN-17085 // RXN-17480
// RXN-7663 // RXN-7673 // RXN-
8788 // RXN-11488 // RXN-11458 //
RXN-18785 // RXN-18786 // RXN-
18811 // RXN-18812 // RXN-18885
// RXN-18977 // RXN-18981 //
2.5.1.32-RXN // RXN-13323 // RXN-
18893 // RXN-19160 // RXN-19235
// RXN-12892 // RXN-14242 // RXN-
18975 // RXN-18891 // RXN-10625
// RXN-7658 // RXN-11772 // RXN-
11628

5-AMINOPENTANOATE

VAGL-RXN

5-AMINOPENTANOATE

CPD-108 PWY-6892 // THISYN- CPD-108
PWY // PWY-7514

RXN-15588 // M-CRESOL- PWY-6892 // THISYN-
METHYLCATECHOL-RXN // RXN- PWY // PWY-7514
16790 // RXN-16204 // 1.17.99.1-
RXN // TRANS-RXN0-500

CPD-16618	CPD-16618	RXN-6002
TRIMETHYLAMINE	TRIMETHYLAMINE	RXN-12900 // RXN-8102 // 1.5.8.2- RXN // TMAOREDUCT-RXN
GLUTATHIONYLSP	GLUTATHIONYLSPERMIDINE	GSPAMID-RXN // 6.3.1.9-RXN
ERMIDINE		PWY-4121
UDP-MANNACA	UDP-MANNACA	UDPMANACATrans-RXN
CPD-18	CPD-18	LINOLEOYL-RXN // 1.14.19.3-RXN // RXN-16094 // RXN-16228 // RXN- 16116
5-HYDROXY-CTP	5-HYDROXY-CTP	RXN-14188
CPD-8259	CPD-8259	RXN-8443
TREHALOSE	TREHALOSE	TREHALA-RXN // RXN-4441 // RXN- 15426 // ALPHAALPHA-TREHALOSE- PHOSPHORYLASE-RXN // RXN-17176 // RXN-17316 // RXN-17315 // TRANS-RXN-168 // 5.4.99.16-RXN // RXN-9603 // RXN-15358
		TRESYN-PWY
CPD-3708	CPD-3708	RXN-14124
CPD-14424	CPD-14424	RXN-13444
METHYLAMINE	METHYLAMINE	1.2.1.4.3-RXN // GLUTAMATE-- METHYLAMINE-LIGASE-RXN // 2.1.1.21-RXN // RXN-2841 // RXN- 8098 // RXN-17574 // RXN-7262 // 1.5.8.1-RXN // N-METHYLALANINE- DEHYDROGENASE-RXN // N-METHYL- 2-OXOGLUTARAMATE-HYDROLASE- RXN // ALKYLAMIDASE-RXN
		PWY-7431
CPD-3724	CPD-3724	RXN-14115
CPD-16491	CPD-16491	

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CPD-582	PWY-5964	CPD-582	PWY-5964
CPD-10017	HEMESYN2-PWY //	CPD-10017	HEMESYN2-PWY //
CH33ADO	PWY0-501 // PWY-7380 // PWY0-1507 //	CH33ADO	PWY0-501 // PWY-7380 // PWY0-1507 // PWY-6890 // PWY-6895 // PWY-6892 // THISYN-PWY
CPD0-2461	THISYN-PWY	CPD0-2461	RXN0-6550 // RXN-15568 // RXN-14304
ENOL-PHENYLPYRUVATE		ENOL-PHENYLPYRUVATE	RXN0-6708
PHENYLPYRUVATE		PHENYLPYRUVATE	PHENYLPYRUVATE-TAUTOMERASE-RXN
CPD-731		CPD-731	RXN-745
CPD-3711		CPD-3711	RXN-14090
CPD-11495		CPD-11495	RXN-18767
CPD-8534		CPD-8534	
CPD-7031		CPD-7031	RXN-7693 // 1.1.1.265-RXN
OH	DETOX1-PWY-1 // P224-PWY	OH	RXN-10688
LINOLENOYL-COA		LINOLENOYL-COA	RXN-13426 // RXN-13441

GDP-MANNOSE PWY-5659 GDP-MANNOSE
GDPMANDEHYDRA-RXN // 2.4.1.217- PWY-5659
RXN // RXN30-663 // 2.4.1.110-RXN
// 2.4.1.54-RXN // RXN-10795 // RXN-
11788 // RXN-11789 // RXN-12040
// RXN-5463 // 2.7.8.9-RXN //
2.4.1.32-RXN // RXN0-5108 //
2.4.1.48-RXN // RXN-7992 // RXN-
8849 // RXN-12029 // GDP-
MANNOSE-6-DEHYDROGENASE-RXN
// RXN-9935 // RXN-16602 // RXN-
17204 // RXN-17311 // RXN-5464 //
RXN-5462 // 2.4.1.142-RXN //
GDPMANMANHYDRO-RXN // RXN-
18607 // RXN-18610 // RXN-18680
// RXN-1882 // RXN-7771 // 2.4.1.57-
RXN // RXN-18771 // RXN-18772 //
RXN-18773 // RXN-18774 // RXN-
18775 // RXN-18776 // 2.4.1.232-
RXN // RXN-18915 // RXN30-9783 //
RXN-19015 // RXN-19016 // RXN-
19017 // 2.4.1.83-RXN // RXN-18684
// MANNPGUANYLTRANGDP-RXN

CPD-14442
CPD-294

MALEYLACETATE-REDUCTASE-RXN //
RXN-9922

CPD-14442
CPD-294
CPD0-1208

N-ACETYL-D- GLUCOSAMINE	PWY0-1261	N-ACETYL-D-GLUCOSAMINE	N-ACYLHEXOSAMINE-OXIDASE-RXN // RXN-15185 // R381-RXN // 2.4.1.211-RXN // RXN0-5243	PWY0-1261
CPD-13759	PWY-6944	CPD-13759	RXN-11397	PWY-6944
CPD-12366	PWY-5695 //	CPD-12366	URATE-OXIDASE-RXN // RXN-11186	PWY-5695 //
URATE	SALVADEHYPOX-PWY // PWY-6608 // PWY- 6353	URATE	// RXN-18354 // TRANS-RXN0-530 // SALVADEHYPOX-PWY //	PWY-6608 // PWY-6353
CPD-1772	PWY0-981	CPD-1772	RXN-11455 // RXN0-901 // TRANS- RXN-207 // URATE-RIBONUCLEOTIDE PHOSPHORYLASE-RXN	PWY0-981
CPD-10774		CPD-10774	RXN-15982 // TRANS-RXN0-454 //	
			TRANS-RXN0-453	

3-5-ADP	PWY-6012 // SO4ASSIM-PWY // SULFATE-CYS-PWY // PWY-5345	3-5-ADP	1.8.4.8-RXN // 325-BISPHOSPHATE- NUCLEOTIDASE-RXN // RXN-10674 // RENILLA-LUCIFERIN- SULFOTRANSFERASE-RXN // ARYLAMINE-SULFOTRANSFERASE- RXN // RXN-17203 // RXN-16759 // RXN-11559 // RXN-10994 // 2.8.2.19- RXN // RXN-15587 // RXN-15589 // RXN-15588 // RXN-14843 // RXN- 8729 // BILE-SALT- SULFOTRANSFERASE-RXN // TYROSINE-ESTER- SULFOTRANSFERASE-RXN // ALCOHOL-SULFOTRANSFERASE-RXN // RXN-10880 // RXN-10879 // RXN- 10811 // CHOLINE- SULFOTRANSFERASE-RXN // ESTRONE-SULFOTRANSFERASE-RXN // CORTISOL-SULFOTRANSFERASE- RXN // RXN-701 // STEROID- SULFOTRANSFERASE-RXN // 2.8.2.7- RXN // THIOL-SULFOTRANSFERASE- RXN // 2.8.2.31-RXN // 2.8.2.34-RXN // 2.8.2.32-RXN	PWY-6012 // SO4ASSIM- PWY // SULFATE-CYS- PWY // PWY-5345
CPD-10776		CPD-10776		RXN-10019
CPD0-1905		CPD0-1905		RXN-14205 // RXN-11396
CPD-12019		CPD-12019		RXN-11068 // RXN-11069
CPD-12557		CPD-12557		
CPD-13912		CPD-13912		

FERULIC-ACID

PWY-6784

FERULIC-ACID

RXN-1121 // 6.2.1.34-RXN // RXN-
14071 // RXN-801 // N-
FERULOYLGLYCINE-DEACYLASE-RXN

PWY-6784

U.S. wounded military personnel (APPENDIX D, strains # 3132-3160 and 3284) as well as 12 non-military isolates representing type strains, different international clonal lineages, strains whose genomes were fully sequenced and annotated as well as strains that were classified as antimicrobial susceptible or MDR (APPENDIX D, strains # 406-3022 and #3161). Additionally, 28 CDC & FDA AR Isolate *A. baumannii* panel were tested. We initially tested the antibiotic susceptibility of all non-WRAIR and non-AR Isolate strains, the identities of which were confirmed using a combination of standard bacteriological methods and modern technology such as MALDI-TOF MS. This analysis showed that this strain set includes isolates, such as *A. baumannii* ATCC SDF, that are susceptible to all tested antibiotics, which included more than six different classes of antimicrobials; isolates that display resistance to some antibiotics, such as ATCC 19606T and ATCC 17978; MDR isolates, such as LUH07672, LUH08809, LUH05875, LUH13000, RUH00134, and RUH00875; and isolates that are resistant to practically all drugs, such as AYE and ACICU; with the latter being the most resistant isolate used in this work (Table 12). The U.S. military strain collection of clinical isolates includes 30 strains, each of which are resistant to most of the 11 antibiotics tested (75).

Growth inhibitory effects of GaPPIX

All tested strains displayed apparent growth when cultured in CAMH broth at 37°C for 18 h using 96-well microtiter plates, although there was some growth variability among them (APPENDIX D). The addition of GaPPIX produced a dose-dependent growth response with several strains growing to higher optical densities in the presence of 5 µg/ml to 20 µg/ml of this non-ferric metalloporphyrin when assayed using an automated two-fold microdilution method. However, bacterial growth was significantly reduced when the

Table 12. *Acinetobacter baumannii* minimal inhibitory concentrations

MIC ($\mu\text{g/ml}$) ^{a,b}	Strains	Penicillins				Cephalosporins									
		AMP ^v	SAM ^v	TZP ^v	CFZ ^v	FEP ^ε	FOX ^v	CAZ ^ε	CRO ^v						
	ATCC 19606 ^T	≥32	R ≤2	S ≤4	S	≥64	R	24	*	≥64	R	12	*	16	I
	ATCC 17978	≥32	R ≤2	S ≤4	S	≥64	R	3	S	≥64	R	6	S	16	I
	LUH07672	≥32	R ≤2	S ≤4	S	≥64	R	32	R	≥64	R	>256	R	≥64	R
	LUH08809	≥32	R 4	S ≥128	R	≥64	R	96	R	≥64	R	192	R	≥64	R
	LUH05875	≥32	R 4	S ≥128	R	≥64	R	>256	R	≥64	R	64	R	≥64	R
	LUH13000	≥32	R 4	S ≥128	R	≥64	R	16	I	≥64	R	≥256	R	≥64	R
	RUH00134	≥32	R ≥32	R 8	S	≥64	R	12	I	≥64	R	6	S	16	I
	RUH00875	≥32	R ≥32	R 16	S	≥64	R	24	I	≥64	R	16	I	16	I
	AYE	≥32	R 8	S >128	R	≥64	R	>256	R	≥64	R	>256	R	≥64	R
	SDF	ND	ND	ND	ND	ND	ND	2	S	ND	ND	4	S	ND	ND
	A118	16	R ≤2	S 8	S	≥64	R	3	S	4	S	6	S	16	I
	ACICU	≥32	R ≥32	R ≥128	R	≥64	R	≥256	R	≥64	R	≥256	R	≥64	R

MIC ($\mu\text{g/ml}$) ^{a,b}														
Strains	Carbapenems			Fluoroquinolones			Aminoglycosides							
	IMP ^β	MEM ^ε		CIP ^ε	LVX ^ε		AMK ^β	GEN ^ε	GEN ^ε	TOB ^ε				
ATCC 19606 ^T	≤1	S	1.5	S	0.75	S	0.5	S	16	S	12	R	3	S
ATCC 17978	1	S	0.75	S	0.25	S	0.19	S	≤4	S	1.5	S	0.5	S
LUH07672	≤1	S	1.5	S	>32	R	24	R	>32	R	>256	R	64	R
LUH08809	≤1	S	8	I	>32	R	>32	R	>32	R	>256	R	>256	R
LUH05875	≤1	S	8	I	>32	R	>32	R	>32	R	>256	R	96	R
LUH13000	2	S	1	S	>32	R	>32	R	>32	R	>256	R	96	R
RUH00134	≤1	S	0.75	S	0.38	S	0.25	S	8	S	≥256	R	1.5	S
RUH00875	≤1	S	2	S	0.75	S	0.38	S	16	S	>256	R	>256	R
AYE	≤1	S	2	S	>32	R	>32	R	>32	R	>256	R	48	R
SDF	≤1	S	1	S	0.25	S	0.25	S	<4	S	0.5	S	0.19	S
A118	≤1	S	0.75	S	0.19	S	0.125	S	≤4	S	1.5	S	0.75	S
ACICU	>8	R	≥32	R	≥32	R	≥32	R	≥32	R	16	R	16	R

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MIC ($\mu\text{g/ml}$) ^{a,b}		Tetracyclines			Miscellaneous		
Strains	TGC* ^ε	DOX ^κ		CST ^ε	SXT ^ε		Ga-PPIX ^τ
ATCC 19606 [†]	2	27	S	0.125	S	>640	R 15 *
ATCC 17978	0.38	26	S	0.38	S	>640	R 17 *
LUH07672	6	12	I	0.125	S	>640	R 18 *
LUH08809	8	12	I	0.125	S	>640	R 20 *
LUH05875	12	14	S	0.125	S	>640	R 19 *
LUH13000	4	6	R	0.25	S	>640	R 20 *
RUH00134	3	6	R	0.25	S	≥32	R 20 *
RUH00875	3	10	I	0.19	S	>640	R 19 *
AYE	3	15	S	0.38	S	>640	R 14 *
SDF	0.5	26	S	0.094	S	5	S 11 *
A118	0.38	27	S	0.125	S	0.75	S 18 *
ACICU	4	15	S	0.125	S	≥32	R 18 *

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^a Amikacin (AMK), Ampicillin (AMP), Ampicillin-Sulbactam (SAM), Cefazolin (CFZ), Cefepime (FEP), Cefoxitin (FOX), Ceftriaxone (CAZ), Ceftriaxone (CRO), Ciprofloxacin (CIP), Colistin (CST), Gentamicin (GEN), Imipenem (IPM), Levofloxacin (LVX), Meropenem (MEM), Piperacillin-tazobactam (TZP), Tigecycline (TGC), Tobramycin (TOB), Trimethoprim-sulfamethoxazole (SXT), Gallium protoporphyrin IX (Ga-PPIX)

^b Susceptible (S), Intermediate (I), Resistant (R), Not

* No interpretative

^ε MIC determined by Etest

^v MIC determined by VITEK-2

^β MIC determined by BD Phoenix

^κ Susceptibility determined by Kirby-

^τ MIC determined by microdilution

CAMH broth contained more than 20 µg/ml GaPPIX making 40 µg/ml the MIC for all 42 strains when tested using this automated approach, which resulted in inocula containing 10⁶ bacteria per sample. A more detailed manual analysis of the non-military isolates following the CLSI standards (10⁵-bacteria inocula and CAMHB) using a 2-fold GaPPIX serial dilution scheme resulted in a MIC value of 20 µg/ml for all of these isolates. Furthermore, a 1 µg/ml resolution scheme performed under the latter experimental conditions resulted in GaPPIX MIC values ranging between 11 µg/ml and 20 µg/ml (Table 12). The median and mean MIC of these non-military isolates was 19 µg/ml and 17.4 µg/ml, respectively. The CDC & FDA AR Isolates were all susceptible at an MIC comparable to all isolates tested. No resistance was noted. The presence of 10% heat-inactivated normal human serum increased the MIC for the ATCC 19606^T and ACICU strains to 62.5 µg/ml, a 3-fold increase when compared with the values obtained in the absence of proteins, without causing the complete inactivation or sequestration of GaPPIX. The GaPPIX susceptibility of these isolates was also tested using disk diffusion assays. All strains tested produced detectable ZOI ranging between 13 mm and 23 mm in diameter when the seeded plates were exposed to sterile filter disks impregnated with 50 µg or 100 µg GaPPIX, respectively (Figure 15), and there were no heteroresistant colonies noted in the ZOI, which is represented in the insets of Figure 15 A and B. This observation is in agreement with the failure to isolate GaPPIX resistant colonies of ATCC 19606^T and ACICU when a population of greater than 9.8x10⁹ bacteria were challenged to 2x (40 µg/ml) or 4x (80 µg/ml) MIC of GaPPIX (data not shown).

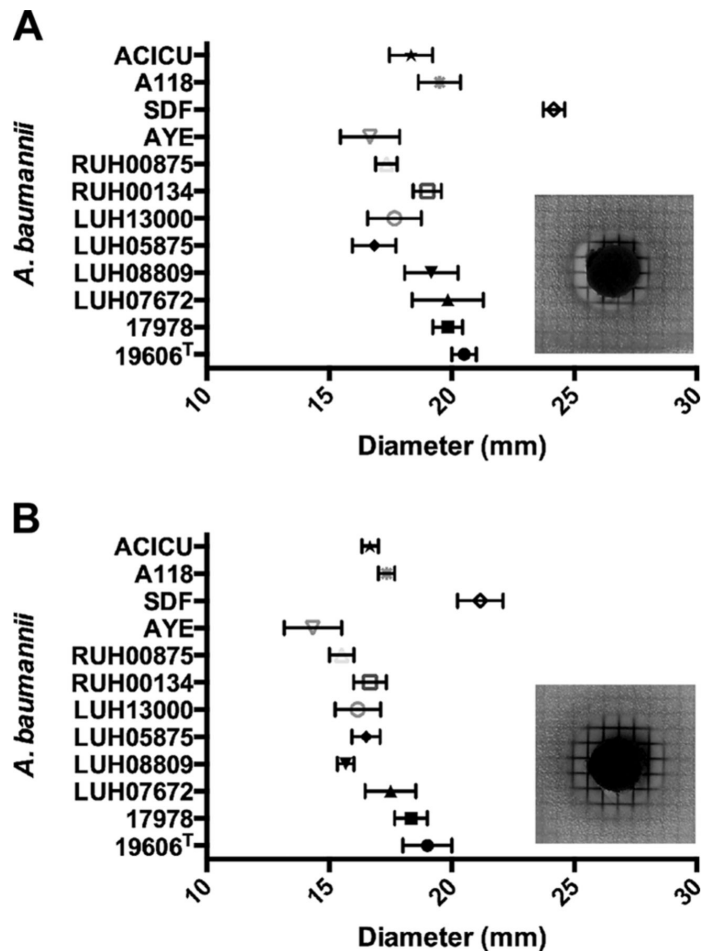


Figure 15. GaPPIX disk diffusion assays. *A. baumannii* bacteria were seeded onto CAMH agar and then disks impregnated with 50 μg (A) or 100 μg (B) of GaPPIX were deposited on the surfaces of the plates. Growth inhibition halos were measured after incubation for 24 h at 37°C. Data are expressed as \pm standard errors of the means (SEM) (error bars) from experiments done twice in triplicate. The insets show the growth inhibition halos observed when the CAMH agar plates were seeded with *A. baumannii* ATCC 19606^T and incubated for 24 h at 37°C.

Comparable results were obtained when the disk assays were conducted using LB agar plates that were supplemented with FeCl₃ or DIP to generate iron-rich and iron-chelated conditions, respectively (data not shown). Furthermore, comparable GaPPIX susceptibility responses were detected with the ATCC 19606^T strain and the isogenic derivatives ATCC 19606^T t6 (strain #1653 in APPENDIX D) and ATCC 19606^T entA (strain #3069 in APPENDIX D), which are affected in the uptake and biosynthesis of acinetobactin due to mutations in the genes coding for the BauA acinetobactin receptor protein and the BasD biosynthetic protein, respectively (109). Additionally, the detailed analysis of *A. baumannii* AB5075 (strain #3156 in APPENDIX D), a MDR isolate recently cultured from an infected wound that has been proposed as a model strain to study the pathobiology of this pathogen (75), showed a GaPPIX MIC of 20 µg/ml when cultured in CAMH broth under CLSI conditions (APPENDIX D Fig. S1, panels A and B).

These experimental data collected using two different methods show that the susceptibility of different *A. baumannii* clinical strains to GaPPIX, with a standard MIC of 20 µg/ml, is independent of their time and site of isolation as well as their overall antimicrobial resistance phenotypes and clonal lineages. The data also indicate that the susceptibility to GaPPIX is independent of the free-iron content of the medium as well as the capacity of bacteria to produce or use acinetobactin, which seems to be the most common siderophore-mediated iron uptake system found in the genome of different *A. baumannii* clinical isolates (110).

GaPPIX time-kill kinetics

The antibacterial activity of GaPPIX was tested by determining its time-kill kinetics using the ATCC 19606^T and ACICU non-military isolates, which are considered non-MDR

and MDR strains, respectively, at a concentration of 0.5, 1 and 2 times the MIC as determined by the microdilution method. Both *A. baumannii* strains showed similar responses, with the addition of 10 µg/ml GaPPIX (0.5 x MIC) causing only a small reduction in bacterial viability (Figure 16). In contrast, the addition of 20 µg/ml (1 x MIC) or 40 µg/ml (2 x MIC) was effective in reducing the viable cells by > 3 logs after four hours.

GaPPIX toxicity to eukaryotic cells and *Galleria mellonella* larvae

The toxicity of GaPPIX was tested using A549 alveolar epithelial tissue culture cells and *G. mellonella* caterpillars. GaPPIX exhibited no statistically significant toxicity for A549 cells at concentrations up to 160 µg/ml, 8 times the MIC, when tested using the Celltiter-Glo luminescent cell viability assay. This assay also showed that there was a statistically significant reduction in A549 viability when the culture medium contained 640 µg/ml ($P \leq 0.0001$) or 320 µg/ml ($P = 0.004$) GaPPIX (Figure 17A), concentrations that are far higher than the MIC values reported in the previous section. The *ex vivo* toxicity is corroborated by *in vivo* experiments using *G. mellonella* larvae (Figure 17B) with comparable body mass (Figure 17B inset). After injection with GaPPIX over a 3-log range, the survival of larvae injected with 25 mM was significantly reduced compared to the control group ($P = 0.0363$) (data not shown). The LC_{50} for GaPPIX in *G. mellonella* was extrapolated by pro-bit analysis from the log-dose response curve to be 157 mg/ml (Figure 17B). Also noted, the injection of high concentrations of GaPPIX resulted in immediate coloration of larvae and subsequently excreted feces were notably pink (data not shown).

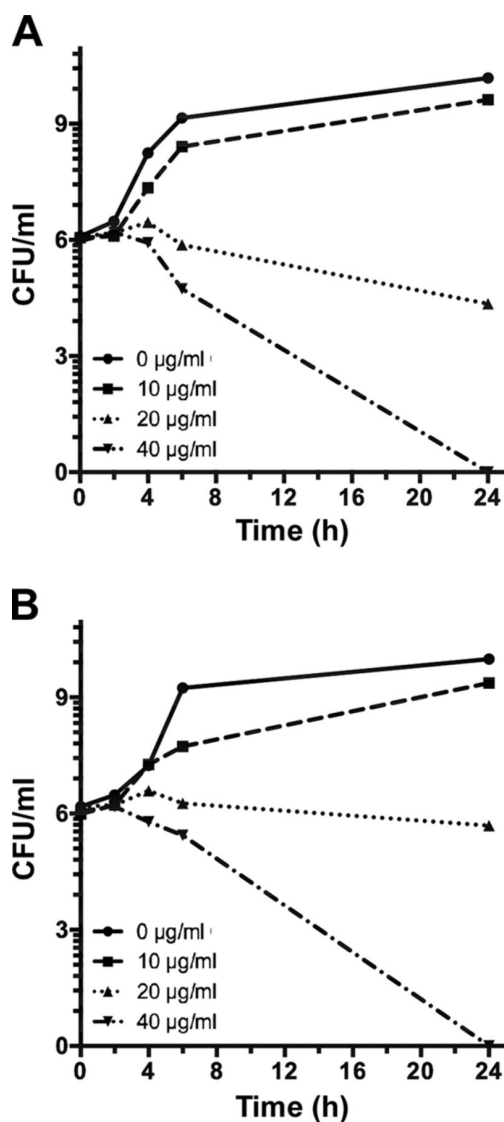


Figure 16. GaPPIX time-kill assays. GaPPIX time-kill kinetics for *A. baumannii* ATCC 19606^T (A) and ACICU (B) was determined after 0, 2, 4, 6, and 24 h of incubation by CFU count after exposure to 0 µg/ml (0X MIC), 10 µg/ml (0.5X MIC), 20 µg/ml (1X MIC), or 40 µg/ml (2X MIC) GaPPIX.

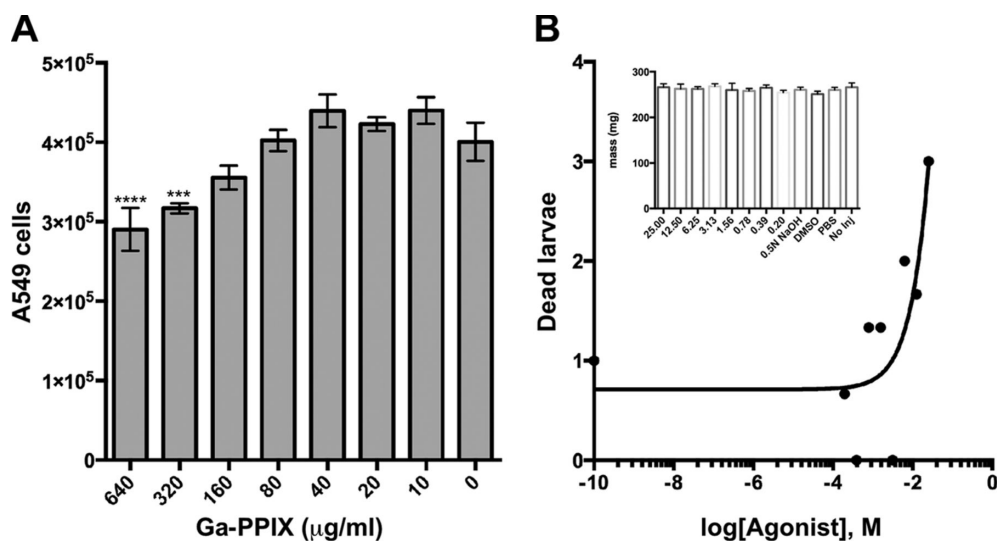


Figure 17. GaPPIX toxicity toward A549 human cells and *G. mellonella* larvae.

GaPPIX toxicity toward A549 human cells and *G. mellonella* larvae. (A) Submerged A549 cell monolayers containing 4×10^5 cells were incubated with increasing concentrations of GaPPIX dissolved in DMSO and added DMEM containing 10% heat-inactivated fetal bovine serum without antibiotics. Cell viability was determined after 24 h of incubation at 37°C in the presence of 5% CO₂. Responses to the presence of GaPPIX were compared to those detected with cells cultured in the absence of this metalloporphyrin derivative. Values that are significantly different from the value for the control (0 µg/ml GaPPIX) are indicated by asterisks as follows: ***, $P = 0.0004$, $P < 0.0001$. (B) Mass-matched *G. mellonella* larvae were injected with 5 µl of twofold dilutions ranging from 0.2 mM to 25 mM GaPPIX solubilized in 0.5 N NaOH and 1.5% DMSO. Larvae injected with 0.5 N NaOH, 1.5% DMSO, PBS or not injected (No Inj) served as controls. The inset shows the mean masses of all animal groups with error bars showing standard errors.

These results demonstrate the ability of eukaryotic cells and organisms to tolerate GaPPIX at concentrations much higher than the MIC values determined using standard methods.

GaPPIX treatment of *ex vivo* and *in vivo* experimental infections

The antibacterial effectiveness of GaPPIX was determined by infecting A549 tissue cultures and *G. mellonella* larvae with the *A. baumannii* ATCC 19606^T type strain or the ACICU MDR strain in the presence or absence of this non-ferric metalloporphyrin derivative. The presence of 20 µg/ml or 40 µg/ml of GaPPIX leads to a statistically significant reduction in CFUs for ATCC 19606^T ($P = 0.037$, $P = 0.014$) and ACICU ($P = 0.0005$, $P = 0.0005$) when compared with the samples incubated in the absence of this non-ferric metalloporphyrin derivative (Figure 18A and 18B). Overall, the addition of 40 µg/ml of GaPPIX led to 701-fold and 145-fold reductions of ATCC 19606^T and ACICU CFUs recovered from the infected monolayers, respectively.

The *G. mellonella in vivo* infection model also showed the antibacterial activity of GaPPIX (Figure 18C and 18D). Infection of larvae with an ATCC 19606^T inoculum containing 20 µg/ml or 40 µg/ml GaPPIX significantly increased animal survival with P values of 0.03 and 0.0003 and log-rank hazard ratios of 2.5 and 8.4 for each GaPPIX concentration tested, respectively, when compared with animals infected in the absence of this metalloporphyrin derivative (Figure 18C). Similar results were obtained with the MDR ACICU strain (Figure 18D), where injection with 20 µg/ml and 40 µg/ml of GaPPIX resulted in significant increases in survival with $P = 0.008$ and 0.001, and log-rank hazard ratios of 3.4 and 5.0 for the respective concentrations. Unfortunately, numerous attempts to test the antibacterial effect of GaPPIX by injecting it after infection failed to produce

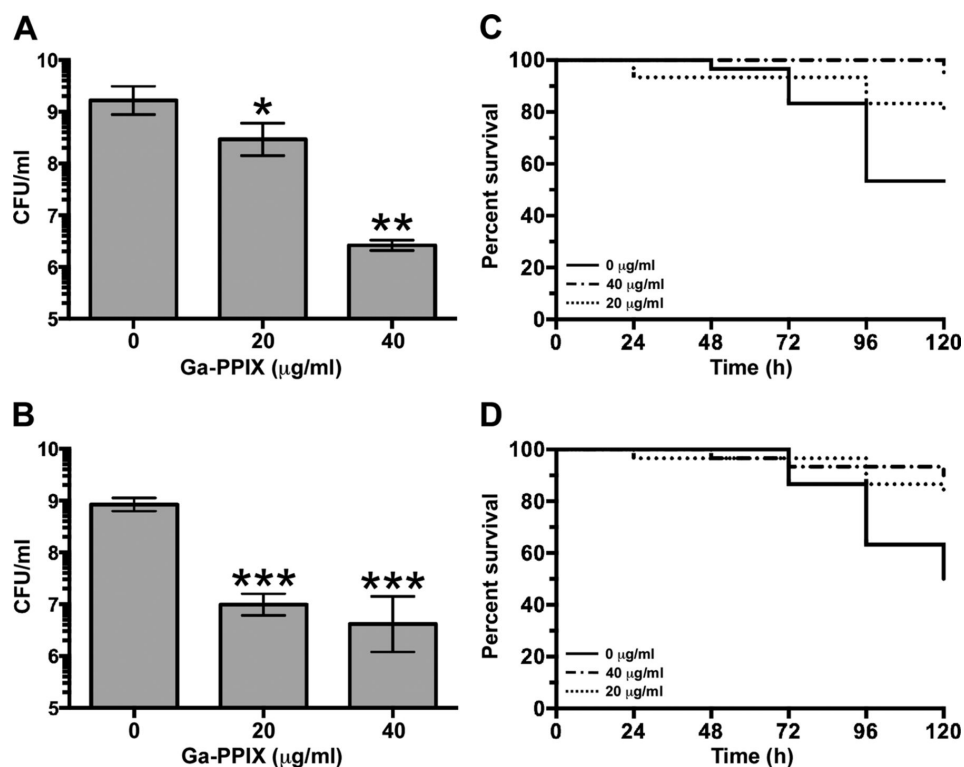


Figure 18. Antibacterial activity of GaPPIX against experimental infections.

Antibacterial activity of GaPPIX against experimental infections. Monolayers of A549 human alveolar epithelial cells (A and B) and *G. mellonella* larvae (C and D) were infected with *A. baumannii* ATCC 19606^T strain (A and C) or ACICU (B and D) in the absence or the presence of either 20 $\mu\text{g/ml}$ or 40 $\mu\text{g/ml}$ of GaPPIX. Data shown in panels A and B represents the means (\pm SEM) of experiments performed twice in octuplet ($n = 16$) using fresh biological samples each time. Responses to the presence of GaPPIX were compared to those detected with bacteria cultured in the absence of this metalloporphyrin derivative. Values that are significantly different from the value for the control (0 $\mu\text{g/ml}$ GaPPIX) are indicated by asterisks as follows: *, $P = 0.037$, $P = 0.014$, $P = 0.005$.

valid experimental data since the death rates of caterpillars injected twice with 5 μ l of sterile PBS, which were used as negative controls, were higher than those we consider acceptable (i.e. no more than two death per sample/per trial). Clearly, this is one limitation of this otherwise convenient experimental virulence model we expect to address in the future by using vertebrate hosts where the volume of the inoculum is not as critical as is in the case of *G. mellonella*.

Taken together, these observations indicate that GaPPIX has antibacterial activity when tested using experimental infection models previously used to show the role of iron-acquisition functions in the virulence of *A. baumannii* (53).

GaPPIX induces a global differential transcriptional response in *A. baumannii*

Conceptually, the host-pathogen interactions and cytotoxicity responses described above involved the coordinated expression of a large number of genes. We predicted that *A. baumannii* would differentially regulate gene expression in the presence of GaPPIX. Therefore, we used RNASeq to examine the global transcriptional response of *A. baumannii* ACICU to the presence of GaPPIX in CAMH broth. Sequencing of cDNA libraries prepared using total RNA isolated from bacteria grown in CAMH or CAMH with 10 μ g/ml GaPPIX generated an average of 35.7 million and 47.4 million total reads, respectively, for the three replicates for each experimental condition, with an overall average length of 99 nucleotides for all six sequenced libraries. The *A. baumannii* ACICU genome was annotated to improve understanding of the results of the RNASeq analysis. The OmicsBox was used to annotate the genome by incorporating blast, InterProt, Gene Ontology, and KEGG ontology. More than 85% of the reads mapped to the genome of *A. baumannii* ACICU. Table 13 shows that the presence of GaPPIX induced a global

Table 13. *Acinetobacter baumannii* ACICU differentially expressed genes in the presence of GaPPIX

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001156616.1	8.02E-06	0.003672384	11.906647	ID=WP_001156616.1;Description=excisionase
WP_000347180.1	1.62E-10	5.28E-08	10.628388	ID=WP_000347180.1;Description=C4-dicarboxylate transporter DctA;Gene=dctA;Gene=dctA_2;Gene=dctA_1;Gene=E5A70_07685;Gene=dctA_3;Ontology_term=plasma membrane,integral component of membrane,symporter activity,dicarboxylic acid transport,transmembrane transport;Ontology_id=GO:0005886,GO:016021,GO:0015293,GO:0006835,GO:0055085

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001207327.1	5.51E-05	0.002487237	10.413801	ID=WP_001207327.1;Description=lipid A phosphoethanolamine transferase;Gene=ABTJ_02705;Gene=eptA_2;Gene=eptA_1;Gene=D0529_12980;Gene=eptA;Gene=EGT34_17180;Gene=A7A62_01225;Ontology_term=integral component of membrane,sulfuric ester hydrolase activity,transferase activity, transferring phosphorus-containing groups;Ontology_id=GO:0016021,GO:0008484,GO:0016772
WP_000042002.1	2.67E-12	1.12E-09	10.368367	ID=WP_000042002.1;Description=EamA family transporter;Gene=yddG_1;Gene=ABAYE1355;Gene=T630_2486;Gene=E5D09_16240;Gene=AB719_22260;Gene=EA682_03685;Gene=DVA79_09760;Gene=F922_01259;Gene=A7M79_12585;Gene=EGT34_04500;Gene=yddG;Gene=ABTJ_01320;Gene=E5F90_17215;Gene=J635_2458;Ontology_term=integral component of membrane;Ontology_id=GO:0016021

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000097866.1	4.80E-13	2.81E-10	10.30043	ID=WP_000097866.1;Description=AraC family transcriptional regulator;Gene=F913_01791;Gene=EGS71_05850;Gene=J608_3305;Gene=FJU8903230;Gene=J552_3472;Gene=T630_2534;Gene=BWP00_06175;Gene=E5D09_16020;Gene=nphR_2;Gene=marA;Gene=ABAYE1307;Gene=nphR_1;Gene=J635_2418;Gene=J524_0754;Gene=ABTJ_01296;Gene=HMREF0010_00102;Gene=D0529_06895;Gene=B4R90_03400;Gene=araC;Gene=F962_01352;Ontology_term=cytoplasm,DNA-binding transcription factor activity,sequence-specific DNA binding,regulation of transcription, DNA-templated;Ontology_id=GO:0005737,GO:0003700,GO:0043565,GO:0006355
WP_000790104.1	1.93E-04	0.007426242	10.151137	ID=WP_000790104.1;Description=protein CsuA

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000345328.1	2.00E-04	0.007426242	10.0626545	ID=WP_000345328.1;Description=mechanosensitive ion channel protein MscS;Gene=mscM;Gene=C3422_02490;Gene=F910_01644;Gene=ABAYE1487;Gene=J512_2144;Gene=J532_2236;Gene=J608_3382;Gene=J506_2628;Gene=F922_01402;Gene=J529_3392;Gene=ybdG;Gene=FJU73_02935;Gene=J596_2017;Gene=HMPREF0010_00263;Gene=EGS71_04855;Gene=BWP00_01935;Gene=mscM_1;Gene=mscM_2;Gene=B9X95_17105;Gene=T630_2715;Gene=EGT34_03435;Gene=FJU81_04405;Gene=F913_01934;Gene=FJU43_02495;Gene=J518_4214;Gene=J517_3666;Gene=J635_3112;Gene=B4R90_04215;Gene=J524_2424;Gene=AB237_1318;Gene=D0529_06185;Gene=J567_3847;Ontology_term=integral component of membrane,mechanosensitive ion channel activity,ion transmembrane transport,cellular response to osmotic stress;Ontology_id=GO:0016021,GO:0008381,GO:0034220,GO:0071470

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001136773.1	4.18E-08	6.81E-06	9.724567	ID=WP_001136773.1;Description=Uncharacterised protein
WP_000204864.1	0.001056525	0.027299693	9.549398	ID=WP_000204864.1;Description=hydroxyethylthiazole kinase;Gene=thiM_1;Gene=thiM;Ontology_term=magnesium ion binding,hydroxyethylthiazole kinase activity,ATP binding,thiamine biosynthetic process,thiamine diphosphate biosynthetic process,phosphorylation;Ontology_id=GO:0000287,GO:004417,GO:0005524,GO:009228,GO:0009229,GO:0016310;Enzyme_code=EC:2.7.1.50;Enzyme_name=Hydroxyethylthiazole kinase
WP_000203146.1	0.001448253	0.032425392	9.537202	ID=WP_000203146.1;Description=GGDEF domain-containing protein;Gene=gmr_1;Gene=gmr_2;Ontology_term=cyclic-guanylate-specific phosphodiesterase activity;Ontology_id=GO:0071111;Enzyme_code=EC:3.1.4.52;Enzyme_name=Cyclic-guanylate-specific phosphodiesterase

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000312223.1	0.001242481	0.030108279	9.496593	ID=WP_000312223.1;Description=AraC family transcriptional regulator;Gene=FJU85_02830;Gene=AB7 19_20325;Gene=rob;Gene=D0529_17810 ;Gene=CSB70_2161;Gene=C3422_02400 ;Gene=C3415_05975;Gene=AB237_1306 ;Gene=ABTJ_01448;Ontology_term=DNA- binding transcription factor activity,sequence-specific DNA binding,regulation of transcription, DNA- templated;Ontology_id=GO:0003700,GO: 0043565,GO:0006355

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000401807.1	2.48E-06	2.27E-04	8.968435	ID=WP_000401807.1;Description=LysR family transcriptional regulator;Gene=cynR_2;Gene=F922_02160;Gene=cynR_3;Gene=cynR_4;Gene=AL533_09405;Gene=F910_02339;Gene=J807_1660;Gene=A7M90_05400;Gene=FJU43_08720;Gene=T630_1581;Gene=J524_0732;Gene=J532_1503;Gene=ABTJ_02242;Gene=mdcR;Gene=J804_0832;Gene=J517_0502;Gene=EKS29_05855;Gene=J529_0163;Gene=J732_0576;Gene=J810_1411;Gene=J596_0978;Gene=C3422_05270;Gene=J813_0687;Gene=J809_1522;Gene=J552_0888;Gene=B4R90_12940;Gene=F913_02668;Gene=HMPREF0010_00946;Gene=J812_2178;Gene=AWW73_03455;Gene=D0529_12210;Gene=J506_1586;Gene=FJU45_01055;Gene=J811_0692;Gene=J567_2937;Gene=J805_0580;Gene=J635_1875;Gene=J806_0558;Gene=EGT34_19410;Ontology_term=DNA binding,DNA-binding transcription factor activity,regulation of transcription, DNA-templated;Ontology_id=GO:0003677,GO:

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000792950.1	1.27E-05	7.76E-04	8.93617	ID=WP_000792950.1;Description=TetR family transcriptional regulator;Gene=FJV16_02195;Gene=J506_3411;Gene=BSF95_02611;Gene=A7A62_16870;Gene=EKS29_07230;Gene=CPI82_06505;Gene=FJV34_16700;Gene=FJU71_05860;Gene=FJU44_06600;Gene=AB71_9_14795;Gene=FJU62_01450;Gene=ABTJ_01311;Gene=FJU55_01565;Gene=D052_9_06980;Ontology_term=DNA binding;Ontology_id=GO:0003677
WP_000956776.1	4.36E-06	3.36E-04	8.880198	ID=WP_000956776.1;Description=LysR family transcriptional regulator;Gene=D0529_00300;Gene=DVA79_13330;Gene=ABTJ_03220;Gene=benM_2;Gene=FJU89_15970;Gene=AB237_2_916;Gene=benM_1;Gene=J608_1597;Gene=FJU72_18915;Ontology_term=DNA binding,DNA-binding transcription factor activity,regulation of transcription, DNA-templated;Ontology_id=GO:0003677,GO:0003700,GO:0006355

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001089196.1	3.15E-04	0.010437371	8.801159	ID=WP_001089196.1;Description=AsnC family transcriptional regulator;Gene=J811_3890;Gene=J813_3 986;Gene=AB719_19605;Gene=J805_398 6;Gene=EGS71_05095;Gene=J807_3962; Gene=J804_3981;Gene=J532_1627;Gene =D0529_06210;Gene=FJU71_05230;Gene =AB237_1314;Gene=DC362_06805;Gene =J635_3450;Gene=J552_3373;Gene=J806 _4030;Gene=T630_2313;Gene=A7M79_1 8745;Gene=HMPREF0010_00257;Gene= ABAYE1478;Gene=J715_4071;Gene=F96 2_01494;Gene=J506_2879;Gene=J529_3 578;Gene=AL533_05520;Gene=lrp_8;Gen e=lrp_7;Gene=lrp_6;Gene=J512_2148;Ge ne=J810_3905;Gene=FJV16_02810;Gene =J518_0923;Gene=J812_3887;Gene=F91 3_01928;Gene=J524_0199;Gene=J608_3 387;Gene=FJV20_01440;Gene=ABTJ_01 457;Gene=F910_01634;Gene=J567_0094; Gene=J809_1220;Gene=EGT34_03460;G ene=J596_2021;Gene=ABSDF1543;Gene= J732_4025;Gene=F922_01395;Gene=C34 22_02465;Gene=ACINNAV82_2370;Gene

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000576999.1	1.02E-04	0.004222449	8.70564	ID=WP_000576999.1;Description=protein CsuA
WP_000471445.1	7.15E-04	0.02015345	8.670773	ID=WP_000471445.1;Description=type VI secretion protein
WP_000654348.1	6.10E-04	0.017711526	7.8080273	ID=WP_000654348.1;Description=Unchar acterised protein
WP_001159802.1	3.30E-04	0.010753279	6.1104164	ID=WP_001159802.1;Description=NADP(H)-dependent aldo-keto reductase;Gene=AB237_2348;Gene=tas;G ene=A7M79_15080;Gene=gpr;Gene=E5D 09_03445;Gene=J552_2339;Gene=J524_ 1948;Gene=D0529_11895;Gene=J567_18 60;Gene=ABSDF1441;Gene=EGT34_178 00;Gene=ABTJ_02548;Gene=J608_3058; Ontology_term=oxidoreductase activity,oxidation-reduction process;Ontology_id=GO:0016491,GO:00 55114

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_002000873.1	2.26E-04	0.008176077	5.2591424	ID=WP_002000873.1;Description=bacterial regulatory helix-turn-helix, lysR family protein;Gene=perR;Gene=AB237_2522;Gene=F962_02742;Gene=J608_0649;Gene=J506_0070;Gene=gcvA_4;Gene=ABAYE2827;Gene=J517_0763;Gene=gcvA_6;Gene=ACINNAV82_1047;Gene=T630_1060;Gene=gcvA_1;Gene=gcvA_2;Gene=gcvA_3;Gene=J532_0767;Gene=ABTJ_02844;Ontology_term=DNA binding,DNA-binding transcription factor activity,regulation of transcription, DNA-templated;Ontology_id=GO:0003677,GO:0003700,GO:0006355

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000054921.1	9.79E-04	0.02563864	4.062698	ID=WP_000054921.1;Description=alpha/beta hydrolase;Gene=FQK03_12845;Gene=D0529_06900;Gene=EGT34_04620;Gene=J608_3306;Gene=phbC_3;Gene=phaC_2;Gene=phbC_2;Gene=J532_2818;Gene=FJU60_10685;Gene=J512_4103;Ontology_term=transferase activity, transferring acyl groups,hydrolase activity;Ontology_id=GO:0016746,GO:0016787

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000059344.1	2.53E-04	0.041509394	3.9894598	ID=WP_000059344.1;Description=Acetyl-CoA hydrolase;Gene=FAU76_00255;Gene=J529_2687;Gene=F913_00252;Gene=E5A70_02330;Gene=FJU84_10870;Gene=J552_3489;Gene=J517_3130;Gene=J532_2874;Gene=F910_00280;Gene=J506_0309;Gene=J518_3671;Gene=EGT34_09925;Gene=ABAYE0257;Gene=ABTJ_00260;Gene=scpC;Gene=HMPREF0010_02483;Gene=F922_00271;Gene=J567_4108;Gene=F962_00273;Gene=J596_1668;Gene=AB237_0246;Gene=FJU85_07305;Gene=J524_1097;Gene=T630_3803;Gene=J635_1075;Gene=B4R90_06360;Gene=C3422_03905;Gene=A7N09_17915;Gene=ACINNAV82_3642;Gene=EGS71_11310;Gene=cat1;Gene=D0529_11505;Gene=J512_0707;Ontology_y_term=acetyl-CoA hydrolase activity,acetate CoA-transferase activity,acetate metabolic process,acetyl-CoA metabolic process,propionate metabolic process,methylcitrate cycle;Ontology_id=GO:0003986,GO:0008

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000494374.1	0.002035032	0.040773496	2.3163848	ID=WP_000494374.1;Description=transcriptional regulator;Gene=AB237_1302;Gene=J552_3387;Gene=T630_2329;Gene=EGT34_03525;Gene=J518_0908;Gene=D0529_17785;Gene=J512_2166;Gene=ABAYE1461;Gene=J532_1644;Gene=J596_2035;Gene=J635_3464;Gene=C3422_02375;Gene=HMPREF0010_00240;Gene=F962_01480;Gene=J524_0213;Gene=ACINNAV82_2383;Gene=J567_0108;Gene=J529_0483;Gene=F910_01615;Gene=FJV01_00185;Gene=B9X95_20630;Gene=FJV14_17055;Gene=NC7C7364_02420;Gene=EGS71_05165;Gene=F913_01914;Gene=acoR_2;Gene=ABTJ_01443;Gene=acoR_1;Gene=J506_2897;Ontology_term=DNA binding,phosphorelay signal transduction system,regulation of transcription, DNA-templated;Ontology_id=GO:0003677,GO:0000160,GO:0006355
WP_001226300.1	7.70E-08	1.08E-05	2.1702454	ID=WP_001226300.1;Description=Uncharacterised protein

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000803005.1	2.20E-04	0.008078461	1.6861771	ID=WP_000803005.1;Description=TonB-dependent receptor;Gene=ABTJ_02706;Gene=EGT34_17175;Gene=BSF95_01156;Gene=A7M79_05730;Gene=D0529_12985;Gene=T630_3273;Gene=FJU95_18135;Gene=J532_4000;Gene=HMPREF0010_02938;Gene=J608_3771;Gene=AB237_2416;Gene=A7M90_14045;Ontology_term=cell outer membrane,integral component of membrane;Ontology_id=GO:0009279,GO:0016021
WP_000064463.1	4.16E-17	6.10E-14	1.6332191	ID=WP_000064463.1;Description=Uncharacterised protein

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000520927.1	3.13E-04	0.010437371	1.6223297	ID=WP_000520927.1;Description=aspartate 4-decarboxylase;Gene=asD;Gene=J608_3670;Gene=C3422_03405;Gene=EGT34_04535;Gene=E5979_18385;Gene=aspD;Gene=FJU43_03240;Gene=D0529_06990;Gene=A7M90_04140;Gene=CHQ89_02915;Gene=ABTJ_01313;Ontology_term=transaminase activity,lyase activity,pyridoxal phosphate binding,biosynthetic process;Ontology_id=GO:0008483,GO:0016829,GO:0030170,GO:0009058
WP_000046989.1	1.06E-05	0.004054906	1.5457501	ID=WP_000046989.1;Description=DUF4102 domain-containing protein;Gene=T630_1140;Gene=AB237_2413;Gene=HMPREF0010_02942;Gene=AB719_17950;Gene=D0529_12970;Gene=EGT34_17190;Gene=MRSN3942C25_140;Gene=BSF95_01160;Gene=ABTJ_02702;Ontology_term=DNA binding,DNA recombination,DNA integration;Ontology_id=GO:0003677,GO:0006310,GO:0015074
WP_000718101.1	1.60E-17	4.69E-14	1.5441679	ID=WP_000718101.1;Description=Uncharacterised protein

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000589038.1	8.37E-06	5.64E-04	1.526801	ID=WP_000589038.1;Description=phage family protein
WP_000602535.1	5.11E-05	0.002378924	1.5201911	ID=WP_000602535.1;Description=Unchar acterised protein
WP_002062678.1	0.001743856	0.03652669	1.4737643	ID=WP_002062678.1;Description=TIGR0 4219 family outer membrane beta-barrel protein
WP_000401163.1	0.00204354	0.040773496	1.4193517	ID=WP_000401163.1;Description=Unchar acterised protein
WP_001263981.1	2.26E-05	0.001167632	1.2705739	ID=WP_001263981.1;Description=D-amino acid dehydrogenase small subunit;Gene=dadA;Gene=dadA_2;Gene=dadA1;Ontology_term=D-amino-acid dehydrogenase activity,D-amino acid catabolic process,oxidation-reduction process;Ontology_id=GO:0008718,GO:0019478,GO:0055114;Enzyme_code=EC:1.4.99.1;Enzyme_name=Acting on the CH-NH(2) group of donors

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000524257.1	6.72E-06	4.81E-04	1.2152873	ID=WP_000524257.1;Description=glutamate 5-kinase;Gene=E5D09_04210;Gene=D0529_17205;Gene=AB719_21275;Ontology_term=kinase activity,phosphorylation;Ontology_id=GO:0016301,GO:0016310
WP_001017220.1	0.002291944	0.044815145	1.1585345	ID=WP_001017220.1;Description=Amino peptidase N;Gene=D0529_17830;Gene=pepN_1;Gene=pepN;Gene=CYQ93_13420;Gene=ABTJ_01452;Ontology_term=aminopeptidase activity,metallopeptidase activity,zinc ion binding,proteolysis;Ontology_id=GO:0004177,GO:0008237,GO:0008270,GO:0006508;Enzyme_code=EC:3.4.11;Enzyme_name=Acting on peptide bonds (peptidases)

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000991232.1	2.92E-04	0.010078773	1.0613412	ID=WP_000991232.1;Description=metal-dependent hydrolase;Gene=FJU40_04135;Gene=FJU44_09345;Gene=BGC29_01650;Gene=CAT59_04245;Gene=A7N09_08335;Gene=ABUW_0620;Gene=E5A70_04185;Gene=CPI82_00535;Gene=EGT34_08275;Gene=SAMEA104305292_01932;Gene=ACINNAV82_3234;Gene=T630_3442;Gene=EGS71_09650;Gene=B9X91_21175;Gene=EA706_01170;Gene=FJU71_09165;Gene=ABTJ_00586;Gene=C3422_06765;Gene=EA763_04835;Gene=D0529_03590;Gene=NCTC7364_03206;Ontology_term=hydrolase activity;Ontology_id=GO:0016787
WP_000277448.1	2.25E-05	0.001167632	1.0495752	ID=WP_000277448.1;Description=Putative bacteriophage protein
WP_000698529.1	9.59E-14	7.03E-11	1.047971	ID=WP_000698529.1;Description=Uncharacterised protein

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_085916999.1	0.001488656	0.032722123	1.035855	ID=WP_085916999.1;Description=septum site-determining protein MinC;Gene=minC;Ontology_term=cell morphogenesis,division septum assembly,regulation of cell septum assembly;Ontology_id=GO:0000902,GO:000917,GO:1901891
WP_000729387.1	1.43E-07	1.83E-05	1.0137999	ID=WP_000729387.1;Description=DUF22 80 domain-containing protein
WP_001019739.1	9.19E-05	0.003850799	1.00137	ID=WP_001019739.1;Description=glycosyl hydrolase 108 family protein;Gene=T630_3274;Gene=J608_3770;Gene=J658_2231;Ontology_term=hydrolase activity;Ontology_id=GO:0016787

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000654846.1	2.49E-04	0.008807146	0.982762	ID=WP_000654846.1;Description=Unchar acterised protein;Gene=C2U32_08705;Gene=FJV11_18380;Gene=J610_0453;Gene=EGS71_06940;Gene=NCTC7412_02871;Gene=FJU85_11800;Gene=D0529_17000;Gene=A7M90_18395;Gene=BGC29_14185;Gene=C3422_07705;Gene=E5D09_04365;Gene=BGC29_08000;Gene=BSF95_01090;Gene=J532_3630;Gene=J608_1841;Gene=F962_01162;Ontology_term=integral component of membrane;Ontology_id=GO:0016021
WP_001144958.1	0.002466972	0.046984594	0.95528287	ID=WP_001144958.1;Description=Unchar acterised protein
WP_000056390.1	7.23E-06	5.05E-04	0.9042812	ID=WP_000056390.1;Description=Unchar acterised protein;Gene=AB237_1065;Ontology_term=hydrolase activity;Ontology_id=GO:0016787
WP_000258012.1	0.001766826	0.03652669	0.87460834	ID=WP_000258012.1;Description=beta- ketoacyl synthase
WP_001984388.1	6.94E-05	0.003037143	0.86446905	ID=WP_001984388.1;Description=Unchar acterised protein

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000048916.1	0.001339482	0.031587694	0.84303313	ID=WP_000048916.1;Description=XRE family transcriptional regulator;Gene=EA685_07990;Gene=ABT J_02759;Gene=BSF95_01102;Gene=FJU6 2_18575;Gene=F910_01204;Gene=LV38 _02492;Gene=CEJ63_13600;Gene=AB23 7_2450;Gene=A7M79_14845;Gene=J567 _4077;Gene=J608_1828;Gene=D0529_17 065;Gene=BFR92_15375;Gene=F985_01 887;Gene=FJV17_18700;Gene=D0529_17 855;Gene=EGS71_18575;Gene=J552_381 8;Gene=J524_3137;Gene=HMPREF0010_ 01592;Gene=ACINWC141_1278;Ontolog y_term=DNA binding;Ontology_id=GO:0003677
WP_000046548.1	1.63E-04	0.006467333	0.82458466	ID=WP_000046548.1;Description=tape measure protein
WP_000378523.1	3.93E-05	0.00195253	0.8232388	ID=WP_000378523.1;Description=Unchar acterised protein

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000733835.1	3.45E-06	2.81E-04	0.82256746	ID=WP_000733835.1;Description=Thiol:d isulfide interchange protein;Gene=F962_00146;Gene=dsbD_3; Gene=B4R90_18325;Gene=dsbD_1;Gene =dsbD;Ontology_term=integral component of membrane,protein-disulfide reductase activity,cytochrome complex assembly,cell redox homeostasis,oxidation- reduction process;Ontology_id=GO:0016021,GO:00 47134,GO:0017004,GO:0045454,GO:005 5114;Enzyme_code=EC:1.8.1.8;Enzyme_ name=Protein-disulfide reductase

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001043531.1	0.002155994	0.042726547	0.80672187	ID=WP_001043531.1;Description=bifunctional tRNA (5-methylaminomethyl-2-thiouridine)(34)-methyltransferase MnmD/FAD-dependent 5-carboxymethylaminomethyl-2-thiouridine(34) oxidoreductase MnmC;Gene=mnmC;Gene=mnmC_1;Gene=mnmC_2;Ontology_term=cytoplasm,tRNA A (5-methylaminomethyl-2-thiouridylate)-methyltransferase activity,oxidoreductase activity, acting on the CH-NH group of donors,flavin adenine dinucleotide binding,tRNA wobble base modification,tRNA methylation,oxidation-reduction process;Ontology_id=GO:0005737,GO:0004808,GO:0016645,GO:0050660,GO:0002097,GO:0030488,GO:0055114;Enzyme_code=EC:2.1.1.61;Enzyme_name=tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
WP_000235282.1	0.001224465	0.030108279	0.80430645	ID=WP_000235282.1;Description=Uncharacterised protein

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000064595.1	8.63E-08	1.15E-05	0.8026618	ID=WP_000064595.1;Description=Unchar acterised protein
WP_025079739.1	2.15E-05	0.001165468	0.7677891	ID=WP_025079739.1;Description=Unchar acterised protein
WP_000248411.1	7.29E-12	2.67E-09	0.76455927	ID=WP_000248411.1;Description=Unchar acterised protein
WP_000094251.1	1.57E-07	1.92E-05	0.7340427	ID=WP_000094251.1;Description=Unchar acterised protein
WP_000155519.1	3.95E-04	0.012060571	0.72062445	ID=WP_000155519.1;Description=DUF20 59 domain-containing protein
WP_001011955.1	7.39E-04	0.02065643	0.67588645	ID=WP_001011955.1;Description=NADH- quinone oxidoreductase subunit N;Gene=nuoN;Gene=nouN;Ontology_term =plasma membrane,integral component of membrane,NADH dehydrogenase (ubiquinone) activity,quinone binding,ATP synthesis coupled electron transport;Ontology_id=GO:0005886,GO:0 016021,GO:0008137,GO:0048038,GO:00 42773;Enzyme_code=EC:7.1.1.2,EC:1.6.5 .11,EC:1.6.99.3;Enzyme_name=NADH:ubi quinone reductase (H(+)- translocating),NADH dehydrogenase (quinone),NADH dehydrogenase

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000852265.1	5.82E-08	8.99E-06	0.67355597	ID=WP_000852265.1;Description=methyltransferase;Gene=CBE85_19180;Gene=D0529_17190;Gene=CHQ89_19080;Gene=AB719_21260;Gene=B9X80_11900;Gene=EA685_18320;Ontology_term=methyltransferase activity,methylation;Ontology_id=GO:0008168,GO:0032259
WP_000932189.1	2.03E-05	0.001121621	0.644518	ID=WP_000932189.1;Description=Uncharacterised protein
WP_000004579.1	8.47E-06	5.64E-04	0.5945353	ID=WP_000004579.1;Description=Uncharacterised protein
WP_000146970.1	4.69E-05	0.002232159	0.5940955	ID=WP_000146970.1;Description=phage head morphogenesis protein
WP_002002228.1	3.37E-04	0.010868087	0.57060635	ID=WP_002002228.1;Description=putative N-acetyltransferase YedL
WP_000301495.1	3.17E-04	0.010437371	0.5639852	ID=WP_000301495.1;Description=DUF4055 domain-containing protein

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000088974.1	0.001563508	0.033482928	0.5264409	ID=WP_000088974.1;Description=DNA-binding protein;Gene=EGM95_15515;Gene=FJV34_08360;Gene=EGS71_18515;Gene=A7M90_18380;Gene=CPI82_12155;Gene=D0529_16985;Gene=FJU95_16695;Gene=C3422_05115;Gene=B9X91_23280;Gene=EGT34_16840;Gene=FJU64_18085;Ontology_term=DNA binding;Ontology_id=GO:0003677
WP_000048052.1	0.001296433	0.030914133	0.4744152	ID=WP_000048052.1;Description=Uncharacterised protein
WP_001226777.1	3.90E-04	0.012046678	0.38546014	ID=WP_001226777.1;Description=methionine--tRNA ligase;Gene=metG;Gene=metG_2;Ontology_term=cytoplasm,tRNA binding,methionine-tRNA ligase activity,ATP binding,metal ion binding,methionyl-tRNA aminoacylation;Ontology_id=GO:0005737,GO:0000049,GO:0004825,GO:0005524,GO:0046872,GO:0006431;Enzyme_code=EC:6.1.1.10;Enzyme_name=Methionine--tRNA ligase

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000276693.1	0.00136573	0.031783223	0.38379666	<p>ID=WP_000276693.1;Description=NADH-quinone oxidoreductase subunit I;Gene=nuoI;Gene=nouI;Ontology_term=plasma membrane,iron ion binding,quinone binding,NADH dehydrogenase (quinone) activity,4 iron, 4 sulfur cluster binding,oxidation-reduction process;Ontology_id=GO:0005886,GO:0005506,GO:0048038,GO:0050136,GO:0051539,GO:0055114;Enzyme_code=EC:1.6.5.11,EC:1.6.99.3;Enzyme_name=NADH dehydrogenase (quinone),NADH dehydrogenase</p>

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_002000896.1	9.00E-04	0.023912225	-0.32908285	ID=WP_002000896.1;Description=primary amine oxidase;Gene=tynA;Gene=ABTJ_01742;Ontology_term=copper ion binding;primary amine oxidase activity;quinone binding;amine metabolic process;oxidation-reduction process;Ontology_id=GO:0005507,GO:0008131,GO:0048038,GO:0009308,GO:0055114;Enzyme_code=EC:1.4.3.21;Enzyme_name=Primary-amine oxidase
WP_001185622.1	0.001846604	0.037352342	-0.35129073	ID=WP_001185622.1;Description=Uncharacterised protein

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001133054.1	8.65E-04	0.023278354	-0.3571878	<p>alpha-ketoacid dehydrogenase subunit beta; Gene=F962_01991; Gene=EA751_03 265; Gene=BFR91_15000; Gene=EXE08_1 0680; Gene=EA682_17250; Gene=AL489_015260; Gene=B9X80_18430; Gene=EGT3 4_01850; Gene=acoB_1; Gene=F910_0203 1; Gene=F931_01047; Gene=EXE07_0960 5; Gene=F922_01896; Gene=C3422_00135 ; Gene=acoB; Gene=CVD06_00445; Gene=ABTJ_01972; Gene=EA756_08180; Gene=DZ985_06575; Gene=SAMN02799632_02 144; Gene=D0529_09185; Ontology_term=oxidoreductase activity, oxidation-reduction process; Ontology_id=GO:0016491, GO:0055114</p>

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001216217.1	0.001376226	0.031783223	-0.35984233	ID=WP_001216217.1;Description=2-C-methyl-D-erythritol 4-phosphate cytidyltransferase;Gene=ispD_2;Gene=FU44_08245;Gene=ispD;Ontology_term=2-C-methyl-D-erythritol 4-phosphate cytidyltransferase activity,terpenoid biosynthetic process,isopentenyl diphosphate biosynthetic process,methylerythritol 4-phosphate pathway;Ontology_id=GO:0050518,GO:016114,GO:0019288;Enzyme_code=EC:2.7.7.60;Enzyme_name=2-C-methyl-D-erythritol 4-phosphate cytidyltransferase

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000044139.1	1.99E-04	0.007426242	-0.38293514	ID=WP_000044139.1;Description=pyridine nucleotide-disulfide oxidoreductase;Gene=yjID;Gene=FJU52_17275;Gene=FJU81_17865;Gene=ABTJ_01784;Gene=A7A54_14660;Gene=AB237_1626;Gene=C3422_01030;Gene=BSF95_02162;Gene=D0529_05240;Ontology_term=oxidoreductase activity,oxidation-reduction process;Ontology_id=GO:0016491,GO:0055114
WP_001187342.1	7.95E-04	0.02166593	-0.39029017	ID=WP_001187342.1;Description=signal recognition particle-docking protein FtsY;Gene=ftsY;Ontology_term=cytoplasm,intrinsic component of plasma membrane,GTPase activity,GTP binding,SRP-dependent cotranslational protein targeting to membrane,cell division;Ontology_id=GO:0005737,GO:0031226,GO:0003924,GO:0005525,GO:0006614,GO:0051301;Enzyme_code=EC:3.6.1.15;Enzyme_name=Nucleoside-triphosphate phosphatase

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000238447.1	0.002524061	0.04776175	-0.39134228	ID=WP_000238447.1;Description=diacetyl
			1	reductase;Gene=ABTJ_01969;Gene=CYQ93_00100;Gene=F913_02401;Gene=A7M79_09795;Gene=EWO92_02370;Gene=B4R90_10505;Gene=C3422_00120;Gene=D0529_09170;Gene=budC;Gene=CHQ89_01470;Gene=budC_3;Gene=budC_4;Gene=budC_1;Gene=budC_2;Gene=FJV00_04465;Ontology_term=(S,S)-butanediol dehydrogenase activity,diacetyl reductase ((S)-acetoin forming) activity,acetoin catabolic process,oxidation-reduction process;Ontology_id=GO:0047512,GO:0052588,GO:0045150,GO:0055114;Enzyme_code=EC:1.1.1.76,EC:1.1.1.304,EC:1.1.1.303;Enzyme_name=(S,S)-butanediol dehydrogenase,Diacetyl reductase ((S)-acetoin forming),Diacetyl reductase ((R)-acetoin forming)

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000407064.1	0.001726193	0.036423918	-0.42069632	ID=WP_000407064.1;Description=4-hydroxy-3-methylbut-2-enyl diphosphate reductase;Gene=ispH_2;Gene=ispH_1;Gene=ispH;Ontology_term=metal ion binding,4 iron, 4 sulfur cluster binding,4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase activity,terpenoid biosynthetic process,isopentenyl diphosphate biosynthetic process,methylerythritol 4-phosphate pathway,dimethylallyl diphosphate biosynthetic process,oxidation-reduction process;Ontology_id=GO:0046872,GO:0051539,GO:0051745,GO:0016114,GO:0019288,GO:0050992,GO:0055114;Enzyme_code=EC:1.17.1,EC:1.17.1.2;Enzyme_name=Acting on CH or CH(2) groups,Acting on CH or CH(2) groups

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000631823.1	0.001493442	0.032722123	-0.42339337	ID=WP_000631823.1;Description=acyl-CoA dehydrogenase;Gene=EGS71_03335;Gene=D0529_05345;Gene=B9X80_13225;Gene=FJV00_05090;Gene=EGT34_02010;Gene=J518_2968;Gene=J524_2607;Gene=bb_sG_1;Gene=FJV27_03390;Gene=J552_2946;Gene=acdA_2;Gene=J567_3794;Gene=AB237_1608;Gene=ABTJ_01763;Gene=carC_2;Gene=FJU90_04895;Gene=J635_3522;Gene=EA682_12660;Ontology_term=(R)-benzylsuccinyl-CoA dehydrogenase activity,flavin adenine dinucleotide binding,oxidation-reduction process;Ontology_id=GO:0033734,GO:0050660,GO:0055114;Enzyme_code=EC:1.3.8.3;Enzyme_name=(R)-benzylsuccinyl-CoA dehydrogenase

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000920736.1	0.001346219	0.031587694	-0.5065032	ID=WP_000920736.1;Description=phage tail protein;Gene=FJU81_15240;Gene=BSF95_02922;Gene=BFR70_08115;Gene=F910_01247;Gene=BFR92_12985;Gene=T630_2673;Gene=FJU94_01390;Gene=J512_0651;Gene=AB719_24505;Gene=EGT34_05135;Gene=EA752_15840;Gene=FJV26_14360;Gene=AB719_16850;Gene=ABTJ_01000;Gene=EA752_14865;Ontology_term=integral component of membrane;Ontology_id=GO:0016021

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000619893.1	0.00109535	0.027695362	-0.5331275	ID=WP_000619893.1;Description=alpha/beta hydrolase;Gene=DOL94_13680;Gene=SA MEA104305320_02030;Gene=AB237_01 10;Gene=ABUW_0104;Gene=ABAYE010 5;Gene=FJU45_03225;Gene=T630_3956; Gene=D1G37_06530;Ontology_term=trigl lyceride lipase activity,lipid catabolic process;Ontology_id=GO:0004806,GO:00 16042;Enzyme_code=EC:3.1.1.1,EC:3.1.1 .3;Enzyme_name=Carboxylesterase,Triacy lglycerol lipase

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000044203.1	0.001401169	0.03195213	-0.54104817	ID=WP_000044203.1;Description=type 1 glutamine amidotransferase domain-containing protein;Gene=EGT34_00605;Gene=AB719_13180;Gene=B9X68_11920;Gene=EXD88_15710;Gene=C3415_13145;Gene=EGS71_03230;Gene=D0529_05245;Gene=ABTJ_01783;Gene=AB237_1625;Gene=hca_1;Gene=FJU81_17860;Ontology_term=peptidase activity,transferase activity,lyase activity,proteolysis,glutamine metabolic process;Ontology_id=GO:0008233,GO:0016740,GO:0016829,GO:0006508,GO:0006541

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001242511.1	1.26E-05	7.76E-04	-0.5550691	ID=WP_001242511.1;Description=lactoyl glutathione lyase;Gene=F910_01093;Gene=F985_01831;Gene=F927_03326;Gene=H125_12790;Gene=gloA;Gene=AC057_04190;Gene=F91926_01489;Gene=F962_01082;Gene=F913_01556;Gene=F958_01783;Gene=F922_01026;Gene=ABTJ_01080;Ontology_term=lactoylglutathione lyase activity,metal ion binding;Ontology_id=GO:0004462,GO:0046872;Enzyme_code=EC:4.4.1.5;Enzyme_name=Lactoylglutathione lyase
WP_001987894.1	0.001515727	0.03293058	-0.5865454	ID=WP_001987894.1;Description=peptidase
				M16;Gene=AB237_1523;Gene=FJV23_06860;Gene=EKS29_08865;Gene=FJV20_02280;Gene=EA706_06690;Ontology_term=metallopeptidase activity,metal ion binding,proteolysis;Ontology_id=GO:0008237,GO:0046872,GO:0006508

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000983821.1	0.001839714	0.037352342	-0.59039754	ID=WP_000983821.1;Description=acineto bactin biosynthesis isochorismate synthase BasJ;Gene=ABTJ_01143;Gene=entC;Gene= =HMPREF0010_02312;Gene=basJ;Gene= DVA79_07645;Gene=D0529_15050;Onto logy_term=isochorismate synthase activity,biosynthetic process;Ontology_id=GO:0008909,GO:00 09058;Enzyme_code=EC:5.4.4.2;Enzyme _name=Isochorismate synthase

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000710404.1	0.001237255	0.030108279	-0.6166958	ID=WP_000710404.1;Description=acetyl-CoA carboxylase carboxyl transferase subunit alpha;Gene=accA_1;Gene=accA;Gene=E5A70_16095;Ontology_term=acetyl-CoA carboxylase complex,acetyl-CoA carboxylase activity,ATP binding,carboxyl-or carbamoyltransferase activity,fatty acid biosynthetic process,malonyl-CoA biosynthetic process;Ontology_id=GO:0009317,GO:0003989,GO:0005524,GO:0016743,GO:0006633,GO:2001295;Enzyme_code=EC:6.4.1.2;Enzyme_name=Acetyl-CoA carboxylase
WP_000738603.1	5.53E-04	0.016387561	-0.64430475	ID=WP_000738603.1;Description=DNA transfer protein p32
WP_000248356.1	3.44E-06	2.81E-04	-0.6459689	ID=WP_000248356.1;Description=glycine zipper containing OmpA-like membrane domain protein

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000580938.1	0.002359672	0.045833886	-0.6546862	ID=WP_000580938.1;Description=fatty acid oxidation complex subunit alpha FadB;Gene=fadB;Gene=fadB_2;Ontology_term=fatty acid beta-oxidation multienzyme complex,3-hydroxyacyl-CoA dehydrogenase activity,dodecenoyl-CoA delta-isomerase activity,enoyl-CoA hydratase activity,3-hydroxybutyryl-CoA epimerase activity,fatty acid beta-oxidation;Ontology_id=GO:0036125,GO:0003857,GO:0004165,GO:0004300,GO:0008692,GO:0006635;Enzyme_code=EC:1.1.1.35,EC:5.3.3.8,EC:4.2.1.17,EC:5.1.2.3;Enzyme_name=3-hydroxyacyl-CoA dehydrogenase,Delta(3)-Delta(2)-enoyl-CoA isomerase,Enoyl-CoA hydratase,3-hydroxybutyryl-CoA epimerase

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001092382.1	6.17E-04	0.017745096	-0.7064901	<p>ID=WP_001092382.1;Description=methyl malonate-semialdehyde</p> <p>dehydrogenase;Gene=J608_0435;Gene=F910_03749;Gene=FJU52_12075;Gene=FJU55_14820;Gene=F913_00736;Gene=mmasA_2;Gene=J552_2804;Gene=mmasA_1;Gene=FJU58_11410;Gene=mmasA_3;Gene=J517_2535;Gene=F962_03570;Gene=FJV01_13745;Gene=mmasA;Ontology_term=methylmalonate-semialdehyde</p> <p>dehydrogenase (acylating) activity,oxidation-reduction process;Ontology_id=GO:0004491,GO:0055114;Enzyme_code=EC:1.2.1.27;Enzyme_name=Methylmalonate-semialdehyde dehydrogenase (CoA acylating)</p>

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000175360.1	7.98E-04	0.02166593	-0.71542174	ID=WP_000175360.1;Description=biotin synthase;Gene=bioB;Ontology_term=biotin synthase activity,iron ion binding,2 iron, 2 sulfur cluster binding,4 iron, 4 sulfur cluster binding,biotin biosynthetic process;Ontology_id=GO:0004076,GO:0005506,GO:0051537,GO:0051539,GO:0009102;Enzyme_code=EC:2.8.1.6;Enzyme_name=Biotin synthase
WP_000344169.1	0.002638294	0.049287368	-0.73331755	ID=WP_000344169.1;Description=DNA recombination/repair protein RecA;Gene=recA;Ontology_term=cytoplasm,damaged DNA binding,single-stranded DNA binding,ATP binding,DNA-dependent ATPase activity,DNA repair,DNA recombination,SOS response;Ontology_id=GO:0005737,GO:0003684,GO:0003697,GO:0005524,GO:0008094,GO:0006281,GO:0006310,GO:0009432;Enzyme_code=EC:3.6.1.3,EC:3.6.1.15;Enzyme_name=Adenosinetriphosphatase,Nucleoside-triphosphate phosphatase

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000095311.1	1.46E-09	3.58E-07	-0.758104	ID=WP_000095311.1;Description=Acetyl-CoA acetyltransferase;Gene=F958_02650;Gene=J582_0129;Gene=J512_1914;Gene=FJU43_13070;Gene=J506_3795;Gene=AL533_07960;Gene=F962_01957;Gene=atoB;Gene=DC362_18060;Gene=F922_01865;Gene=J518_4024;Gene=T630_1880;Gene=J567_0564;Gene=ACINNAV82_1953;Gene=J524_1561;Gene=AL489_015110;Gene=EGS71_02255;Gene=thlA_2;Gene=J529_1501;Gene=J633_0705;Gene=ACIN5021_2037;Gene=thlA_1;Gene=B9X80_18575;Gene=J552_0448;Gene=HMPREF0010_00646;Gene=FJU87_04235;Gene=J517_2898;Gene=D0529_09030;Gene=ABAYE1916;Gene=ABTJ_01941;Ontology_term=acetyl-CoA C-acetyltransferase activity;Ontology_id=GO:0003985;Enzyme_code=EC:2.3.1.16,EC:2.3.1.9;Enzyme_name=Acetyl-CoA C-acetyltransferase,Acetyl-CoA C-acetyltransferase

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000966689.1	4.75E-04	0.014353403	-0.86548406	ID=WP_000966689.1;Description=type II toxin-antitoxin system HicB family antitoxin
WP_002027464.1	9.05E-04	0.023912225	-0.86918676	ID=WP_002027464.1;Description=Unchar acterised protein
WP_001274814.1	1.26E-05	7.76E-04	-0.87745297	ID=WP_001274814.1;Description=malonyl CoA-acyl carrier protein transacylase;Gene=F913_03383;Gene=fabD;Gene=F958_03705;Gene=HI25_05196;Gene=F962_02936;Gene=fabD_1;Gene=F910_03067;Gene=ABTJ_02996;Gene=J608_1486;Ontology_term=[acyl-carrier-protein] S-malonyltransferase activity;Ontology_id=GO:0004314;Enzyme_code=EC:2.3.1.85,EC:2.3.1.39;Enzyme_name=Fatty-acid synthase system,[Acyl-carrier-protein] S-malonyltransferase
WP_000677531.1	0.001061086	0.027299693	-0.88523954	ID=WP_000677531.1;Description=Unchar acterised protein

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000140309.1	2.24E-08	3.86E-06	-0.8855904	ID=WP_000140309.1;Description=30S ribosomal protein S1;Gene=FJV16_06775;Gene=F958_02783;Gene=AL533_08665;Gene=F913_02520;Gene=C3422_00715;Gene=EGT34_20220;Gene=F910_02187;Gene=EGS71_22050;Gene=D0529_09770;Gene=ABTJ_02088;Gene=E5A70_11125;Gene=tpsA;Gene=J608_0175;Gene=FJU94_06900;Gene=FJV19_05675;Gene=F962_02098;Gene=F922_02011;Gene=AL489_015795;Ontology_term=ribosome,RNA binding,structural constituent of ribosome,translation;Ontology_id=GO:0005840,GO:0003723,GO:0003735,GO:0006412
WP_000126114.1	1.70E-06	1.72E-04	-0.8982569	ID=WP_000126114.1;Description=TENA/THI-4 domain protein;Gene=tenA_1;Ontology_term=thiaminase activity;Ontology_id=GO:0050334;Enzyme_name=EC:3.5.99.2;Enzyme_name=Am inopyrimidine aminohydrolase

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001018264.1	7.75E-04	0.021430947	-0.91587734	ID=WP_001018264.1;Description=isochorismatase;Gene=F962_01134;Gene=BWP00_11900;Gene=EA706_09140;Gene=J552_3206;Gene=F910_01168;Gene=EGS71_07085;Gene=D0529_15085;Gene=J567_2640;Gene=ACINNAV82_2674;Gene=C3422_15360;Gene=entB_1;Gene=EGT34_05775;Gene=entB;Gene=J524_3313;Gene=ABTJ_01136;Gene=basF;Gene=A7M79_07915;Ontology_term=isochorismatase activity,lyase activity,2,3-dihydroxybenzoate-serine ligase activity;Ontology_id=GO:0008908,GO:0016829,GO:0047527;Enzyme_code=EC:3.3.2.6,EC:3.3.2.1,EC:6.3.2.14;Enzyme_name=Leukotriene-A(4) hydrolase,Isochorismatase,Enterobactin synthase
WP_002001156.1	3.60E-04	0.011464594	-0.9351417	ID=WP_002001156.1;Description=cell division protein;Gene=CYQ93_14530;Ontology_term=peptidoglycan binding,cell division;Ontology_id=GO:0042834,GO:0051301

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001284535.1	0.002579984	0.048506998	-0.9517948	ID=WP_001284535.1;Description=putative lipoprotein
WP_000952702.1	2.09E-06	1.98E-04	-0.95821935	ID=WP_000952702.1;Description=ATP-dependent Clp protease ATP-binding subunit ClpA;Gene=F922_01634;Gene=clpA;Gene=F913_02178;Gene=clpA_1;Gene=ABTJ_01689;Ontology_term=ATP binding,peptidase activity,ATPase activity,proteolysis,protein unfolding;Ontology_id=GO:0005524,GO:0008233,GO:0016887,GO:0006508,GO:0043335;Enzyme_code=EC:3.6.1.3,EC:3.6.1.15;Enzyme_name=Adenosinetriphosphatase,Nucleoside-triphosphate phosphatase

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001024697.1	3.70E-06	2.93E-04	-0.9716357	ID=WP_001024697.1;Description=YbaB/ EbfC family nucleoid-associated protein;Gene=DC362_19930;Gene=J690_0424;Gene=J733_1942;Gene=AL533_08215;Gene=ACINNAV82_1899;Gene=AOLE_10365;Gene=F958_02697;Gene=J610_0659;Gene=J552_0399;Gene=ABAYE1967;Gene=ABSDF1914;Gene=BDGL_001041;Gene=SAMN04487817_101468;Gene=J608_6074;Gene=ABTJ_01990;Gene=J517_0028;Gene=DBL02_01240;Gene=J580_0525;Gene=ABBFA_001813;Gene=J529_1452;Gene=CVD06_00355;Gene=EGS71_01965;Gene=SAMN02799632_02123;Gene=J810_2002;Gene=J806_2176;Gene=J512_2459;Gene=CAT59_03035;Gene=J732_2063;Gene=J608_2603;Gene=CIL08_12375;Gene=J807_2264;Gene=J635_0580;Gene=AB57_1909;Gene=F913_02422;Gene=F935_01351;Gene=A9988_01000;Gene=C3422_00225;Gene=APC53_13720;Gene=H125_00955;Gene=J524_1610;Gene=J567_0515;Gene=J812_3919;Gene=J532_1377;Gene=FJV00_04360;Gene=J551_020

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_012297364.1	2.46E-04	0.008794453	-0.9717406	ID=WP_012297364.1;Description=translation initiation factor IF-3;Gene=infC;Ontology_term=cytoplasm,translation initiation factor activity,translational initiation;Ontology_id=GO:0005737,GO:0003743,GO:0006413

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000678311.1	3.04E-10	8.93E-08	-0.9891874	ID=WP_000678311.1;Description=recomb inase family protein;Gene=C7E16_15620;Gene=F905_00032;Gene=F923_00154;Gene=D9K80_17565;Gene=C0119_15640;Gene=CF596_13395;Gene=B9X91_27950;Gene=EA74_8_16560;Gene=J658_3407;Gene=CDG60_00650;Gene=D7V31_16445;Gene=MF46_40_14810;Gene=P253_02863;Gene=C9E89_020550;Gene=FJU72_18070;Gene=F899_00051;Gene=B7Z24_02440;Gene=FJU63_18630;Gene=F897_03205;Gene=FJU52_16705;Gene=HMPREF0017_02990;Gene=F893_00103;Gene=ABWEK_A0209;Gene=AHTJR_17515;Gene=J577_2939;Gene=cinH;Gene=GS19_19250;Gene=F947_00104;Gene=J504_3531;Gene=F884_00084;Gene=CWI32_14690;Gene=F955_00087;Gene=CDG55_00915;Gene=EA752_20205;Gene=EXE08_20360;Gene=EGK59_14830;Gene=F909_00017;Gene=J500_3465;Gene=EGT68_15265;Gene=CDG68_02000;Gene=P253_02879;Gene=PA3_38240;Ontology_term=recombinase

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000331712.1	2.82E-05	0.001425077	-1.0402814	ID=WP_000331712.1;Description=Fe-S cluster assembly scaffold
				IscU;Gene=iscU_2;Gene=A9988_00805;Gene=MF4642_13645;Gene=DH17_12990;Gene=DT74_07160;Gene=F964_03017;Gene=F886_02153;Gene=B9T36_09250;Gene=iscU;Gene=CVD06_15335;Gene=CQZ96_02425;Gene=F910_02098;Gene=ASC84_01605;Gene=F960_02852;Gene=SAMN04487817_101426;Gene=nifU;Gene=ABTJ_02049;Gene=AAV97_05250;Gene=DBL02_01480;Gene=SAMN02799632_02085;Gene=F981_01951;Gene=A3F63_00075;Gene=AMS70_09070;Gene=F913_02481;Gene=CIL08_12170;Gene=A0J50_09335;Gene=NDM229_010115;Gene=AOLE_10590;Gene=DFR99_1446;Gene=F963_02365;Gene=F958_02745;Gene=F938_00483;Gene=F935_01394;Gene=F937_02726;Gene=RZ95_08005;Gene=C3422_00525;Gene=F931_01105;Gene=F922_01973;Gene=AC057_10825;Gene=A0A0A8TP30;Gene=F962_02060;Gene=ASF86_04160;Gene=MF4640_04610;Gene=C5B72_01085;

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000027403.1	1.83E-06	1.78E-04	-1.0492111	ID=WP_000027403.1;Description=Uncharacterised protein
WP_001057073.1	0.00244462	0.0468632	-1.0590403	ID=WP_001057073.1;Description=acyl-CoA desaturase;Gene=EWO92_05875;Gene=EGT34_06060;Gene=FJV27_05355;Gene=des6;Gene=J517_1475;Gene=F913_01526;Gene=EGS71_07390;Gene=F922_00996;Gene=J596_3062;Gene=ABTJ_01050;Gene=J518_1277;Gene=J635_0297;Gene=HMPREF0010_02246;Gene=J524_1002;Gene=J567_1513;Gene=J552_1496;Gene=J512_1369;Gene=D0529_02475;Gene=C3422_06060;Gene=T630_2953;Gene=desA3_2;Gene=ACINNAV82_2739;Gene=desA3_1;Gene=F910_01062;Gene=J529_3381;Gene=AB237_0908;Gene=ABAYE1018;Gene=ABSDF1089;Gene=J506_0576;Gene=F962_01051;Gene=J532_1232;Ontology_term=oxidoreductase activity,lipid metabolic process,oxidation-reduction process;Ontology_id=GO:0016491,GO:006629,GO:0055114

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000581860.1	4.83E-04	0.014455954	-1.1215156	ID=WP_000581860.1;Description=signal peptide
WP_001083446.1	3.47E-09	7.82E-07	-1.138651	ID=WP_001083446.1;Description=Uncharacterised protein
WP_001145693.1	0.001702967	0.036194213	-1.2047936	ID=WP_001145693.1;Description=iron-containing redox enzyme family protein
WP_001072861.1	0.001563983	0.033482928	-1.2049487	ID=WP_001072861.1;Description=thiamine biosynthesis protein ThiC;Gene=thiC;Ontology_term=zinc ion binding,carbon-carbon lyase activity,4 iron, 4 sulfur cluster binding,thiamine biosynthetic process,thiamine diphosphate biosynthetic process;Ontology_id=GO:0008270,GO:0016830,GO:0051539,GO:0009228,GO:0009229

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000994352.1	6.27E-06	4.60E-04	-1.2210395	ID=WP_000994352.1;Description=tricarba llylate utilization protein B;Gene=citB;Gene=tcuB;Gene=T630_079 2;Gene=BSF95_00736;Gene=ABTJ_0310 8;Ontology_term=integral component of membrane,iron-sulfur cluster binding;Ontology_id=GO:0016021,GO:00 51536
WP_000995508.1	1.92E-12	9.37E-10	-1.2219255	ID=WP_000995508.1;Description=thioest erase

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001097630.1	6.15E-05	0.002733185	-1.2319436	ID=WP_001097630.1;Description=putative methionine/alanine importer small subunit;Gene=F987_03215;Gene=J610_1741;Gene=J551_0542;Gene=F909_00881;Gene=J552_1643;Gene=J567_3114;Gene=J532_1268;Gene=EGS71_12795;Gene=ABTJ_00024;Gene=DZ985_03050;Gene=J635_0835;Gene=J580_2668;Gene=BDGL_002930;Gene=ABSDF3650;Gene=F887_03661;Gene=J508_1537;Gene=J733_2965;Gene=C5B41_02210;Gene=DGS69_02130;Gene=DBL02_03740;Gene=J518_0951;Gene=AOLE_00090;Gene=ABAYE0020;Gene=F886_00213;Gene=AC2117_00025;Gene=EGT34_11215;Gene=J619_01566;Gene=F942_03116;Gene=D0529_00680;Gene=J596_3218;Gene=EGS47_07240;Gene=J500_3321;Gene=J529_1238;Gene=BSF95_03873;Gene=F962_00023;Gene=J658_1987;Gene=HMPREF0012_02568;Gene=J507_2209;Gene=D7V21_14905;Gene=A9988_02820;Gene=J622_00370;Gene=SAMN02799632_02959;Gene=J663_1841;Gene=J517_3195;Gene=CIL08_19010;

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000160878.1	0.001494976	0.032722123	-1.3096582	ID=WP_000160878.1;Description=Sidero phore-interacting protein;Gene=FJU54_05240;Gene=CBE85_00775;Gene=viuB;Gene=E5H25_05920;Gene=ABTJ_01123;Gene=J608_3557;Gene=viuB_1;Gene=FJU73_01320;Gene=bauF;Gene=D0529_15140;Ontology_term=oxidoreductase activity,oxidation-reduction process;Ontology_id=GO:0016491,GO:0055114
WP_000271409.1	7.94E-05	0.003375971	-1.3412734	ID=WP_000271409.1;Description=50S ribosomal protein L21;Gene=rpIU;Ontology_term=ribosome, structural constituent of ribosome,rRNA binding,translation;Ontology_id=GO:0005840,GO:0003735,GO:0019843,GO:0006412
WP_001034851.1	0.00125108	0.030108279	-1.3592234	ID=WP_001034851.1;Description=DNA transfer protein p32
WP_001037927.1	0.001206698	0.030108279	-1.375168	ID=WP_001037927.1;Description=YARH G domain-containing protein
RF00010	0.001405327	0.03195213	-1.3839862	#N/A

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001017546.1	6.07E-04	0.017711526	-1.4143065	ID=WP_001017546.1;Description=MFS transporter;Gene=D0529_02865;Gene=ABTJ_02307;Gene=AB237_2133;Gene=BSF95_01555;Gene=B9X91_16325;Gene=DVA79_07380;Ontology_term=oxidoreductase activity, acting on the aldehyde or oxo group of donors,oxidation-reduction process;Ontology_id=GO:0016903,GO:0055114

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000362312.1	1.19E-04	0.004828119	-1.4348513	ID=WP_000362312.1;Description=RNA polymerase sigma factor;Gene=C3422_08135;Gene=EGS71_07955;Gene=E5A70_05625;Gene=F910_00952;Gene=J582_1317;Gene=AL533_02750;Gene=FJU79_09760;Gene=J512_2300;Gene=J635_0172;Gene=CYQ93_11390;Gene=sigX;Gene=EA682_16525;Gene=J567_1772;Gene=ABAYE0897;Gene=J524_1386;Gene=NCTC7364_02899;Gene=J506_3837;Gene=J532_2257;Gene=FJU41_06145;Gene=ACIN5021_3087;Gene=D0529_01940;Gene=sigE;Gene=F962_00894;Gene=J552_1579;Gene=H125_13434;Gene=ABSDF0903;Gene=HMPREF0010_02138;Gene=EGT34_06600;Gene=AB237_0809;Gene=ACINNAV82_2877;Gene=T630_3075;Gene=ABTJ_00874;Gene=FJU95_01770;Gene=F922_00880;Ontology_term=sigma factor activity,DNA binding,DNA-binding transcription factor activity,DNA-directed 5'-3' RNA polymerase activity,regulation of DNA-templated transcription,

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000048256.1	0.001073828	0.027387282	-1.4432069	ID=WP_000048256.1;Description=50S ribosomal protein L28;Gene=rpmB;Ontology_term=ribosome,structural constituent of ribosome,translation;Ontology_id=GO:0005840,GO:0003735,GO:0006412
WP_002000179.1	8.77E-07	9.19E-05	-1.4571362	ID=WP_002000179.1;Description=glycosyltransferase 20 family protein;Gene=J529_0873;Gene=otsA_1;Gene=F962_02953;Gene=otsA;Gene=F913_03399;Gene=T630_0876;Gene=J517_1089;Gene=HMPREF0010_01305;Gene=F922_02930;Gene=ABTJ_03010;Gene=J552_0705;Gene=J518_1410;Gene=J567_2388;Gene=J506_0772;Gene=J635_2015;Gene=ACINNAV82_0872;Gene=J524_1753;Gene=J532_1861;Gene=J596_2911;Ontology_term=alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity,trehalose biosynthetic process;Ontology_id=GO:0003825,GO:0005992;Enzyme_code=EC:2.4.1.15;Enzyme_name=Alpha,alpha-trehalose-phosphate synthase (UDP-forming)

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000830363.1	1.26E-04	0.005057523	-1.4955359	ID=WP_000830363.1;Description=amino acid ABC transporter substrate-binding protein
WP_001205343.1	0.001446554	0.032425392	-1.5105021	ID=WP_001205343.1;Description=RepB family plasmid replication initiator protein;Gene=repB;Gene=p2ABAYE0001;Gene=repE_1;Gene=J524_4089;Gene=FJU37_18385;Gene=F923_00004;Gene=RZ95_19315;Gene=ABIBUN_P10004;Gene=F969_03487;Gene=AJ0707_03469;Gene=T630_4219;Gene=repAci1;Ontology_term=DNA-directed DNA polymerase activity,DNA replication initiation,DNA biosynthetic process;Ontology_id=GO:0003887,GO:006270,GO:0071897;Enzyme_code=EC:2.7.7.7;Enzyme_name=DNA-directed DNA polymerase

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_032488579.1	0.002195229	0.04321213	-1.5405669	ID=WP_032488579.1;Description=AAC(6'-Ib family aminoglycoside 6'-N-acetyltransferase; Gene=AN672_29365; Gene=A0A240EUE7; Gene=acc(6')-Ib; Gene=W5XIZ6; Gene=HMPREF1611_03330; Gene=BFW41_15865; Gene=A0A0G3AYQ9; Gene=aac(6')-Ib-cr; Gene=aacA4; Gene=A0A142IIS2; Gene=blaOXA-30; aacA4; Gene=aacA4cr; Gene=A0A0F7IDE3; Gene=A0A0E3DSI7; Gene=AacA4; Gene=aac(6)-Ib; Gene=A0A2U8T0R2; Gene=A0A0E3MTQ7; Gene=aac(6')-Ib; Gene=A0A482M0L0; Gene=AAC(6')-Ib; Ontology_term=nucleotidyltransferase activity, metal ion binding, aminoglycoside 6'-N-acetyltransferase activity, N6-hydroxylysine O-acetyltransferase activity; Ontology_id=GO:0016779, GO:0046872, GO:0047663, GO:0050133; Enzyme_code=EC:2.3.1.5, EC:2.3.1.82, EC:2.3.1.102; Enzyme_name=Arylamine N-acetyltransferase, Aminoglycoside 6'-N-

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000209410.1	3.82E-04	0.011923935	-1.5623051	ID=WP_000209410.1;Description=glutamyl-tRNA amidotransferase;Gene=AB237_1186;Gene=F913_01767;Gene=F910_01441;Gene=J512_2440;Gene=ABAYE1285;Gene=J506_2607;Gene=ABTJ_01271;Gene=F922_01204;Gene=yqeY;Gene=J529_1251;Gene=EA722_04305;Gene=D0529_06790;Gene=HMPREF0010_00082;Gene=J532_1982;Gene=J596_0119;Gene=FJU54_05690;Gene=ABSDF1282;Gene=BSF95_02652;Gene=EGS71_06015;Gene=F962_01327;Gene=ACINNAV82_2517;Gene=T630_2558;Gene=J518_1622;Gene=J552_2863;Gene=EGT34_04785;Gene=J517_3489;Gene=J567_0893;Gene=J524_0781;Gene=J635_2146;Gene=C3422_03130;Ontology_term=transferase activity,carbon-nitrogen ligase activity, with glutamine as amido-N-donor;Ontology_id=GO:0016740,GO:0016884

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001229357.1	3.73E-04	0.011752947	-1.5857126	ID=WP_001229357.1;Description=30S ribosomal protein S15;Gene=rpsO;Ontology_term=ribosome, structural constituent of ribosome,rRNA binding,translation;Ontology_id=GO:0005840,GO:0003735,GO:0019843,GO:0006412

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001147894.1	5.32E-05	0.002436451	-1.6029129	ID=WP_001147894.1;Description=oxidoreductase;Gene=CYQ93_11935;Gene=FJV01_05865;Gene=ABUW_1104;Gene=J517_1474;Gene=EGS71_07395;Gene=EGT34_06065;Gene=B9X95_15195;Gene=F913_01525;Gene=J596_3061;Gene=F922_00995;Gene=ACINNAV82_2740;Gene=HMPREF0010_02245;Gene=SAMEA104305283_01511;Gene=J512_1370;Gene=D0529_02470;Gene=J567_1512;Gene=J524_1003;Gene=C3422_06065;Gene=J552_1495;Gene=NCTC7412_00998;Gene=BSF95_02873;Gene=A7M79_07630;Gene=T630_2954;Gene=EA706_05210;Gene=C3415_13875;Gene=ABAYE1017;Gene=AB237_0907;Gene=J506_0575;Gene=F962_01050;Gene=LV38_02025;Gene=ABTJ_01049;Gene=J532_1233;Ontology_term=electron transfer activity,metal ion binding,2 iron,2 sulfur cluster binding,electron transport chain;Ontology_id=GO:0009055,GO:0046872,GO:0051537,GO:0022900

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000543705.1	0.001768425	0.03652669	-1.6698135	ID=WP_000543705.1;Description=Unchar acterised protein;Gene=ABAYE3041;Gene=J529_2 207;Gene=J635_2051;Gene=F962_02987; Gene=J532_0627;Gene=F910_03128;Gen e=T630_0842;Gene=NT90_07625;Gene=J 517_1054;Gene=EGS71_16995;Gene=NC TC7364_00796;Gene=J518_1374;Gene= D0529_14520;Gene=J506_0807;Gene=E GT34_14875;Gene=J596_1640;Gene=J52 4_0631;Gene=ACINNAV82_0837;Gene=F JV30_10755;Gene=J512_1100;Gene=BSF 95_00799;Gene=F913_03436;Gene=C342 2_11550;Gene=EA677_06670;Gene=J552 _0739;Gene=A7M79_13210;Gene=J567_ 0212;Gene=ABTJ_03045;Gene=F922_02 965;Gene=SAMEA104305268_01928;Ont ology_term=integral component of membrane;Ontology_id=GO:0016021
WP_001103036.1	1.42E-05	8.32E-04	-1.6968595	ID=WP_001103036.1;Description=Unchar acterised protein

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001143890.1	0.001252373	0.030108279	-1.762776	ID=WP_001143890.1;Description=superoxide dismutase;Gene=C3422_04360;Gene=EGT34_09470;Gene=J517_2102;Gene=F910_00366;Gene=sodC;Gene=D0529_11050;Gene=F913_00339;Gene=F922_00359;Gene=EGS71_10860;Gene=FJV07_03090;Gene=EW092_14560;Gene=F962_00362;Gene=J608_2266;Ontology_term=superoxide dismutase activity,metal ion binding,removal of superoxide radicals,oxidation-reduction process;Ontology_id=GO:0004784,GO:0046872,GO:0019430,GO:0055114;Enzyme_code=EC:1.15.1.1;Enzyme_name=Superoxide dismutase
WP_001016788.1	6.59E-04	0.01876271	-1.7848924	ID=WP_001016788.1;Description=phenylacetate-CoA oxygenase subunit PaaI;Gene=paaC;Gene=H125_01910;Gene=paaI;Gene=ABTJ_02369;Ontology_term=phenylacetate catabolic process;Ontology_id=GO:0010124

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000119670.1	3.07E-04	0.010437371	-1.8545033	ID=WP_000119670.1;Description=addicti on module antitoxin;Gene=reIE;Ontology_term=hydr olase activity;Ontology_id=GO:0016787
WP_001984048.1	1.17E-05	7.64E-04	-1.8583783	ID=WP_001984048.1;Description=1,2- phenylacetyl-CoA epoxidase subunit B;Gene=E5A70_12385;Gene=FJU43_080 60;Gene=FJU47_11270;Gene=FJU45_003 95;Gene=FJV00_09270;Ontology_term=p henylacetyl-CoA 1,2-epoxidase activity,oxidation-reduction process;Ontology_id=GO:0097266,GO:00 55114;Enzyme_code=EC:1.14.13,EC:1.14 .13.149;Enzyme_name=Acting on paired donors, with incorporation or reduction of molecular oxygen. The oxygen incorporated need not be derived from O(2),Phenylacetyl-CoA 1,2-epoxidase

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000135049.1	7.38E-05	0.003183417	-1.8643708	ID=WP_000135049.1;Description=DNA-directed RNA polymerase subunit omega;Gene=rpz;Ontology_term=DNA binding,DNA-directed 5'-3' RNA polymerase activity,transcription, DNA-templated;Ontology_id=GO:0003677,GO:0003899,GO:0006351;Enzyme_code=EC:2.7.7.6;Enzyme_name=DNA-directed RNA polymerase

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000892936.1	4.19E-05	0.002048833	-1.8828888	ID=WP_000892936.1;Description=phenyl acetic acid degradation bifunctional protein PaaZ;Gene=ABTJ_02372;Gene=J608_298 8;Gene=paaZ;Gene=paaZ_1;Ontology_ter m=aldehyde dehydrogenase (NAD+) activity,glyceraldehyde-3-phosphate dehydrogenase (NAD+) (non- phosphorylating) activity,oxidation- reduction process;Ontology_id=GO:0004029,GO:00 43878,GO:0055114;Enzyme_code=EC:1. 2.1.5,EC:1.2.1.3;Enzyme_name=Aldehyde dehydrogenase (NAD(P)(+)),Aldehyde dehydrogenase (NAD(+))

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000906487.1	0.001781905	0.03654774	-1.8976054	ID=WP_000906487.1;Description=carbon storage regulator; Gene=csrA; Ontology_term=cytoplasm,mRNA 5'-UTR binding,regulation of carbohydrate metabolic process,mRNA catabolic process,negative regulation of translational initiation,positive regulation of translational initiation; Ontology_id=GO:0005737,GO:0048027,GO:0006109,GO:0006402,GO:0045947,GO:0045948
WP_000744381.1	1.95E-04	0.007426242	-1.9047738	ID=WP_000744381.1;Description=2,3-dihydroxybenzoate-AMP ligase; Gene=J517_2070; Gene=D0529_15090; Gene=entE; Gene=dhbE; Gene=ABTJ_01135; Ontology_term=(2,3-dihydroxybenzoyl)adenylate synthase activity,2,3-dihydroxybenzoate-serine ligase activity,siderophore biosynthetic process; Ontology_id=GO:0008668,GO:0047527,GO:0019290; Enzyme_code=EC:2.7.7.58,EC:6.3.2.14; Enzyme_name=(2,3-dihydroxybenzoyl)adenylate synthase,Enterobactin synthase

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000920230.1	4.15E-07	4.68E-05	-1.9990343	ID=WP_000920230.1;Description=putative lipoprotein;Gene=HMPREF0010_00610; Gene=ABAYE1876;Ontology_term=integral component of membrane;Ontology_id=GO:0016021

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000431126.1	1.35E-05	8.06E-04	-2.0047789	ID=WP_000431126.1;Description=1,2-phenylacetyl-CoA epoxidase subunit A;Gene=B9X80_09160;Gene=paaG;Gene=paaA;Gene=EGT34_18735;Gene=F910_02484;Gene=EA685_02755;Gene=F913_02816;Gene=BFR91_04320;Gene=ABTJ_02371;Gene=EGS71_20555;Gene=D0529_03195;Gene=EA752_13275;Gene=F922_02285;Gene=AL489_017205;Ontology_term=phenylacetyl-CoA 1,2-epoxidase activity,phenylacetate catabolic process,oxidation-reduction process;Ontology_id=GO:0097266,GO:0010124,GO:0055114;Enzyme_code=EC:1.14.13,EC:1.14.13.149;Enzyme_name=Acting on paired donors, with incorporation or reduction of molecular oxygen. The oxygen incorporated need not be derived from O(2),Phenylacetyl-CoA 1,2-epoxidase

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000735356.1	3.42E-16	3.34E-13	-2.093011	ID=WP_000735356.1;Description=5-methyltetrahydropteroyltriglutamate--homocysteine methyItransferase;Gene=J512_1734;Gene=F962_03017;Gene=T630_0806;Gene=J529_2701;Gene=xecA1_1;Gene=ACINNAV82_0807;Gene=xecA1_2;Gene=FJU45_18275;Gene=CHQ89_11975;Gene=ABTJ_03095;Gene=AL533_13770;Gene=J518_2321;Gene=FJV13_16090;Gene=HMPREF001_01234;Gene=metE;Gene=F922_02995;Gene=EGT34_14670;Gene=J608_1982;Gene=xecA1;Gene=J552_3412;Gene=J532_0661;Gene=EGS71_16800;Gene=J506_0838;Gene=D0529_14255;Gene=FJU50_11475;Gene=J635_3719;Gene=J567_1345;Gene=J517_3249;Gene=AL489_001905;Gene=J524_0581;Ontology_term=5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity,zinc ion binding,methionine synthase activity,2-hydroxypropyl-CoM lyase activity,methionine biosynthetic process,methylation;Ontology_id=GO:000

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_085916956.1	5.88E-10	1.57E-07	-2.097932	ID=WP_085916956.1;Description=sell repeat family protein

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000185571.1	2.74E-06	2.43E-04	-2.1412187	ID=WP_000185571.1;Description=Uncharacterised protein;Gene=BSF95_02287;Gene=F913_02150;Gene=ABSDF2083;Gene=HI25_14219;Gene=EGT34_02510;Gene=F922_01608;Gene=J813_3309;Gene=J811_3813;Gene=J567_3630;Gene=J715_1691;Gene=J506_3513;Gene=J732_2512;Gene=D0529_08270;Gene=J608_1620;Gene=FJU85_03585;Gene=SAMEA104305229_06802;Gene=AB237_1511;Gene=J582_0658;Gene=F910_01779;Gene=AL533_06600;Gene=FJV01_01430;Gene=J804_3911;Gene=J596_1032;Gene=F958_02407;Gene=J518_3420;Gene=AL489_013900;Gene=J532_0009;Gene=C3422_01550;Gene=ACINNA_V82_2193;Gene=J806_2657;Gene=NCTC_7364_02198;Gene=J517_2464;Gene=A7M79_14530;Gene=T630_2098;Gene=J807_2418;Gene=J512_3076;Gene=FJU50_16495;Gene=J805_2357;Gene=ACIN5021_2332;Gene=J524_2253;Gene=ABAYE1629;Gene=J635_2877;Gene=EGS71_03840;Gene=J633_0109;Gene=J809_3200;Gene

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000353163.1	4.72E-05	0.002232159	-2.1822917	<p>ID=WP_000353163.1;Description=4-hydroxyphenylpyruvate dioxygenase;Gene=A0A0E3H184;Gene=F962_00068;Gene=F910_00072;Gene=F922_00071;Gene=F913_00069;Gene=ABTJ_00066;Gene=A0A0E3MV38;Gene=hppD;Gene=hpd;Ontology_term=4-hydroxyphenylpyruvate dioxygenase activity,metal ion binding,aromatic amino acid family metabolic process,oxidation-reduction process;Ontology_id=GO:0003868,GO:0046872,GO:0009072,GO:0055114;Enzyme_code=EC:1.13.11,EC:1.13.11.27;Enzyme_name=Acting on single donors with incorporation of molecular oxygen (oxygenases). The oxygen incorporated need not be derived from O(2),4-hydroxyphenylpyruvate dioxygenase</p>

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_001260033.1	1.81E-05	0.001018781	-2.2145717	ID=WP_001260033.1;Description=ATP-dependent Clp protease adapter ClpS;Gene=clpS_2;Ontology_term=peptidase activity,proteolysis,protein catabolic process;Ontology_id=GO:0008233,GO:006508,GO:0030163

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000956973.1	1.80E-08	3.31E-06	-2.3010402	ID=WP_000956973.1;Description=Acetyltransferase;Gene=AB237_1841;Gene=J608_0931;Gene=J506_1052;Gene=J518_1939;Gene=FJU97_00900;Gene=FJU44_12870;Gene=J517_0063;Gene=J567_2284;Gene=FJU83_00635;Gene=ABSDF1874;Gene=ABTJ_02024;Gene=J635_0615;Gene=mbtK;Gene=EGS71_01760;Gene=B9X95_11380;Gene=J529_1423;Gene=E5A70_10805;Gene=EGT34_00385;Gene=T630_1800;Gene=J552_0364;Gene=EWO92_02650;Gene=J512_2495;Gene=J532_1415;Gene=J524_2702;Gene=C3422_00400;Gene=ABAYE1997;Gene=J596_0743;Gene=D0529_09450;Ontology_term=ribosome,transferase activity, transferring acyl groups;Ontology_id=GO:0005840,GO:0016746
WP_000086293.1	1.36E-08	2.66E-06	-2.3794029	ID=WP_000086293.1;Description=Transcriptional regulator
WP_000108365.1	1.53E-05	8.78E-04	-2.494533	ID=WP_000108365.1;Description=Uncharacterised protein

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000966850.1	2.14E-07	2.50E-05	-2.5382326	ID=WP_000966850.1;Description=Uncharacterised protein;Gene=ASF86_03695;Gene=AB237_1984;Gene=J551_0067;Gene=AC057_10360;Gene=F935_01487;Gene=DFR99_1539;Gene=AOLE_11055;Gene=A9988_00340;Gene=F931_01197;Gene=D0529_12685;Gene=AC2117_02078;Gene=NCTC7364_01728;Gene=J567_3833;Gene=F985_02936;Gene=F962_02153;Gene=H125_00245;Gene=ABSDF2122;Gene=J810_2249;Gene=DH17_13455;Gene=ACINNAV82_1746;Gene=J733_2125;Gene=F958_02840;Gene=J663_2349;Gene=J518_3827;Gene=C3422_18465;Gene=J529_1083;Gene=HMPREF0012_00822;Gene=SAMN02799632_02251;Gene=J596_1515;Gene=A7M79_18100;Gene=F922_02066;Gene=SAMEA104305215_02631;Gene=J811_1251;Gene=J610_0794;Gene=A0J50_09800;Gene=JF913_02575;Gene=F937_02819;Gene=J512_3277;Gene=T630_1682;Gene=J584_1828;Gene=ABTJ_02144;Gene=ABAYE2119;Gene=J608_5921;Gene=J635_0735;G

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000132044.1	7.23E-08	1.06E-05	-2.5671737	ID=WP_000132044.1;Description=putative surface antigen
WP_000942498.1	2.55E-04	0.008889574	-2.9303553	ID=WP_000942498.1;Description=Uncharacterised protein
WP_000138830.1	2.27E-05	0.001167632	-3.0730064	ID=WP_000138830.1;Description=monotrophic glutaredoxin, Grx4 family;Gene=ABTJ_01658;Gene=SAMN02799632_01664;Gene=F962_01665;Gene=grxD;Gene=F913_02145;Gene=J608_1615;Gene=A0J50_07505;Gene=F910_01773;Gene=grxD_2;Gene=A9988_08750;Gene=F958_02402;Gene=H125_14244;Gene=F931_00685;Gene=F985_02463;Gene=ABYE1624;Gene=J608_5314;Gene=AB237_1507;Gene=ABSDF2089;Ontology_term=electron transfer activity,protein disulfide oxidoreductase activity,metal ion binding,2 iron, 2 sulfur cluster binding,electron transport chain,cell redox homeostasis;Ontology_id=GO:0009055,GO:0015035,GO:0046872,GO:0051537,GO:0022900,GO:0045454

Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000031355.1	3.13E-06	2.70E-04	-3.2350273	ID=WP_000031355.1;Description=DUF1852 domain-containing protein
WP_000644342.1	0.002432283	0.0468632	-3.8140364	ID=WP_000644342.1;Description=DUF4142 domain-containing protein
WP_000129799.1	8.19E-07	8.89E-05	-7.859184	ID=WP_000129799.1;Description=Uncharacterised protein
WP_000365972.1	1.90E-04	0.007426242	-7.9913087	ID=WP_000365972.1;Description=putative membrane protein;Gene=AB237_1501;Gene=BSF95_02299;Gene=J524_2241;Gene=NCTC7364_02210;Gene=F910_01766;Gene=J608_1609;Gene=J567_3251;Gene=J517_2453;Gene=J552_1102;Gene=EGT34_02570;Gene=J635_2889;Gene=D0529_08330;Gene=J512_3063;Gene=T630_2110;Gene=ABAYE1616;Gene=C3422_01610;Gene=AMEA104305229_02507;Gene=A7N09_14130;Gene=ABUW_1774;Gene=ABTJ_01651;Gene=F922_01596;Gene=CBI29_02195;Gene=FJU71_04595;Gene=EGS71_03900;Ontology_term=integral component of membrane;Ontology_id=GO:0016021

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Protein Id	P-value	FDR	Log2 Fold Change	Annotation
WP_000640864.1	4.82E-06	3.63E-04	-9.375482	ID=WP_000640864.1;Description=Unchar acterised protein
WP_000616034.1	5.86E-09	1.23E-06	-9.783564	ID=WP_000616034.1;Description=Unchar acterised protein

differential transcriptional response, which encompasses a total of 160 predicted protein-coding genes that were differentially transcribed, but only 36 and 64 transcriptional units up- and down-regulated when the data were analyzed using statistically significant difference values ($P \leq 0.05$). Gene Ontology (GO) annotation of the differentially expressed genes resulted 18 ontology groups for up-regulated and 44 ontology groups for down-regulated genes. These groupings revealed a great proportion of up-regulated genes being transcription factors and participating in DNA binding. There was upregulation of signal transduction genes that included those exhibiting kinase activity and cyclic-guanylate-specific phosphodiesterase activity. Additionally, genes involved in magnesium ion binding are overexpressed (Table 14 and Figure 19). The presence of GaPPIX in the culture medium decreased the expression of genes in Gene ontology (GO) groups, including oxidation-reduction, electron carrier/transport and cellular and macromolecular metabolic processes, as well as porins. Notably, groups important in metal acquisition were decreased, including iron, zinc, and copper. (2,3-dihydroxybenzoyl)adenylate synthase activity group has been shown to be responsible for siderophore production and are closely associated with central metabolism were also decreased in expression (Table 15 and Figure 20). Of the 64 down-regulated genes, 76.6% were annotated using KEGG Ontology (KO) annotation. Most were involved in genetic information processing, carbohydrate metabolism, amino acid metabolism, and lipid metabolism had lower expression than cells grown without GaPPIX in the culture medium (Table 16 and Figure 21). Over half of the 36 up-regulated genes (55.6%) were annotated with KO annotations. The majority of groups were important in the genetic information processing and metabolism (Table 17 and Figure 22). Taken together, these results indicate that the

Table 14. Gene Ontology of Genes Overexpressed in the Presence of GaPPIX

Gene Ontology Group	Term ID	Description	Frequency	Log10 p-value	Uniqueness
Molecular Function	GO:0000287	magnesium ion binding	1.20%	-2.9761	0.828
		transcription factor activity, sequence-specific			
	GO:0003700	specific DNA binding	9.29%	-3.5017	0.855
	GO:0008168	methyltransferase activity	2.50%	-7.2351	0.654
	GO:0003986	acetyl-CoA hydrolase activity	0.03%	-3.5976	0.727
	GO:0008718	D-amino-acid dehydrogenase activity	0.08%	-4.6459	0.803
	GO:0016787	hydrolase activity	19.38%	-5.1409	0.8
	GO:0016491	oxidoreductase activity	16.63%	-3.4815	0.797
	GO:0003677	DNA binding	15.71%	-2.8059	0.85
	GO:0004177	aminopeptidase activity	0.31%	-2.6398	0.745
	GO:0008483	transaminase activity	0.97%	-3.5045	0.668
	GO:0016301	kinase activity	4.48%	-5.1726	0.646
		cyclic-guanylate-specific phosphodiesterase activity			
	GO:0071111	activity	0.28%	-2.8392	0.716
	GO:0016746	transferase activity, transferring acyl groups	3.31%	-3.0092	0.65
Cellular Component	GO:0009279	cell outer membrane	3.64%	-3.6576	0.237
	GO:0005737	cytoplasm	31.27%	-3.4089	0.531
	GO:0016021	integral component of membrane	48.87%	-5.4622	0.516
	GO:0005886	plasma membrane	22.21%	-2.8646	0.256
Biological Process	GO:0000902	cell morphogenesis	0.87%	-2.8272	1

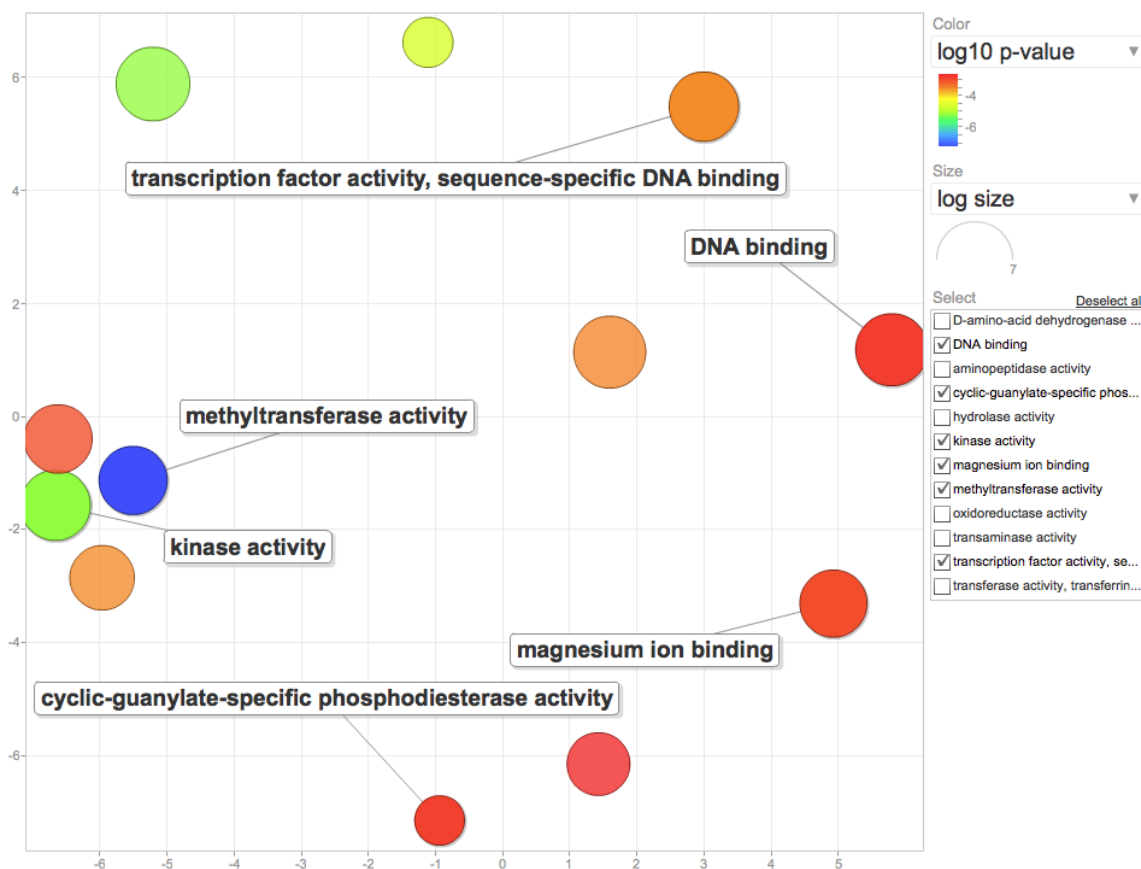


Figure 19. Molecular functions overexpressed in the presence of GaPPIX.

Genes that were determined to be differentially expressed to a higher level in cells grown in 10 $\mu\text{g/ml}$ by RNASeq were characterized using gene ontology. An enrichment analysis shows increased abundance of transcripts responsible for multiple molecular functions. Many are associated with gene regulation. Interestingly, the transcripts associated with magnesium ion binding were also upregulated.

Table 15. Gene ontology of genes underexpressed in the presence of GaPPIX

Gene Ontology Group	Term_ID	Description	Frequency	Log10 p-value	Uniqueness
Molecular Function	GO:0003871	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity	0.03%	-15.466	0.849
	GO:0005506	iron ion binding	2.28%	-4.5498	0.826
	GO:0008270	zinc ion binding	1.56%	-2.8058	0.83
	GO:0009055	electron carrier activity	2.81%	-4.644	0.947
	GO:0016987	sigma factor activity	0.72%	-3.9245	0.946
	GO:0000150	recombinase activity	0.03%	-9.5171	0.914
	GO:0008909	isochorismate synthase activity	0.03%	-2.7352	0.914
	GO:0050334	thiaminase activity	0.54%	-5.7696	0.862
	GO:0097266	phenylacetyl-CoA 1,2-epoxidase activity	0.06%	-4.8697	0.844
	GO:0004462	lactoylglutathione lyase activity	0.08%	-4.8996	0.912
	GO:0016787	hydrolase activity	19.38%	-3.5129	0.897
	GO:0042834	peptidoglycan binding	0.17%	-3.4437	0.908
	GO:0016491	oxidoreductase activity	16.63%	-2.8254	0.897
	GO:0016740	transferase activity	19.10%	-3.4179	0.897
	GO:0003677	DNA binding	15.71%	-4.1319	0.911
	GO:0003985	acetyl-CoA C-acetyltransferase activity	0.03%	-8.8356	0.835
	GO:0003825	alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity	0.04%	-6.057	0.846
	GO:0004076	biotin synthase activity	0.03%	-3.098	0.849
	GO:0008668	(2,3-dihydroxybenzoyl)adenylate synthase activity	0.04%	-3.71	0.802
	GO:0003868	4-hydroxyphenylpyruvate dioxygenase activity	0.03%	-4.3261	0.848
	GO:0047512	(S,S)-butanediol dehydrogenase activity	0.05%	-2.5979	0.845

Gene Ontology Group	Term_ID	Description	Frequency	Log ₁₀ p-value	Uniqueness
	GO:0004806	triglyceride lipase activity	0.03%	-2.9604	0.877
	GO:0008908	isochorismatase activity	0.03%	-3.1107	0.877
	GO:0004784	superoxide dismutase activity	0.06%	-2.9023	0.844
	GO:0004029	aldehyde dehydrogenase (NAD) activity	0.20%	-4.3778	0.809
	GO:0004491	methylmalonate-semialdehyde dehydrogenase (acylating) activity	0.08%	-3.2097	0.815
	GO:0016903	oxidoreductase activity, acting on the aldehyde or oxo group of donors	0.92%	-3.2168	0.823
	GO:0033734	(R)-benzylsuccinyl-CoA dehydrogenase activity	0.20%	-2.8258	0.835
	GO:0008233	peptidase activity	3.06%	-4.7423	0.85
	GO:0008237	metallopeptidase activity	1.06%	-2.8194	0.857
	GO:0005524	ATP binding	11.79%	-5.6799	0.858
	GO:0016779	nucleotidyltransferase activity	1.86%	-2.6585	0.787
	GO:0004314	[acyl-carrier-protein] S-malonyltransferase activity	0.06%	-4.8996	0.831
	GO:0050518	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase activity	0.06%	-2.8613	0.798
	GO:0046872	metal ion binding	15.18%	-2.7629	0.842
	GO:0003887	DNA-directed DNA polymerase activity	0.36%	-2.8397	0.781
	GO:0005507	copper ion binding	0.39%	-3.0458	0.843
Cellular Component	GO:0005840	ribosome	2.31%	-7.7447	0.248
	GO:0016021	integral component of membrane	48.87%	-3.7212	0.761
	GO:0005737	cytoplasm	31.27%	-2.7491	0.498
	GO:0036125	fatty acid beta-oxidation multienzyme complex	0.04%	-2.6271	0.354

Gene Ontology Group	Term_ID	Description	Frequency	Log10 p-value	Uniqueness
	GO:0009317	acetyl-CoA carboxylase complex	0.16%	-2.9075	0.287
Biological Process	GO:0010124	phenylacetate catabolic process	0.08%	-3.1811	1

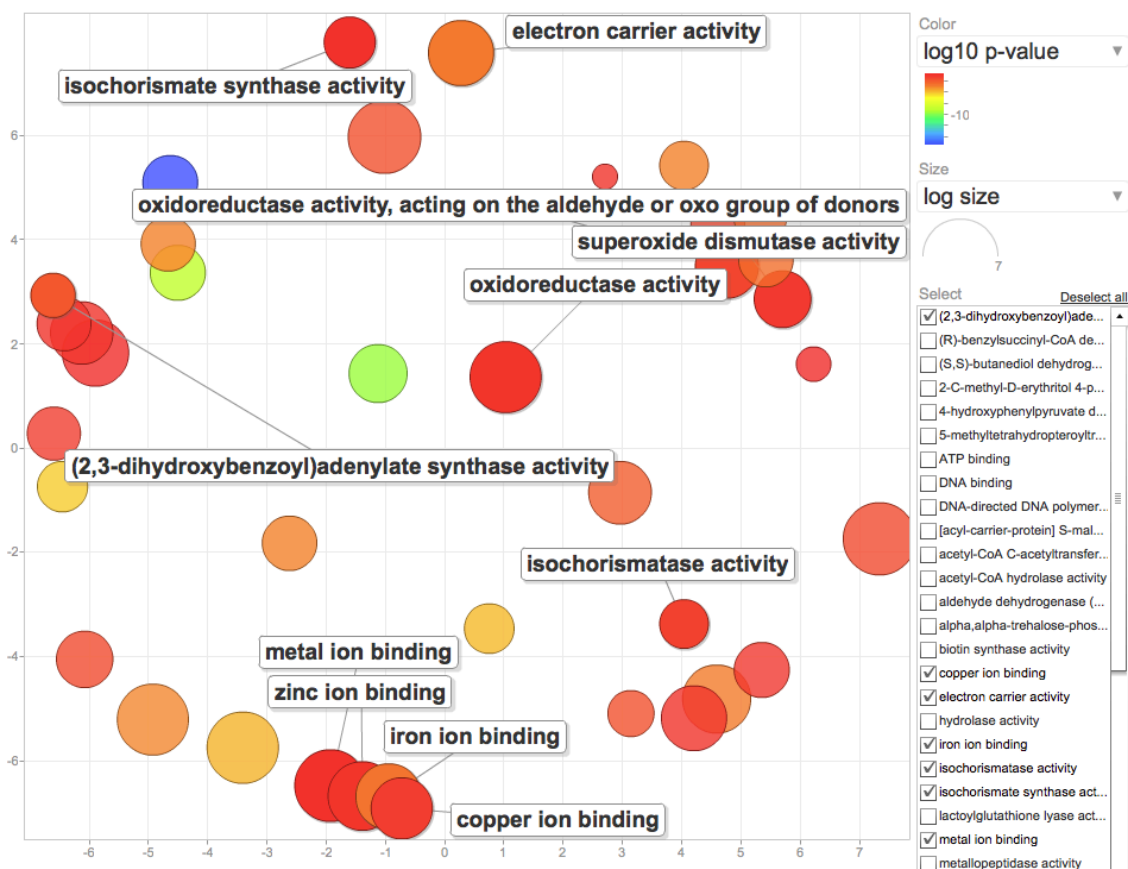


Figure 20. Molecular functions underexpressed in the presence of GaPPIX.

Genes that were determined to be differentially expressed to a lower level in cells grown in 10 $\mu\text{g/ml}$ by RNASeq were characterized using gene ontology. An enrichment analysis shows decreased abundance of transcripts responsible for multiple molecular functions. A highly significant set of transcripts are related to metal binding functions. Transcripts related to binding iron, copper, zinc, and metal binding are greatly decreased in cells grown in GaPPIX. Additionally, electron transport and respiratory molecular function transcripts are reduced. Superoxide dismutase transcripts are also significantly reduced.

Table 16. KEGG ontology of genes underexpressed in the presence of GaPPIX

Protein ID	KO	Definition	Score
WP_002000896.1	K00276	AOC3; primary-amine oxidase [EC:1.4.3.21]	667
WP_001133054.1	K21417	acoB; acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit beta [EC:1.1.1.-]	335
WP_001216217.1	K00991	ispD; 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase [EC:2.7.7.60]	269
WP_000044139.1	K03885	ndh; NADH dehydrogenase [EC:1.6.99.3]	336
WP_001187342.1	K03110	ftsY; fused signal recognition particle receptor butA; meso-butenediol dehydrogenase / (S,S)-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.- 1.1.1.76 1.1.1.304]	330
WP_000238447.1	K03366	diacetyl reductase [EC:1.1.1.- 1.1.1.76 1.1.1.304]	240
WP_000407064.1	K03527	ispH; 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase [EC:1.17.7.4]	308
WP_000631823.1	K00249	ACADM; acyl-CoA dehydrogenase [EC:1.3.8.7]	312
WP_000920736.1			108
WP_000619893.1			300
WP_000044203.1			283
WP_001242511.1	K01759	GLO1; lactoylglutathione lyase [EC:4.4.1.5]	131
WP_001987894.1	K06972	PITRM1; presequence protease [EC:3.4.24.-]	923
WP_000983821.1	K02361	entC; isochorismate synthase [EC:5.4.4.2] accA; acetyl-CoA carboxylase carboxyl transferase subunit alpha [EC:6.4.1.2]	249
WP_000710404.1	K01962	2.1.3.15]	377
WP_000580938.1	K01825	5.1.2.3 5.3.3.8] fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase [EC:1.1.1.35 4.2.1.17]	687
WP_001092382.1	K00140	mmsA; malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27]	505

Protein ID	KO	Definition	Score
WP_000175360.1	K01012	bioB; biotin synthase [EC:2.8.1.6]	327
WP_000344169.1	K03553	recA; recombination protein RecA	333
WP_000095311.1	K00626	ACAT; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	375
WP_001274814.1	K00645	fabD; [acyl-carrier-protein] S-malonyltransferase [EC:2.3.1.39]	429
WP_000140309.1	K02945	RP-S1; small subunit ribosomal protein S1	541
WP_000126114.1			322
		entB; bifunctional isochorismate lyase / aryl carrier protein [EC:3.3.2.1]	
WP_001018264.1	K01252	6.3.2.14]	346
WP_002001156.1			234
WP_000952702.1	K03694	clpA; ATP-dependent Clp protease ATP-binding subunit ClpA	744
WP_001024697.1	K09747	uncharacterized protein	104
WP_012297364.1	K02520	infC; translation initiation factor IF-3	240
WP_000678311.1			133
WP_000331712.1	K04488	iscU; nitrogen fixation protein NifU and related proteins	128
WP_001057073.1	K00508	E1.14.19.3; linoleoyl-CoA desaturase [EC:1.14.19.3]	514
WP_001072861.1	K03147	thiC; phosphomethylpyrimidine synthase [EC:4.1.99.17]	627
WP_000994352.1	K13795	citB; citrate/tricarballoylate utilization protein	353
WP_001097630.1			31
WP_000160878.1			182
WP_000271409.1	K02888	RP-L21; large subunit ribosomal protein L21	101
WP_001017546.1	K04090	E1.2.7.8; indolepyruvate ferredoxin oxidoreductase [EC:1.2.7.8]	1403
WP_000362312.1	K03088	rpoE; RNA polymerase sigma-70 factor, ECF subfamily	190
WP_000048256.1	K02902	RP-L28; large subunit ribosomal protein L28	113
WP_002000179.1	K00697	otsA; trehalose 6-phosphate synthase [EC:2.4.1.15 2.4.1.347]	435
WP_001205343.1			270
WP_032488579.1	K19278	aac6-Ib; aminoglycoside 6'-N-acetyltransferase Ib [EC:2.3.1.82]	158

Protein ID	KO	Definition	Score
WP_000209410.1	K09117	uncharacterized protein	137
WP_001229357.1	K02956	RP-S15; small subunit ribosomal protein S15	125
WP_001147894.1	K22770	stearoyl-CoA 9-desaturase NADPH oxidoreductase	220
WP_000543705.1			16
WP_001143890.1	K04565	SOD1; superoxide dismutase, Cu-Zn family [EC:1.15.1.1]	220
WP_001016788.1	K02611	paaC; ring-1,2-phenylacetyl-CoA epoxidase subunit PaaC [EC:1.14.13.149]	317
WP_000119670.1	K06218	relE; mRNA interferase RelE/StbE	41
WP_001984048.1	K02610	paaB; ring-1,2-phenylacetyl-CoA epoxidase subunit PaaB	121
WP_000135049.1	K03060	rpoZ; DNA-directed RNA polymerase subunit omega [EC:2.7.7.6]	131
		paaZ; oxepin-CoA hydrolase / 3-oxo-5,6-dehydrosuberyl-CoA semialdehyde	
WP_000892936.1	K02618	dehydrogenase [EC:3.3.2.12 1.2.1.91]	643
WP_000906487.1	K03563	csrA; carbon storage regulator	102
WP_000744381.1	K02363	entE; 2,3-dihydroxybenzoate-AMP ligase [EC:6.3.2.14 2.7.7.58]	481
WP_000920230.1			31
WP_000431126.1	K02609	paaA; ring-1,2-phenylacetyl-CoA epoxidase subunit PaaA [EC:1.14.13.149]	431
		metE; 5-methyltetrahydropteroyltryptylglutamate--homocysteine	
WP_000735356.1	K00549	methyltransferase [EC:2.1.1.14]	340
WP_000185571.1			105
WP_000353163.1	K00457	HPD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]	341
WP_001260033.1	K06891	clpS; ATP-dependent Clp protease adaptor protein ClpS	192
WP_000956973.1			31
WP_000966850.1			51
WP_000138830.1	K07390	grxD; monothiol glutaredoxin	113
WP_000365972.1			155

Table 16 page 3 of 3

Your BlastKOALA job

Query dataset: 64 entries
 Taxonomy group: Prokaryotes
 KEGG database searched: species_prokaryotes.pep
 Job submitted: Tue Apr 28 03:46:06 JST 2020
 Job completed: Tue Apr 28 03:54:58 JST 2020

Annotation data [View](#) | [Download](#)

Summary 49 entries (76.6%) annotated

Functional
category

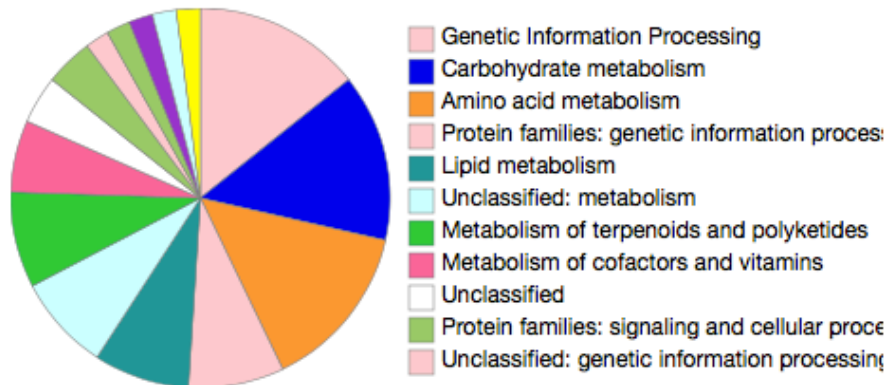


Figure 21. KEGG ontology distribution of underexpressed genes in functional groups. Functional analysis was performed on 64 underexpressed genes from *A. baumannii* ACICU treated with 10 $\mu\text{g/ml}$ GaPPIX and 77% were placed in functional categories. Genetic information processing and carbohydrate metabolism were most abundant of groups effected by the presence of GaPPIX.

Table 17. KEGG ontology of genes overexpressed in the presence of GaPPIX

Protein ID	KO	Definition	Score
WP_000347180.1	K11103	dctA; aerobic C4-dicarboxylate transport protein	311
WP_001207327.1	K03760	eptA; lipid A ethanolaminophosphotransferase [EC:2.7.8.43]	247
WP_000042002.1			160
WP_000097866.1			155
WP_000345328.1	K16053	ybdG; miniconductance mechanosensitive channel	299
WP_000204864.1	K00878	thiM; hydroxyethylthiazole kinase [EC:2.7.1.50]	119
WP_000203146.1			196
WP_000312223.1	K13652	AraC family transcriptional regulator	167
		mdcR; LysR family transcriptional regulator, malonate utilization transcriptional	
WP_000401807.1	K13928	regulator	163
WP_000792950.1			22
WP_000956776.1			103
WP_001089196.1	K03719	lrp; Lrp/AsnC family transcriptional regulator, leucine-responsive regulatory protein	84
WP_001159802.1			300
WP_002000873.1			142
WP_000054921.1	K03821	phbC; polyhydroxyalkanoate synthase subunit PhaC [EC:2.3.1.-]	175
WP_000059344.1	K18118	aarC; succinyl-CoA:acetate CoA-transferase [EC:2.8.3.18]	377
WP_000494374.1			169
WP_000803005.1	K02014	TC.FEV.OM; iron complex outermembrane receptor protein	117
WP_000520927.1	K09758	asdA; aspartate 4-decarboxylase [EC:4.1.1.12]	411
WP_000046989.1			77
WP_001263981.1	K00285	dadA; D-amino-acid dehydrogenase [EC:1.4.5.1]	312
WP_000524257.1			29
WP_001017220.1	K01256	pepN; aminopeptidase N [EC:3.4.11.2]	435
WP_000991232.1	K07044	uncharacterized protein	123

Protein ID	KO	Definition	Score
WP_085916999.1	K03610	minC; septum site-determining protein MinC	55
WP_001019739.1			87
WP_000654846.1			12
WP_000056390.1			13
WP_000048916.1			5
WP_000733835.1	K04084	dsbD; thioredoxin:protein disulfide reductase [EC:1.8.4.16]	138
		mnmC; tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein	
WP_001043531.1	K15461	[EC:2.1.1.61 1.5.-.-]	194
WP_001011955.1	K00343	nuoN; NADH-quinone oxidoreductase subunit N [EC:7.1.1.2]	242
WP_000852265.1			159
WP_000088974.1			9
WP_001226777.1	K01874	MARS; methionyl-tRNA synthetase [EC:6.1.1.10]	463
WP_000276693.1	K00338	nuoI; NADH-quinone oxidoreductase subunit I [EC:7.1.1.2]	150

Your BlastKOALA job

Query dataset: 36 entries
 Taxonomy group: Prokaryotes,Bacteria
 KEGG database searched: genus_prokaryotes.pep
 Job submitted: Tue Apr 28 04:49:36 JST 2020
 Job completed: Tue Apr 28 04:51:44 JST 2020

Annotation data [View](#) | [Download](#)

Summary 20 entries (55.6%) annotated

Functional
category

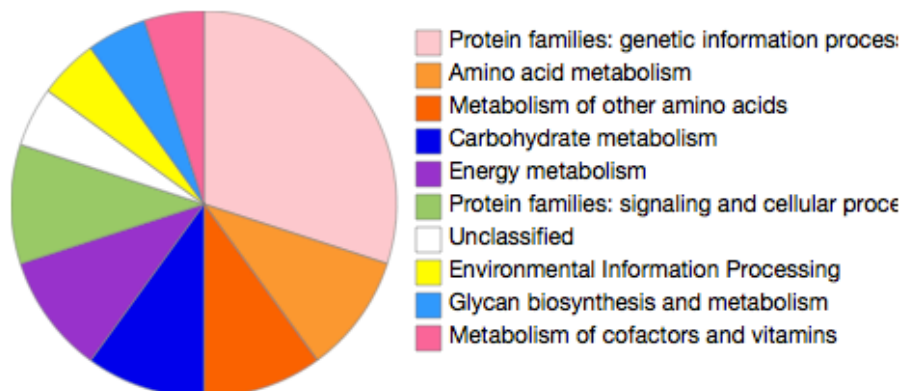


Figure 22. KEGG ontology distribution of overexpressed genes in functional groups. Functional analysis was performed on 36 overexpressed genes from *A. baumannii* ACICU treated with 10 $\mu\text{g/ml}$ GaPPIX and 56% were placed in functional categories. Genetic information processing was the most enriched group. This indicates a great deal of gene regulation related to the presence of GaPPIX. Metabolism of amino acids and carbohydrates were also enriched.

presence of GaPPIX in the extracellular environment affects the overall physiology of *A. baumannii*. This effect could be similar to that of heme B or the other gallium-containing compounds, additional studies will be required to parse the differences. Interestingly, genes on the plasmid pACICU1 were down (panel A of Figure 23) and the ACICU_p0019 gene, bla-oxa58, that is responsible for conferring carbapenem resistance was found to be significantly downregulated (Figure 23, panel B).

ICP-MS of whole cells

The quantity of biologically pertinent metals were measured by mass spectroscopy (Figure 24). The amount of gallium present was approaching the limit of quantitation for the instrument. The increase of GaPPIX directly correlated with the measured Ga present in digested whole bacterial cells. Mn and Cu showed significant decreases in concentration as Ga increased. The degree of quantification of these metals is uncertain as the concentrations are approaching parts per trillion. In spite of Mn and Cu having lower quantitation limits than other mid-atomic mass elements.

GaPPIX inhibits catalase activity

Considering the similarities in structures of GaPPIX to heme B, it is likely GaPPIX will be incorporated into pockets that are normally occupied by heme. This would lead to a dysfunction of the enzyme because Ga will not undergo the same redox as Fe and inhibit catalysis. In clinical assessments, *A. baumannii* is a catalase positive organism. This fact was tested to determine if the characteristic positive catalase reaction of *A. baumannii* was reduced in the presence of GaPPIX. Figure 25 panels A and B show the results of a single experiment for *A. baumannii* ATCC 19606^T and ACICU, respectively. The presence of 15 µg/ml GaPPIX causes a ten-fold reduction in catalase activity compared to cell lysates

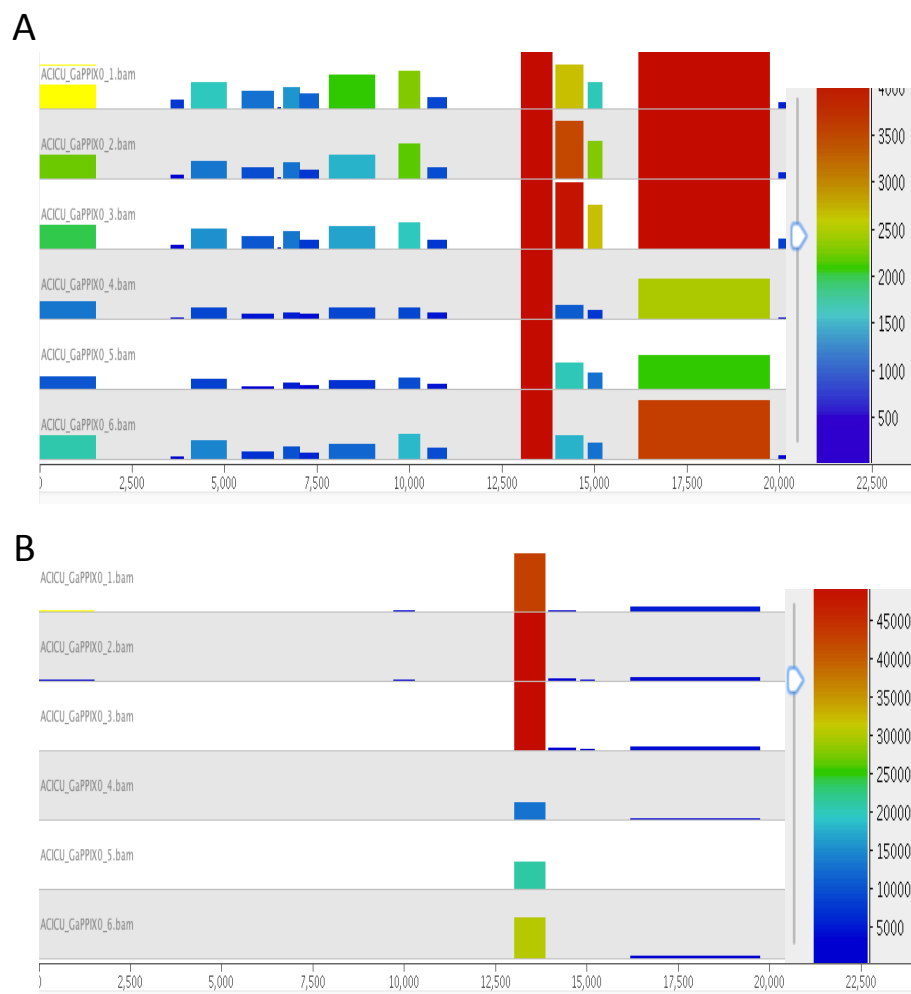


Figure 23. Differential gene expression of pACICU1. Gene expression is reduced in the presence of 10 $\mu\text{g/ml}$ GaPPIX as determined by RNASeq. A significant reduction of OXA-58 expression was seen when *A. baumannii* ACICU was grown in the presence of GaPPIX. The overall decreased expression of genes present on the plasmid is seen in panel A. Oxa-58 is a highly expressed gene in ACICU and contributes to the strains carbapenem resistance. The reduced expression of OXA-58 can be seen in panel B.

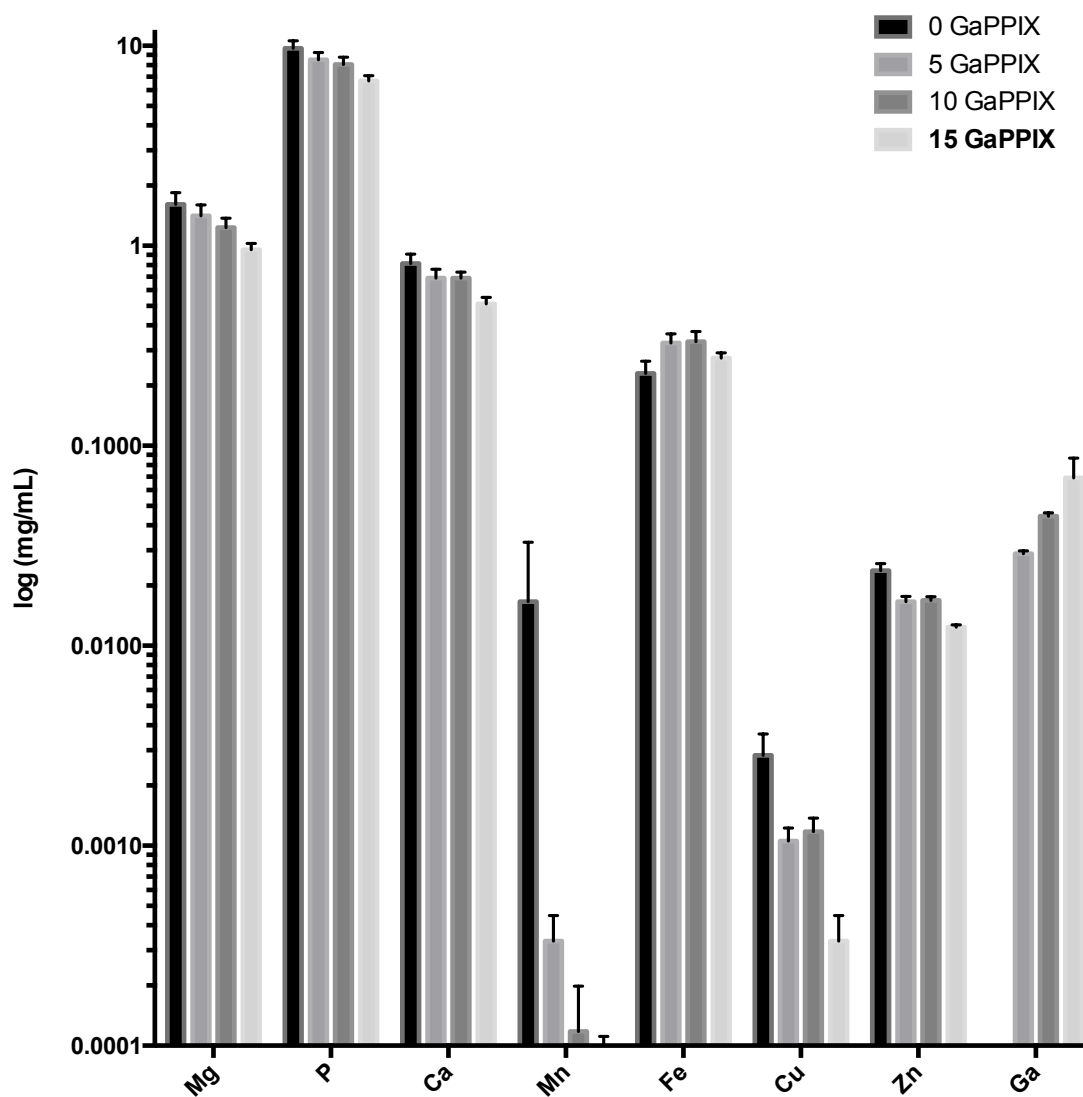


Figure 24. Quantification of biologically relevant metal ions in *A. baumannii* treated with GaPPIX. *A. baumannii* ACICU was grown with 0, 5, 10, or 15 $\mu\text{g/ml}$ GaPPIX in CAMH broth for 24 h. ICP-MS was used to simultaneously determine the concentration of metal ions commonly found in biological systems. Distinct inverse correlations appear, as Ga concentrations increase Mg, P, Mn, Ca, Cu, and Zn concentrations decrease. Interestingly Fe concentration did not decrease.

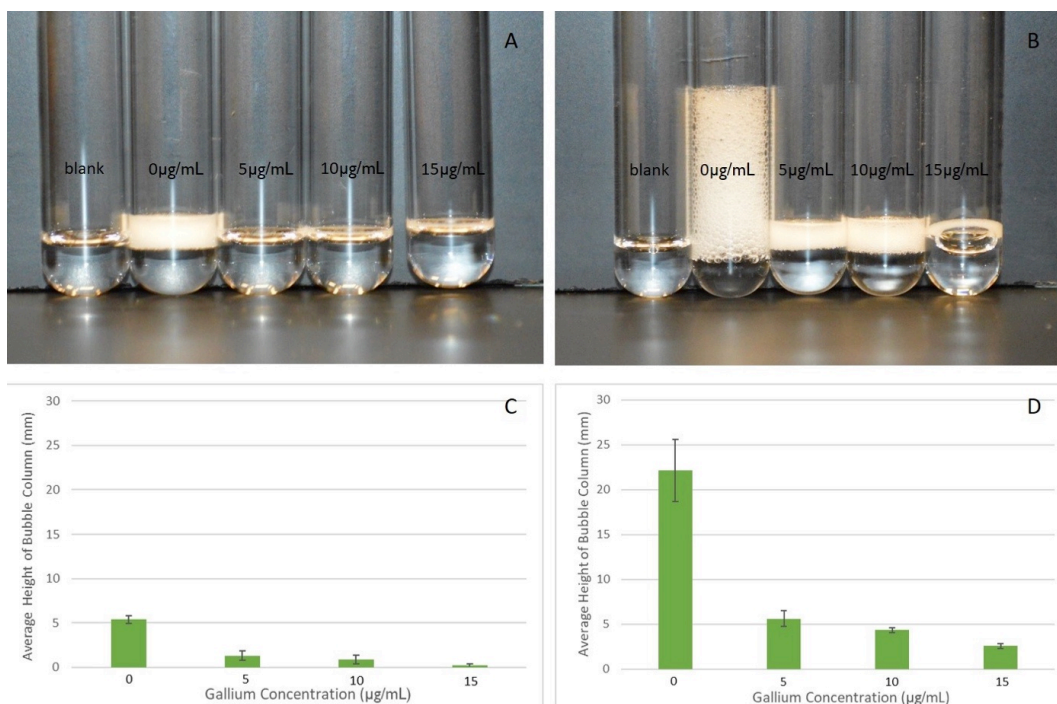


Figure 25. Catalase activity of normalized total cell lysates. The *A. baumannii* type strain, ATCC19606^T, and multidrug resistant strain, ACICU, were grown in CAMH broth with 0, 5, 10, or 15 µg/ml GaPPIX. Normalized total cell lysates were then assayed for catalase activity by the formation of bubbles in the presence of hydrogen peroxide. Catalase activity decreased almost 5 fold in the presence of 5 µg/ml of GaPPIX with no noticeable decrease in growth. These results suggest preferential inhibition of catalase over general toxicity to *A. baumannii*.

without GaPPIX in the media. Interestingly, the more recent and drug-resistant clinical isolate had approximately five times more catalase activity than the type strain.

The decreased enzyme activity supported further enrichment of catalase from cells grown with and without GaPPIX. Fractions with catalase activity were assayed using SDS-PAGE to visualize the enrichment of proteins (Figure 26, panel A). Panel B of Figure 26 shows the increase in activity after enrichment. It should be noted that catalase activity could not be measured for the cognate samples grown with 15 $\mu\text{g/ml}$ GaPPIX. It was recognized through the course of enrichment that chromatograms for proteins being size-fractionated by SEC were markedly different (Figure 26, Panel C). A primary peak with catalase activity (denoted with asterisk in Figure 26, panel C) present in protein fraction from cells grown without GaPPIX was notably absent in proteins from cells grown in the presence of GaPPIX. Catalase subunits are known to form homotetrameric complexes and this may help explain the characteristics of peaks seen in panel C (111). This may indicate that GaPPIX disrupts the quaternary structure of catalase.

GaPPIX docking to *Acinetobacter baumannii* catalase model

Computational modeling of surface binding of catalase by heme and GaPPIX identified many sites that one or both molecules exhibited favorable binding energies (Figure 27 panel A). Interestingly despite tremendous similarities in the molecules, only 5 of the top positions were favorable for both heme and GaPPIX. When considering the core binding associated with the tyrosine residue at position 415, heme and GaPPIX both had very favorable binding energies for this bona fide catalytic pocket of -9.3 kcal/mol and -8.3 kcal/mol, respectively (Figure 27, panels B and C).

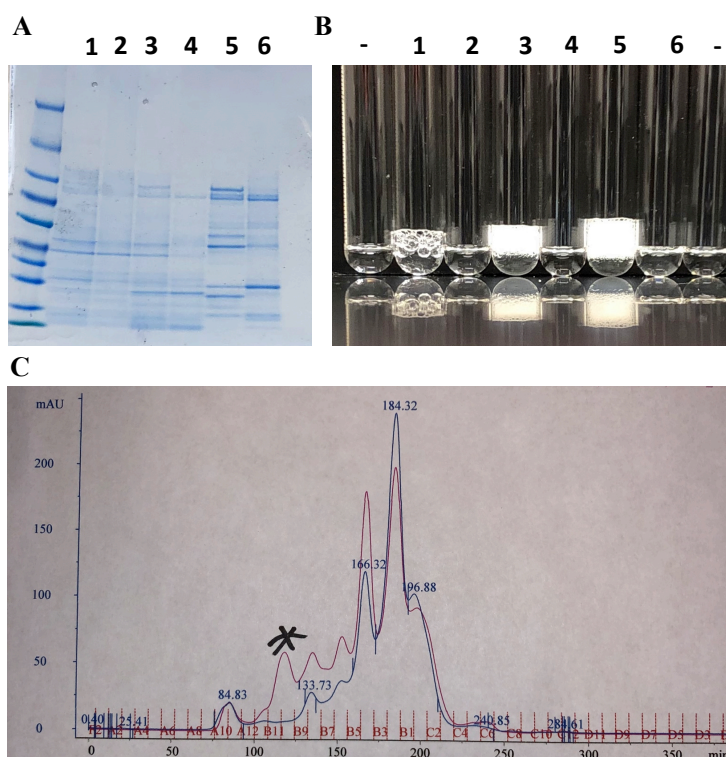


Figure 26. Effects of GaPPIX on enriched fractions with catalase activity. Panel A shows 1 µg of SDS-PAGE size fractionated of EtOH-fractionated total cell lysate (1 and 2), DEAE fractions collected based on catalase activity (3, 4), and SEC fractions collected based on catalase activity. For both panels A and B, fractions 1,3, and 5 were from *A. baumannii* ACICU grown in CAMH broth without GaPPIX and fractions 2, 4, and 6 were grown with 15 µg/ml GaPPIX. The enrichment resulted in increased concentration of higher weight proteins (panel A) and corresponding increased catalase activity from fractions 1, 3, and 5. GaPPIX fractions were collected based on activity of untreated samples. The SEC chromatogram in panel C shows a difference in profiles from the pink (0 µg/ml GaPPIX) and blue (15 µg/ml GaPPIX). A notable absence of a higher molecular weight peak is noted by an asterisk. These are representative of repeated measures.

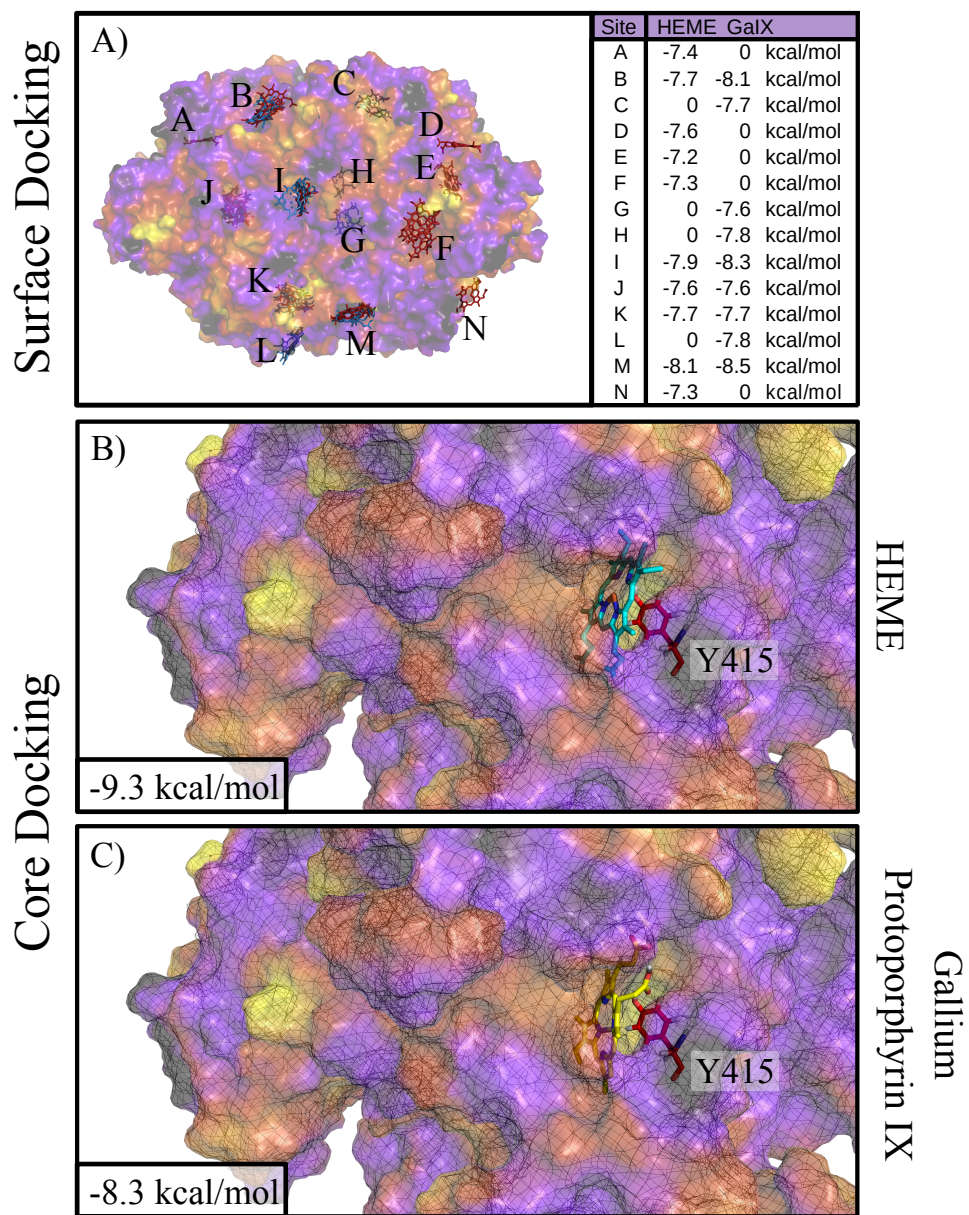


Figure 27. Molecular modeling of GaPPIX binding catalase. Surface binding affinities of heme B compared to GaPPIX are shown in A). The binding and affinities of heme and GaPPIX in the *bona fide* catalytic pocket can be seen in panels B) and C), respectively.

DISCUSSION

Our previous work has shown that iron acquisition is a critical *A. baumannii* virulence trait when tested using *ex vivo* and *in vivo* experimental infection models (53). Furthermore, we observed that the presence of hemin promoted the growth of ATCC 19606^T when cultured in the presence of the synthetic iron chelator 2,2'-dipyridyl. This response is independent of the expression of the acinetobactin-mediated system (69), which is the only complete siderophore-mediated system that allows this strain to prosper under iron-limiting conditions when tested using *in vitro*, *ex vivo* and *in vivo* experimental conditions (53). All these observations strongly indicate that this strain expresses siderophore and hemin transport and utilization functions that could be targeted to treat *A. baumannii* infections, particularly those caused by MDR isolates. Our initial work (69) and unpublished preliminary observations indicate that the antibacterial activity of Ga nitrate is variable among all strains tested and depends on the free-iron content of the medium as has been reported before (112). These findings and the recent report that hypervirulent strains tolerate high concentrations of Ga nitrate (113) prompted us to study the antibacterial activity of GaPPIX against an *A. baumannii* strain collection that includes isolates obtained from different sources at different times, representing different clonal lineages and expressing different antibiotic resistance phenotypes. Our work demonstrated that all tested *A. baumannii* strains, including the *A. baumannii* AB5075 MDR military isolate recently proposed as a working model strain (75), displayed similar MIC values, which ranged between 11 and 20 $\mu\text{g/ml}$, when tested under standard laboratory conditions following CLSI guidelines. Furthermore, our data show that GaPPIX susceptibility is independent of the free-iron content and active expression of siderophore-mediated iron

acquisition functions, while the presence of proteins in the *in vitro*, *ex vivo*, and *in vivo* susceptibility assays showed that they do not drastically affect the antibacterial activity of GaPPIX. Our data also showed that GaPPIX displays bactericidal activity relatively quickly, particularly when used at twice the MIC (40 $\mu\text{g/ml}$) under standard laboratory conditions, without causing any detectable cytotoxic effects on human cells and *G. mellonella* caterpillars. These findings are relevant since patients suffering from severe wound and soft tissue infections require immediate and effective antimicrobial chemotherapy. Equally concerning is the emergence of *A. baumannii* isolates with increased and/or altered virulence, such as the LAC-4 strain and isolates obtained from deadly cases of necrotizing fasciitis, respectively (49, 114, 115). These infections require immediate and effective antimicrobial treatment not only because of the devastating nature of these infections, but also because of the alarming MDR phenotype of the bacterial agents responsible for these diseases.

Our recent observation that the GaPPIX susceptible strain AYE produces the hydroxamate siderophore baumannoferrin (115, 116), but not acinetobactin or any catechol-derived siderophore due to a natural *entA* natural mutation (116) shows that the antibacterial activity of this non-ferric metalloporphyrin extends beyond those strains that produce and use acinetobactin to acquire iron. More recently, it was reported that the *A. baumannii* ATCC 17978 strain, which could rely on the production and use of acinetobactin and fimsbactins to grow under free-iron limiting conditions (117), is also susceptible to GaPPIX. These observations further demonstrate that the antibacterial activity of GaPPIX is independent of the type or number of high-affinity iron chelators produced by a particular isolate. Whether these conditions also apply to the LAC-4

hypervirulent strain, which proved to be susceptible to GaPPIX (113), is currently unknown since the siderophore-mediated iron acquisition system or systems expressed by this isolate is/are unknown.

The fact that GaPPIX displays bactericidal activity even in a medium such as LB agar, which has enough free iron to inhibit the expression of the acinetobactin system in the ATCC 19606^T strain (118), demonstrates the antibacterial effectiveness of this non-iron metalloporphyrin derivative even under conditions that inhibit the expression of critical iron-regulated bacterial functions, including those required for iron acquisition via siderophore- or hemin-uptake processes. However, the mechanisms by which GaPPIX is transported into the bacterial cytoplasm and affects iron metabolism are not fully understood. Pioneering work done by Stoljiljkovic *et al.* showed that Gram-negative bacteria, such as *Yersinia enterocolitica*, are susceptible to GaPPIX when expressing hemin acquisition functions under low iron conditions (65). Similarly, work done by Moriwaki *et al.* showed that the *S. aureus* IsdH-NEAT3 hemin receptor interacts with GaPPIX in a fashion similar to the natural hemin ligand (119). However, these results are unlike our observations that GaPPIX displays antibacterial activity against bacteria cultured in iron-rich media such as LB agar or broth, which should significantly inhibit the expression of hemin transport functions according to data collected with *Y. enterocolitica* and *E. coli* (65). Taken together, these results argue in favor of the hypothesis that GaPPIX could reach the periplasmic and cytoplasmic spaces either by using unknown low-affinity or TonB-independent hemin receptors or passive diffusion through bacterial membranes (65). Those hypotheses are supported by our data showing that the *A. baumannii* strains AYE and ATCC 17978, which lack the 8-gene cluster coding for putative hemin oxygenase and

hemin utilization proteins recently described by de Léséleuc *et al.* (113), and ATCC 19606^T, which does not have an identifiable *hemO* ortholog and therefore lacks this cluster, were as susceptible as the ACICU, SDF and AB0057 strains, all of which harbor the aforementioned 8-gene cluster. The GaPPIX susceptibility of AYE, ATCC 17978 and ATCC 19606^T could also be explained by the presence of a 12-gene cluster (iron-uptake gene cluster #2), which codes for predicted hemin uptake functions but lacks a canonical *hemO* ortholog, that is also present in the genome of the ACICU, SDF and AB0057 strains (70). Together, these observations indicate that the wide spread susceptibility of *A. baumannii* to GaPPIX is mediated by more than one cellular process, a property that will most likely not favor the emergence of resistant derivatives at least in the short term as it could be predicted from our work, which failed to detect a resistance phenotype using disk diffusion assays, broth MIC, or mutation rate studies.

Previous studies have described the role that host factors such as mucin plays in the regulation of the bacterial gene expression. It is interesting to juxtapose findings with mucin to GaPPIX since GaPPIX could be considered to be analogous to heme B. Heme B is very abundant in the circulatory system of humans and hemolymph in *G. mellonella*. This abundance makes it very likely that invading bacteria will come in contact with heme B and many pathogens have been shown to have a responsive regulatory network when heme is present in the environment. The consequence of providing GaPPIX in the presence of mucin may function to counter some of the pathogenic effects of this organism.

Ohneck *et al.* showed mucin triggers the expression of virulence-associated genes that are important in persistence and pathogenicity of *A. baumannii* by RNASeq. Specifically, the presence of mucin increased transcription of eight genes coding for

proteins involved in phenylacetate degradation. That was further supported by qRT-PCR transcriptional analysis which showed that *paaH* expression increased when grown in the presence of mucin particularly when grown in aerobic conditions. Also noted in Ohneck *et al.*, the putative *paaA-paaI* polycistronic operon had variation in gene expression. That study showed that the last eight genes were significantly induced, while the first five genes were not as responsive to mucin. This indicates this operon may have intricate gene expression regulation in response to external signals (120).

It has been suggested that products of the Paa pathway may also be involved in the reduction of reactive oxygen species in neutrophils (121), as this supports the correlation of overexpression of this pathway with increased virulence. In a zebrafish infection model the deletion of *paaA* was shown to lead to the increase in a neutrophil chemoattractant, phenylacetate, leading to increased clearing of bacteria burden (122). Expression of this novel *A. baumannii* virulence function results in a decrease host immune response. In contrast to mucin, GaPPIX leads to a decrease in phenylacetate catabolism gene expression of *paaA*, *paaI*, and *paaZ*. This decrease could lead to bacteria that are less capable of evading the innate immune system of the host and being less capable of dealing with oxidative stress.

The role of external appendages has been studied in *A. baumannii*. Pili such as the Csu have been shown to be important in adherence and affect motility. The importance of secretion systems has also been described including the type VI secretion system. Environmental stimuli have been shown to cause gene expression changes in these operons. For example, mucin up-regulated 13 genes related to the production of T6SS. All sequenced *A. baumannii* strains as well as non-pathogenic *Acinetobacter* strains show the

presence of core T6SS genes (123), but some *A. baumannii* isolates are unable to secrete the Hemolysin Correlated Protein (Hcp) effector protein without a functional T6SS (123). Like mucin, the presence of GaPPIX upregulates a gene encoding a type VI secretion protein. This is supported by previous studies that show mucin, extracellular phosphate, and iron concentrations lead to modulated expression of this secretion system (124, 125). The expression of the *P. aeruginosa* H2-T6SS, which modulates the interaction of this pathogen with eukaryotic host cells, is repressed by high iron concentrations via a Fur-mediated process (126). GaPPIX may lead to a response that is mediated by Fur transcriptional regulators, but in a way that is regulated differently than *P. aeruginosa* or *E. coli*. This is supported by WP_000471445.1, a type VI secretion protein, being upregulated 407-fold in the presence of GaPPIX. It should be noted that the functionality of *A. baumannii* ACICU type VI secretion system has not been determined experimentally, so the upregulation of this gene may not directly correlate to virulence toward eukaryotic cells. However, in *A. nosocomialis* the T6SS was shown to provide a competitive advantage against other prokaryotic cells (127). This may turn out to be true for ACICU as genes known to be important in single species biofilm, such as *csuA*, are upregulated in the presence of GaPPIX.

Interestingly, metal acquisition systems are repressed in the presence of GaPPIX. This supports the finding that GaPPIX is being utilized as other metals would in the cells. It is easy to speculate that the presence of GaPPIX leads to liberation of Ga from the porphyrin ring. This is likely a chokepoint in the heme metabolism of the cells and may be considered for further targeted study. Additionally, genes important in synthesis of siderophores are down regulated. This could support the liberation of Ga and subsequent

binding of Ga to FUR, which then represses iron acquisition. This could be the same mechanism for Ga binding to the zinc uptake regulator, ZUR.

Previous work with mucin showed that two ATCC 19606^T genes coding for proteases were up-regulated in the presence of mucin, including ClpX. Interestingly, the gene that codes for the proteolytic subunit of ClpXP, ClpP (A1S_0476), is necessary for persistence of *A. baumannii* within the lung (128). Since GaPPIX causes a decrease of the ClpA and ClpS encoding genes, it may be reasonable to hypothesize that the cells treated with GaPPIX may not be as fit to cause infection. These gene downregulations may be the explanation of the effectiveness of GaPPIX for decreasing *ex vivo* cell toxicity in A549 cells and *in vivo* survival of *G. mellonella*. Developing a further understanding of how *A. baumannii* interacts with the host factors, such as the interactions observed in this work with a heme B analog, GaPPIX, is crucial particularly for MDR isolates.

Conclusion

The World Health Organization listed carbapenem-resistant *Acinetobacter* as a critical group that is of high-priority for development of new antimicrobials makes these studies important (34). The increase in multidrug resistance frequency of *A. baumannii* has become a large threat for the healthcare system, highlighting the need for a new treatment. Determining the mode of function for a compound is critical in the discovery effort of new therapeutics. Our modeling supports GaPPIX association with the catalase of *A. baumannii* and is supported by a decrease in catalase activity. However, the RNASeq analysis suggest the bacteria may be sensing less oxidative stress. This could be the result of GaPPIX incorporating into the PAS domain of WP_000203146.1 of *A. baumannii* ACICU that is potentially a cyclic-GMP signaling protein because of the presence of a

GGDEF domain. This could be a regulatory step to allow *A. baumannii* to respond to changes in oxygen tension. This incidentally may be an important regulatory mechanism for *A. baumannii* to respond to oxidative stresses in the host. Additionally, RNASeq and to a lesser extent ICP-MS data suggest the active metal uptake is diminished in cells grown in the presence of GaPPIX. This may indicate GaPPIX is not only directly incorporated into active sites as a cofactor, but Ga is also liberated to be used as free ions. This likely leads the bacterial cells to sense higher internal metal ion concentrations while Ga interacts with ferric uptake regulator (FUR) and zinc uptake regulator (ZUR) transcription regulators. This would likely mean an increased binding of Ga and potentially Fe and Zn to these transcriptional regulators leading to repression of genes that actively acquire metal ions from the environment. FUR has also been shown to regulate virulence factors in *A. baumannii* (71, 129).

In summary, our work shows that *A. baumannii* strains are susceptible to GaPPIX regardless of their clonal lineages, site and time of isolation, antimicrobial resistance phenotypes, expression of iron acquisition systems, the iron content of the medium or the presence of proteins in *in vitro* and *ex vivo* tissue culture susceptibility assays. All these properties make this non-ferric metalloporphyrin derivative a potentially valuable and convenient antimicrobial agent that affects the viability of bacterial cells not only by interfering with critical physiological processes that depend on the redox properties of iron, but also making bacterial cells more susceptible to oxidative stresses due to the presence of reactive oxygen species produced by bacteria growing under aerobic conditions as well as by the host in response to infection due to decrease in superoxide dismutase transcripts and decreased catalase activity (65). However, the relatively low solubility of GaPPIX in

aqueous solutions is one obstacle that must be overcome before this compound is introduced as a viable therapeutic option, either alone or in synergistic combination with current antibiotics. Our findings suggest the possibility that GaPPIX may increase susceptibility to carbapenems and aminoglycosides, this would greatly aid treatment of *A. baumannii* infections, particularly those caused by isolates that are highly resistant to current antimicrobial agents. Additionally, the greater molecular understanding the physiologic response of *A. baumannii* to GaPPIX will add to the basic understanding of the heme and metal metabolism of the organism.

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Title: Antimicrobial Activity of Gallium Protoporphyrin IX against Acinetobacter baumannii Strains Displaying Different Antibiotic Resistance Phenotypes

Author: Brock A. Arivett, Steven E. Fiester, Emily J. Ohneck, William F. Penwell, Cynthia M. Kaufman, Ryan F. Relich, Luis A. Actis

Publication: Antimicrobial Agents and Chemotherapy

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APPENDIX C: Curriculum Vitae

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Educational Background:

Ph.D. 2015-current Middle Tennessee State University, Molecular and Bioscience
 M.S. 2014 Middle Tennessee State University, Biology
 B.S. 2005 Middle Tennessee State University, Microbiology, minor Chemistry

Relevant Appointments:

Graduate Teaching Assistant, 2015-Current, Department of Biology, Middle Tennessee State University, Murfreesboro, TN, Interim Chair: Dennis Mullen, Ph.D.
Research Associate, 2012 – 2015, Department of Microbiology, Miami University, Oxford, OH, Supervisor: Luis A. Actis, Ph.D.
Research Assistant, 2010 – 2012, Department of Microbiology, Miami University, Oxford, OH, Supervisor: Luis A. Actis, Ph.D.
Research Assistant I, 2007 – 2008, Center for Human Genetics Research DNA Core, Vanderbilt Medical Center, Nashville, TN, Supervisor: Cara B Sutcliffe

Current Research Focus:

- Elucidation of the factors dictating the virulence of multidrug resistant *Acinetobacter baumannii*
- Evaluation of the mechanisms by which *A. baumannii* acquires iron such as the uncharacterized hemin utilization system
- Translocation of virulence-associated proteins to the outer membrane and the secretion of virulence factors in *A. baumannii*
- Mechanisms of *A. baumannii* cytotoxicity to eukaryotic cells
- Use of novel therapeutics that target virulence mechanisms to treat *A. baumannii* infections

Publications :

1. **Arivett BA, Charnot-Katsikas A, Bethel C, Fiester SE, Actis LA.** 2020. Draft Genome Sequences of Two *Acinetobacter baumannii* Isolates from a Fatal Case of Necrotizing Fasciitis. *Microbiology Resource Announcements* **9**:e00047-00020.
2. **Ramirez MS, Penwell WF, Traglia GM, Zimble DL, Gaddy JA, Nikolaidis N, Arivett BA, Adams MD, Bonomo RA, Actis LA, Tolmasky ME.** 2019.

- Identification of Potential Virulence Factors in the Model Strain *Acinetobacter baumannii* A118. *Front Microbiol* **10**:1599.
3. **Hosain NA, Ghosh R, Bryant DL, Arivett BA, Farone AL, Kline PC.** 2019. Isolation, structure elucidation, and immunostimulatory activity of polysaccharide fractions from *Boswellia carterii frankincense* resin. *Int J Biol Macromol* **133**:76-85.
 4. **Ghosh R, Smith SA, Nwangwa EE, Arivett BA, Bryant DL, Fuller ML, Hayes D, Bowling JL, Nelson DE, DuBois JD, Altman E, Kline PC, Farone AL.** 2019. *Panax quinquefolius* (North American ginseng) cell suspension culture as a source of bioactive polysaccharides: Immunostimulatory activity and characterization of a neutral polysaccharide AGC1. *Int J Biol Macromol* **139**:221-232.
 5. **Fiester SE, Arivett BA, Beckett AC, Wagner BR, Ohneck EJ, Schmidt RE, Grier JT, Actis LA.** 2019. Miltefosine Reduces the Cytolytic Activity and Virulence of *Acinetobacter baumannii*. *Antimicrob Agents Chemother* **63**.
 6. **Chapagain P, Arivett B, Cleveland BM, Walker DM, Salem M.** 2019. Analysis of the fecal microbiota of fast- and slow-growing rainbow trout (*Oncorhynchus mykiss*). *BMC Genomics* **20**:788.
 7. **Alqahtani FM, Arivett BA, Taylor ZE, Handy ST, Farone AL, Farone MB.** 2019. Chemogenomic profiling to understand the antifungal action of a bioactive aurone compound. *PloS one* **14**.
 8. **Tran T, Chiem K, Jani S, Arivett BA, Lin DL, Lad R, Jimenez V, Farone MB, Debevec G, Santos R, Giulianotti M, Pinilla C, Tolmasky ME.** 2018. Identification of a small molecule inhibitor of the aminoglycoside 6'-N-acetyltransferase type Ib [AAC(6')-Ib] using mixture-based combinatorial libraries. *Int J Antimicrob Agents* **51**:752-761.
 9. **Ohneck EJ, Arivett BA, Fiester SE, Wood CR, Metz ML, Simeone GM, Actis LA.** 2018. Mucin acts as a nutrient source and a signal for the differential expression of genes coding for cellular processes and virulence factors in *Acinetobacter baumannii*. *PLoS One* **13**:e0190599.
 10. **Rumbo-Feal S, Perez A, Ramelot TA, Alvarez-Fraga L, Vallejo JA, Beceiro A, Ohneck EJ, Arivett BA, Merino M, Fiester SE, Kennedy MA, Actis LA, Bou G, Poza M.** 2017. Contribution of the *A. baumannii* A1S_0114 Gene to the Interaction with Eukaryotic Cells and Virulence. *Front Cell Infect Microbiol* **7**:108.
 11. **Park HS, Nelson DE, Taylor ZE, Hayes JB, Cunningham KD, Arivett BA, Ghosh R, Wolf LC, Taylor KM, Farone MB, Handy ST, Farone AL.** 2017. Suppression of LPS-induced NF-kappaB activity in macrophages by the synthetic aurone, (Z)-2-((5-(hydroxymethyl) furan-2-yl) methylene) benzofuran-3(2H)-one. *Int Immunopharmacol* **43**:116-128.
 12. **Kidane DT, Arivett BA, Crigler J, Vick EJ, Farone AL, Farone MB.** 2017. Draft Genome Sequence of *Gardnerella vaginalis* Strain ATCC 49145 Associated with Bacterial Vaginosis. *Genome Announc* **5**.
 13. **Mehari YT, Arivett BA, Farone AL, Gunderson JH, Farone MB.** 2016. Draft Genome Sequences of Two Novel Amoeba-Resistant Intranuclear Bacteria, "Candidatus *Berkiella cookevillensis*" and "Candidatus *Berkiella aquae*". *Genome Announc* **4**.

14. **Fiester SE, Arivett BA, Schmidt RE, Beckett AC, Ticak T, Carrier MV, Ghosh R, Ohneck EJ, Metz ML, Sellin Jeffries MK, Actis LA.** 2016. Iron-Regulated Phospholipase C Activity Contributes to the Cytolytic Activity and Virulence of *Acinetobacter baumannii*. *PLoS One* **11**:e0167068.
15. **Arivett BA, Ream DC, Fiester SE, Kidane D, Actis LA.** 2016. Draft Genome Sequences of *Escherichia coli* Isolates from Wounded Military Personnel. *Genome Announc* **4**.
16. **Arivett BA, Ream DC, Fiester SE, Kidane D, Actis LA.** 2016. Draft Genome Sequences of *Pseudomonas aeruginosa* Isolates from Wounded Military Personnel. *Genome Announc* **4**.
17. **Arivett BA, Ream DC, Fiester SE, Kidane D, Actis LA.** 2016. Draft Genome Sequences of *Acinetobacter baumannii* Isolates from Wounded Military Personnel. *Genome Announc* **4**.
18. **Ticak T, Hariraju D, Arcelay MB, Arivett BA, Fiester SE, Ferguson DJ, Jr.** 2015. Isolation and characterization of a tetramethylammonium-degrading *Methanococcoides* strain and a novel glycine betaine-utilizing *Methanobolus* strain. *Arch Microbiol* **197**:197-209.
19. **Penwell WF, DeGrace N, Tentarelli S, Gauthier L, Gilbert CM, Arivett BA, Miller AA, Durand-Reville TF, Joubran C, Actis LA.** 2015. Discovery and Characterization of New Hydroxamate Siderophores, Baumannoferrin A and B, produced by *Acinetobacter baumannii*. *Chembiochem* **16**:1896-1904.
20. **Lopez C, Arivett BA, Actis LA, Tolmasky ME.** 2015. Inhibition of AAC(6')-Ib-mediated resistance to amikacin in *Acinetobacter baumannii* by an antisense peptide-conjugated 2',4'-bridged nucleic acid-NC-DNA hybrid oligomer. *Antimicrob Agents Chemother* **59**:5798-5803.
21. **Fiester SE, Nwugo CC, Penwell WF, Neary JM, Beckett AC, Arivett BA, Schmidt RE, Geiger SC, Connerly PL, Menke SM, Tomaras AP, Actis LA.** 2015. Role of the carboxy terminus of SecA in iron acquisition, protein translocation, and virulence of the bacterial pathogen *Acinetobacter baumannii*. *Infect Immun* **83**:1354-1365.
22. **Arivett BA, Ream DC, Fiester SE, Mende K, Murray CK, Thompson MG, Kanduru S, Summers AM, Roth AL, Zurawski DV, Actis LA.** 2015. Draft Genome Sequences of *Klebsiella pneumoniae* Clinical Type Strain ATCC 13883 and Three Multidrug-Resistant Clinical Isolates. *Genome Announc* **3**.
23. **Arivett BA, Fiester SE, Ream DC, Centron D, Ramirez MS, Tolmasky ME, Actis LA.** 2015. Draft Genome of the Multidrug-Resistant *Acinetobacter baumannii* Strain A155 Clinical Isolate. *Genome Announc* **3**.
24. **Arivett BA, Fiester SE, Ohneck EJ, Penwell WF, Kaufman CM, Relich RF, Actis LA.** 2015. Antimicrobial Activity of Gallium Protoporphyrin IX against *Acinetobacter baumannii* Strains Displaying Different Antibiotic Resistance Phenotypes. *Antimicrob Agents Chemother* **59**:7657-7665.
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26. **Arivett B, Farone M, Masiragani R, Burden A, Judge S, Osinloye A, Minici C, Degano M, Robinson M, Kline P.** 2014. Characterization of inosine-uridine nucleoside hydrolase (RihC) from *Escherichia coli*. *Biochim Biophys Acta* **1844**:656-662.
27. **Zimblar DL, Arivett BA, Beckett AC, Menke SM, Actis LA.** 2013. Functional features of TonB energy transduction systems of *Acinetobacter baumannii*. *Infect Immun* **81**:3382-3394.
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31. **Gaddy JA, Arivett BA, McConnell MJ, Lopez-Rojas R, Pachon J, Actis LA.** 2012. Role of acinetobactin-mediated iron acquisition functions in the interaction of *Acinetobacter baumannii* strain ATCC 19606T with human lung epithelial cells, *Galleria mellonella* caterpillars, and mice. *Infect Immun* **80**:1015-1024.
32. **Mussi MA, Gaddy JA, Cabruja M, Arivett BA, Viale AM, Rasia R, Actis LA.** 2010. The opportunistic human pathogen *Acinetobacter baumannii* senses and responds to light. *J Bacteriol* **192**:6336-6345.

Presentations:

127th meeting of the Tennessee Academy of Science, Heme-like gallium protoporphyrin IX inhibits catalase activity in *Acinetobacter baumannii*, Martin, TN. November 2017

Miami University Center for Bioinformatics and Functional Genomics, Next Generation Sequencing workshop, Next Generation Sequencing in the CBF: My Seek, Brock Arivett, August 2014.

Awards:

Department of Energy Argonne National Laboratory Grant-in-kind. GUP-48369 Novel approach to inactivating *Acinetobacter*, a relevant human pathogen: How Gallium Protoporphyrin IX can disrupt Iron Homeostasis in *Acinetobacter baumannii*. 72 hours of beamline 9-1b usage for single-cell metallomics. Argonne, IL. October 2017.

5th Annual UAB Workshop on Metabolomics Travel Fellowship. National Institute of General Medical Sciences NIH Common Fund Metabolomics initiative. Birmingham AL. July 2017.

National Science Foundation Innovation Corps-537001. Microbial Biopanel for High-Throughput Screening to Facilitate Drug Discovery. Entrepreneurial Lead. 2016-2017.

Middle Tennessee State University. Bioremediation of Parking Lot Runoff for Stormwater Reclamation. Murfreesboro, TN. 2015-2017.

Honors:

American Society for Microbiology. Microbe Rapid Fire Talk (Outside the Box Therapeutics): Hexadecylphosphocholine Reduces *Acinetobacter Baumannii* Virulence. ASM Microbe Atlanta GA. Presented by Steve Fiester. June 2018.

Middle Tennessee State University. MTSU Business Plan Competition 2nd place. Murfreesboro, TN. April 2018.

Middle Tennessee State University. MTSU Business Plan Competition Best Written Business Plan. Murfreesboro, TN. April 2018.

Middle Tennessee State University. The Clouse-Elrod Foundation, Inc Agricultural Technology Award. Murfreesboro, TN. April 2018.

127th meeting of the Tennessee Academy of Science, First Place in the Microbiology Student Oral Presentation of Heme-like gallium protoporphyrin IX inhibits catalase activity in *Acinetobacter baumannii*, Martin, TN. November 2017.

Kentucky-Tennessee Branch of American Society for Microbiology. Outstanding Graduate Poster for Use of synchrotron radiation to investigate heme-like gallium protoporphyrin IX in *Acinetobacter baumannii*. Cookeville, TN. November 2017.

Middle Tennessee State University. MTSU Business Plan Competition Best Elevator Pitch. Murfreesboro, TN. April 2017.

Middle Tennessee State University. MTSU Business Plan Competition 4th place. Murfreesboro, TN. April 2016.

Peer Reviews:

Ad hoc reviewer: BioMed Research International, BMC Microbiology, Cellular Physiology and Biochemistry, Frontiers in Microbiology, International Journal of Biological Macromolecules

Publons: <https://publons.com/researcher/1599680/brock-arivett/metrics/>

Poster Presentations :

BA Arivett, JT Grier, JA Bigner, EJ Ohneck, ML Metz, CR Wood, RF Relich, LA Actis and SE Fiester. Increased twitching motility, biofilm formation and virulence of *Acinetobacter baumannii* associated with necrotizing fasciitis. American Society for Microbiology Microbe. San Francisco, CA. June 2019.

J Griner, **BA Arivett**, PC Kline. Kinetic Characterization for Inosine-Uridine Nucleoside Hydrolases (IU-NH) found in *Crithidia fasciculata*, *Arabidopsis thaliana*, and *Escherichia coli*. Kentucky-Tennessee Branch meeting of American Society for Microbiology. Murfreesboro, TN. November 2018.

R Ghosh, S Smith, E Nwangwa, **BA Arivett**, DL Bryant, E Altman, PC Kline, A Farone. *Panax quinquefolius* (North American Ginseng) Callus Culture as a Source of Bioactive Polysaccharides: Characterization of an Immunostimulatory Neutral Polysaccharide AGC1. American Society of Pharmacognosy. Lexington, KY. July 2018

SE Fiester, **BA Arivett**, AC Beckett, BR Wagner, EJ Ohneck, RE Schmidt, LA Actis. Hexadecylphosphocholine reduces *Acinetobacter baumannii* virulence. American Society for Microbiology Microbe. Atlanta, GA. June 2018.

BA Arivett, T Gerke, SE Fiester, A Farone. Use of synchrotron radiation to investigate heme-like gallium protoporphyrin IX in *Acinetobacter baumannii*. Kentucky-Tennessee Branch meeting of American Society for Microbiology. Cookeville, TN. November 2017.

EJ Ohneck, **BA Arivett**, SE Fiester, GM Simeone, MM Metz, LA Actis. Investigating the role of the *Acinetobacter baumannii* two-component system BfmRS in sensing and responding to mucin. 22nd Midwest Microbial Pathogenesis Conference, Indianapolis, IN. September 2015.

C Lopez, **BA Arivett**, LA Actis, ME Tolmasky. Antisense Inhibition of an Aminoglycoside Modifying Enzyme Expression Restores Susceptibility. Annual Biomedical Research Conference for Minority Students. Seattle, WA. 2015.

WF Penwell, N DeGrace, S Tentarelli, L Gauthier, CM Gilbert, **BA Arivett**, AA Miller, TF Durand-Reville, C Joubran and LA Actis. Discovery and characterization of novel hydroxamate siderophores, baumannoferrin –A and –B, produced by *Acinetobacter baumannii*. 115th General Meeting of the American Society for Microbiology, New Orleans, LA, May 2015.

A Tomaras, J Crandon, C McPherson, WF Penwell, SE Fiester, **BA Arivett**, LA Actis, D Nicolau. Lack of correlation between *in vitro* activity and *in vivo* efficacy of MB-1, a siderophore- β -lactam conjugate, against multiple strains of *Acinetobacter baumannii*. ICAAC 2014, Washington, DC, September 2014.

SC Geiger, **BA Arivett**, SE Fiester, LA Actis. Determining the antimicrobial mode of action of GaPPIX on *Acinetobacter baumannii*, 12th Annual Cell, Molecular and Structural Biology (CMSB) Symposium, Miami University, Oxford, OH, May 2014.

BA Arivett, WF Penwell, CM Kaufman, RF Relich, SE Fiester, LA Actis. Gallium protoporphyrin IX inhibits growth of multidrug-resistant *Acinetobacter baumannii*, 114th General Meeting of the American Society for Microbiology, Boston, MA, May 2014.

SE Fiester, CC Nwugo, WF Penwell, J Neary, AC Beckett, **BA Arivett**, PL Connerly, SM Menke, AP Tomaras, and LA Actis. Role of the carboxyl terminus of SecA in iron acquisition, protein translocation and virulence in the bacterial pathogen *Acinetobacter baumannii*, 114th General Meeting of the American Society for Microbiology, Boston, MA, May 2014.

SE Fiester, CC Nwugo, WF Penwell, JM Neary, AC Beckett, ML Metz, **BA Arivett**, PM Connerly, SM Menke, AP Tomaras, LA Actis. Role of the carboxyl terminus of SecA in iron acquisition, protein translocation and virulence of the bacterial pathogen *Acinetobacter baumannii*, Ohio Branch of the American Society for Microbiology Annual Meeting, Columbus, OH, April 2014.

SE Fiester, **BA Arivett**, AC Beckett, RE Schmidt, ML Metz, MV Carrier, LA Actis. Iron-regulated cytolitic activity plays a role in the virulence of the human pathogen *Acinetobacter baumannii*, Ohio Branch of the American Society for Microbiology Annual Meeting, Columbus, OH, April 2014.

GM Simeone, EJ Ohneck, **BA Arivett**, SE Fiester, LA Actis. *Acinetobacter baumannii* sensor kinase BfmS is involved in sensing pulmonary surfactant components, Ohio Branch of the American Society for Microbiology Annual Meeting, Columbus, OH, April 2014.

SC Geiger, **BA Arivett**, SE Fiester, LA Actis. Determining the antimicrobial mode of action of GaPPIX on *Acinetobacter baumannii*, Ohio Branch of the American Society for Microbiology Annual Meeting, Columbus, OH, April 2014.

WF Penwell, DL Zimble, AC Beckett, AM Richards, **BA Arivett**, EJ Ohneck, SE Fiester, DV Zurawski, LA Actis. Variability of virulence factors among *Acinetobacter baumannii* isolates obtained from wounded military personnel, 20th Annual Midwest Microbial Pathogenesis Conference, Columbus, OH, August 2013.

SE Fiester, CC Nwugo, J Neary, WF Penwell, **BA Arivett**, AC Beckett, S Menke, AP Tomaras, LA Actis. Role of the C-terminus of SecA in iron acquisition and protein translocation by *Acinetobacter baumannii* ATCC 19606^T, Cell, Molecular and Structural Biology (CMSB) Symposium, Miami University, Oxford, OH, May 2013.

ML Metz, **BA Arivett**, AC Beckett, MV Carrier, WF Penwell, SE Fiester, LA Actis. Phosphatidylcholine-specific phospholipase C activity is responsible for the hemolytic activity of *A. baumannii*, Cell, Molecular and Structural Biology (CMSB) Symposium, Miami University, Oxford, OH, May 2013.

SE Fiester, CC Nwugo, J Neary, WF Penwell, **BA Arivett**, AC Beckett, S Menke, AP Tomaras, LA Actis. Role of the C-terminus of SecA in iron acquisition and protein translocation by *Acinetobacter baumannii* ATCC 19606^T, Ohio Branch of the American Society for Microbiology Annual Meeting, Ashland, OH, April 2013.

ML Metz, **BA Arivett**, AC Beckett, MV Carrier, WF Penwell, SE Fiester, LA Actis. Phosphatidylcholine-specific phospholipase C activity is responsible for the hemolytic activity of *A. baumannii*, Ohio Branch of the American Society for Microbiology Annual Meeting, Ashland, OH April 2013.

ML Metz, **BA Arivett**, AC Beckett, MV Carrier, WF Penwell, SE Fiester, LA Actis. Examining hemolytic activity in *Acinetobacter baumannii*, Undergraduate Research Forum, Miami University, Oxford, OH, April 2013.

MK Sellin-Jeffries, **BA Arivett**, SE Fiester, DD Coffey, LM Thornton, AW Smith, LA Actis, JT Oris. Development of two small fish species, *Pimephales promelas* and *Cyprinodon variegates*, as model organisms for immunotoxicity, Society of Toxicology and Environmental Chemistry North America 33rd Annual Meeting, Long Beach, CA, November 2012.

SE Fiester, **BA Arivett**, MV Carrier, AC Beckett, LA Actis. Hemolytic activity of *Acinetobacter baumannii*, 19th Annual Midwest Microbial Pathogenesis Conference, Milwaukee, WI, September 2012.

BA Arivett, SE Fiester, WF Penwell, DL Zimble, LA Actis. Exploiting an iron vein: *Acinetobacter baumannii*'s acquisition of iron from erythrocytes, 19th Annual Midwest Microbial Pathogenesis Conference, Milwaukee, WI, September 2012.

EJ Ohneck, DL Zimble, SE Fiester, **BA Arivett**, LA Actis. *Acinetobacter baumannii* two-component regulatory system *bfmRS* is involved in biofilm formation on both biotic and abiotic surfaces, 19th Annual Midwest Microbial Pathogenesis Conference, Milwaukee, WI, September 2012.

AC Beckett, MV Carrier, **BA Arivett**, SE Fiester and LA Actis. Hemolytic activity of *Acinetobacter baumannii*, Cell, Molecular and Structural Biology (CMSB) Symposium, Miami University, Oxford, OH, June 2012.

MV Carrier, **BA Arivett**, SE Fiester, LA Actis. Analysis of uncharacterized hemolytic activity expressed by *Acinetobacter baumannii*, Ohio Branch of the American Society for Microbiology Annual Meeting, Mason, OH, April 2012.

WF Penwell, AC Beckett, **BA Arivett**, DL Zimble, LA Actis. Characterization of acinetobactin secretion in *Acinetobacter baumannii* ATCC 19606^T. 19th Annual Midwest Microbial Pathogenesis Conference, Milwaukee, Wisconsin, 2012.

A Richards, **BA Arivett**, C Nwugo, N Finely, LA Actis. Blue-light sensing protein in *Acinetobacter baumannii* mitigates oxidative stress and the role of glutathione. 18th Annual Midwest Microbial Pathogenesis Conference, Ann Arbor, Michigan, 2011.

WF Penwell, **BA Arivett**, LA Actis. Involvement of EntA in acinetobactin biosynthesis in *Acinetobacter baumannii*. 111th General Meeting of the American Society for Microbiology, New Orleans, Louisiana, 2011.

DL Zimbler, TM Park, **BA Arivett**, LA Actis. A *nfuA*-like gene deals with iron starvation and oxidative stress in *Acinetobacter baumannii*. 17th Annual Undergraduate Research Forum, Miami University, April 2011

A Richards, **BA Arivett**, JA Gaddy, LA Actis. Light at the end of the tunnel or a train: blue light induced virulence of *Acinetobacter baumannii* ATCC 17978. Annual meeting, Ohio Branch American Society for Microbiology, Ohio University, Athens, Ohio. 2011.

DL Zimbler, TM Park, **BA Arivett**, LA Actis. A *nfuA*-like gene deals with iron starvation and oxidative stress in *Acinetobacter baumannii* ATCC 17978. Annual meeting, Ohio Branch American Society for Microbiology, Ohio University, Athens, Ohio 2011

CC Nwugo, JA Gaddy, **BA Arivett**, DL Zimbler, LA Actis. Proteomic analysis of ethanol-induced virulence response in *Acinetobacter baumannii*. 17th Annual Midwest Microbial Pathogenesis Conference, Saint Louis, Missouri, 2010.

BA Arivett, WF Penwell, LA Actis. *Galleria mellonella* as a model to study the virulence role of the *Acinetobacter baumannii* acinetobactin-mediated iron acquisition system. 16th Annual Midwest Microbial Pathogenesis Conference, Purdue University, West Lafayette, IN, 2009.

BA Arivett, PC Kline, M Farone, A Farone, T Quinn, A Khaliq, Z Sinkala. Site-directed mutagenesis of nucleoside hydrolase from *Escherichia coli*. ACS 235th National meeting. New Orleans, LA, 2008.

BA Arivett. The Detection of *Mycobacterium* in a Water Distribution System and the Association with Amoebae. KY/TN ASM meeting. Corbin, TN, 2007.

BA Arivett. Site-directed mutagenesis of inosine-uridine hydrolase of *Escherichia coli*. ASM 107th general meeting. Toronto, Canada. 2007. (MTSU Graduate Travel Award)

BA Arivett. The isolation and identification of a bacterial pathogen from a hot tub amoebae. MTSU Scholars Day. Murfreesboro, TN 2005.

APPENDIX D: GaPPIX Supplement 1

TABLE S1 *A. baumannii* clinical isolates used in this work

Strain	Strain Name	Sequenced	Relevant characteristic(s)	Source	Ref.
406	ATCC 19606 ^T	*	Type strain	ATCC	(1)
1653	ATCC 19606 ^T t6		ATCC 19606 ^T <i>bauA</i> mutant	Lab stock	(2)
3069	ATCC 19606 ^T <i>entA</i>		ATCC 19606 ^T <i>entA</i> mutant	Lab stock	(2)
2488	ATCC 17978	*		ATCC	(1)
2886	LUH07672		EU clone III	L. Dijkshoorn	(3)
2887	LUH08809		EU clone I	L. Dijkshoorn	(4)
2888	LUH05875		EU clone III	L. Dijkshoorn	(5)
2889	LUH13000		EU clone II	L. Dijkshoorn	(6)
2890	RUH00134		EU clone II	L. Dijkshoorn	(6)
2891	RUH00875		EU clone I	L. Dijkshoorn	(6)
2997	AYE	*		ATCC	(7)
2998	SDF	*		ATCC	(7)
3022	A118	*		M. Tolmasky	(8)
3132	AB967			D. Zurawski	(9)
3133	AB2828			D. Zurawski	(9)
3134	AB3340			D. Zurawski	(9)
3135	AB3560			D. Zurawski	(9)
3136	AB3638			D. Zurawski	(9)
3137	AB3785			D. Zurawski	(9)
3138	AB3806			D. Zurawski	(9)
3139	AB3927			D. Zurawski	(9)
3140	AB4025			D. Zurawski	(9)
3141	AB4026			D. Zurawski	(9)
3142	AB4027			D. Zurawski	(9)
3143	AB4052			D. Zurawski	(9)
3144	AB4269			D. Zurawski	(9)
3145	AB4448			D. Zurawski	(9)
3146	AB4456			D. Zurawski	(9)
3147	AB4490			D. Zurawski	(9)
3148	AB4498			D. Zurawski	(9)
3149	AB4795			D. Zurawski	(9)
3150	AB4857	*		D. Zurawski	(9)
3151	AB4878			D. Zurawski	(9)
3152	AB4932			D. Zurawski	(9)
3153	AB4957			D. Zurawski	(9)
3154	AB4991			D. Zurawski	(9)
3155	AB5001			D. Zurawski	(9)
3156	AB5075	*		D. Zurawski	(9)
3157	AB5197			D. Zurawski	(9)
3158	AB5256	*		D. Zurawski	(9)
3159	AB5674			D. Zurawski	(9)
3160	AB5711	*		D. Zurawski	(9)

3161	ACICU	*	D. Zurawski	(10)
3284	AB0057	*	D. Zurawski	(11)

* Genome sequence is publicly available

TABLE S2 Automated microdilution MIC screening of GaPPIX against *A. baumannii* strains

Strain #	Strain name	Bacterial growth determined by OD ₆₀₀ *						
		GaPPIX added to the culture medium (µg/ml)						
		0	5	10	20	40	80	160
406	ATCC 19606 ^T	0.231	0.264	0.240	0.248	-0.002	0.006	0.003
2488	ATCC 17978	0.379	0.424	0.420	0.444	0.005	0.011	0.006
2886	LUH07672	0.426	0.309	0.357	0.379	-0.001	0.004	0.006
2887	LUH08809	0.493	0.365	0.327	0.339	0.000	0.009	0.022
2888	LUH05875	0.328	0.263	0.321	0.329	0.014	0.010	0.004
2889	LUH13000	0.407	0.428	0.388	0.363	0.202	0.075	-0.014
2890	RUH00134	0.341	0.380	0.394	0.409	0.003	0.005	0.006
2891	RUH00875	0.393	0.476	0.520	0.623	0.109	0.012	0.012
2997	AYE	0.417	0.499	0.522	0.575	0.115	0.003	0.009
2998	SDF	0.386	0.297	0.252	0.224	0.004	0.013	0.016
3022	A118	0.313	0.391	0.375	0.404	-0.001	0.001	-0.001
3132	AB967	0.439	0.505	0.526	0.598	0.023	0.008	0.003
3133	AB2828	0.134	0.160	0.161	0.169	0.002	0.006	0.006
3134	AB3340	0.354	0.409	0.389	0.434	0.003	0.004	0.005
3135	AB3560	0.362	0.411	0.376	0.443	0.001	0.002	0.005
3136	AB3638	0.404	0.425	0.508	0.516	0.000	0.003	0.007
3137	AB3785	0.480	0.511	0.549	0.566	0.003	0.005	0.010
3138	AB3806	0.368	0.406	0.391	0.450	0.009	0.001	0.005
3139	AB3927	0.444	0.512	0.508	0.471	0.001	0.003	0.005
3140	AB4025	0.342	0.344	0.353	0.382	0.044	0.012	0.008
3141	AB4026	0.382	0.417	0.422	0.419	0.013	0.009	0.006
3142	AB4027	0.412	0.371	0.249	0.272	0.023	0.006	0.035
3143	AB4052	0.196	0.379	0.398	0.427	0.002	0.013	0.011
3144	AB4269	0.389	0.409	0.438	0.514	0.002	0.006	0.003
3145	AB4448	0.459	0.556	0.529	0.622	0.011	0.020	0.018
3146	AB4456	0.432	0.570	0.569	0.585	0.005	0.014	0.024
3147	AB4490	0.328	0.378	0.379	0.406	0.063	0.021	0.007
3148	AB4498	0.420	0.473	0.473	0.497	0.001	0.016	0.007
3149	AB4795	0.307	0.403	0.377	0.302	0.003	0.009	0.007
3150	AB4857	0.496	0.540	0.498	0.636	0.003	0.025	0.020
3151	AB4878	0.504	0.530	0.550	0.624	0.010	0.023	0.023
3152	AB4932	0.306	0.383	0.393	0.418	0.006	0.010	0.003
3153	AB4957	0.475	0.565	0.518	0.669	0.031	0.067	0.017
3154	AB4991	0.299	0.344	0.348	0.398	0.004	0.004	0.003
3155	AB5001	0.511	0.575	0.414	0.625	0.051	0.013	0.019

3156	AB5075	0.467	0.516	0.433	0.619	0.002	0.010	0.009
3157	AB5197	0.415	0.498	0.473	0.526	0.008	0.019	0.007
3158	AB5256	0.463	0.533	0.470	0.548	0.079	0.035	0.026
3159	AB5674	0.347	0.405	0.349	0.459	0.003	0.004	0.001
3160	AB5711	0.254	0.261	0.156	0.312	0.021	0.013	0.021
3161	ACICU	0.357	0.301	0.178	0.205	0.017	0.072	0.004
3284	AB0057	0.358	0.404	0.386	0.445	0.016	0.018	0.001

*Average of three determinations done in triplicate each time (n=9)

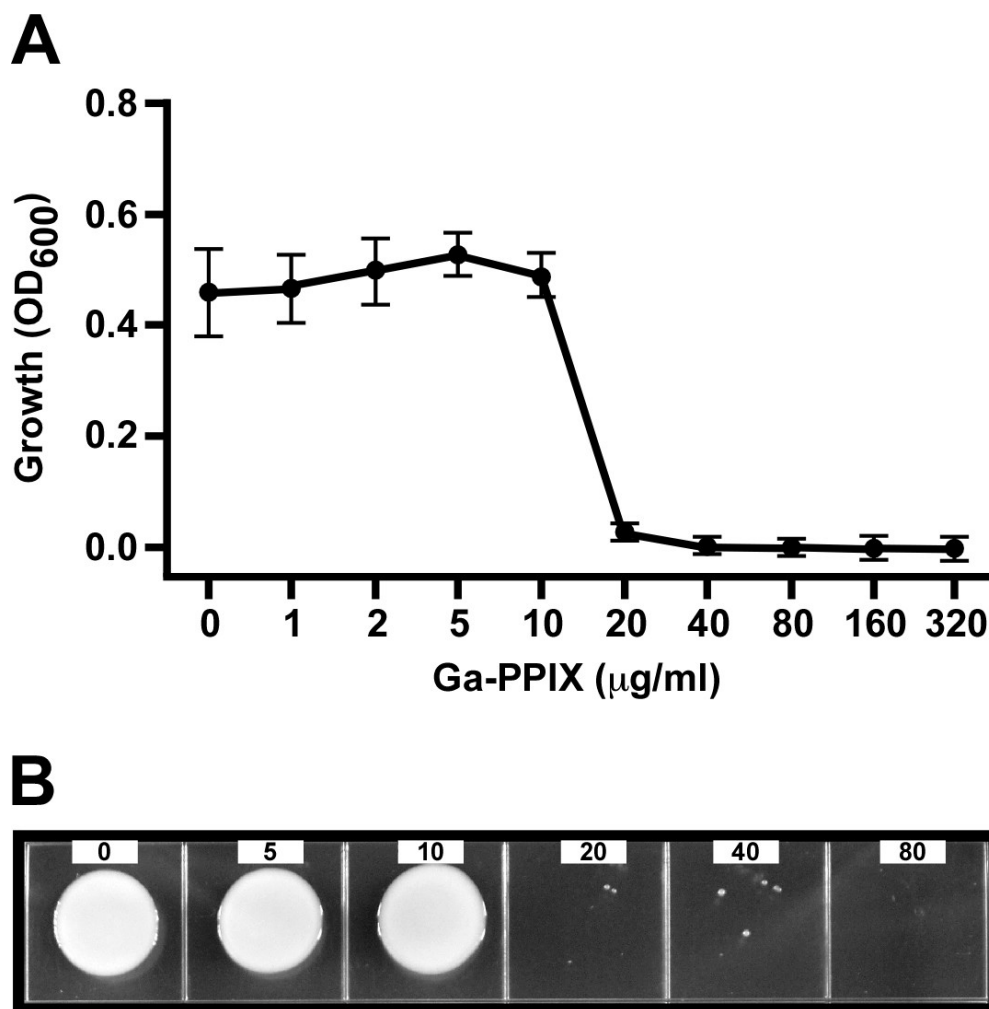


FIG S1. Susceptibility of *A. baumannii* AB5075 to GaPPIX. The MIC of GaPPIX was determined by the microdilution method in microtiter plates containing CAMHB inoculated with 10^5 AB5075 bacteria following CLSI guidelines (A). (B) MIC cultures were spotted onto MH agar to confirm cell viability.

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APPENDIX E: AR_0274 full annotation

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00001	CDS	hypothetical protein		
SAMN04901664_00002	CDS	1.14.13.- putative HTH-type	monooxygenase	
SAMN04901664_00003	CDS	transcriptional regulator		
SAMN04901664_00004	CDS	zapE	Cell division protein ZapE	
SAMN04901664_00005	CDS	glcB	2.3.3.9	Malate synthase G
SAMN04901664_00006	CDS	bltD	2.3.1.57	Spermine/spermidine acetyltransferase
SAMN04901664_00007	CDS	exbD_1	ExbD	
SAMN04901664_00008	CDS	exbD_2	ExbD	
SAMN04901664_00009	CDS	exbB_1	ExbB	
SAMN04901664_00010	CDS	hypothetical protein		
SAMN04901664_00011	CDS	cirA_1	Colicin I receptor	
SAMN04901664_00012	CDS	hypothetical protein		
SAMN04901664_00013	CDS	hbpA	Heme-binding protein A	
SAMN04901664_00014	CDS	oppA_1	OppA	
SAMN04901664_00015	CDS	prlC_1	3.4.24.70	Oligopeptidase A
SAMN04901664_00016	CDS	gsiC	Glutathione transport system permease protein GsiC	
SAMN04901664_00017	CDS	oppC	Oligopeptide transport system permease protein OppC	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00018	CDS	gsiA_1	3.6.3.-	Glutathione import ATP-binding protein GsiA
SAMN04901664_00019	CDS	hypothetical protein		
SAMN04901664_00020	CDS	hypothetical protein		
SAMN04901664_00021	CDS	cysQ	3.1.3.7	3'(2'),5'-bisphosphate nucleotidase CysQ
SAMN04901664_00022	CDS	hypothetical protein		
SAMN04901664_00023	CDS	rpsT	30S ribosomal protein S20	
SAMN04901664_00024	CDS	hypothetical protein		
SAMN04901664_00025	CDS	4.1.3.17	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase	
SAMN04901664_00026	CDS	hypothetical protein		
SAMN04901664_00027	CDS	yfeX_1	1.11.1.-	putative deferrochelataase/peroxidase YfeX
SAMN04901664_00028	CDS	hypothetical protein		
SAMN04901664_00029	CDS	mfd	3.6.4.-	Transcription-repair-coupling factor
SAMN04901664_00030	CDS	hypothetical protein		
SAMN04901664_00031	CDS	cyaA	4.6.1.1	Adenylate cyclase 1
SAMN04901664_00032	CDS	fdx_1	2Fe-2S ferredoxin	
SAMN04901664_00033	CDS	hscA	Chaperone protein HscA	
SAMN04901664_00034	CDS	hscB	Co-chaperone protein HscB	
SAMN04901664_00035	CDS	iscA	Iron-binding protein IscA	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00036	CDS	iscU	Iron-sulfur cluster assembly scaffold protein IscU	
SAMN04901664_00037	CDS	iscS	2.8.1.7	Cysteine desulfurase IscS
SAMN04901664_00038	CDS	iscR_1	HTH-type transcriptional regulator IscR	
SAMN04901664_00039	CDS	hypothetical protein		
SAMN04901664_00040	CDS	hypothetical protein		
SAMN04901664_00041	CDS	hupB	DNA-binding protein HU-beta	
SAMN04901664_00042	CDS	ppiD	5.2.1.8	Peptidyl-prolyl cis-trans isomerase D
SAMN04901664_00043	CDS	relR	RCS-specific HTH-type transcriptional activator RelR	
SAMN04901664_00044	CDS	alkB	1.14.15.3	Alkane 1-monoxygenase
SAMN04901664_00045	CDS	bcd	1.3.8.1	Acyl-CoA dehydrogenase, short-chain specific
SAMN04901664_00046	CDS	acdA	1.3.99.-	Acyl-CoA dehydrogenase
SAMN04901664_00047	CDS	ubiB_1	2.7.-.-	putative protein kinase UbiB
SAMN04901664_00048	CDS	hypothetical protein		
SAMN04901664_00049	CDS	ybaK	4.2.-.-	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase YbaK
SAMN04901664_00050	CDS	iucA	6.3.2.38	N(2)-citryl-N(6)-acetyl-N(6)-hydroxylysine synthase
SAMN04901664_00051	CDS	iucD_1	1.14.13.59	L-lysine N6-monoxygenase
SAMN04901664_00052	CDS	ribZ	Riboflavin transporter RibZ	
SAMN04901664_00053	CDS	iucC_1	6.3.2.39	Aerobactin synthase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00054	CDS	iucC_2	6.3.2.39	Aerobactin synthase
SAMN04901664_00055	CDS	hypothetical protein		
SAMN04901664_00056	CDS	4.1.3.17	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase	
SAMN04901664_00057	CDS	iutA_1	Ferric aerobactin receptor	
SAMN04901664_00058	CDS	hypothetical protein		
SAMN04901664_00059	CDS	hypothetical protein		
SAMN04901664_00060	CDS	hypothetical protein		
SAMN04901664_00061	CDS	mbtK	2.3.1.-	Lysine N-acyltransferase MbtK
SAMN04901664_00062	CDS	3.1.3.-	Phosphorylated carbohydrates phosphatase	
SAMN04901664_00063	CDS	hypothetical protein		
SAMN04901664_00064	CDS	cobP	2.7.1.156	Bifunctional adenosylcobalamin biosynthesis protein CobP
SAMN04901664_00065	CDS	cobT_1	2.4.2.21	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
SAMN04901664_00066	CDS	pspB	3.1.3.3	Putative phosphoserine phosphatase 2
SAMN04901664_00067	CDS	hypothetical protein		
SAMN04901664_00068	CDS	cobS_1	2.7.8.26	Adenosylcobinamide-GDP ribazoletransferase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00069	CDS	aroF_1	2.5.1.54	Phospho-2-dehydro-3-deoxyheptonate aldolase, Tyr-sensitive
SAMN04901664_00070	CDS	hypothetical protein		
SAMN04901664_00071	CDS	hypothetical protein		
SAMN04901664_00072	CDS	hypothetical protein		
SAMN04901664_00073	CDS	hypothetical protein		
SAMN04901664_00074	CDS	fhuE_1	FhuE receptor	
SAMN04901664_00075	CDS	lpxB	2.4.1.182	Lipid-A-disaccharide synthase
SAMN04901664_00076	CDS	yttP	putative HTH-type transcriptional regulator YttP	
SAMN04901664_00077	CDS	mdtN	MdtN	
SAMN04901664_00078	CDS	ybhF	putative ABC transporter ATP-binding protein YbhF	
SAMN04901664_00079	CDS	ybhS	Inner membrane transport permease YbhS	
SAMN04901664_00080	CDS	ybhR_1	Inner membrane transport permease YbhR	
SAMN04901664_00081	CDS	hypothetical protein		
SAMN04901664_00082	CDS	hypothetical protein		
SAMN04901664_00083	CDS	hypothetical protein		
SAMN04901664_00084	CDS	porB	P.IB	
SAMN04901664_00085	CDS	putative HIT-like protein		
SAMN04901664_00086	CDS	hypothetical protein		
SAMN04901664_00087	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00088	CDS	hypothetical protein		
SAMN04901664_00089	CDS	hypothetical protein		
SAMN04901664_00090	CDS	hypothetical protein		
SAMN04901664_00091	CDS	ycgJ	2.1.1.-	putative methyltransferase YcgJ
SAMN04901664_00092	CDS	phaC_1	2.3.1.-	Poly(3-hydroxyalkanoate) polymerase subunit PhaC
SAMN04901664_00093	CDS	metZ	2.5.1.-	O-succinylhomoserine sulfhydrilase
SAMN04901664_00094	CDS	hypothetical protein		
SAMN04901664_00095	CDS	ybaB	YbaB	
SAMN04901664_00096	CDS	recR	Recombination protein RecR	
SAMN04901664_00097	CDS	rnd_1	3.1.13.5	Ribonuclease D
SAMN04901664_00098	CDS	hypothetical protein		
SAMN04901664_00099	CDS	hypothetical protein		
SAMN04901664_00100	CDS	hypothetical protein		
SAMN04901664_00101	CDS	ycgL	Protein YcgL	
SAMN04901664_00102	CDS	hypothetical protein		
SAMN04901664_00103	CDS	hypothetical protein		
SAMN04901664_00104	CDS	hypothetical protein		
SAMN04901664_00105	CDS	trpB_1	4.2.1.20	Tryptophan synthase beta chain
SAMN04901664_00106	CDS	prnB	2.1.1.298	50S ribosomal protein L3
SAMN04901664_00107	CDS	arcC	4.2.3.5	glutamine methyltransferase Chorismate synthase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00108	CDS	cph2_1	Phytochrome-like protein cph2	
SAMN04901664_00109	CDS	tenA_1	3.5.99.2	Aminopyrimidine aminohydrolase
SAMN04901664_00110	CDS	acoR_1	Acetoin dehydrogenase operon transcriptional activator AcoR	
SAMN04901664_00111	CDS	lipA_1	2.8.1.8	Lipoyl synthase
SAMN04901664_00112	CDS	acoA	1.1.1.-	Acetoin:2,6- dichlorophenolindophenol oxidoreductase subunit alpha
SAMN04901664_00113	CDS	acoB	1.1.1.-	Acetoin:2,6- dichlorophenolindophenol oxidoreductase subunit beta
SAMN04901664_00114	CDS	pdhC	2.3.1.12	Dihydropyridyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex
SAMN04901664_00115	CDS	1.8.1.4	Dihydropyridyl dehydrogenase	
SAMN04901664_00116	CDS	budC_1	1.1.1.304	Diacetyl reductase [(S)-acetoin forming]
SAMN04901664_00117	CDS	gutB	1.1.1.14	Sorbitol dehydrogenase
SAMN04901664_00118	CDS	hypothetical protein	NR(I)	
SAMN04901664_00119	CDS	glnG_1		
SAMN04901664_00120	CDS	blh_1	3.-.-.-	Beta-lactamase hydrolase-like protein

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00121	CDS	blh_2	3.-.-.-	Beta-lactamase hydrolase-like protein
SAMN04901664_00122	CDS	hypothetical protein		
SAMN04901664_00123	CDS	hom_1	1.1.1.3	Homoserine dehydrogenase
SAMN04901664_00124	CDS	hypothetical protein		
SAMN04901664_00125	CDS	tetD	Transposon Tn10 TetD protein	
SAMN04901664_00126	CDS	hxIR_1	HTH-type transcriptional activator HxIR	
SAMN04901664_00127	CDS	azoR1	1.7.-.-	FMN-dependent NADH-azoreductase 1
SAMN04901664_00128	CDS	chrA1_1	Chromate transport protein	
SAMN04901664_00129	CDS	yvoA_1	HTH-type transcriptional repressor YvoA	
SAMN04901664_00130	CDS	aprA	1.8.99.2	Adenylylsulfate reductase subunit alpha
SAMN04901664_00131	CDS	aprB	Adenylylsulfate reductase subunit beta	
SAMN04901664_00132	CDS	ssuA_1	Putative aliphatic sulfonates-binding protein	
SAMN04901664_00133	CDS	cmpB	Bicarbonate transport system permease protein CmpB	
SAMN04901664_00134	CDS	tauB_1	3.6.3.36	Taurine import ATP-binding protein TauB
SAMN04901664_00135	CDS	hypothetical protein		
SAMN04901664_00136	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00137	CDS	kgtP_1	Alpha-ketoglutarate permease	
SAMN04901664_00138	CDS	fcuA_1	Ferrichrome receptor FcuA	
SAMN04901664_00139	CDS	aspA	4.3.1.1	Aspartate ammonia-lyase
SAMN04901664_00140	CDS	hypothetical protein		
SAMN04901664_00141	CDS	hypothetical protein		
SAMN04901664_00142	CDS	yjiE	HTH-type transcriptional regulator YjiE	
SAMN04901664_00143	CDS	pcpR	transcriptional activation protein	
SAMN04901664_00144	CDS	thlA_1	2.3.1.9	Acetyl-CoA acetyltransferase
SAMN04901664_00145	CDS	atoE	Putative short-chain fatty acid transporter	
SAMN04901664_00146	CDS	scoB	2.8.3.5	putative succinyl-CoA:3-ketoacid coenzyme A transferase subunit B
SAMN04901664_00147	CDS	scoA	2.8.3.5	putative succinyl-CoA:3-ketoacid coenzyme A transferase subunit A
SAMN04901664_00148	CDS	gltC_1	HTH-type transcriptional regulator GltC	
SAMN04901664_00149	CDS	hypothetical protein		
SAMN04901664_00150	CDS	hypothetical protein		
SAMN04901664_00151	CDS	uvrA	UvrABC system protein A	
SAMN04901664_00152	CDS	nemR_1	HTH-type transcriptional repressor NemR	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00153	CDS	qorA	1.6.5.5	Quinone oxidoreductase I
SAMN04901664_00154	CDS	hypothetical protein		
SAMN04901664_00155	CDS	ydgC		Inner membrane protein YdgC
SAMN04901664_00156	CDS	tenA_2	3.5.99.2	Aminopyrimidine aminohydrolase
SAMN04901664_00157	CDS	hypothetical protein		
SAMN04901664_00158	CDS	yajR		Inner membrane transport protein YajR
SAMN04901664_00159	CDS	ssb_1		Single-stranded DNA-binding protein
SAMN04901664_00160	CDS	hypothetical protein		
SAMN04901664_00161	CDS	hypothetical protein		
SAMN04901664_00162	CDS	sutR_1		HTH-type transcriptional regulator SutR
SAMN04901664_00163	CDS	gabP_1		GABA permease
SAMN04901664_00164	CDS	gabR_1		HTH-type transcriptional regulatory protein GabR
SAMN04901664_00165	CDS	puuE	2.6.1.19	4-aminobutyrate aminotransferase PuuE
SAMN04901664_00166	CDS	gabD_1	1.2.1.79	Succinate-semialdehyde dehydrogenase [NADP(+)] GabD
SAMN04901664_00167	CDS	dmlR_1		HTH-type transcriptional regulator DmlR
SAMN04901664_00168	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00169	CDS	yhhW_1	1.13.11.24	Quercetin 2,3-dioxygenase
SAMN04901664_00170	CDS	hypothetical protein		Erythromycin 3"-O-methyltransferase
SAMN04901664_00171	CDS	eryG	2.1.1.254	
SAMN04901664_00172	CDS	hypothetical protein		
SAMN04901664_00173	CDS	hypothetical protein		
SAMN04901664_00174	tRNA	tRNA-Thr(tgt)		
SAMN04901664_00175	CDS	ynfM		Inner membrane transport protein YnfM
SAMN04901664_00176	CDS	hcaR_1		Hca operon transcriptional activator HcaR
SAMN04901664_00177	CDS	hypothetical protein		
SAMN04901664_00178	CDS	hypothetical protein		
SAMN04901664_00179	CDS	hypothetical protein		
SAMN04901664_00180	CDS	yhdN	1.1.1.-	General stress protein 69
SAMN04901664_00181	CDS	adaA		Bifunctional transcriptional activator/DNA repair enzyme AdaA
SAMN04901664_00182	CDS	hypothetical protein	2.1.1.-	
SAMN04901664_00183	CDS	esiB_1		Secretory immunoglobulin A-binding protein EsiB
SAMN04901664_00184	CDS	hypothetical protein		
SAMN04901664_00185	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00186	CDS	hxIR_2	HTH-type transcriptional activator HxIR	
SAMN04901664_00187	CDS	ywrO	1.6.99.-	General stress protein 14
SAMN04901664_00188	CDS	hypothetical protein		
SAMN04901664_00189	CDS	hypothetical protein		
SAMN04901664_00190	tRNA	tRNA-Ser(gga)		
SAMN04901664_00191	CDS	kup	Low affinity potassium transport system protein kup	
SAMN04901664_00192	CDS	hypothetical protein		
SAMN04901664_00193	CDS	nucA	3.1.30.-	Nuclease
SAMN04901664_00194	CDS	eamB_1	protein	
SAMN04901664_00195	CDS	hypothetical protein		
SAMN04901664_00196	CDS	aqpZ2	Aquaporin Z 2	
SAMN04901664_00197	CDS	virS_1	HTH-type transcriptional regulator VirS	
SAMN04901664_00198	CDS	hypothetical protein		
SAMN04901664_00199	CDS	hisF	4.1.3.-	Imidazole glycerol phosphate synthase subunit HisF
SAMN04901664_00200	CDS	thrB	2.7.1.39	Homoserine kinase
SAMN04901664_00201	CDS	hypothetical protein		
SAMN04901664_00202	CDS	hypothetical protein		
SAMN04901664_00203	CDS	hypothetical protein		
SAMN04901664_00204	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00205	CDS	sutR_2	HTH-type transcriptional regulator SutR	
SAMN04901664_00206	CDS	hisA	5.3.1.16	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase
SAMN04901664_00207	CDS	rnd_2	3.1.13.5	Ribonuclease D
SAMN04901664_00208	CDS	yhaI_1	Inner membrane protein YhaI	
SAMN04901664_00209	CDS	hisH	2.4.2.-	Imidazole glycerol phosphate synthase subunit HisH
SAMN04901664_00210	CDS	hisB	Histidine biosynthesis bifunctional protein HisB	
SAMN04901664_00211	CDS	panM	PanD maturation factor	
SAMN04901664_00212	tRNA	tRNA tRNA-Phe(gaa)		
SAMN04901664_00213	tRNA	tRNA tRNA-Phe(gaa)		
SAMN04901664_00214	CDS	ypeA	2.3.1.-	Acetyltransferase YpeA
SAMN04901664_00215	CDS	catI	2.8.3.-	Succinyl-CoA:coenzyme A transferase
SAMN04901664_00216	CDS	envZ	2.7.13.3	Osmolarity sensor protein EnvZ
SAMN04901664_00217	CDS	ompR	Transcriptional regulatory protein OmpR	
SAMN04901664_00218	CDS	yugI	General stress protein 13	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00219	CDS	bicA_1	Bicarbonate transporter BicA	
SAMN04901664_00220	CDS	acr1	1.2.1.-	Fatty acyl-CoA reductase
SAMN04901664_00221	CDS	mgI	4.4.1.11	L-methionine gamma-lyase
SAMN04901664_00222	CDS	ettA	Energy-dependent translational throttle protein EttA	
SAMN04901664_00223	CDS	hypothetical protein		
SAMN04901664_00224	CDS	hypothetical protein		
SAMN04901664_00225	CDS	hypothetical protein		
SAMN04901664_00226	CDS	hypothetical protein		
SAMN04901664_00227	CDS	hypothetical protein		
SAMN04901664_00228	CDS	hypothetical protein		
SAMN04901664_00229	CDS	czcC	Cobalt-zinc-cadmium resistance protein CzcC	
SAMN04901664_00230	CDS	czcB	Cobalt-zinc-cadmium resistance protein CzcB	
SAMN04901664_00231	CDS	czcA_1	Cobalt-zinc-cadmium resistance protein CzcA	
SAMN04901664_00232	CDS	czcD_1	Metal cation efflux system protein CzcD	
SAMN04901664_00233	CDS	hypothetical protein		
SAMN04901664_00234	CDS	hypothetical protein		
SAMN04901664_00235	tRNA	tRNA tRNA-Glu(ttc)		
SAMN04901664_00236	tRNA	tRNA tRNA-Glu(ttc)		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00237	CDS	hypothetical protein		
SAMN04901664_00238	CDS	rocC_1	Amino-acid permease RocC	
SAMN04901664_00239	tRNA	tRNA-Glu(ttc)		
SAMN04901664_00240	tRNA	tRNA-Ala(ggc)		
SAMN04901664_00241	CDS	gltX	6.1.1.17	Glutamate--tRNA ligase
SAMN04901664_00242	CDS	hypothetical protein		
SAMN04901664_00243	CDS	sbp_1	Sulfate-binding protein	
SAMN04901664_00244	CDS	rsmH	2.1.1.199	Ribosomal RNA small subunit methyltransferase H
SAMN04901664_00245	CDS	ftsL	Cell division protein FtsL	
SAMN04901664_00246	CDS	ftsI	3.4.16.4	Peptidoglycan D,D-transpeptidase FtsI
SAMN04901664_00247	CDS	murE	6.3.2.13	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase
SAMN04901664_00248	CDS	murF	6.3.2.10	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase
SAMN04901664_00249	CDS	mraY	2.7.8.13	Phospho-N-acetylmuramoyl-pentapeptide-transferase
SAMN04901664_00250	CDS	hypothetical protein		
SAMN04901664_00251	CDS	rlmA	2.1.1.187	23S rRNA (guanine(745)-N(1))-methyltransferase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00252	CDS	mrca	Penicillin-binding protein 1A	
SAMN04901664_00253	CDS	ftsA_1	Cell division protein FtsA	
SAMN04901664_00254	CDS	hypothetical protein		
SAMN04901664_00255	CDS	hypothetical protein		
SAMN04901664_00256	CDS	hypothetical protein		
SAMN04901664_00257	CDS	pilQ	Type IV pilus biogenesis and competence protein PilQ	
SAMN04901664_00258	CDS	aroK	2.7.1.71	Shikimate kinase 1
SAMN04901664_00259	CDS	aroB	4.2.3.4	3-dehydroquinate synthase
SAMN04901664_00260	CDS	hypothetical protein		
SAMN04901664_00261	CDS	gltB	1.4.1.13	Glutamate synthase [NADPH] large chain
SAMN04901664_00262	CDS	gltD	1.4.1.13	Glutamate synthase [NADPH] small chain
SAMN04901664_00263	CDS	hypothetical protein		
SAMN04901664_00264	CDS	hypothetical protein		
SAMN04901664_00265	CDS	anoR	Transcriptional activator protein AnoR	
SAMN04901664_00266	CDS	hypothetical protein		
SAMN04901664_00267	CDS	abaI	2.3.1.184	Acyl-homoserine-lactone synthase
SAMN04901664_00268	CDS	yhjE_1	Inner membrane metabolite transport protein YhjE	
SAMN04901664_00269	CDS	crt_1	4.2.1.150	Short-chain-enoyl-CoA hydratase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00270	CDS	echA8_1	4.2.1.17	putative enoyl-CoA hydratase echA8
SAMN04901664_00271	CDS	mmgC_1	1.3.99.-	Acyl-CoA dehydrogenase
SAMN04901664_00272	CDS	acsA_1	6.2.1.1	Acetyl-coenzyme A synthetase
SAMN04901664_00273	CDS	mmsB	1.1.1.31	3-hydroxyisobutyrate dehydrogenase
SAMN04901664_00274	CDS	mmsA	1.2.1.27	Methylmalonate-semialdehyde dehydrogenase [acylating]
SAMN04901664_00275	CDS	gltR_1	HTH-type transcriptional regulator GltR	
SAMN04901664_00276	CDS	cycA_1	D-serine/D-alanine/glycine transporter	
SAMN04901664_00277	CDS	cycA_2	D-serine/D-alanine/glycine transporter	
SAMN04901664_00278	CDS	amnD	3.5.99.5	2-aminomuconate deaminase
SAMN04901664_00279	CDS	dadX_1	5.1.1.1	Alanine racemase, catabolic
SAMN04901664_00280	CDS	dadA1	1.4.99.-	D-amino acid dehydrogenase 1
SAMN04901664_00281	CDS	lrp_1	protein	
SAMN04901664_00282	CDS	hypothetical protein	Ferrichrome-iron receptor	
SAMN04901664_00283	CDS	fhuA_1	activity B	
SAMN04901664_00284	CDS	hypothetical protein		
SAMN04901664_00285	CDS	rraB_1		
SAMN04901664_00286	CDS	rluA_1	5.4.99.28	Ribosomal large subunit pseudouridine synthase A
SAMN04901664_00287	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00288	CDS	nepI_1	Purine ribonucleoside efflux pump NepI	
SAMN04901664_00289	CDS	comR_1	HTH-type transcriptional repressor ComR	
SAMN04901664_00290	CDS	1.-.-.-	putative oxidoreductase	3-oxoacyl-[acyl-carrier-protein] synthase 1
SAMN04901664_00291	CDS	fabB_1	2.3.1.41	
SAMN04901664_00292	CDS	hypothetical protein		
SAMN04901664_00293	CDS	hypothetical protein		
SAMN04901664_00294	CDS	hypothetical protein		
SAMN04901664_00295	CDS	hypothetical protein		
SAMN04901664_00296	CDS	hypothetical protein		
SAMN04901664_00297	CDS	acnD	4.2.1.117	2-methylcitrate dehydratase (2-methyl-trans-aconitate forming)
SAMN04901664_00298	CDS	prpC	2.3.3.5	2-methylcitrate synthase
SAMN04901664_00299	CDS	prpB	4.1.3.30	2-methylisocitrate lyase
SAMN04901664_00300	CDS	gntR_1	operon transcriptional repressor	
SAMN04901664_00301	CDS	tyrB	2.6.1.57	Aromatic-amino-acid aminotransferase
SAMN04901664_00302	CDS	dld	1.1.1.28	D-lactate dehydrogenase
SAMN04901664_00303	CDS	lldD	1.1.-.-	L-lactate dehydrogenase
SAMN04901664_00304	CDS	lldR_1	dehydrogenase operon regulatory protein	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00305	CDS	lldP	L-lactate permease	
SAMN04901664_00306	CDS	algC_1	5.4.2.2	Phosphomannomutase/phosphoglucomutase
SAMN04901664_00307	CDS	galE_1	5.1.3.2	UDP-glucose 4-epimerase
SAMN04901664_00308	CDS	pgi	5.3.1.9	Glucose-6-phosphate isomerase
SAMN04901664_00309	CDS	rkpK	1.1.1.22	UDP-glucose 6-dehydrogenase
SAMN04901664_00310	CDS	galU	2.7.7.9	UTP--glucose-1-phosphate uridylyltransferase
SAMN04901664_00311	CDS	epsL	2.-.-.-	putative sugar transferase EpsL
SAMN04901664_00312	CDS	wbbD	2.4.1.303	UDP-Gal:alpha-D-GlcNAc-diphosphoundecaprenol beta-1,3-galactosyltransferase
SAMN04901664_00313	CDS	hypothetical protein		
SAMN04901664_00314	CDS	hypothetical protein		
SAMN04901664_00315	CDS	hypothetical protein		
SAMN04901664_00316	CDS	hypothetical protein		
SAMN04901664_00317	CDS	hypothetical protein		
SAMN04901664_00318	CDS	pseI	2.5.1.97	Pseudaminic acid synthase
SAMN04901664_00319	CDS	hypothetical protein		
SAMN04901664_00320	CDS	pseG	3.6.1.57	UDP-2,4-diacetamido-2,4,6-trideoxy-beta-L-altropyranose hydrolase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00321	CDS	neuA	2.7.7.82	CMP-N,N'-diacetyllegionaminic acid synthase
SAMN04901664_00322	CDS	pseC	2.6.1.92	UDP-4-amino-4,6-dideoxy-N-acetyl-beta-L-altrosamine transaminase
SAMN04901664_00323	CDS	pseB	4.2.1.115	UDP-N-acetylglucosamine 4,6-dehydratase (inverting)
SAMN04901664_00324	CDS	wbpA	1.1.1.136	UDP-N-acetyl-D-glucosamine 6-dehydrogenase
SAMN04901664_00325	CDS	hypothetical protein		
SAMN04901664_00326	CDS	ptp	3.1.3.48	Low molecular weight protein-tyrosine-phosphatase Ptp
SAMN04901664_00327	CDS	ptk	2.7.10.-	Tyrosine-protein kinase ptk
SAMN04901664_00328	CDS	fkpA_1	5.2.1.8	putative FKBP-type peptidyl-prolyl cis-trans isomerase FkpA
SAMN04901664_00329	CDS	fkpA_2	5.2.1.8	putative FKBP-type peptidyl-prolyl cis-trans isomerase FkpA
SAMN04901664_00330	CDS	murJ	putative lipid II flippase	MurJ
SAMN04901664_00331	CDS	ampD	3.5.1.28	1,6-anhydro-N-acetylmuramyl-L-alanine amidase AmpD
SAMN04901664_00332	CDS	nadC	2.4.2.19	Nicotinate-nucleotide pyrophosphorylase [carboxylating]

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00333	CDS	hypothetical protein		
SAMN04901664_00334	CDS	plcN_1	3.1.4.3	Non-hemolytic phospholipase C
SAMN04901664_00335	CDS	plcN_2	3.1.4.3	Non-hemolytic phospholipase C
SAMN04901664_00336	CDS	rph	2.7.7.56	Ribonuclease PH
SAMN04901664_00337	CDS	desA3_1	1.14.19.-	NADPH-dependent stearyl-CoA 9-desaturase
SAMN04901664_00338	CDS	1.-.-.-	NADPH oxidoreductase	
SAMN04901664_00339	CDS	fabR_1	HTH-type transcriptional repressor FabR	
SAMN04901664_00340	CDS	hypothetical protein		
SAMN04901664_00341	CDS	dsbA	Thiol:disulfide interchange protein DsbA	
SAMN04901664_00342	CDS	ubiG_1	2.1.1.222	Ubiquinone biosynthesis O-methyltransferase
SAMN04901664_00343	CDS	gph_1	3.1.3.18	Phosphoglycolate phosphatase
SAMN04901664_00344	CDS	yciK	1.-.-.-	putative oxidoreductase YciK
SAMN04901664_00345	CDS	hypothetical protein		
SAMN04901664_00346	CDS	hypothetical protein		
SAMN04901664_00347	CDS	argA	2.3.1.1	Amino-acid acetyltransferase
SAMN04901664_00348	CDS	ssuA_2	Putative aliphatic sulfonates-binding protein	
SAMN04901664_00349	CDS	ssuA_3	Putative aliphatic sulfonates-binding protein	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00350	CDS	ssuD_1	1.14.14.5	Alkanesulfonate monooxygenase
SAMN04901664_00351	CDS	ssuC_1	transport permease protein SsuC	
SAMN04901664_00352	CDS	ssuB_1	3.6.3.-	Aliphatic sulfonates import ATP-binding protein SsuB
SAMN04901664_00353	CDS	rutR	HTH-type transcriptional regulator RutR	
SAMN04901664_00354	CDS	mtnN_1	3.2.2.9	5'-methylthioadenosine/S- adenosylhomocysteine nucleosidase
SAMN04901664_00355	CDS	hypothetical protein		
SAMN04901664_00356	CDS	ribF	RibF	
SAMN04901664_00357	CDS	ileS	6.1.1.5	Isoleucine--tRNA ligase
SAMN04901664_00358	CDS	lspA	3.4.23.36	Lipoprotein signal peptidase
SAMN04901664_00359	CDS	fkpB	5.2.1.8	FKBP-type 16 kDa peptidyl- prolyl cis-trans isomerase
SAMN04901664_00360	CDS	azr	1.7.-.-	FMN-dependent NADPH- azoreductase
SAMN04901664_00361	rRNA	5S ribosomal RNA		
SAMN04901664_00362	CDS	uppP	3.6.1.27	Undecaprenyl-diphosphatase
SAMN04901664_00363	CDS	virF	Virulence regulon transcriptional activator VirF	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00364	CDS	ppsC	2.3.1.41	Phthiocerol/phenolphthiocerol synthesis polyketide synthase type I PpsC
SAMN04901664_00365	CDS	hchA_1	4.2.1.130	Molecular chaperone Hsp31 and glyoxalase 3
SAMN04901664_00366	tRNA	tRNA-Arg(cct)		
SAMN04901664_00367	CDS	aroP_1		Aromatic amino acid transport protein AroP
SAMN04901664_00368	CDS	prpF	5.3.3.-	2-methyl-aconitate isomerase
SAMN04901664_00369	CDS	ispA	2.5.1.10	Farnesyl diphosphate synthase
SAMN04901664_00370	CDS	hypothetical protein		
SAMN04901664_00371	CDS	hfIK		HfIK
SAMN04901664_00372	CDS	hypothetical protein		
SAMN04901664_00373	CDS	putative NTE family protein		
SAMN04901664_00374	CDS	hypothetical protein		
SAMN04901664_00375	CDS	hypothetical protein		
SAMN04901664_00376	CDS	hypothetical protein		
SAMN04901664_00377	CDS	eptA_1	2.7.-.-	Phosphoethanolamine transferase EptA
SAMN04901664_00378	CDS	qseB_1		
SAMN04901664_00379	CDS	qseC_1		
SAMN04901664_00380	CDS	hypothetical protein		
			Transcriptional regulatory protein QseB	
			2.7.13.3	Sensor protein QseC

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00381	CDS	amtB_1	Ammonia channel	
SAMN04901664_00382	CDS	cmpR_1	HTH-type transcriptional activator CmpR	
SAMN04901664_00383	CDS	hypothetical protein		
SAMN04901664_00384	CDS	hypothetical protein		
SAMN04901664_00385	CDS	cmoA_1	2.1.1.-	tRNA (cmo5U34)-methyltransferase
SAMN04901664_00386	CDS	vals	6.1.1.9	Valine--tRNA ligase
SAMN04901664_00387	CDS	hypothetical protein		
SAMN04901664_00388	CDS	fabG_1	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase FabG
SAMN04901664_00389	CDS	hypothetical protein		
SAMN04901664_00390	CDS	hypothetical protein		
SAMN04901664_00391	CDS	hypothetical protein		
SAMN04901664_00392	CDS	oprM_1	Outer membrane protein OprM	
SAMN04901664_00393	CDS	mexB_1	MexB	
SAMN04901664_00394	CDS	acrA	AcrA	
SAMN04901664_00395	CDS	hypothetical protein		
SAMN04901664_00396	CDS	hypothetical protein		
SAMN04901664_00397	CDS	sdsA	2.5.1.84	All-trans-nonaprenyl-diphosphate synthase (geranyl-diphosphate specific)
SAMN04901664_00398	CDS	rplU	50S ribosomal protein L21	
SAMN04901664_00399	CDS	rpmA	50S ribosomal protein L27	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00400	CDS	lola_1	Outer-membrane lipoprotein carrier protein	
SAMN04901664_00401	CDS	hypothetical protein		
SAMN04901664_00402	CDS	serS	6.1.1.11	Serine--tRNA ligase
SAMN04901664_00403	CDS	cysG	Siroheme synthase	
SAMN04901664_00404	CDS	trmL	2.1.1.207	tRNA (cytidine(34)-2'-O)-methyltransferase
SAMN04901664_00405	CDS	yybR_1	putative HTH-type transcriptional regulator YybR	
SAMN04901664_00406	CDS	pnpB_1	1.6.5.2	p-benzoquinone reductase
SAMN04901664_00407	CDS	plaP	importer PlaP	
SAMN04901664_00408	CDS	dhaT_1	1.1.1.202	1,3-propanediol dehydrogenase
SAMN04901664_00409	CDS	hypothetical protein		
SAMN04901664_00410	CDS	lipB	2.3.1.181	Octanoyltransferase
SAMN04901664_00411	CDS	hypothetical protein		
SAMN04901664_00412	CDS	rpoD	RpoD	
SAMN04901664_00413	CDS	hypothetical protein		
SAMN04901664_00414	CDS	hypothetical protein		
SAMN04901664_00415	CDS	hypothetical protein		
SAMN04901664_00416	CDS	glpE_1	2.8.1.1	Thiosulfate sulfurtransferase GlpE
SAMN04901664_00417	CDS	hypothetical protein		
SAMN04901664_00418	CDS	gltA_1	2.3.3.16	Citrate synthase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00419	CDS	sdhC	Succinate dehydrogenase cytochrome b556 subunit	
SAMN04901664_00420	CDS	sdhD	Succinate dehydrogenase hydrophobic membrane anchor subunit	
SAMN04901664_00421	CDS	sdhA	1.3.5.1	Succinate dehydrogenase flavoprotein subunit
SAMN04901664_00422	CDS	sdhB	1.3.5.1	Succinate dehydrogenase iron-sulfur subunit
SAMN04901664_00423	CDS	sucA	1.2.4.2	2-oxoglutarate dehydrogenase E1 component
SAMN04901664_00424	CDS	sucB	2.3.1.61	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex
SAMN04901664_00425	CDS	lpdG	1.8.1.4	Dihydrolipoyl dehydrogenase
SAMN04901664_00426	CDS	sucC	6.2.1.5	Succinate--CoA ligase [ADP-forming] subunit beta
SAMN04901664_00427	CDS	sucD	6.2.1.5	Succinate--CoA ligase [ADP-forming] subunit alpha
SAMN04901664_00428	CDS	trpS2	6.1.1.2	Tryptophan--tRNA ligase 2
SAMN04901664_00429	CDS	yedI	Inner membrane protein YedI	
SAMN04901664_00430	CDS	hypothetical protein		
SAMN04901664_00431	CDS	nhaP	Na(+)/H(+) antiporter NhaP	
SAMN04901664_00432	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00433	CDS	hypothetical protein		
SAMN04901664_00434	CDS	hypothetical protein		
SAMN04901664_00435	CDS	lysO	Lysine exporter LysO	
SAMN04901664_00436	CDS	pyrF	4.1.1.23	Orotidine 5'-phosphate decarboxylase
SAMN04901664_00437	CDS	lapA	Lipopolysaccharide assembly protein A	
SAMN04901664_00438	CDS	ihfB	beta	
SAMN04901664_00439	CDS	rpsA	30S ribosomal protein S1	
SAMN04901664_00440	CDS	cmk	2.7.4.25	Cytidylate kinase
SAMN04901664_00441	CDS	hypothetical protein		
SAMN04901664_00442	CDS	tadA	3.5.4.33	tRNA-specific adenosine deaminase
SAMN04901664_00443	CDS	crt_2	4.2.1.150	Short-chain-enoyl-CoA hydratase
SAMN04901664_00444	CDS	ung	3.2.2.27	Uracil-DNA glycosylase
SAMN04901664_00445	CDS	hypothetical protein		
SAMN04901664_00446	CDS	gspK	Putative type II secretion system protein K	
SAMN04901664_00447	CDS	xcpW	protein J	
SAMN04901664_00448	CDS	xcpV	protein I	
SAMN04901664_00449	CDS	pulG	protein G	
SAMN04901664_00450	CDS	hypothetical protein		
SAMN04901664_00451	CDS	ycfH	3.1.-.-	putative metal-dependent hydrolase YcfH

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00452	CDS	hypothetical protein		
SAMN04901664_00453	CDS	dnaX_1	2.7.7.7	DNA polymerase III subunit tau
SAMN04901664_00454	CDS	kdsB	2.7.7.38	3-deoxy-manno-octulosonate cytidyltransferase
SAMN04901664_00455	CDS	lpxK	2.7.1.130	Tetraacyldisaccharide 4'-kinase
SAMN04901664_00456	CDS	msbA	3.6.3.-	Lipid A export ATP-binding/permease protein MsbA
SAMN04901664_00457	CDS	hypothetical protein	ExbB	
SAMN04901664_00458	CDS	exbB_2	putative chromosome-partitioning protein ParB	
SAMN04901664_00459	CDS	parB		
SAMN04901664_00460	CDS	soj_1	3.6.-.-	Sporulation initiation inhibitor protein Soj
SAMN04901664_00461	CDS	rsmG	2.1.1.170	Ribosomal RNA small subunit methyltransferase G
SAMN04901664_00462	CDS	cugP	2.7.7.9	UTP--glucose-1-phosphate uridylyltransferase
SAMN04901664_00463	CDS	hypothetical protein		
SAMN04901664_00464	CDS	lptD	LPS-assembly protein LptD	
SAMN04901664_00465	CDS	surA	5.2.1.8	Chaperone SurA
SAMN04901664_00466	CDS	fbaA	4.1.2.13	Fructose-bisphosphate aldolase class 2
SAMN04901664_00467	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00468	CDS	pgk	2.7.2.3	Phosphoglycerate kinase
SAMN04901664_00469	CDS	hypothetical protein		
SAMN04901664_00470	CDS	yceF	Maf-like protein YceF	
SAMN04901664_00471	CDS	1.14.11.-	putative ribosomal oxygenase	
SAMN04901664_00472	CDS	yxaf_1	putative HTH-type	
SAMN04901664_00473	CDS	bigR	transcriptional regulator YxaF	
SAMN04901664_00474	CDS	sstI	repressor	
SAMN04901664_00475	CDS	hypothetical protein	SstI	
SAMN04901664_00476	CDS	hypothetical protein		
SAMN04901664_00477	CDS	3.6.3.-	Putative multidrug export ATP-binding/permease protein	
SAMN04901664_00478	CDS	hypothetical protein		
SAMN04901664_00479	CDS	putative HTH-type		
SAMN04901664_00480	CDS	transcriptional regulator		
SAMN04901664_00481	CDS	gcvH	protein	
SAMN04901664_00482	CDS	cobB	3.5.1.-	NAD-dependent protein deacylase
SAMN04901664_00483	CDS	putP	Sodium/proline symporter	
SAMN04901664_00484	CDS	lrp_2	protein	
SAMN04901664_00485	CDS	putA	Bifunctional protein PutA	
SAMN04901664_00486	CDS	hypothetical protein		
SAMN04901664_00487	CDS	trmA	2.1.1.-	tRNA/tmRNA (uracil-C(5))-methyltransferase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00488	CDS	hypothetical protein		
SAMN04901664_00489	CDS	hypothetical protein		
SAMN04901664_00490	CDS	ycel	Protein Ycel	
SAMN04901664_00491	CDS	hypothetical protein		
SAMN04901664_00492	CDS	tktA	2.2.1.1	Transketolase 1
SAMN04901664_00493	CDS	metK	2.5.1.6	S-adenosylmethionine synthase
SAMN04901664_00494	CDS	hypothetical protein		
SAMN04901664_00495	CDS	hypothetical protein		
SAMN04901664_00496	CDS	hypothetical protein		
SAMN04901664_00497	CDS	3.5.2.6	Beta-lactamase OXA-133	
SAMN04901664_00498	CDS	2.3.1.-	methionine sulfone acetyltransferase	
SAMN04901664_00499	CDS	sutR_3	HTH-type transcriptional regulator SutR	
SAMN04901664_00500	CDS	ruvC_1	3.1.22.4	Crossover junction endodeoxyribonuclease RuvC
SAMN04901664_00501	CDS	nnr	Bifunctional NAD(P)H-hydrate repair enzyme Nnr	
SAMN04901664_00502	CDS	queG	1.17.99.6	Epoxyqueuosine reductase
SAMN04901664_00503	CDS	bioB	2.8.1.6	Biotin synthase
SAMN04901664_00504	CDS	hypothetical protein		
SAMN04901664_00505	CDS	hypothetical protein		
SAMN04901664_00506	CDS	6.2.1.-	Long-chain-fatty-acid--AMP ligase FadD32	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00507	CDS	1.3.8.10	Cyclohex-1-ene-1-carbonyl-CoA dehydrogenase	
SAMN04901664_00508	CDS	pkSN	2.3.1.-	Polyketide synthase PksN
SAMN04901664_00509	CDS	cmdD	Chondramide synthase cmdD	
SAMN04901664_00510	CDS	dhbF_1	Dimodular nonribosomal peptide synthase	
SAMN04901664_00511	CDS	srpB	Solvent-resistant pump membrane transporter SrpB	
SAMN04901664_00512	CDS	hypothetical protein		
SAMN04901664_00513	CDS	menH_1	4.2.99.20	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase
SAMN04901664_00514	CDS	sfp_1	2.7.8.-	4'-phosphopantetheinyl transferase sfp
SAMN04901664_00515	tRNA	tRNA tRNA-Gly(gcc)		
SAMN04901664_00516	tRNA	tRNA tRNA-Gly(gcc)		
SAMN04901664_00517	CDS	bolA	DNA-binding transcriptional regulator BolA	
SAMN04901664_00518	CDS	hypothetical protein		
SAMN04901664_00519	CDS	para	Chromosome partitioning protein ParA	
SAMN04901664_00520	CDS	hypothetical protein		
SAMN04901664_00521	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00522	CDS	putative membrane protein		
SAMN04901664_00523	CDS	yqjF	Inner membrane protein YqjF	
SAMN04901664_00524	CDS	hypothetical protein		
SAMN04901664_00525	CDS	guaA_1	6.3.5.2	GMP synthase [glutamine-hydrolyzing]
SAMN04901664_00526	CDS	ant1_1	2.7.7.47	Streptomycin 3"-adenylyltransferase
SAMN04901664_00527	CDS	yqjI	Transcriptional regulator YqjI	
SAMN04901664_00528	CDS	hypothetical protein		
SAMN04901664_00529	CDS	yhhW_2	1.13.11.24	Quercetin 2,3-dioxygenase
SAMN04901664_00530	CDS	hypothetical protein		
SAMN04901664_00531	CDS	dcmA	4.5.1.3	Dichloromethane dehalogenase
SAMN04901664_00532	CDS	ftsN_1	Cell division protein FtsN	
SAMN04901664_00533	CDS	argS	6.1.1.19	Arginine--tRNA ligase
SAMN04901664_00534	CDS	macA	1.1.1.38	NAD-dependent malic enzyme
SAMN04901664_00535	CDS	hypothetical protein		
SAMN04901664_00536	CDS	yfeX_2	1.1.1.1.-	putative deferochelatase/peroxidase YfeX
SAMN04901664_00537	CDS	rhtB_1	Homoserine/homoserine lactone efflux protein	
SAMN04901664_00538	CDS	znuB	system membrane protein ZnuB	
SAMN04901664_00539	CDS	znuC	3.6.3.-	Zinc import ATP-binding protein ZnuC

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00540	CDS	zur		Zinc uptake regulation protein
SAMN04901664_00541	CDS	znuA		High-affinity zinc uptake system protein ZnuA
SAMN04901664_00542	CDS	hypothetical protein		
SAMN04901664_00543	CDS	atpB		ATP synthase subunit a
SAMN04901664_00544	CDS	atpE		ATP synthase subunit c
SAMN04901664_00545	CDS	atpF		ATP synthase subunit b
SAMN04901664_00546	CDS	atpH		ATP synthase subunit delta
SAMN04901664_00547	CDS	atpA	3.6.3.14	ATP synthase subunit alpha
SAMN04901664_00548	CDS	atpG		ATP synthase gamma chain
SAMN04901664_00549	CDS	atpD1	3.6.3.14	ATP synthase subunit beta 1
SAMN04901664_00550	CDS	atpC		
SAMN04901664_00551	CDS	hypothetical protein		
SAMN04901664_00552	CDS	btuE	1.11.1.15	Thioredoxin/glutathione peroxidase BtuE
SAMN04901664_00553	CDS	nimR_1		HTH-type transcriptional regulator NimR
SAMN04901664_00554	CDS	nepI_2		Purine ribonucleoside efflux pump NepI
SAMN04901664_00555	CDS	comR_2		HTH-type transcriptional repressor ComR
SAMN04901664_00556	CDS	hypothetical protein		
SAMN04901664_00557	CDS	tsaC	2.7.7.87	Threonylcarbamoyl-AMP synthase
SAMN04901664_00558	CDS	dprA		DNA processing protein DprA

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00559	CDS	hypothetical protein		
SAMN04901664_00560	CDS	def_1	3.5.1.88	Peptide deformylase
SAMN04901664_00561	CDS	hypothetical protein		
SAMN04901664_00562	CDS	btuB_1	Vitamin B12 transporter BtuB	
SAMN04901664_00563	CDS	hypothetical protein		
SAMN04901664_00564	CDS	lep	1.13.-.-	Rubber oxygenase
		putative HTH-type		
SAMN04901664_00565	CDS	transcriptional regulator		
SAMN04901664_00566	CDS	hypothetical protein		
SAMN04901664_00567	CDS	hypothetical protein		
SAMN04901664_00568	CDS	hypothetical protein		
SAMN04901664_00569	CDS	hypothetical protein		
SAMN04901664_00570	CDS	hypothetical protein		
SAMN04901664_00571	CDS	hypothetical protein		
SAMN04901664_00572	CDS	hypothetical protein		
SAMN04901664_00573	CDS	hypothetical protein		
SAMN04901664_00574	CDS	hypothetical protein		
SAMN04901664_00575	CDS	hypothetical protein		
SAMN04901664_00576	CDS	hypothetical protein		
SAMN04901664_00577	CDS	hypothetical protein		
SAMN04901664_00578	CDS	hypothetical protein		
SAMN04901664_00579	CDS	hypothetical protein		
SAMN04901664_00580	CDS	hypothetical protein		
SAMN04901664_00581	CDS	hypothetical protein		
SAMN04901664_00582	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00583	CDS	hypothetical protein		
SAMN04901664_00584	CDS	hypothetical protein		
SAMN04901664_00585	CDS	xerC_1		Tyrosine recombinase XerC
SAMN04901664_00586	CDS	hypothetical protein		
SAMN04901664_00587	CDS	hypothetical protein		
SAMN04901664_00588	CDS	hypothetical protein		
SAMN04901664_00589	CDS	hypothetical protein		
SAMN04901664_00590	CDS	hypothetical protein		
SAMN04901664_00591	CDS	hypothetical protein		
SAMN04901664_00592	CDS	hypothetical protein		
SAMN04901664_00593	CDS	hypothetical protein		
SAMN04901664_00594	CDS	hypothetical protein		
SAMN04901664_00595	CDS	hypothetical protein		
SAMN04901664_00596	CDS	hypothetical protein		
SAMN04901664_00597	CDS	hypothetical protein		
SAMN04901664_00598	CDS	hypothetical protein		
SAMN04901664_00599	CDS	hypothetical protein		
SAMN04901664_00600	CDS	hypothetical protein		
SAMN04901664_00601	CDS	hypothetical protein		
SAMN04901664_00602	CDS	hypothetical protein		
SAMN04901664_00603	CDS	hypothetical protein		
SAMN04901664_00604	CDS	hypothetical protein		
SAMN04901664_00605	CDS	hypothetical protein		
SAMN04901664_00606	CDS	hypothetical protein		
SAMN04901664_00607	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00608	CDS	hypothetical protein		
SAMN04901664_00609	CDS	hypothetical protein		
SAMN04901664_00610	CDS	hypothetical protein		
SAMN04901664_00611	CDS	hypothetical protein		
SAMN04901664_00612	CDS	hypothetical protein		
SAMN04901664_00613	CDS	hypothetical protein		
SAMN04901664_00614	CDS	hypothetical protein		
SAMN04901664_00615	CDS	hypothetical protein		
SAMN04901664_00616	CDS	hypothetical protein		
SAMN04901664_00617	CDS	hypothetical protein		
SAMN04901664_00618	CDS	hypothetical protein		
SAMN04901664_00619	tRNA	tRNA-Arg(tct)		
SAMN04901664_00620	CDS	hypothetical protein		
SAMN04901664_00621	CDS	hypothetical protein		
SAMN04901664_00622	CDS	hypothetical protein		
SAMN04901664_00623	CDS	hypothetical protein		
SAMN04901664_00624	CDS	hypothetical protein		
SAMN04901664_00625	CDS	hypothetical protein		
SAMN04901664_00626	CDS	hypothetical protein		
SAMN04901664_00627	CDS	hypothetical protein		
SAMN04901664_00628	CDS	dnaB_1	3.6.4.12	Replicative DNA helicase
SAMN04901664_00629	CDS	hypothetical protein		
SAMN04901664_00630	CDS	hypothetical protein		
SAMN04901664_00631	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00632	CDS	putative HTH-type transcriptional regulator		
SAMN04901664_00633	CDS	hypothetical protein		
SAMN04901664_00634	CDS	hypothetical protein		
SAMN04901664_00635	CDS	hypothetical protein		
SAMN04901664_00636	CDS	hypothetical protein		
SAMN04901664_00637	CDS	hypothetical protein		
SAMN04901664_00638	CDS	hypothetical protein		
SAMN04901664_00639	CDS	hypothetical protein		
SAMN04901664_00640	CDS	hypothetical protein		
SAMN04901664_00641	CDS	hypothetical protein		
SAMN04901664_00642	CDS	hypothetical protein		
SAMN04901664_00643	CDS	hypothetical protein		
SAMN04901664_00644	CDS	6.3.3.2 ligase		
SAMN04901664_00645	CDS	ompA		Outer membrane protein A
SAMN04901664_00646	CDS	ata		Adhesin Ata autotransporter
SAMN04901664_00647	CDS	tyrS		6.1.1.1 Tyrosine--tRNA ligase
SAMN04901664_00648	CDS	anmK		2.7.1.170 Anhydro-N-acetylmuramic acid kinase
SAMN04901664_00649	CDS	ephA		3.3.2.10 Epoxide hydrolase A
SAMN04901664_00650	CDS	erpA		Iron-sulfur cluster insertion protein ErpA
SAMN04901664_00651	CDS	hypothetical protein		
SAMN04901664_00652	CDS	hypothetical protein		
SAMN04901664_00653	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00654	CDS	yheS_1	putative ABC transporter ATP-binding protein YheS	
SAMN04901664_00655	CDS	putative membrane protein		
SAMN04901664_00656	CDS	cybC	Soluble cytochrome b562	
SAMN04901664_00657	CDS	gyrB	5.99.1.3	DNA gyrase subunit B
SAMN04901664_00658	CDS	recF_1	DNA replication and repair protein RecF	
SAMN04901664_00659	CDS	dnaN	2.7.7.7	DNA polymerase III subunit beta
SAMN04901664_00660	CDS	dnaA	Chromosomal replication initiator protein DnaA	
SAMN04901664_00661	CDS	rpmH	50S ribosomal protein L34	
SAMN04901664_00662	CDS	mpaA	3.1.26.5	Ribonuclease P protein component
SAMN04901664_00663	CDS	yidD	Putative membrane protein insertion efficiency factor	
SAMN04901664_00664	CDS	yidC	YidC	
SAMN04901664_00665	CDS	mmnE	3.6.-.-	tRNA modification GTPase MmnE
SAMN04901664_00666	CDS	renR	Transcriptional repressor RenR	
SAMN04901664_00667	CDS	czcD_2	Cadmium, cobalt and zinc/H(+)-K(+) antiporter	
SAMN04901664_00668	CDS	dsbC_1	putative thiol:disulfide interchange protein DsbC	
SAMN04901664_00669	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00670	CDS	hpt	2.4.2.8	Hypoxanthine phosphoribosyltransferase
SAMN04901664_00671	CDS	hypothetical protein		
SAMN04901664_00672	CDS	guaD_1	3.5.4.3	Guanine deaminase
SAMN04901664_00673	CDS	ndmA	1.14.13.178	Methylxanthine N1-demethylase NdmA
SAMN04901664_00674	CDS	ygiC	6.3.1.-	Putative acid--amine ligase YgiC
SAMN04901664_00675	CDS	hypothetical protein		
SAMN04901664_00676	CDS	alx	Inner membrane protein alx	
SAMN04901664_00677	CDS	ybjG	3.6.1.27	Putative undecaprenyl-diphosphatase YbjG
SAMN04901664_00678	CDS	hypothetical protein		
SAMN04901664_00679	CDS	mpl	6.3.2.45	UDP-N-acetylmuramate--L-alanyl-gamma-D-glutamyl-meso-2,6-diaminoheptandioate ligase
SAMN04901664_00680	CDS	hypothetical protein		
SAMN04901664_00681	CDS	purE	5.4.99.18	N5-carboxyaminoimidazole ribonucleotide mutase
SAMN04901664_00682	CDS	purK	6.3.4.18	N5-carboxyaminoimidazole ribonucleotide synthase
SAMN04901664_00683	CDS	mltB_1	4.2.2.-	Membrane-bound lytic murein transglycosylase B
SAMN04901664_00684	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00685	CDS	hypothetical protein		
SAMN04901664_00686	CDS	hypothetical protein		
SAMN04901664_00687	CDS	dnaK	Chaperone protein DnaK	
SAMN04901664_00688	CDS	grpE	Protein GrpE	
SAMN04901664_00689	CDS	dmlR_2	HTH-type transcriptional regulator DmlR	
SAMN04901664_00690	CDS	hypothetical protein		
SAMN04901664_00691	CDS	hypothetical protein		
SAMN04901664_00692	CDS	hypothetical protein		
SAMN04901664_00693	CDS	nlhH_1	3.1.1.1	Carboxylesterase NlhH
SAMN04901664_00694	CDS	ppiA	5.2.1.8	Peptidyl-prolyl cis-trans isomerase A
SAMN04901664_00695	rRNA	16S ribosomal RNA		
SAMN04901664_00696	tRNA	tRNA-Ile(gat)		
SAMN04901664_00697	CDS	hypothetical protein		
SAMN04901664_00698	CDS	hypothetical protein		
SAMN04901664_00699	CDS	hypothetical protein		
SAMN04901664_00700	CDS	hypothetical protein		
SAMN04901664_00701	CDS	hypothetical protein		
SAMN04901664_00702	CDS	hypothetical protein		
SAMN04901664_00703	CDS	hypothetical protein		
SAMN04901664_00704	CDS	hypothetical protein		
SAMN04901664_00705	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00706	CDS	hypothetical protein		
SAMN04901664_00707	CDS	hypothetical protein		
SAMN04901664_00708	CDS	hypothetical protein		
SAMN04901664_00709	CDS	hypothetical protein		
SAMN04901664_00710	CDS	hypothetical protein		
SAMN04901664_00711	CDS	hypothetical protein		
SAMN04901664_00712	CDS	hypothetical protein		
SAMN04901664_00713	CDS	hypothetical protein		
SAMN04901664_00714	CDS	hypothetical protein		
SAMN04901664_00715	CDS	hypothetical protein		
SAMN04901664_00716	CDS	hypothetical protein		
SAMN04901664_00717	CDS	hcaT		putative 3-phenylpropionic acid transporter
SAMN04901664_00718	CDS	hypothetical protein		
SAMN04901664_00719	CDS	accC_1	6.3.4.14	Biotin carboxylase
SAMN04901664_00720	CDS	accB		Biotin carboxyl carrier protein
SAMN04901664_00721	CDS	aroQ	4.2.1.10	of acetyl-CoA carboxylase
SAMN04901664_00722	CDS	dinB1	2.7.7.7	3-dehydroquinate dehydratase
SAMN04901664_00723	CDS	cmpC	3.6.3.-	DNA polymerase IV I Bicarbonate transport ATP-binding protein CmpC
SAMN04901664_00724	CDS	pdtaR		putative transcriptional regulatory protein pdtaR
SAMN04901664_00725	CDS	hypothetical protein		
SAMN04901664_00726	CDS	nasD_1	1.7.1.4	Nitrite reductase [NAD(P)H]

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00727	CDS	nasD_2	1.7.1.4	Nitrite reductase [NAD(P)H]
SAMN04901664_00728	CDS	nasA	1.7.99.4	Nitrate reductase
SAMN04901664_00729	CDS	mobA	2.7.7.77	Molybdenum cofactor guanylyltransferase
SAMN04901664_00730	CDS	fdhF	1.1.99.33	Formate dehydrogenase H
SAMN04901664_00731	CDS	moaA	4.1.99.22	GTP 3',8-cyclase
SAMN04901664_00732	CDS	hypothetical protein		
SAMN04901664_00733	CDS	moaE1	2.8.1.12	Molybdopterin synthase catalytic subunit 1
SAMN04901664_00734	CDS	moaC2	4.6.1.17	Cyclic pyranopterin monophosphate synthase 2
SAMN04901664_00735	CDS	moaA	2.10.1.1	Molybdopterin molybdenumtransferase
SAMN04901664_00736	CDS	putative HTH-type transcriptional regulator		
SAMN04901664_00737	CDS	norG_1		HTH-type transcriptional regulator NorG
SAMN04901664_00738	CDS	hypothetical protein		
SAMN04901664_00739	CDS	tusE	2.8.1.-	Sulfurtransferase TusE
SAMN04901664_00740	CDS	hypothetical protein		
SAMN04901664_00741	CDS	hypothetical protein		
SAMN04901664_00742	CDS	tusD	2.8.1.-	Sulfurtransferase TusD
SAMN04901664_00743	CDS	galE_2	5.1.3.2	UDP-glucose 4-epimerase
SAMN04901664_00744	CDS	fumC	4.2.1.2	Fumarate hydratase class II
SAMN04901664_00745	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00746	CDS	hypothetical protein		
SAMN04901664_00747	CDS	hypothetical protein		
SAMN04901664_00748	CDS	dadA	1.4.99.-	D-amino acid dehydrogenase
SAMN04901664_00749	CDS	hypothetical protein		
SAMN04901664_00750	CDS	ispF	4.6.1.12	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
SAMN04901664_00751	CDS	hypothetical protein		
SAMN04901664_00752	CDS	argF	2.1.3.3	Ornithine carbamoyltransferase
SAMN04901664_00753	CDS	hypothetical protein		
SAMN04901664_00754	CDS	yadV_1	YadV	
SAMN04901664_00755	CDS	htrE_1	HtrE	
SAMN04901664_00756	CDS	mrkD_1	Fimbria adhesin protein	
SAMN04901664_00757	CDS	hypothetical protein		
SAMN04901664_00758	CDS	frmA_1	1.1.1.284	S-(hydroxymethyl)glutathione dehydrogenase
SAMN04901664_00759	CDS	hypothetical protein		
SAMN04901664_00760	CDS	cat_1	1.11.1.6	Catalase
SAMN04901664_00761	CDS	hypothetical protein		
SAMN04901664_00762	CDS	hypothetical protein		
SAMN04901664_00763	CDS	clsC_1	2.7.8.-	Cardiolipin synthase C
SAMN04901664_00764	CDS	hypothetical protein		
SAMN04901664_00765	CDS	hypothetical protein		
SAMN04901664_00766	CDS	hypothetical protein		
SAMN04901664_00767	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00768	CDS	mftC	2.-.-.-	Putative mycofactacin radical SAM maturase MftC
SAMN04901664_00769	CDS	pqqD	protein D	
SAMN04901664_00770	CDS	pqqC	1.3.3.11	Pyroloquinoline-quinone synthase
SAMN04901664_00771	CDS	pqqB	protein B	
SAMN04901664_00772	CDS	ppk_1	2.7.4.1	Polyphosphate kinase
SAMN04901664_00773	CDS	yhcR	3.1.31.-	Endonuclease YhcR
SAMN04901664_00774	CDS	fur_1	Ferric uptake regulation protein	
SAMN04901664_00775	CDS	vibB	3.3.2.1	Vibriobactin-specific isochorismatase
SAMN04901664_00776	CDS	dhbA	1.3.1.28	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
SAMN04901664_00777	CDS	cysA_1	3.6.3.25	Sulfate/thiosulfate import ATP-binding protein CysA
SAMN04901664_00778	CDS	modB	Molybdenum transport system permease protein ModB	
SAMN04901664_00779	CDS	modA	Molybdate-binding periplasmic protein	
SAMN04901664_00780	CDS	mopA	Molybdenum-pterin-binding protein MopA	
SAMN04901664_00781	CDS	antA_1	1.14.12.1	Anthranilate 1,2-dioxygenase large subunit

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00782	CDS	antB	1.14.12.1	Anthranilate 1,2-dioxygenase small subunit
SAMN04901664_00783	CDS	antC	Anthranilate 1,2-dioxygenase electron transfer component	
SAMN04901664_00784	CDS	rhaS	HTH-type transcriptional activator RhaS	
SAMN04901664_00785	CDS	hypothetical protein		
SAMN04901664_00786	CDS	C1-hpah_1	1.5.1.36	p-hydroxyphenylacetate 3-hydroxylase, reductase component
SAMN04901664_00787	CDS	styA	1.14.14.11	Styrene monooxygenase StyA
SAMN04901664_00788	CDS	bacC_1	1.1.1.385	Dihydroantcapsin 7-dehydrogenase
SAMN04901664_00789	CDS	c1cD_1	3.1.1.45	Carboxymethylenebutenolidase
SAMN04901664_00790	CDS	pcaK_1	PcaK	
SAMN04901664_00791	CDS	pchR	Regulatory protein PchR	
SAMN04901664_00792	CDS	hypothetical protein		
SAMN04901664_00793	CDS	minE	Cell division topological specificity factor	
SAMN04901664_00794	CDS	minD	Septum site-determining protein MinD	
SAMN04901664_00795	CDS	minC	Septum site-determining protein MinC	
SAMN04901664_00796	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00797	CDS	yihG	2.3.-.-	putative acyltransferase YihG
SAMN04901664_00798	CDS	yiaD_1	putative lipoprotein	YiaD
SAMN04901664_00799	CDS	hypothetical protein		
SAMN04901664_00800	CDS	rep_1	3.6.4.12	ATP-dependent DNA helicase Rep
SAMN04901664_00801	CDS	dut	3.6.1.23	Deoxyuridine 5'-triphosphate nucleotidohydrolase
SAMN04901664_00802	CDS	algC_2	5.4.2.2	Phosphomannomutase/phosphoglucomutase
SAMN04901664_00803	CDS	argB	2.7.2.8	Acetylglutamate kinase
SAMN04901664_00804	CDS	hypothetical protein		
SAMN04901664_00805	CDS	yafJ	2.4.2.-	Putative glutamine amidotransferase YafJ
SAMN04901664_00806	CDS	Bacteriohemerythrin		
SAMN04901664_00807	CDS	hypothetical protein		
SAMN04901664_00808	CDS	pasI	Persistence and stress-resistance antitoxin	PasI
SAMN04901664_00809	CDS	bamE	Outer membrane protein assembly factor	BamE
SAMN04901664_00810	CDS	fur_2	Ferric uptake regulation protein	
SAMN04901664_00811	CDS	pilT_1	Twitching mobility protein	
SAMN04901664_00812	CDS	pilT_2	Twitching mobility protein	
SAMN04901664_00813	CDS	hypothetical protein		
SAMN04901664_00814	CDS	sbcC	Nuclease SbcCD subunit C	
SAMN04901664_00815	CDS	sbcD	Nuclease SbcCD subunit D	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00816	CDS	hypothetical protein		
SAMN04901664_00817	CDS	hypothetical protein		
SAMN04901664_00818	CDS	hypothetical protein		
SAMN04901664_00819	CDS	Epimerase family protein		
SAMN04901664_00820	CDS	thiO	1.4.3.19	Glycine oxidase
SAMN04901664_00821	CDS	hemB	4.2.1.24	Delta-aminolevulinic acid dehydratase
SAMN04901664_00822	CDS	hypothetical protein		
SAMN04901664_00823	CDS	emrK		putative multidrug resistance protein EmrK
SAMN04901664_00824	CDS	emrB_1		Multidrug export protein EmrB
SAMN04901664_00825	CDS	ggt	2.3.2.2	Gamma-glutamyltranspeptidase
SAMN04901664_00826	tmRN	A		
SAMN04901664_00827	A	ssrA		transfer-messenger RNA, SsrA
SAMN04901664_00828	CDS	emrA_1		Multidrug export protein EmrA
SAMN04901664_00829	CDS	emrB_2		Multidrug export protein EmrB
SAMN04901664_00830	CDS	hypothetical protein		
SAMN04901664_00831	CDS	hypothetical protein		
SAMN04901664_00832	CDS	bepC		BepC
SAMN04901664_00833	CDS	hypothetical protein		
SAMN04901664_00834	CDS	surE_1	3.1.3.5	5'-nucleotidase SurE
SAMN04901664_00835	CDS	hypothetical protein		
SAMN04901664_00835	CDS	spoT_1		Bifunctional (p)ppGpp synthase/hydrolase SpoT

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00836	CDS	hypothetical protein		
SAMN04901664_00837	CDS	hypothetical protein		
SAMN04901664_00838	CDS	hypothetical protein		
SAMN04901664_00839	CDS	hypothetical protein		
SAMN04901664_00840	CDS	hypothetical protein		
SAMN04901664_00841	CDS	hypothetical protein		
SAMN04901664_00842	CDS	hypothetical protein		
SAMN04901664_00843	CDS	hypothetical protein		
SAMN04901664_00844	CDS	limC	1.1.1.-	(-)-trans-carveol dehydrogenase
SAMN04901664_00845	CDS	fabG2	1.-.-	putative oxidoreductase
SAMN04901664_00846	CDS	hypothetical protein		
SAMN04901664_00847	CDS	virS_2	HTH-type transcriptional regulator VirS	
SAMN04901664_00848	CDS	hypothetical protein		
SAMN04901664_00849	CDS	baeS_1	2.7.13.3	Signal transduction histidine-protein kinase BaeS
SAMN04901664_00850	CDS	srrA	Transcriptional regulatory protein SrrA	
SAMN04901664_00851	CDS	mexA	MexA	
SAMN04901664_00852	CDS	acrB	AcrB	
SAMN04901664_00853	CDS	oprM_2	Outer membrane protein OprM	
SAMN04901664_00854	CDS	3.1.1.23	Monoacylglycerol lipase	
SAMN04901664_00855	CDS	1.14.13.-	monoxygenase	
SAMN04901664_00856	CDS	pao	1.4.3.24	Pseudooxynicotine oxidase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00857	CDS	lysDH	1.4.1.18	Lysine 6-dehydrogenase
SAMN04901664_00858	CDS	ethR	HTH-type transcriptional regulator EthR	
SAMN04901664_00859	CDS	puuB_1	1.4.3.-	Gamma-glutamylputrescine oxidoreductase
SAMN04901664_00860	CDS	hypothetical protein		
SAMN04901664_00861	CDS	hypothetical protein		
SAMN04901664_00862	rRNA	5S ribosomal RNA		
SAMN04901664_00863	CDS	aac	2.3.1.-	Aminoglycoside 2'-N-acetyltransferase
SAMN04901664_00864	CDS	srpG	2.5.1.47	Cysteine synthase
SAMN04901664_00865	CDS	slt_1	4.2.2.-	Soluble lytic murein transglycosylase
SAMN04901664_00866	CDS	pnpB_2	1.6.5.2	p-benzoquinone reductase
SAMN04901664_00867	CDS	hypothetical protein		
SAMN04901664_00868	CDS	cueR	HTH-type transcriptional regulator CueR	
SAMN04901664_00869	CDS	hypothetical protein		
SAMN04901664_00870	CDS	rimO_1	2.8.4.4	Ribosomal protein S12 methylthiotransferase RimO
SAMN04901664_00871	CDS	hypothetical protein		
SAMN04901664_00872	CDS	RutC family protein		
SAMN04901664_00873	CDS	dinB	2.7.7.7	DNA polymerase IV
SAMN04901664_00874	CDS	acm	3.2.1.17	Lysozyme M1

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00875	CDS	hsrA		putative transport protein HsrA
SAMN04901664_00876	CDS	yvdD_1		LOG family protein YvdD
SAMN04901664_00877	CDS	corC_1		Magnesium and cobalt efflux protein CorC
SAMN04901664_00878	CDS	hypothetical protein		
SAMN04901664_00879	CDS	hypothetical protein		
SAMN04901664_00880	CDS	naiP_1		Putative niacin/nicotinamide transporter NaiP
SAMN04901664_00881	CDS	parC	5.99.1.3	DNA topoisomerase 4 subunit A
SAMN04901664_00882	CDS	fadD	6.2.1.3	Long-chain-fatty-acid--CoA ligase
SAMN04901664_00883	CDS	hypothetical protein		
SAMN04901664_00884	CDS	hypothetical protein		
SAMN04901664_00885	CDS	ppa	3.6.1.1	Inorganic pyrophosphatase
SAMN04901664_00886	CDS	oprD	3.4.21.-	Porin D
SAMN04901664_00887	CDS	hypothetical protein		
SAMN04901664_00888	CDS	hypothetical protein		
SAMN04901664_00889	CDS	dapA_1	4.3.3.7	4-hydroxy-tetrahydrodipicolinate synthase
SAMN04901664_00890	CDS	novR	4.1.-.-	Decarboxylase NovR
SAMN04901664_00891	CDS	gabR_2		HTH-type transcriptional regulatory protein GabR
SAMN04901664_00892	CDS	comM_1		Competence protein ComM
SAMN04901664_00893	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00894	CDS	tnsB_1	Transposon Tn7 transposition protein TnsB	
SAMN04901664_00895	CDS	araC_1	4.2.1.25	L-arabonate dehydratase
SAMN04901664_00896	CDS	hypothetical protein		
SAMN04901664_00897	CDS	gbpR	HTH-type transcriptional regulator GbpR	
SAMN04901664_00898	CDS	putative epimerase/dehydratase		
SAMN04901664_00899	CDS	ttuB_1	Putative tartrate transporter	
SAMN04901664_00900	CDS	glxR_1	1.1.1.60	2-hydroxy-3-oxopropionate reductase
SAMN04901664_00901	CDS	exsA	Exoenzyme S synthesis regulatory protein ExsA	
SAMN04901664_00902	CDS	hypothetical protein		
SAMN04901664_00903	CDS	hypothetical protein		
SAMN04901664_00904	CDS	adhA	1.1.1.-	putative formaldehyde dehydrogenase AdhA
SAMN04901664_00905	CDS	yciQ_1	putative ABC transporter solute-binding protein YciQ	
SAMN04901664_00906	CDS	putative ABC transporter permease protein		
SAMN04901664_00907	CDS	fepC	Ferric enterobactin transport ATP-binding protein FepC	
SAMN04901664_00908	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00909	CDS	nimR_2	HTH-type transcriptional regulator NimR	
SAMN04901664_00910	CDS	hypothetical protein		
SAMN04901664_00911	CDS	prs2	2.7.6.1	Ribose-phosphate pyrophosphokinase 2
SAMN04901664_00912	CDS	hypothetical protein		
SAMN04901664_00913	CDS	hypothetical protein		
SAMN04901664_00914	CDS	hypothetical protein		
SAMN04901664_00915	CDS	hypothetical protein		
SAMN04901664_00916	CDS	hypothetical protein		
SAMN04901664_00917	CDS	hypothetical protein		
SAMN04901664_00918	CDS	hypothetical protein		
SAMN04901664_00919	CDS	hypothetical protein		
SAMN04901664_00920	CDS	hypothetical protein		
SAMN04901664_00921	CDS	hypothetical protein		
SAMN04901664_00922	CDS	hypothetical protein		
SAMN04901664_00923	CDS	hypothetical protein		
SAMN04901664_00924	CDS	hypothetical protein		
SAMN04901664_00925	CDS	hypothetical protein		
SAMN04901664_00926	CDS	hypothetical protein		
SAMN04901664_00927	CDS	hypothetical protein		
SAMN04901664_00928	CDS	mdlY	3.5.1.86	Mandelamide hydrolase
SAMN04901664_00929	CDS	hypothetical protein		
SAMN04901664_00930	CDS	1.14.13.-	monooxygenase	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00931	CDS	budC_2	1.1.1.304	Diacetyl reductase [(S)-acetoin forming]
SAMN04901664_00932	CDS	hypothetical protein	HTH-type transcriptional repressor Bm3R1	
SAMN04901664_00933	CDS	bm3R1_1	1.13.11.24	Quercetin 2,3-dioxygenase
SAMN04901664_00934	CDS	yhhW_3		
SAMN04901664_00935	CDS	hypothetical protein		
SAMN04901664_00936	CDS	hypothetical protein		
SAMN04901664_00937	CDS	ephD_1	1.-.-	putative oxidoreductase EphD
SAMN04901664_00938	CDS	1.14.13.-	monooxygenase	
SAMN04901664_00939	CDS	hypothetical protein		
SAMN04901664_00940	CDS	adeP	Adenine permease AdeP	
SAMN04901664_00941	CDS	3.5.4.2	Adenine deaminase	
SAMN04901664_00942	CDS	yceJ_1	Cytochrome b561	
SAMN04901664_00943	CDS	hypothetical protein		
SAMN04901664_00944	CDS	rnhB	3.1.26.4	Ribonuclease HII
SAMN04901664_00945	CDS	csrA	Carbon storage regulator	
SAMN04901664_00946	CDS	2.7.2.4	Aspartate kinase	
SAMN04901664_00947	CDS	alaS	6.1.1.7	Alanine--tRNA ligase
SAMN04901664_00948	CDS	epd	1.2.1.72	D-erythrose-4-phosphate dehydrogenase
SAMN04901664_00949	CDS	hisZ	phosphoribosyltransferase regulatory subunit	
SAMN04901664_00950	CDS	purA	6.3.4.4	Adenylosuccinate synthetase
SAMN04901664_00951	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00952	CDS	loiP	3.4.24.-	Metalloprotease LoiP
SAMN04901664_00953	CDS	gpr	1.1.1.-	L-glyceraldehyde 3-phosphate reductase
SAMN04901664_00954	CDS	hypothetical protein		
SAMN04901664_00955	CDS	hypothetical protein		
SAMN04901664_00956	CDS	hypothetical protein		
SAMN04901664_00957	CDS	hypothetical protein		
SAMN04901664_00958	CDS	wecD	2.3.1.210	dTDP-fucosamine acetyltransferase
SAMN04901664_00959	CDS	hypothetical protein		
SAMN04901664_00960	CDS	nimT	2-nitroimidazole transporter	
SAMN04901664_00961	CDS	guaD_2	3.5.4.3	Guanine deaminase
SAMN04901664_00962	CDS	hypothetical protein		
SAMN04901664_00963	CDS	gltC_2	HTH-type transcriptional regulator GltC	
SAMN04901664_00964	CDS	cwIK	3.4.-.-	Peptidoglycan L-alanyl-D-glutamate endopeptidase CwIK
SAMN04901664_00965	CDS	hypothetical protein		
SAMN04901664_00966	CDS	hypothetical protein		
SAMN04901664_00967	CDS	hypothetical protein		
SAMN04901664_00968	CDS	hypothetical protein		
SAMN04901664_00969	CDS	clpB_1	Chaperone protein ClpB	
SAMN04901664_00970	CDS	hypothetical protein		
SAMN04901664_00971	CDS	viaD_2	putative lipoprotein YiaD	
SAMN04901664_00972	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00973	CDS	hypothetical protein		
SAMN04901664_00974	CDS	hypothetical protein		
SAMN04901664_00975	CDS	hypothetical protein		
SAMN04901664_00976	CDS	hypothetical protein		
SAMN04901664_00977	CDS	hypothetical protein		
SAMN04901664_00978	CDS	hypothetical protein		
SAMN04901664_00979	CDS	hypothetical protein		
SAMN04901664_00980	CDS	hypothetical protein		
SAMN04901664_00981	CDS	hypothetical protein		
SAMN04901664_00982	CDS	hypothetical protein		
SAMN04901664_00983	CDS	mprA	MprA	
SAMN04901664_00984	CDS	hypothetical protein		
SAMN04901664_00985	CDS	hypothetical protein		
SAMN04901664_00986	CDS	fruA	PTS system fructose-specific EIIB'BC component	Tagatose-6-phosphate kinase
SAMN04901664_00987	CDS	lacC	2.7.1.144	Phosphoenolpyruvate-protein phosphotransferase
SAMN04901664_00988	CDS	ptsI	2.7.3.9	
SAMN04901664_00989	CDS	hypothetical protein		
SAMN04901664_00990	CDS	hypothetical protein		
SAMN04901664_00991	CDS	hypothetical protein		
SAMN04901664_00992	CDS	hypothetical protein		
SAMN04901664_00993	CDS	brnQ	transport system 2 carrier protein	
SAMN04901664_00994	CDS	map_1	3.4.11.18	Methionine aminopeptidase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_00995	CDS	dmlR_3	HTH-type transcriptional regulator DmlR	
SAMN04901664_00996	CDS	hypothetical protein		
SAMN04901664_00997	CDS	grxD	Glutaredoxin 4	
SAMN04901664_00998	CDS	argD	2.6.1.11	Acetylornithine aminotransferase
SAMN04901664_00999	CDS	guaB_1	1.1.1.205	Inosine-5'-monophosphate dehydrogenase
SAMN04901664_01000	CDS	hypothetical protein		
SAMN04901664_01001	CDS	hypothetical protein		
SAMN04901664_01002	CDS	hypothetical protein		
SAMN04901664_01003	CDS	hypothetical protein		
SAMN04901664_01004	CDS	ftsY	Signal recognition particle receptor FtsY	
SAMN04901664_01005	CDS	hypothetical protein		
SAMN04901664_01006	CDS	hypothetical protein		
SAMN04901664_01007	CDS	hypothetical protein		
SAMN04901664_01008	CDS	hypothetical protein		
SAMN04901664_01009	CDS	cydX	1.10.3.14	Cytochrome bd-I ubiquinol oxidase subunit X
SAMN04901664_01010	CDS	cydB_1	1.10.3.14	Cytochrome bd-I ubiquinol oxidase subunit 2
SAMN04901664_01011	CDS	cydA_1	1.10.3.-	Cytochrome bd ubiquinol oxidase subunit 1
SAMN04901664_01012	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01013	CDS	hypothetical protein		
SAMN04901664_01014	CDS	hypothetical protein		
SAMN04901664_01015	CDS	hypothetical protein		
SAMN04901664_01016	CDS	pheP	permease	
SAMN04901664_01017	CDS	kynU	3.7.1.3	Kynureninase
SAMN04901664_01018	CDS	decR_1	DNA-binding transcriptional activator	DecR
SAMN04901664_01019	CDS	hypothetical protein		
SAMN04901664_01020	CDS	hypothetical protein		
SAMN04901664_01021	CDS	hypothetical protein		
SAMN04901664_01022	CDS	hypothetical protein		
SAMN04901664_01023	CDS	yrfG	3.1.3.5	GMP/IMP nucleotidase YrfG
SAMN04901664_01024	CDS	hsIR	Heat shock protein 15	
SAMN04901664_01025	CDS	recA_1	Protein RecA	
SAMN04901664_01026	CDS	recX	Regulatory protein RecX	
SAMN04901664_01027	CDS	cpoB	Cell division coordinator CpoB	
SAMN04901664_01028	CDS	lpxA	2.3.1.129	Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase
SAMN04901664_01029	CDS	fabZ	4.2.1.59	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ
SAMN04901664_01030	CDS	lpxD	2.3.1.-	UDP-3-O-acylglucosamine N-acyltransferase
SAMN04901664_01031	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01032	CDS	bamA	Outer membrane protein assembly factor BamA	
SAMN04901664_01033	CDS	rseP	3.4.24.-	Regulator of sigma-E protease RseP
SAMN04901664_01034	CDS	dxr	1.1.1.267	1-deoxy-D-xylulose 5-phosphate reductoisomerase
SAMN04901664_01035	CDS	cdsA	2.7.7.41	Phosphatidate cytidyltransferase
SAMN04901664_01036	CDS	uppS	2.5.1.31	Ditrans,polycis-undecaprenyl-diphosphate synthase ((2E,6E)-farnesyl-diphosphate specific)
SAMN04901664_01037	CDS	frf	Ribosome-recycling factor	
SAMN04901664_01038	CDS	pyrH	2.7.4.22	Uridylate kinase
SAMN04901664_01039	CDS	rimO_2	2.8.4.4	Ribosomal protein S12 methylthiotransferase RimO
SAMN04901664_01040	CDS	glnL	2.7.13.3	Nitrogen regulation protein NR(II)
SAMN04901664_01041	CDS	glnG_2	NR(I)	
SAMN04901664_01042	CDS	comR_3	HTH-type transcriptional repressor ComR	
SAMN04901664_01043	CDS	hypothetical protein		
SAMN04901664_01044	CDS	hypothetical protein		
SAMN04901664_01045	CDS	hypothetical protein		
SAMN04901664_01046	CDS	yhaI_2	Inner membrane protein YhaI	
SAMN04901664_01047	CDS	acsA_2	6.2.1.1	Acetyl-coenzyme A synthetase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01048	CDS	sttH	3.5.2.19	Streptothricin hydrolase
SAMN04901664_01049	CDS	lrpC	HTH-type transcriptional regulator LrpC	
SAMN04901664_01050	CDS	hypothetical protein		
SAMN04901664_01051	CDS	ssuD_2	1.14.14.5	Alkanesulfonate monooxygenase
SAMN04901664_01052	CDS	msuE	1.5.1.38	FMN reductase (NADPH)
SAMN04901664_01053	CDS	exaE	protein ExaE	
SAMN04901664_01054	CDS	hypothetical protein		
SAMN04901664_01055	CDS	rpfC	2.7.13.3	Sensory/regulatory protein RpfC
SAMN04901664_01056	CDS	yjch_1	Inner membrane protein Yjch	
SAMN04901664_01057	CDS	actP_1	Cation/acetate symporter ActP	
SAMN04901664_01058	CDS	hypothetical protein		
SAMN04901664_01059	CDS	Glycine betaine transporter		
SAMN04901664_01060	CDS	hypothetical protein		
SAMN04901664_01061	CDS	pleD_1	Response regulator PleD	
SAMN04901664_01062	CDS	hypothetical protein		
SAMN04901664_01063	CDS	hypothetical protein		
SAMN04901664_01064	CDS	yqiJ	Inner membrane protein YqiJ	
SAMN04901664_01065	CDS	hcaC	acid dioxygenase ferredoxin subunit	
SAMN04901664_01066	CDS	kdgK	2.7.1.45	2-dehydro-3-deoxygluconokinase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01067	CDS	bfrD_1	putative TonB-dependent receptor BfrD	
SAMN04901664_01068	CDS	hypothetical protein		
SAMN04901664_01069	CDS	3.1.1.32	Putative phospholipase A1	
SAMN04901664_01070	CDS	ktrB	Ktr system potassium uptake protein B	
SAMN04901664_01071	CDS	ktrA	Ktr system potassium uptake protein A	
SAMN04901664_01072	CDS	ilvA	4.3.1.19	L-threonine dehydratase biosynthetic IlvA
SAMN04901664_01073	CDS	rpiA	5.3.1.6	Ribose-5-phosphate isomerase A
SAMN04901664_01074	CDS	hypothetical protein		
SAMN04901664_01075	CDS	hypothetical protein		
SAMN04901664_01076	CDS	argC	1.2.1.38	N-acetyl-gamma-glutamyl-phosphate reductase
SAMN04901664_01077	CDS	hypothetical protein		
SAMN04901664_01078	CDS	clpS	ATP-dependent Clp protease adapter protein ClpS	
SAMN04901664_01079	CDS	tufB	Elongation factor Tu 2	
SAMN04901664_01080	tRNA	tRNA-Trp(cca)		
SAMN04901664_01081	CDS	secE	SecE	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01082	CDS	nusG		
SAMN04901664_01083	CDS	rplK		
SAMN04901664_01084	CDS	rplA		
SAMN04901664_01085	CDS	rplJ		
SAMN04901664_01086	CDS	rplL		
SAMN04901664_01087	CDS	rpoB		
SAMN04901664_01088	CDS	rpoC		
SAMN04901664_01089	CDS	hypothetical protein		
SAMN04901664_01090	CDS	hypothetical protein		
SAMN04901664_01091	CDS	hypothetical protein		
SAMN04901664_01092	CDS	hypothetical protein		
SAMN04901664_01093	CDS	intS		
SAMN04901664_01094	CDS	hypothetical protein		
SAMN04901664_01095	CDS	hypothetical protein		
SAMN04901664_01096	CDS	hypothetical protein		
SAMN04901664_01097	CDS	hypothetical protein		
SAMN04901664_01098	CDS	hypothetical protein		
SAMN04901664_01099	CDS	hypothetical protein		
SAMN04901664_01100	CDS	hypothetical protein		
SAMN04901664_01101	CDS	hypothetical protein		
SAMN04901664_01102	CDS	hypothetical protein		
			Transcription	
			termination/antitermination	
			protein NusG	
			50S ribosomal protein L11	
			50S ribosomal protein L1	
			50S ribosomal protein L10	
			50S ribosomal protein L7/L12	
			2.7.7.6	DNA-directed RNA polymerase subunit beta
			2.7.7.6	DNA-directed RNA polymerase subunit beta'
				Prophage integrase IntS

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01103	CDS	ssb_2		
SAMN04901664_01104	CDS	hypothetical protein		Single-stranded DNA-binding protein
SAMN04901664_01105	CDS	hypothetical protein		
SAMN04901664_01106	CDS	hypothetical protein		
SAMN04901664_01107	CDS	hypothetical protein		
SAMN04901664_01108	CDS	hypothetical protein		
SAMN04901664_01109	CDS	putative signaling protein		
		Putative universal stress protein		
SAMN04901664_01110	CDS	protein		
SAMN04901664_01111	CDS	gdhB_1		Quinoprotein glucose dehydrogenase B
SAMN04901664_01112	CDS	hypothetical protein	1.1.5.2	
SAMN04901664_01113	CDS	bicA_2		Bicarbonate transporter BicA
SAMN04901664_01114	CDS	3.4.21.-		Extracellular serine proteinase
				putative HTH-type transcriptional regulator YxaF
SAMN04901664_01115	CDS	yxaF_2		
SAMN04901664_01116	CDS	hypothetical protein		
SAMN04901664_01117	tRNA	tRNA-Met(cat)		
SAMN04901664_01118	CDS	hypothetical protein		
SAMN04901664_01119	CDS	hypothetical protein		
SAMN04901664_01120	CDS	allS		HTH-type transcriptional activator AllS
SAMN04901664_01121	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01122	CDS	hypothetical protein		
SAMN04901664_01123	CDS	hypothetical protein		
SAMN04901664_01124	CDS	yijE_1	YijE	
SAMN04901664_01125	CDS	pgrR_1	HTH-type transcriptional regulator PgrR	
SAMN04901664_01126	CDS	hypothetical protein		
SAMN04901664_01127	CDS	mrkD_2	Fimbria adhesin protein	
SAMN04901664_01128	CDS	htrE_2	HtrE	
SAMN04901664_01129	CDS	yadV_2	YadV	
SAMN04901664_01130	CDS	smf-1_1	Major fimbrial subunit SMF-1 protein	
SAMN04901664_01131	CDS	eamB_2	Multiple antibiotic resistance protein MarA	
SAMN04901664_01132	CDS	marA		
SAMN04901664_01133	CDS	phaC_2		Poly(3-hydroxyalkanoate) polymerase subunit PhaC
SAMN04901664_01134	CDS	gltS	2.3.1.-	
SAMN04901664_01135	CDS	hypothetical protein	Sodium/glutamate symporter	
SAMN04901664_01136	CDS	lldR_2	dehydrogenase operon regulatory protein	
SAMN04901664_01137	CDS	hypothetical protein		
SAMN04901664_01138	CDS	betl_1	HTH-type transcriptional regulator Betl	
SAMN04901664_01139	CDS	hypothetical protein		
SAMN04901664_01140	CDS	hypothetical protein		
SAMN04901664_01141	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01142	CDS	hypothetical protein		
SAMN04901664_01143	CDS	hypothetical protein		
SAMN04901664_01144	CDS	hypothetical protein		
SAMN04901664_01145	CDS	hypothetical protein		
SAMN04901664_01146	CDS	hypothetical protein		
SAMN04901664_01147	CDS	1.2.1.26		Alpha-ketoglutaric semialdehyde dehydrogenase
SAMN04901664_01148	CDS	bm3R1_2		HTH-type transcriptional repressor Bm3R1
SAMN04901664_01149	CDS	emrY_1		putative multidrug resistance protein EmrY
SAMN04901664_01150	CDS	emrA_2		Multidrug export protein EmrA
SAMN04901664_01151	CDS	hypothetical protein		
SAMN04901664_01152	CDS	hypothetical protein		
SAMN04901664_01153	CDS	hypothetical protein		
SAMN04901664_01154	CDS	hypothetical protein		
SAMN04901664_01155	CDS	hypothetical protein		
SAMN04901664_01156	CDS	hypothetical protein		
SAMN04901664_01157	CDS	hypothetical protein		
SAMN04901664_01158	CDS	hypothetical protein		
SAMN04901664_01159	CDS	hypothetical protein		
SAMN04901664_01160	CDS	hypothetical protein		
SAMN04901664_01161	CDS	hypothetical protein		
SAMN04901664_01162	CDS	hypothetical protein		
SAMN04901664_01163	CDS	hin_1		DNA-invertase hin

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01164	CDS	hypothetical protein		
SAMN04901664_01165	CDS	bla	3.5.2.6	Beta-lactamase TEM
SAMN04901664_01166	CDS	tnpR	Transposon Tn3 resolvase	
SAMN04901664_01167	CDS	hypothetical protein		
SAMN04901664_01168	CDS	hypothetical protein		
SAMN04901664_01169	CDS	ant1_2	2.7.7.47	Streptomycin 3"-adenylyltransferase
SAMN04901664_01170	CDS	emrE_1	Multidrug transporter EmrE	
SAMN04901664_01171	CDS	folP_1	2.5.1.15	Dihydropteroate synthase
SAMN04901664_01172	CDS	hypothetical protein		
SAMN04901664_01173	CDS	hypothetical protein		
SAMN04901664_01174	CDS	hypothetical protein		
SAMN04901664_01175	CDS	hypothetical protein		
SAMN04901664_01176	CDS	hypothetical protein		
SAMN04901664_01177	CDS	hypothetical protein		
SAMN04901664_01178	CDS	hypothetical protein		
SAMN04901664_01179	CDS	hypothetical protein		
SAMN04901664_01180	CDS	hypothetical protein		
SAMN04901664_01181	CDS	hypothetical protein		
SAMN04901664_01182	CDS	bicA_3	Bicarbonate transporter BicA	
SAMN04901664_01183	CDS	hypothetical protein		
SAMN04901664_01184	CDS	hypothetical protein		
SAMN04901664_01185	CDS	hypothetical protein		
SAMN04901664_01186	CDS	hypothetical protein		
SAMN04901664_01187	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01188	CDS	hypothetical protein		
SAMN04901664_01189	CDS	tnsB_2	Transposon Tn7 transposition protein TnsB	
SAMN04901664_01190	CDS	hypothetical protein		
SAMN04901664_01191	CDS	folP_2	2.5.1.15	Dihydropteroate synthase
SAMN04901664_01192	CDS	glmM_1	5.4.2.10	Phosphoglucosamine mutase
SAMN04901664_01193	CDS	hypothetical protein		
SAMN04901664_01194	CDS	tnsB_3	Transposon Tn7 transposition protein TnsB	
SAMN04901664_01195	CDS	hypothetical protein		
SAMN04901664_01196	CDS	bdhA	1.1.1.30	D-beta-hydroxybutyrate dehydrogenase
SAMN04901664_01197	CDS	hypothetical protein		
SAMN04901664_01198	CDS	hypothetical protein		
SAMN04901664_01199	CDS	neo_1	2.7.1.95	Aminoglycoside 3'-phosphotransferase
SAMN04901664_01200	CDS	hypothetical protein		
SAMN04901664_01201	CDS	hypothetical protein		
SAMN04901664_01202	CDS	smf-1_2	Major fimbrial subunit SMF-1	
SAMN04901664_01203	CDS	hypothetical protein		
SAMN04901664_01204	CDS	hypothetical protein		
SAMN04901664_01205	CDS	smf-1_3	Major fimbrial subunit SMF-1	
SAMN04901664_01206	CDS	hypothetical protein		
SAMN04901664_01207	CDS	neo_2	2.7.1.95	Aminoglycoside 3'-phosphotransferase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01208	CDS	hypothetical protein		
SAMN04901664_01209	CDS	hypothetical protein		
SAMN04901664_01210	rRNA	23S ribosomal RNA (partial)		
SAMN04901664_01211	CDS	hypothetical protein		
SAMN04901664_01212	rRNA	23S ribosomal RNA (partial)		
SAMN04901664_01213	CDS	hypothetical protein		
SAMN04901664_01214	tRNA	tRNA-Thr(ggt)		
SAMN04901664_01215	tRNA	tRNA-Gly(tcc)		
SAMN04901664_01216	tRNA	tRNA-Tyr(gta)		
SAMN04901664_01217	tRNA	tRNA-Thr(tgt)		
SAMN04901664_01218	CDS	trpE	4.1.3.27	Anthranilate synthase component 1
SAMN04901664_01219	CDS	gph_2	3.1.3.18	Phosphoglycolate phosphatase
SAMN04901664_01220	CDS	fhaA	FHA domain-containing protein FhaA	
SAMN04901664_01221	CDS	xcpQ	protein D	
SAMN04901664_01222	CDS	hypothetical protein		
SAMN04901664_01223	CDS	hypothetical protein		
SAMN04901664_01224	CDS	hvrA	HvrA	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01225	CDS	3.1.-.-	Putative esterase	
SAMN04901664_01226	CDS	hypothetical protein		
SAMN04901664_01227	CDS	hypothetical protein		
SAMN04901664_01228	CDS	hemD	4.2.1.75	Uroporphyrinogen-III synthase
SAMN04901664_01229	CDS	hemC	2.5.1.61	Porphobilinogen deaminase
SAMN04901664_01230	CDS	yehT	Transcriptional regulatory protein YehT	
SAMN04901664_01231	CDS	ypdA	2.7.13.3	Sensor histidine kinase YpdA
SAMN04901664_01232	CDS	argH	4.3.2.1	Argininosuccinate lyase
SAMN04901664_01233	CDS	putative Fe(2+)-trafficking protein		
SAMN04901664_01234	CDS	phoU	Phosphate-specific transport system accessory protein PhoU	
SAMN04901664_01235	CDS	tolC_1	Outer membrane protein TolC	
SAMN04901664_01236	CDS	hypothetical protein		
SAMN04901664_01237	CDS	hypothetical protein		
SAMN04901664_01238	CDS	hypothetical protein		
SAMN04901664_01239	CDS	thiC	4.1.99.17	Phosphomethylpyrimidine synthase
SAMN04901664_01240	CDS	nudF	3.6.1.13	ADP-ribose pyrophosphatase
SAMN04901664_01241	CDS	cpdA_1	3.1.4.53	3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01242	CDS	dkSA	RNA polymerase-binding transcription factor DksA	
SAMN04901664_01243	CDS	gluQ	6.1.1.-	Glutamyl-Q tRNA(Asp) synthetase
SAMN04901664_01244	CDS	ftsW	2.4.1.129	putative peptidoglycan glycosyltransferase FtsW
SAMN04901664_01245	CDS	murD	6.3.2.9	UDP-N-acetylmuramoylalanine-D-glutamate ligase
SAMN04901664_01246	CDS	hypothetical protein		
SAMN04901664_01247	CDS	feoB	Fe(2+) transporter FeoB	
SAMN04901664_01248	CDS	hypothetical protein		
SAMN04901664_01249	CDS	xerD_1	Tyrosine recombinase XerD	
SAMN04901664_01250	CDS	dsbC_2	Thiol:disulfide interchange protein DsbC	
SAMN04901664_01251	CDS	hom_2	1.1.1.3	Homoserine dehydrogenase
SAMN04901664_01252	CDS	thrC	4.2.3.1	Threonine synthase
SAMN04901664_01253	CDS	pbpG	3.4.21.-	D-alanyl-D-alanine endopeptidase
SAMN04901664_01254	CDS	uvrY	Response regulator UvrY	
SAMN04901664_01255	CDS	kinE	2.7.13.3	Sporulation kinase E
SAMN04901664_01256	CDS	zraR	Transcriptional regulatory protein ZraR	
SAMN04901664_01257	CDS	3.4.21.-	protease	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01258	CDS	gpmI	5.4.2.12	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
SAMN04901664_01259	CDS	lptG	Lipopolysaccharide export system permease protein LptG	
SAMN04901664_01260	CDS	lptF	Lipopolysaccharide export system permease protein LptF	
SAMN04901664_01261	CDS	pepA	3.4.11.1	Cytosol aminopeptidase
SAMN04901664_01262	CDS	hypothetical protein		
SAMN04901664_01263	CDS	hypothetical protein		
SAMN04901664_01264	CDS	hypothetical protein		
SAMN04901664_01265	CDS	ribE	2.5.1.9	Riboflavin synthase
SAMN04901664_01266	CDS	fokIM	2.1.1.72	Modification methylase FokI
SAMN04901664_01267	CDS	ribD	RibD	
SAMN04901664_01268	CDS	nrdR	Transcriptional repressor NrdR	
SAMN04901664_01269	CDS	amtB_2	Ammonia channel	
SAMN04901664_01270	CDS	glnK	II 2	
SAMN04901664_01271	CDS	hypothetical protein		
SAMN04901664_01272	CDS	comM_2	Competence protein ComM	
SAMN04901664_01273	CDS	hypothetical protein		
SAMN04901664_01274	CDS	neo_3	2.7.1.95	Aminoglycoside 3'-phosphotransferase
SAMN04901664_01275	CDS	hypothetical protein		
SAMN04901664_01276	CDS	hypothetical protein		
SAMN04901664_01277	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01278	CDS	hypothetical protein		
SAMN04901664_01279	CDS	tetR		Tetracycline repressor protein class B from transposon Tn10
SAMN04901664_01280	CDS	tetA		Tetracycline resistance protein, class B
SAMN04901664_01281	CDS	hypothetical protein		
SAMN04901664_01282	CDS	hypothetical protein		
SAMN04901664_01283	CDS	bicA_4		Bicarbonate transporter BicA
SAMN04901664_01284	CDS	hypothetical protein		
SAMN04901664_01285	CDS	hypothetical protein		
SAMN04901664_01286	CDS	hypothetical protein		
SAMN04901664_01287	CDS	hypothetical protein		
SAMN04901664_01288	CDS	hypothetical protein		
SAMN04901664_01289	CDS	hypothetical protein		
SAMN04901664_01290	CDS	hypothetical protein		
SAMN04901664_01291	CDS	hypothetical protein		
SAMN04901664_01292	CDS	hypothetical protein		
SAMN04901664_01293	CDS	hypothetical protein		
SAMN04901664_01294	CDS	hypothetical protein		
SAMN04901664_01295	CDS	hypothetical protein		
SAMN04901664_01296	CDS	hypothetical protein		
SAMN04901664_01297	CDS	hypothetical protein		
SAMN04901664_01298	CDS	hypothetical protein		
SAMN04901664_01299	CDS	hypothetical protein		
SAMN04901664_01300	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01301	CDS	hypothetical protein		
SAMN04901664_01302	CDS	hypothetical protein		
SAMN04901664_01303	CDS	hypothetical protein		
SAMN04901664_01304	CDS	hypothetical protein		
SAMN04901664_01305	CDS	hypothetical protein		
SAMN04901664_01306	CDS	hypothetical protein		
SAMN04901664_01307	CDS	hypothetical protein		
SAMN04901664_01308	CDS	hypothetical protein		
SAMN04901664_01309	CDS	hypothetical protein		
SAMN04901664_01310	CDS	hypothetical protein		
SAMN04901664_01311	CDS	hypothetical protein		
SAMN04901664_01312	CDS	hypothetical protein		
SAMN04901664_01313	CDS	hypothetical protein		
SAMN04901664_01314	CDS	hypothetical protein		
SAMN04901664_01315	CDS	hypothetical protein		
SAMN04901664_01316	CDS	hypothetical protein		
SAMN04901664_01317	CDS	hypothetical protein		
SAMN04901664_01318	CDS	hypothetical protein		
SAMN04901664_01319	CDS	hypothetical protein		
SAMN04901664_01320	CDS	hypothetical protein		
SAMN04901664_01321	CDS	hypothetical protein		
SAMN04901664_01322	CDS	rhtC_1		Threonine efflux protein
SAMN04901664_01323	CDS	ftsK		DNA translocase FtsK
SAMN04901664_01324	CDS	4.3.1.9		Glucosaminiate ammonia-lyase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01325	CDS	aat	2.3.2.6	Leucyl/phenylalanyl-tRNA--protein transferase
SAMN04901664_01326	CDS	ate	2.3.2.8	Putative arginyl-tRNA--protein transferase
SAMN04901664_01327	CDS	rimI	2.3.1.128	Ribosomal-protein-alanine acetyltransferase
SAMN04901664_01328	CDS	hypothetical protein		
SAMN04901664_01329	CDS	hypothetical protein		
SAMN04901664_01330	CDS	tufI	Elongation factor Tu	
SAMN04901664_01331	CDS	hypothetical protein		
SAMN04901664_01332	CDS	hypothetical protein		
SAMN04901664_01333	CDS	hypothetical protein		
SAMN04901664_01334	CDS	hypothetical protein		
SAMN04901664_01335	CDS	hypothetical protein		
SAMN04901664_01336	CDS	hypothetical protein		
SAMN04901664_01337	CDS	hypothetical protein		
SAMN04901664_01338	CDS	hypothetical protein		
SAMN04901664_01339	CDS	hypothetical protein		
SAMN04901664_01340	CDS	hypothetical protein		
SAMN04901664_01341	CDS	hypothetical protein		
SAMN04901664_01342	CDS	hypothetical protein		
SAMN04901664_01343	CDS	hypothetical protein		
SAMN04901664_01344	CDS	hypothetical protein		
SAMN04901664_01345	CDS	hypothetical protein		
SAMN04901664_01346	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01347	CDS	hypothetical protein		
SAMN04901664_01348	CDS	hypothetical protein		
SAMN04901664_01349	CDS	hypothetical protein		
SAMN04901664_01350	CDS	hypothetical protein		
SAMN04901664_01351	CDS	hypothetical protein		
SAMN04901664_01352	CDS	hypothetical protein		
SAMN04901664_01353	CDS	hypothetical protein		
SAMN04901664_01354	CDS	hypothetical protein		
SAMN04901664_01355	CDS	hypothetical protein		
SAMN04901664_01356	CDS	hypothetical protein		
SAMN04901664_01357	CDS	hypothetical protein		
SAMN04901664_01358	CDS	hypothetical protein		
SAMN04901664_01359	CDS	hypothetical protein		
SAMN04901664_01360	CDS	hypothetical protein		
SAMN04901664_01361	CDS	hypothetical protein		
SAMN04901664_01362	CDS	hypothetical protein		
SAMN04901664_01363	CDS	tnsB_4		Transposon Tn7 transposition protein TnsB
SAMN04901664_01364	CDS	hypothetical protein		
SAMN04901664_01365	CDS	hypothetical protein		
SAMN04901664_01366	CDS	hypothetical protein		
SAMN04901664_01367	CDS	hypothetical protein		
SAMN04901664_01368	CDS	xerC_2		Tyrosine recombinase XerC
SAMN04901664_01369	CDS	hypothetical protein		
SAMN04901664_01370	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01371	CDS	hypothetical protein		
SAMN04901664_01372	CDS	hypothetical protein		
SAMN04901664_01373	CDS	hypothetical protein		
SAMN04901664_01374	CDS	bicA_5	Bicarbonate transporter BicA	
SAMN04901664_01375	CDS	hypothetical protein		
SAMN04901664_01376	CDS	hypothetical protein		
SAMN04901664_01377	CDS	hypothetical protein		
SAMN04901664_01378	CDS	aacC1	2.3.1.60	Gentamicin 3-N-acetyltransferase
SAMN04901664_01379	CDS	xerD_2	Tyrosine recombinase XerD	
SAMN04901664_01380	CDS	hypothetical protein		
SAMN04901664_01381	CDS	hin_2	DNA-invertase hin	
SAMN04901664_01382	CDS	hypothetical protein		
SAMN04901664_01383	CDS	hypothetical protein		
SAMN04901664_01384	CDS	hypothetical protein		
SAMN04901664_01385	CDS	hypothetical protein		
SAMN04901664_01386	tRNA	tRNA-Arg(acg)		
SAMN04901664_01387	CDS	hypothetical protein		
SAMN04901664_01388	CDS	hypothetical protein		
SAMN04901664_01389	CDS	nagK	3.7.1.20	Fumarylpyruvate hydrolase
SAMN04901664_01390	CDS	nimR_3	HTH-type transcriptional regulator NimR	
SAMN04901664_01391	CDS	yijE_2	YijE	
SAMN04901664_01392	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01393	CDS	1.6.5.2	(quinone)	
SAMN04901664_01394	CDS	xpt	2.4.2.22	Xanthine phosphoribosyltransferase
SAMN04901664_01395	CDS	hypothetical protein		
SAMN04901664_01396	CDS	hypothetical protein		
SAMN04901664_01397	CDS	hypothetical protein		
SAMN04901664_01398	CDS	ybeY	3.1.-.-	Endoribonuclease YbeY
SAMN04901664_01399	CDS	PhoH-like protein		
SAMN04901664_01400	CDS	miaB	2.8.4.3	tRNA-2-methylthio-N(6)-dimethylallyladenine synthase
SAMN04901664_01401	CDS	slt_2	4.2.2.-	Soluble lytic murein transglycosylase
SAMN04901664_01402	CDS	hypothetical protein		
SAMN04901664_01403	CDS	mdh	1.1.1.37	Malate dehydrogenase
SAMN04901664_01404	CDS	hypothetical protein		
SAMN04901664_01405	CDS	hypothetical protein		
SAMN04901664_01406	CDS	hypothetical protein		
SAMN04901664_01407	CDS	rlmJ	2.1.1.266	Ribosomal RNA large subunit methyltransferase J
SAMN04901664_01408	CDS	hypothetical protein		
SAMN04901664_01409	CDS	hypothetical protein		
SAMN04901664_01410	rRNA	16S ribosomal RNA		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01411	tRNA	tRNA-Ile(gat)		
SAMN04901664_01412	rRNA	5S ribosomal RNA		
		23S ribosomal RNA		
SAMN04901664_01413	rRNA	rRNA (partial)		
SAMN04901664_01414	CDS	hypothetical protein		
SAMN04901664_01415	CDS	hypothetical protein		
SAMN04901664_01416	CDS	capA	CapA	
SAMN04901664_01417	CDS	hypothetical protein		
SAMN04901664_01418	CDS	DNA base-flipping protein		
SAMN04901664_01419	CDS	teaD	TRAP-T-associated universal stress protein TeaD	
SAMN04901664_01420	CDS	cat_2	2.3.1.28	Chloramphenicol acetyltransferase
SAMN04901664_01421	CDS	greA	GreA	
SAMN04901664_01422	CDS	carB	6.3.5.5	Carbamoyl-phosphate synthase large chain
SAMN04901664_01423	CDS	carA	6.3.5.5	Carbamoyl-phosphate synthase small chain
SAMN04901664_01424	CDS	hypothetical protein		
SAMN04901664_01425	CDS	hypothetical protein		
SAMN04901664_01426	CDS	RNA-binding protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01427	CDS	rImE	2.1.1.166	Ribosomal RNA large subunit methyltransferase E
SAMN04901664_01428	CDS	ftsH	3.4.24.-	ATP-dependent zinc metalloprotease FtsH
SAMN04901664_01429	CDS	folP_3	2.5.1.15	Dihydropteroate synthase
SAMN04901664_01430	CDS	hypothetical protein		
SAMN04901664_01431	CDS	hypothetical protein		
SAMN04901664_01432	tRNA	tRNA-Leu(taa)		
SAMN04901664_01433	CDS	phoD	3.1.3.1	Alkaline phosphatase D
SAMN04901664_01434	tRNA	tRNA-Leu(taa)		
SAMN04901664_01435	tRNA	tRNA-Cys(gca)		
SAMN04901664_01436	CDS	folD	protein	
SAMN04901664_01437	CDS	prmA_1	2.1.1.-	Ribosomal protein L11 methyltransferase
SAMN04901664_01438	CDS	hypothetical protein		
SAMN04901664_01439	CDS	kgp_2	Alpha-ketoglutarate permease	
SAMN04901664_01440	CDS	glpK	2.7.1.30	Glycerol kinase
SAMN04901664_01441	CDS	glpD	1.1.5.3	Aerobic glycerol-3-phosphate dehydrogenase
SAMN04901664_01442	CDS	pkcG	4.1.1.32	Phosphoenolpyruvate carboxykinase [GTP]
SAMN04901664_01443	CDS	bmrU	2.7.1.-	Putative lipid kinase BmrU

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01444	CDS	cpdA_2	3.1.4.53	3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA
SAMN04901664_01445	CDS	hypothetical protein		
SAMN04901664_01446	CDS	groS	10 kDa chaperonin	
SAMN04901664_01447	CDS	groL	60 kDa chaperonin	
SAMN04901664_01448	CDS	dgkA	2.7.1.107	Diacylglycerol kinase
SAMN04901664_01449	CDS	ytnP	3.1.1.-	putative quorum-quenching lactonase YtnP
SAMN04901664_01450	CDS	glpQ	3.1.4.46	Glycerophosphodiester phosphodiesterase, periplasmic
SAMN04901664_01451	CDS	mexB_2	MexB	
SAMN04901664_01452	CDS	hypothetical protein		
SAMN04901664_01453	CDS	htpX_1	3.4.24.-	Protease HtpX
SAMN04901664_01454	CDS	slt_3	4.2.2.-	Soluble lytic murein transglycosylase
SAMN04901664_01455	CDS	ttcA	tRNA 2-thiocytidine biosynthesis protein TtcA	
SAMN04901664_01456	CDS	hypothetical protein		
SAMN04901664_01457	CDS	mIfF	4.2.2.-	Membrane-bound lytic murein transglycosylase F
SAMN04901664_01458	CDS	greB	GreB	
SAMN04901664_01459	tRNA	tRNA tRNA-Ser(iga)		
SAMN04901664_01460	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01461	CDS	dhbF_2		
SAMN04901664_01462	CDS	hypothetical protein		
SAMN04901664_01463	CDS	hypothetical protein		
SAMN04901664_01464	CDS	hypothetical protein		
SAMN04901664_01465	CDS	hypothetical protein		
SAMN04901664_01466	CDS	mhqN		Putative NAD(P)H nitroreductase MhqN
SAMN04901664_01467	CDS	isfD	1.-.-	Sulfoacetaldehyde reductase
SAMN04901664_01468	CDS	hypothetical protein	1.1.1.313	
SAMN04901664_01469	CDS	garK	2.7.1.165	Glycerate 2-kinase
SAMN04901664_01470	CDS	1.-.-	putative oxidoreductase	
SAMN04901664_01471	CDS	fdhD	Sulfurtransferase FdhD	
SAMN04901664_01472	CDS	hypothetical protein		
SAMN04901664_01473	CDS	pdxB	1.1.1.290	Erythronate-4-phosphate dehydrogenase
SAMN04901664_01474	CDS	epmA	6.3.1.-	Elongation factor P--(R)-beta-lysine ligase
SAMN04901664_01475	CDS	hypothetical protein		
SAMN04901664_01476	CDS	radA	3.6.4.-	DNA repair protein RadA
SAMN04901664_01477	CDS	cycA_3		
SAMN04901664_01478	CDS	hypothetical protein	D-serine/D-alanine/glycine transporter	
SAMN04901664_01479	CDS	lysA	4.1.1.20	Diaminopimelate decarboxylase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01480	CDS	dapF	5.1.1.7	Diaminopimelate epimerase
SAMN04901664_01481	CDS	rhtB_2	Homoserine/homoserine lactone efflux protein	
SAMN04901664_01482	CDS	xerC_3	Tyrosine recombinase XerC	
SAMN04901664_01483	CDS	etfB	Electron transfer flavoprotein subunit beta	
SAMN04901664_01484	CDS	etfA	Electron transfer flavoprotein subunit alpha	
SAMN04901664_01485	CDS	gyrA	5.99.1.3	DNA gyrase subunit A
SAMN04901664_01486	CDS	arnT	2.4.2.43	Undecaprenyl phosphate-alpha- 4-amino-4-deoxy-L-arabinose arabinosyl transferase
SAMN04901664_01487	CDS	hypothetical protein	putative glycosyltransferase	
SAMN04901664_01488	CDS	2.4.-.-	Carbohydrate deacetylase	
SAMN04901664_01489	CDS	3.5.1.-	Inner membrane transport permease YbhR	
SAMN04901664_01490	CDS	ybhR_2		
SAMN04901664_01491	CDS	hypothetical protein		
SAMN04901664_01492	CDS	emrA_3	Multidrug export protein EmrA	
SAMN04901664_01493	CDS	hypothetical protein		
SAMN04901664_01494	CDS	serC	2.6.1.52	Phosphoserine amino transferase
SAMN04901664_01495	CDS	hypothetical protein		
SAMN04901664_01496	CDS	hypothetical protein		
SAMN04901664_01497	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01498	CDS	yedA	putative inner membrane transporter YedA	
SAMN04901664_01499	CDS	loIE	Lipoprotein-releasing system transmembrane protein LoIE	
SAMN04901664_01500	CDS	lolD_1	3.6.3.-	Lipoprotein-releasing system
SAMN04901664_01501	CDS	comEC	ComE operon protein 3	Lipoprotein-releasing system ATP-binding protein LolD
SAMN04901664_01502	CDS	lpxL_1	2.3.1.241	Lipid A biosynthesis lauroyltransferase
SAMN04901664_01503	CDS	sppA	3.4.21.-	Putative signal peptide peptidase SppA
SAMN04901664_01504	CDS	hypothetical protein		
SAMN04901664_01505	CDS	purN	2.1.2.2	Phosphoribosylglycinamide formyltransferase
SAMN04901664_01506	CDS	purM	6.3.3.1	Phosphoribosylformylglycinamide cyclase
SAMN04901664_01507	CDS	tqsA	AI-2 transport protein TqsA	
SAMN04901664_01508	CDS	hda	Hda	
SAMN04901664_01509	CDS	hypothetical protein		
SAMN04901664_01510	CDS	hypothetical protein		
SAMN04901664_01511	CDS	hypothetical protein		
SAMN04901664_01512	CDS	hypothetical protein		
SAMN04901664_01513	CDS	sigE	ECF RNA polymerase sigma factor SigE	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01514	CDS	rlmB_1	2.1.1.185	23S rRNA (guanosine-2'-O-)-methyltransferase RlmB
SAMN04901664_01515	CDS	fbp_1	3.1.3.11	Fructose-1,6-bisphosphatase class 1
SAMN04901664_01516	CDS	hypothetical protein		
SAMN04901664_01517	CDS	pal	lipoprotein	
SAMN04901664_01518	CDS	tolB	Protein TolB	
SAMN04901664_01519	CDS	rtxA	3.4.22.-	Multifunctional-autoprocessing repeats-in-toxin
SAMN04901664_01520	CDS	exbD_3	ExbD	
SAMN04901664_01521	CDS	exbB_3	ExbB	
SAMN04901664_01522	CDS	ybgC	3.1.2.-	Acyl-CoA thioesterase YbgC
SAMN04901664_01523	CDS	yxeP_1	3.-.-	putative hydrolase YxeP
SAMN04901664_01524	CDS	ruvB	3.6.4.12	Holliday junction ATP-dependent DNA helicase RuvB
SAMN04901664_01525	CDS	ruvA	3.6.4.12	Holliday junction ATP-dependent DNA helicase RuvA
SAMN04901664_01526	CDS	dgt	3.1.5.1	Deoxyguanosinetriphosphate triphosphohydrolase
SAMN04901664_01527	CDS	purL	6.3.5.3	Phosphoribosylformylglycinamide synthase
SAMN04901664_01528	CDS	bcr_1	protein	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01529	CDS	hypothetical protein		
SAMN04901664_01530	CDS	GTP cyclohydrolase 1 type 2		2,3-dehydroadipyl-CoA hydratase
SAMN04901664_01531	CDS	paaF_1	4.2.1.17	
SAMN04901664_01532	CDS	Bifunctional NMN adenyltransferase/Nudix hydrolase		
SAMN04901664_01533	CDS	hypothetical protein		
SAMN04901664_01534	CDS	bcp	1.1.1.15	Putative peroxiredoxin bcp
SAMN04901664_01535	CDS	hypothetical protein		
SAMN04901664_01536	CDS	hypothetical protein		
SAMN04901664_01537	CDS	queC	6.3.4.20	7-cyano-7-deazaguanine synthase
SAMN04901664_01538	CDS	queE	4.3.99.3	7-carboxy-7-deazaguanine synthase
SAMN04901664_01539	CDS	dapD	2.3.1.117	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase
SAMN04901664_01540	CDS	hypothetical protein		
SAMN04901664_01541	CDS	cbI		HTH-type transcriptional regulator cbI
SAMN04901664_01542	CDS	cysA_2	3.6.3.25	Sulfate/thiosulfate import ATP-binding protein CysA

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01543	CDS	cysW	Sulfate transport system permease protein CysW	
SAMN04901664_01544	CDS	cysT	Sulfate transport system permease protein CysT	
SAMN04901664_01545	CDS	hypothetical protein		
SAMN04901664_01546	CDS	sbp_2	Sulfate-binding protein	
SAMN04901664_01547	CDS	pabC	4.1.3.38	Aminodeoxychorismate lyase
SAMN04901664_01548	CDS	mltG	4.2.2.-	Endolytic murein transglycosylase
SAMN04901664_01549	CDS	tmk_1	2.7.4.9	Thymidylate kinase
SAMN04901664_01550	CDS	hypothetical protein		
SAMN04901664_01551	CDS	nadB	1.4.3.16	L-aspartate oxidase
SAMN04901664_01552	CDS	degQ	3.4.21.107	Periplasmic pH-dependent serine endoprotease DegQ
SAMN04901664_01553	CDS	hypothetical protein		
SAMN04901664_01554	CDS	lepA	3.6.5.-	Elongation factor 4
SAMN04901664_01555	CDS	lepB	3.4.21.89	Signal peptidase I
SAMN04901664_01556	CDS	hypothetical protein		
SAMN04901664_01557	CDS	rnc	3.1.26.3	Ribonuclease 3
SAMN04901664_01558	CDS	era	GTPase Era	
SAMN04901664_01559	CDS	hypothetical protein		
SAMN04901664_01560	CDS	recO	DNA repair protein RecO	
SAMN04901664_01561	CDS	pdxJ	2.6.99.2	Pyridoxine 5'-phosphate synthase
SAMN04901664_01562	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01563	CDS	ydfG	1.1.1.381	NADP-dependent 3-hydroxy acid dehydrogenase YdfG
SAMN04901664_01564	tRNA	tRNA-Asn(gtt)		
SAMN04901664_01565	CDS	hypothetical protein		
SAMN04901664_01566	CDS	hypothetical protein		
SAMN04901664_01567	CDS	hypothetical protein		
SAMN04901664_01568	CDS	2.6.1.1	Aspartate aminotransferase	
SAMN04901664_01569	CDS	hypothetical protein		
SAMN04901664_01570	CDS	ydaM_1	2.7.7.65	putative diguanylate cyclase YdaM
SAMN04901664_01571	CDS	hypothetical protein		
SAMN04901664_01572	CDS	uvrB_1	UvrABC system protein B	
SAMN04901664_01573	CDS	blc	Blc	
SAMN04901664_01574	CDS	hypothetical protein		
SAMN04901664_01575	CDS	gap2	1.2.1.-	Glyceraldehyde-3-phosphate dehydrogenase-like protein
SAMN04901664_01576	CDS	hypothetical protein		
SAMN04901664_01577	CDS	hypothetical protein		
SAMN04901664_01578	CDS	obg	3.6.5.-	GTPase Obg
SAMN04901664_01579	CDS	proB	2.7.2.11	Glutamate 5-kinase
SAMN04901664_01580	CDS	hypothetical protein		
SAMN04901664_01581	CDS	hypothetical protein		
SAMN04901664_01582	CDS	dus	1.3.1.-	putative tRNA-dihydrouridine synthase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01583	CDS	1.13.12.-	Putative monooxygenase	
SAMN04901664_01584	CDS	hypothetical protein		
SAMN04901664_01585	CDS	hypothetical protein		
SAMN04901664_01586	CDS	mmaA	5.1.3.14	UDP-N-acetylglucosamine 2-epimerase
SAMN04901664_01587	CDS	hypothetical protein		
SAMN04901664_01588	CDS	hypothetical protein		
SAMN04901664_01589	CDS	icaA	2.4.1.-	Poly-beta-1,6-N-acetyl-D-glucosamine synthase
SAMN04901664_01590	CDS	hypothetical protein		
SAMN04901664_01591	CDS	hypothetical protein		
SAMN04901664_01592	CDS	phrB	4.1.99.3	Deoxyribodipyrimidine photolyase
SAMN04901664_01593	CDS	slyD	5.2.1.8	FKBP-type peptidyl-prolyl cis-trans isomerase SlyD
SAMN04901664_01594	CDS	ndh	1.6.99.3	NADH dehydrogenase
SAMN04901664_01595	CDS	dacD	3.4.16.4	D-alanyl-D-alanine carboxypeptidase DacD
SAMN04901664_01596	CDS	hypothetical protein		
SAMN04901664_01597	CDS	icd_1	1.1.1.42	Isocitrate dehydrogenase [NADP]
SAMN04901664_01598	CDS	rluE	5.4.99.20	Ribosomal large subunit pseudouridine synthase E
SAMN04901664_01599	CDS	icd_2	1.1.1.42	Isocitrate dehydrogenase [NADP]

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01600	CDS	hypothetical protein		
SAMN04901664_01601	CDS	hypothetical protein		
SAMN04901664_01602	CDS	hypothetical protein		
SAMN04901664_01603	CDS	glrR_2	HTH-type transcriptional regulator GltR	
SAMN04901664_01604	CDS	teyP	L-cystine uptake protein TcyP	
SAMN04901664_01605	CDS	yddE_1	5.1.-.-	putative isomerase YddE
SAMN04901664_01606	CDS	3.4.24.-	putative zinc protease	
SAMN04901664_01607	CDS	hypothetical protein		
SAMN04901664_01608	CDS	hypothetical protein		
SAMN04901664_01609	CDS	ygiF	3.6.1.25	Inorganic triphosphatase
SAMN04901664_01610	CDS	hypothetical protein		
SAMN04901664_01611	CDS	thiE	2.5.1.3	Thiamine-phosphate synthase
SAMN04901664_01612	CDS	hemL	5.4.3.8	Glutamate-1-semialdehyde 2,1-aminomutase
SAMN04901664_01613	CDS	dhbB	3.3.2.1	Isochorismatase
SAMN04901664_01614	CDS	rluA_2	5.4.99.28	Ribosomal large subunit pseudouridine synthase A
SAMN04901664_01615	CDS	rapA	3.6.4.-	RNA polymerase-associated protein RapA
SAMN04901664_01616	CDS	hypothetical protein		
SAMN04901664_01617	CDS	fabR_2	HTH-type transcriptional repressor FabR	
SAMN04901664_01618	CDS	1.-.-	NADPH oxidoreductase	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01619	CDS	desA3_2	1.14.19.-	NADPH-dependent stearyl-CoA 9-desaturase
SAMN04901664_01620	CDS	hypothetical protein		
SAMN04901664_01621	CDS	hypothetical protein		
SAMN04901664_01622	CDS	hypothetical protein		
SAMN04901664_01623	CDS	dat	2.6.1.76	Diaminobutyrate--2-oxoglutarate aminotransferase
SAMN04901664_01624	CDS	ddc	4.1.1.86	L-2,4-diaminobutyrate decarboxylase
SAMN04901664_01625	CDS	styD	1.2.1.39	Phenylacetaldehyde dehydrogenase
SAMN04901664_01626	CDS	lrp_3	protein	
SAMN04901664_01627	CDS	ipdC	4.1.1.74	Indole-3-pyruvate decarboxylase
SAMN04901664_01628	CDS	aroP_2	Aromatic amino acid transport protein AroP	
SAMN04901664_01629	CDS	pstS	PstS	
SAMN04901664_01630	CDS	pstC1	Phosphate transport system permease protein PstC 1	
SAMN04901664_01631	CDS	pstA	Phosphate transport system permease protein PstA	
SAMN04901664_01632	CDS	pstB	3.6.3.27	Phosphate import ATP-binding protein PstB
SAMN04901664_01633	CDS	sohB	3.4.21.-	putative protease SohB
SAMN04901664_01634	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01635	CDS	yjdf	Inner membrane protein YjdF	
SAMN04901664_01636	CDS	purB	4.3.2.2	Adenylosuccinate lyase
SAMN04901664_01637	CDS	hfID	High frequency lysogenization protein HfID	
SAMN04901664_01638	CDS	mmmA	2.8.1.13	tRNA-specific 2-thiouridylylase MmmA
SAMN04901664_01639	CDS	nudJ	3.6.1.-	Phosphatase NudJ
SAMN04901664_01640	CDS	caiE	Carnitine operon protein CaiE	
SAMN04901664_01641	CDS	dacA	3.4.16.4	D-alanyl-D-alanine carboxypeptidase DacA
SAMN04901664_01642	CDS	hypothetical protein		
SAMN04901664_01643	CDS	hypothetical protein		
SAMN04901664_01644	CDS	surE_2	3.1.3.5	5'-nucleotidase SurE
SAMN04901664_01645	CDS	nlpD	NlpD	
SAMN04901664_01646	CDS	dmIR_4	HTH-type transcriptional regulator DmIR	
SAMN04901664_01647	CDS	lon2	3.4.21.53	Lon protease 2
SAMN04901664_01648	CDS	hypothetical protein		
SAMN04901664_01649	CDS	gloA	4.4.1.5	Lactoylglutathione lyase
SAMN04901664_01650	CDS	hypothetical protein		
SAMN04901664_01651	CDS	rpmE	50S ribosomal protein L31	
SAMN04901664_01652	CDS	hypothetical protein		
SAMN04901664_01653	CDS	hypothetical protein		
SAMN04901664_01654	CDS	epmB	5.4.3.-	L-lysine 2,3-aminomutase
SAMN04901664_01655	CDS	efp	Elongation factor P	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01656	CDS	cstA	Carbon starvation protein A	
SAMN04901664_01657	CDS	hypothetical protein		
SAMN04901664_01658	tRNA	tRNA-Val(gac)		
SAMN04901664_01659	CDS	hypothetical protein		
SAMN04901664_01660	CDS	hypothetical protein		
SAMN04901664_01661	CDS	hypothetical protein		
SAMN04901664_01662	CDS	hypothetical protein		
SAMN04901664_01663	CDS	hypothetical protein		
SAMN04901664_01664	CDS	pmfR	Transcriptional activator PmfR	
SAMN04901664_01665	CDS	puuB_2	1.4.3.-	Gamma-glutamylputrescine oxidoreductase
SAMN04901664_01666	CDS	hypothetical protein		
SAMN04901664_01667	CDS	bauC_1	1.2.1.-	Putative 3-oxopropanoate dehydrogenase
SAMN04901664_01668	CDS	gabP_2	GABA permease	
SAMN04901664_01669	CDS	gcvA_1	Glycine cleavage system transcriptional activator	
SAMN04901664_01670	CDS	betS	Glycine betaine/proline betaine transporter BetS	
SAMN04901664_01671	CDS	betL	BetL	
SAMN04901664_01672	CDS	absAa	1.14.12.14	2-aminobenzenesulfonate 2,3-dioxygenase subunit alpha
SAMN04901664_01673	CDS	gbsA	1.2.1.8	Betaine aldehyde dehydrogenase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01674	CDS	rubB_1	1.18.1.1	Rubredoxin-NAD(+) reductase
SAMN04901664_01675	CDS	puuB_3	1.4.3.-	Gamma-glutamylputrescine oxidoreductase
SAMN04901664_01676	CDS	eutQ	EutQ	
SAMN04901664_01677	CDS	hypothetical protein		
SAMN04901664_01678	CDS	hypothetical protein		
SAMN04901664_01679	CDS	yddG_1	YddG	
SAMN04901664_01680	CDS	hypothetical protein		
SAMN04901664_01681	CDS	hypothetical protein		
SAMN04901664_01682	CDS	ygcs	Inner membrane metabolite transport protein Ygcs	
SAMN04901664_01683	CDS	4.2.1.-	dehydratase	
SAMN04901664_01684	CDS	ctrA2	1.3.1.86	Crotonyl-CoA reductase
SAMN04901664_01685	CDS	ysaF_3	putative HTH-type transcriptional regulator YxaF	
SAMN04901664_01686	CDS	betl_2	HTH-type transcriptional regulator Betl	
SAMN04901664_01687	CDS	hypothetical protein		
SAMN04901664_01688	CDS	yhhW_4	1.13.11.24	Quercetin 2,3-dioxygenase
SAMN04901664_01689	CDS	psdht	4.2.1.-	Phenylserine dehydratase
SAMN04901664_01690	CDS	tdcB_1	4.3.1.19	L-threonine dehydratase catabolic TdcB
SAMN04901664_01691	CDS	dauR	Transcriptional regulator DauR	
SAMN04901664_01692	CDS	viuB	ViuB	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01693	CDS	angR		Anguibactin system regulator
SAMN04901664_01694	CDS	dhbF_3		Dimodular nonribosomal peptide synthase
SAMN04901664_01695	CDS	hypothetical protein		
SAMN04901664_01696	CDS	hypothetical protein		
SAMN04901664_01697	CDS	hmuU		Hemin transport system permease protein HmuU
SAMN04901664_01698	CDS	yfhA		putative siderophore transport system permease protein YfhA
SAMN04901664_01699	CDS	yusV		system ATP-binding protein YusV
SAMN04901664_01700	CDS	yciQ_2		putative ABC transporter solute-binding protein YciQ
SAMN04901664_01701	CDS	feuA_2		Ferrichrome receptor FcuA
SAMN04901664_01702	CDS	iucD_2	1.14.13.59	L-lysine N6-monooxygenase
SAMN04901664_01703	CDS	mbtB	6.3.2.-	Phenylloxazoline synthase MbtB
SAMN04901664_01704	CDS	entE	6.3.2.14	Enterobactin synthase component E
SAMN04901664_01705	CDS	entB	6.3.2.14	Enterobactin synthase component B
SAMN04901664_01706	CDS	hdc	4.1.1.22	Histidine decarboxylase
SAMN04901664_01707	CDS	hypothetical protein		
SAMN04901664_01708	CDS	putative ABC transporter ATP-binding protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01709	CDS	ndvA	3.6.3.42	Beta-(1-->2)glucan export ATP-binding/permease protein NdvA
SAMN04901664_01710	CDS	lgrE	1.1.-.-	Linear gramicidin dehydrogenase LgrE
SAMN04901664_01711	CDS	entD	2.7.8.-	Enterobactin synthase component D
SAMN04901664_01712	CDS	entC	5.4.4.2	Isochorismate synthase EntC
SAMN04901664_01713	CDS	ykuD	2.-.-.-	Putative L,D-transpeptidase YkuD
SAMN04901664_01714	CDS	hemE	4.1.1.37	Uroporphyrinogen decarboxylase
SAMN04901664_01715	CDS	hypothetical protein		
SAMN04901664_01716	CDS	hypothetical protein		
SAMN04901664_01717	CDS	hypothetical protein		
SAMN04901664_01718	CDS	ampC	3.5.2.6	Beta-lactamase
SAMN04901664_01719	rRNA	5S ribosomal RNA		
SAMN04901664_01720	CDS	rpoN	factor	
SAMN04901664_01721	CDS	hpf	Ribosome hibernation promoting factor	
SAMN04901664_01722	CDS	ibaG	Acid stress protein IbaG	
SAMN04901664_01723	CDS	murA	2.5.1.7	UDP-N-acetylglucosamine 1-carboxyvinyltransferase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01724	CDS	hisG	2.4.2.17	ATP phosphoribosyltransferase
SAMN04901664_01725	CDS	hisD	1.1.1.23	Histidinol dehydrogenase
SAMN04901664_01726	CDS	hisC	2.6.1.9	Histidinol-phosphate aminotransferase
SAMN04901664_01727	CDS	pabB	2.6.1.85	Aminodeoxychorismate synthase component I
SAMN04901664_01728	CDS	hypothetical protein		
SAMN04901664_01729	CDS	hypothetical protein		
SAMN04901664_01730	CDS	hypothetical protein		
SAMN04901664_01731	CDS	hypothetical protein		
SAMN04901664_01732	CDS	hypothetical protein		
SAMN04901664_01733	CDS	hypothetical protein		
SAMN04901664_01734	CDS	hypothetical protein		
SAMN04901664_01735	CDS	nudC_1	3.6.1.22	NADH pyrophosphatase
SAMN04901664_01736	CDS	nudL	3.6.1.-	putative Nudix hydrolase NudL
SAMN04901664_01737	CDS	2.3.1.-	Putative acetyltransferase	
SAMN04901664_01738	CDS	tsaB	threonylcarbamoyladenine biosynthesis protein TsaB	
SAMN04901664_01739	CDS	rsmJ	2.1.1.242	Ribosomal RNA small subunit methyltransferase J
SAMN04901664_01740	CDS	hypothetical protein		
SAMN04901664_01741	CDS	fghA	3.1.2.12	S-formylglutathione hydrolase
SAMN04901664_01742	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01743	CDS	rpe	5.1.3.1	Ribulose-phosphate 3-epimerase
SAMN04901664_01744	CDS	ybiV	3.1.3.23	Sugar phosphatase YbiV
SAMN04901664_01745	CDS	hypothetical protein		
SAMN04901664_01746	CDS	copA	Copper resistance protein A	
SAMN04901664_01747	CDS	copB	Copper resistance protein B	
SAMN04901664_01748	CDS	zitB	Zinc transporter ZitB	
SAMN04901664_01749	CDS	sugE	compound-resistance protein SugE	
SAMN04901664_01750	CDS	ogt	2.1.1.63	Methylated-DNA--protein-cysteine methyltransferase
SAMN04901664_01751	CDS	argJ	Arginine biosynthesis bifunctional protein ArgJ	
SAMN04901664_01752	CDS	nadA	2.5.1.72	Quinolinate synthase A
SAMN04901664_01753	tRNA	tRNA-Pro(tgg)		
SAMN04901664_01754	tRNA	tRNA-Arg(tct)		
SAMN04901664_01755	tRNA	tRNA-His(gtg)		
SAMN04901664_01756	tRNA	tRNA-Pro(tgg)		
SAMN04901664_01757	CDS	add2	3.5.4.40	Aminodeoxyfutalosine deaminase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01758	CDS	eltD	1.1.1.-	Erythritol/L-threitol dehydrogenase
SAMN04901664_01759	CDS	gcvA_2	Glycine cleavage system transcriptional activator	
SAMN04901664_01760	CDS	mmgC_2	1.3.99.-	Acyl-CoA dehydrogenase
SAMN04901664_01761	CDS	yjhB_1	Putative metabolite transport protein YjhB	
SAMN04901664_01762	CDS	uctC_1	2.8.3.19	Acetyl-CoA:oxalate CoA-transferase
SAMN04901664_01763	CDS	hypothetical protein		Fumarate reductase flavoprotein subunit
SAMN04901664_01764	CDS	ifcA	1.3.5.4	
SAMN04901664_01765	CDS	gltC_3	HTH-type transcriptional regulator GltC	
SAMN04901664_01766	CDS	ais	5.3.3.7	Aconitate isomerase
SAMN04901664_01767	CDS	proP_1	Proline/betaine transporter	
SAMN04901664_01768	CDS	gltC_4	HTH-type transcriptional regulator GltC	
SAMN04901664_01769	CDS	hypothetical protein		
SAMN04901664_01770	CDS	yxep_2	3.-.-.-	putative hydrolase YxeP
SAMN04901664_01771	CDS	putative HTH-type transcriptional regulator		
SAMN04901664_01772	CDS	hypothetical protein		
SAMN04901664_01773	CDS	leuE_1	Leucine efflux protein	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01774	CDS	gcvA_3	Glycine cleavage system transcriptional activator	
SAMN04901664_01775	CDS	hypothetical protein		
SAMN04901664_01776	CDS	xecA1	4.4.1.23	2-hydroxypropyl-CoM lyase
SAMN04901664_01777	CDS	rutF	1.5.1.42	FMN reductase (NADH) RutF
SAMN04901664_01778	CDS	betl_3	HTH-type transcriptional regulator Betl	
SAMN04901664_01779	CDS	hypothetical protein		
SAMN04901664_01780	CDS	hypothetical protein		
SAMN04901664_01781	CDS	dmlR_5	HTH-type transcriptional regulator DmlR	
SAMN04901664_01782	CDS	yddE_2	5.1.-.-	putative isomerase YddE
SAMN04901664_01783	CDS	hypothetical protein		
SAMN04901664_01784	CDS	hypothetical protein		
SAMN04901664_01785	CDS	hypothetical protein		
SAMN04901664_01786	CDS	quiA_1	1.1.5.8	Quinate/shikimate dehydrogenase (quinone)
SAMN04901664_01787	CDS	hypothetical protein		
SAMN04901664_01788	CDS	hypothetical protein		
SAMN04901664_01789	CDS	hypothetical protein		
SAMN04901664_01790	CDS	hypothetical protein		
SAMN04901664_01791	CDS	hypothetical protein		
SAMN04901664_01792	CDS	hypothetical protein		
SAMN04901664_01793	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01794	CDS	hypothetical protein		
SAMN04901664_01795	CDS	hypothetical protein		
SAMN04901664_01796	CDS	hypothetical protein		
SAMN04901664_01797	CDS	hypothetical protein		
SAMN04901664_01798	CDS	hypothetical protein		
SAMN04901664_01799	CDS	hypothetical protein		
SAMN04901664_01800	CDS	gchK	2.7.13.3	Globin-coupled histidine kinase
SAMN04901664_01801	CDS	nrdB_1	1.17.4.1	Ribonucleoside-diphosphate reductase subunit beta
SAMN04901664_01802	CDS	hypothetical protein		
SAMN04901664_01803	CDS	nrdA_1	1.17.4.1	Ribonucleoside-diphosphate reductase 1 subunit alpha
SAMN04901664_01804	CDS	rstA	Transcriptional regulatory protein RstA	
SAMN04901664_01805	CDS	rstB	2.7.13.3	Sensor protein RstB
SAMN04901664_01806	CDS	hypothetical protein		
SAMN04901664_01807	CDS	ydaM_2	2.7.7.65	putative diguanylate cyclase YdaM
SAMN04901664_01808	CDS	ndhC	1.6.5.-	NAD(P)H-quinone oxidoreductase subunit 3
SAMN04901664_01809	CDS	nuoB	1.6.5.11	NADH-quinone oxidoreductase subunit B
SAMN04901664_01810	CDS	nuoC	1.6.5.11	NADH-quinone oxidoreductase subunit C/D

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01811	CDS	nuoE	1.6.5.11	NADH-quinone oxidoreductase subunit E
SAMN04901664_01812	CDS	nuoF	1.6.5.11	NADH-quinone oxidoreductase subunit F
SAMN04901664_01813	CDS	nuoG	1.6.5.11	NADH-quinone oxidoreductase subunit G
SAMN04901664_01814	CDS	nuoH	1.6.5.11	NADH-quinone oxidoreductase subunit H
SAMN04901664_01815	CDS	nuoI	1.6.5.11	NADH-quinone oxidoreductase subunit I
SAMN04901664_01816	CDS	nuoJ	1.6.5.11	NADH-quinone oxidoreductase subunit J
SAMN04901664_01817	CDS	nuoK	1.6.5.11	NADH-quinone oxidoreductase subunit K
SAMN04901664_01818	CDS	nuoL	1.6.5.11	NADH-quinone oxidoreductase subunit L
SAMN04901664_01819	CDS	nuoM	1.6.5.11	NADH-quinone oxidoreductase subunit M
SAMN04901664_01820	CDS	nuoN	1.6.5.11	NADH-quinone oxidoreductase subunit N
SAMN04901664_01821	CDS	upp	2.4.2.9	Uracil phosphoribosyltransferase
SAMN04901664_01822	CDS	hypothetical protein		
SAMN04901664_01823	CDS	cmpR_2		
				HTH-type transcriptional activator CmpR

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01824	CDS	fpr_1	1.18.1.2	Ferredoxin--NADP reductase
SAMN04901664_01825	CDS	hypothetical protein		
SAMN04901664_01826	CDS	hypothetical protein		
SAMN04901664_01827	CDS	hypothetical protein		
SAMN04901664_01828	CDS	hypothetical protein		
SAMN04901664_01829	CDS	5.3.1.29	enzyme	
SAMN04901664_01830	CDS	dcyD	4.4.1.15	D-cysteine desulphydrase
SAMN04901664_01831	CDS	emrA_4	Multidrug export protein EmrA	
SAMN04901664_01832	CDS	emrY_2	putative multidrug resistance protein EmrY	
SAMN04901664_01833	CDS	hypothetical protein		
SAMN04901664_01834	CDS	rhtC_2	Threonine efflux protein	
SAMN04901664_01835	CDS	hypothetical protein		
SAMN04901664_01836	CDS	metG	6.1.1.10	Methionine--tRNA ligase
SAMN04901664_01837	CDS	hypothetical protein		
SAMN04901664_01838	CDS	apbC	protein	
SAMN04901664_01839	CDS	mtmN_2	3.2.2.9	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
SAMN04901664_01840	CDS	hypothetical protein		
SAMN04901664_01841	CDS	hypothetical protein		
SAMN04901664_01842	CDS	dcd	3.5.4.13	dCTP deaminase
SAMN04901664_01843	CDS	hypothetical protein		
SAMN04901664_01844	CDS	hypothetical protein		
SAMN04901664_01845	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01846	CDS	hypothetical protein		
SAMN04901664_01847	CDS	hypothetical protein		
SAMN04901664_01848	CDS	dusC	1.3.1.-	tRNA-dihydrouridine(16) synthase
SAMN04901664_01849	CDS	ypjD	Inner membrane protein YpjD	
SAMN04901664_01850	CDS	ffh	protein	
SAMN04901664_01851	CDS	coaX	2.7.1.33	Type III pantothenate kinase
SAMN04901664_01852	CDS	birA_1	6.3.4.15	Bifunctional ligase/repressor BirA
SAMN04901664_01853	CDS	hypothetical protein		
SAMN04901664_01854	CDS	rspR_1	HTH-type transcriptional repressor RspR	
SAMN04901664_01855	CDS	smc_1	Smc	
SAMN04901664_01856	CDS	zipA	Cell division protein ZipA	
SAMN04901664_01857	CDS	ligA	6.5.1.2	DNA ligase
SAMN04901664_01858	CDS	bfr_1	1.16.3.1	Bacterioferritin
SAMN04901664_01859	CDS	ybjJ	Inner membrane protein YbjJ	
SAMN04901664_01860	CDS	otsA	2.4.1.15	Trehalose-6-phosphate synthase
SAMN04901664_01861	CDS	otsB	3.1.3.12	Trehalose-6-phosphate phosphatase
SAMN04901664_01862	CDS	bioH	3.1.1.85	Pimeloyl-[acyl-carrier protein] methyl ester esterase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01863	CDS	bioA	2.6.1.62	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
SAMN04901664_01864	CDS	bioF	2.3.1.47	8-amino-7-oxononanoate synthase
SAMN04901664_01865	CDS	bioC	2.1.1.197	Malonyl-[acyl-carrier protein] O-methyltransferase
SAMN04901664_01866	CDS	bioD1	6.3.3.3	ATP-dependent dethiobiotin synthetase BioD 1
SAMN04901664_01867	CDS	rluB	5.4.99.22	Ribosomal large subunit pseudouridine synthase B
SAMN04901664_01868	CDS	scpB	Segregation and condensation protein B	
SAMN04901664_01869	CDS	scpA	Segregation and condensation protein A	
SAMN04901664_01870	CDS	2.7.7.87	Putative threonylcarbamoyl-AMP synthase	
SAMN04901664_01871	CDS	epmC	1.14.-.-	Elongation factor P hydroxylase
SAMN04901664_01872	CDS	yceD	Large ribosomal RNA subunit accumulation protein YceD	
SAMN04901664_01873	CDS	rpmF	50S ribosomal protein L32	
SAMN04901664_01874	CDS	fabD_1	2.3.1.39	Malonyl CoA-acyl carrier protein transacylase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01875	CDS	fabG_2	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase FabG
SAMN04901664_01876	CDS	acpP_1	Acyl carrier protein	
SAMN04901664_01877	CDS	hypothetical protein		
SAMN04901664_01878	CDS	thiD	2.7.1.49	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase
SAMN04901664_01879	CDS	3.1.3.5	5'-nucleotidase	
SAMN04901664_01880	CDS	ribB	4.1.99.12	3,4-dihydroxy-2-butanone 4-phosphate synthase
SAMN04901664_01881	CDS	hypothetical protein		
SAMN04901664_01882	CDS	hypothetical protein		
SAMN04901664_01883	CDS	panD	4.1.1.11	Aspartate 1-decarboxylase
SAMN04901664_01884	CDS	pth	3.1.1.29	Peptidyl-tRNA hydrolase
SAMN04901664_01885	CDS	rplY	50S ribosomal protein L25	
SAMN04901664_01886	CDS	prs	2.7.6.1	Ribose-phosphate pyrophosphokinase
SAMN04901664_01887	tRNA	tRNA-Gln(ttg)		
SAMN04901664_01888	tRNA	tRNA-Gln(ttg)		
SAMN04901664_01889	tRNA	tRNA-Gln(ttg)		
SAMN04901664_01890	tRNA	tRNA-Gln(ttg)		
SAMN04901664_01891	CDS	loIB	LoIB	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01892	CDS	bepA_1	3.4.-.-	Beta-barrel assembly-enhancing protease
SAMN04901664_01893	CDS	hema	1.2.1.70	Glutamyl-tRNA reductase
SAMN04901664_01894	CDS	dnaG_1	2.7.7.-	DNA primase
SAMN04901664_01895	CDS	bamD	Outer membrane protein assembly factor BamD	
SAMN04901664_01896	CDS	rluD	5.4.99.23	Ribosomal large subunit pseudouridine synthase D
SAMN04901664_01897	CDS	yfiH	Laccase domain protein YfiH	
SAMN04901664_01898	CDS	pnpB_3	1.6.5.2	p-benzoquinone reductase
SAMN04901664_01899	CDS	smpB	SsrA-binding protein	
SAMN04901664_01900	CDS	coaD	2.7.7.3	Phosphopantetheine adenylyltransferase
SAMN04901664_01901	CDS	fdx_2	Ferredoxin	
SAMN04901664_01902	tRNA	tRNA-Met(cat)		
SAMN04901664_01903	CDS	hypothetical protein	HTH-type transcriptional regulator DmlR	
SAMN04901664_01904	CDS	dmlR_6		
SAMN04901664_01905	CDS	dmlA	1.1.1.83	D-malate dehydrogenase [decarboxylating]
SAMN04901664_01906	CDS	caiT	L-carnitine/gamma-butyrobetaine antiporter	
SAMN04901664_01907	CDS	nlhH_2	3.1.1.1	Carboxylesterase NlhH

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01908	CDS	antA_2	1.14.12.1	Anthranilate 1,2-dioxygenase large subunit
SAMN04901664_01909	CDS	gabD_2	1.2.1.79	Succinate-semialdehyde dehydrogenase [NADP(+)] GabD
SAMN04901664_01910	CDS	pobB	1.-.-.-	Phenoxybenzoate dioxygenase subunit beta
SAMN04901664_01911	tRNA	tRNA-Met(cat)		
SAMN04901664_01912	CDS	hypothetical protein		
SAMN04901664_01913	CDS	nadE	6.3.5.1	Glutamine-dependent NAD(+) synthetase
SAMN04901664_01914	CDS	hypothetical protein		
SAMN04901664_01915	CDS	1.13.11.24	dioxygenase	
SAMN04901664_01916	CDS	hypothetical protein		
SAMN04901664_01917	CDS	fabB_2	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase 1
SAMN04901664_01918	CDS	hypothetical protein		
SAMN04901664_01919	CDS	rpsL	30S ribosomal protein S12	
SAMN04901664_01920	CDS	rpsG	30S ribosomal protein S7	
SAMN04901664_01921	CDS	fusA	Elongation factor G	
SAMN04901664_01922	CDS	hypothetical protein		
SAMN04901664_01923	CDS	yebC	putative transcriptional regulatory protein YebC	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01924	CDS	decR_2	DNA-binding transcriptional activator DecR	
SAMN04901664_01925	CDS	hypothetical protein		
SAMN04901664_01926	CDS	glnQ_1	Glutamine transport ATP-binding protein GlnQ	
SAMN04901664_01927	CDS	gltK_1	Glutamate/aspartate import permease protein GltK	
SAMN04901664_01928	CDS	gltK_2	Glutamate/aspartate import permease protein GltK	
SAMN04901664_01929	CDS	gltI	Glutamate/aspartate import solute-binding protein	
SAMN04901664_01930	CDS	hypothetical protein		
SAMN04901664_01931	CDS	soxC_1	Dibenzothiophene desulfurization enzyme C	
SAMN04901664_01932	CDS	soxC_2	Dibenzothiophene desulfurization enzyme C	
SAMN04901664_01933	CDS	dmoA_1	1.14.13.131	Dimethyl-sulfide monooxygenase
SAMN04901664_01934	CDS	metQ_1	D-methionine-binding lipoprotein MetQ	
SAMN04901664_01935	CDS	metQ_2	D-methionine-binding lipoprotein MetQ	
SAMN04901664_01936	CDS	metN_1	3.6.3.-	Methionine import ATP-binding protein MetN

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01937	CDS	metI_1	D-methionine transport system permease protein MetI	
SAMN04901664_01938	CDS	ychF	YchF	
SAMN04901664_01939	CDS	hypothetical protein	HTH-type transcriptional regulator Cmr	
SAMN04901664_01940	CDS	cmr		
SAMN04901664_01941	CDS	hypothetical protein		
SAMN04901664_01942	CDS	hypothetical protein		
SAMN04901664_01943	CDS	ygaZ_1	Inner membrane protein YgaZ	
SAMN04901664_01944	CDS	hypothetical protein		
SAMN04901664_01945	CDS	hypothetical protein		
SAMN04901664_01946	CDS	purT	2.1.2.-	Formate-dependent phosphoribosylglycinamide formyltransferase
SAMN04901664_01947	CDS	glnD	Bifunctional uridylyltransferase/uridylyl-removing enzyme	
SAMN04901664_01948	CDS	dapL	2.6.1.83	LL-diaminopimelate aminotransferase
SAMN04901664_01949	CDS	rhtC_3	Threonine efflux protein	
SAMN04901664_01950	CDS	ada_1	activator/DNA repair enzyme Ada	
SAMN04901664_01951	CDS	gpx1	1.11.1.22	Hydroperoxy fatty acid reductase gpx1

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01952	CDS	msrB	1.8.4.12	Peptide methionine sulfoxide reductase MsrB
SAMN04901664_01953	CDS	alaA	2.6.1.2	Glutamate-pyruvate aminotransferase AlaA
SAMN04901664_01954	CDS	gltT	Proton/sodium-glutamate symport protein	
SAMN04901664_01955	CDS	ansB	3.5.1.38	Glutaminase-asparaginase
SAMN04901664_01956	CDS	dnaE_1	2.7.7.7	DNA polymerase III subunit alpha
SAMN04901664_01957	CDS	trmJ	2.1.1.200	tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmJ
SAMN04901664_01958	CDS	cysE_1	2.3.1.30	Serine acetyltransferase
SAMN04901664_01959	CDS	hypothetical protein		
SAMN04901664_01960	CDS	hypothetical protein		
SAMN04901664_01961	CDS	ahpF_1	1.8.1.-	Alkyl hydroperoxide reductase subunit F
SAMN04901664_01962	CDS	chrA1_2	Chromate transport protein	
SAMN04901664_01963	CDS	chrA1_3	Chromate transport protein	
SAMN04901664_01964	CDS	benM_1	HTH-type transcriptional regulator BenM	
SAMN04901664_01965	CDS	acr3	Acr3	
SAMN04901664_01966	CDS	arsR1	Arsenic resistance transcriptional regulator ArsR1	
SAMN04901664_01967	CDS	arsC	1.20.4.1	Arsenate reductase
SAMN04901664_01968	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01969	CDS	nfdA	3.5.1.91	N-substituted formamide deformylase
SAMN04901664_01970	CDS	hypothetical protein		
SAMN04901664_01971	CDS	dmlR_7	HTH-type transcriptional regulator DmlR	
SAMN04901664_01972	CDS	rspR_2	HTH-type transcriptional repressor RspR	
SAMN04901664_01973	CDS	pucI	putative allantoin permease	
SAMN04901664_01974	CDS	murI_1	5.1.1.3	Glutamate racemase
SAMN04901664_01975	CDS	tauD	1.14.11.17	Alpha-ketoglutarate-dependent taurine dioxygenase
SAMN04901664_01976	CDS	ssuC_2	transport permease protein SsuC	
SAMN04901664_01977	CDS	tauB_2	3.6.3.36	Taurine import ATP-binding protein TauB
SAMN04901664_01978	CDS	tauA	protein	
SAMN04901664_01979	CDS	hypothetical protein		
SAMN04901664_01980	CDS	ydjE	Inner membrane metabolite transport protein YdjE	
SAMN04901664_01981	CDS	dmoA_2	1.14.13.131	Dimethyl-sulfide monooxygenase
SAMN04901664_01982	CDS	soxC_3	Dibenzothiophene desulfurization enzyme C	
SAMN04901664_01983	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01984	CDS	cydA_2	1.10.3.14	Cytochrome bd-I ubiquinol oxidase subunit 1
SAMN04901664_01985	CDS	cydB_2	1.10.3.14	Cytochrome bd-I ubiquinol oxidase subunit 2
SAMN04901664_01986	CDS	hypothetical protein	HTH-type transcriptional regulator NorG	
SAMN04901664_01987	CDS	norG_2	HTH-type transcriptional regulator CynR	
SAMN04901664_01988	CDS	cynR_1		
SAMN04901664_01989	CDS	hypothetical protein		
SAMN04901664_01990	CDS	hypothetical protein		
SAMN04901664_01991	CDS	fabD_2	2.3.1.39	Malonyl CoA -acyl carrier protein transacylase
SAMN04901664_01992	CDS	mdcG	2.7.7.66	Phosphoribosyl-dephospho-CoA transferase
SAMN04901664_01993	CDS	madD	2.1.3.10	Malonyl-S-ACP:biotin-protein carboxyltransferase MADD
SAMN04901664_01994	CDS	madC	2.1.3.10	Malonyl-S-ACP:biotin-protein carboxyltransferase MADC
SAMN04901664_01995	CDS	mdcC	Malonate decarboxylase acyl carrier protein	
SAMN04901664_01996	CDS	citG	2.4.2.52	2-(5"-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_01997	CDS	madA	2.3.1.187	Acetyl-S-ACP:malonate ACP transferase
SAMN04901664_01998	CDS	rflnT	Riboflavin transporter RflnT	
SAMN04901664_01999	CDS	hypothetical protein		
SAMN04901664_02000	CDS	paiB	Protease synthase and sporulation protein PAI 2	
SAMN04901664_02001	CDS	gabR_3	HTH-type transcriptional regulatory protein GabR	
SAMN04901664_02002	CDS	cidB_1	Holin-like protein CidB	
SAMN04901664_02003	CDS	cidA	Holin-like protein CidA	
SAMN04901664_02004	CDS	gltC_5	HTH-type transcriptional regulator GltC	
SAMN04901664_02005	CDS	yfcF	2.5.1.18	Glutathione S-transferase YfcF
SAMN04901664_02006	CDS	yghU	1.8.4.-	Disulfide-bond oxidoreductase YghU
SAMN04901664_02007	CDS	dmlR_8	HTH-type transcriptional regulator DmlR	
SAMN04901664_02008	CDS	fabG_3	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase FabG
SAMN04901664_02009	CDS	glpE_2	2.8.1.1	Thiosulfate sulfurtransferase GlpE
SAMN04901664_02010	CDS	cysE_2	2.3.1.30	Serine acetyltransferase
SAMN04901664_02011	CDS	mmpI	Major membrane protein I	
SAMN04901664_02012	CDS	sufS	2.8.1.7	Cysteine desulfurase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02013	CDS	rhtC_4		Threonine efflux protein
SAMN04901664_02014	CDS	dmlR_9		HTH-type transcriptional regulator DmlR
SAMN04901664_02015	CDS	glnH_1		ABC transporter glutamine-binding protein GlnH
SAMN04901664_02016	CDS	glnH_2		ABC transporter glutamine-binding protein GlnH
SAMN04901664_02017	CDS	glnQ_2		Glutamine transport ATP-binding protein GlnQ
SAMN04901664_02018	CDS	glnP		transporter permease protein GlnP
SAMN04901664_02019	CDS	glnM		transporter permease protein GlnM
SAMN04901664_02020	CDS	hypothetical protein		
SAMN04901664_02021	CDS	pleD_2		Response regulator PleD
SAMN04901664_02022	CDS	luxQ		Autoinducer 2 sensor
SAMN04901664_02023	CDS	hypothetical protein	2.7.13.3	kinase/phosphatase LuxQ
SAMN04901664_02024	CDS	lrp_4		protein
SAMN04901664_02025	CDS	rhtB_3		Homoserine/homoserine
SAMN04901664_02026	CDS	lexA		lactone efflux protein
SAMN04901664_02027	CDS	hypothetical protein	3.4.21.88	LexA repressor
SAMN04901664_02028	CDS	hypothetical protein		
SAMN04901664_02029	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02030	CDS	ydaD	1.-.-.-	General stress protein 39
SAMN04901664_02031	CDS	katE	1.11.1.6	Catalase HP11
SAMN04901664_02032	CDS	hypothetical protein		
SAMN04901664_02033	CDS	cinA	CinA-like protein	
SAMN04901664_02034	CDS	hypothetical protein		
SAMN04901664_02035	CDS	hypothetical protein		
SAMN04901664_02036	CDS	hypothetical protein		
SAMN04901664_02037	CDS	hypothetical protein		
SAMN04901664_02038	CDS	hypothetical protein		
SAMN04901664_02039	CDS	hypothetical protein		
SAMN04901664_02040	CDS	hypothetical protein		
SAMN04901664_02041	CDS	dmrR_10	HTH-type transcriptional regulator DmrR	
SAMN04901664_02042	CDS	hypothetical protein		
SAMN04901664_02043	CDS	hypothetical protein		
SAMN04901664_02044	CDS	cmoA_2	2.1.3.-	Carboxy-S-adenosyl-L-methionine synthase
SAMN04901664_02045	CDS	fadD3	6.2.1.41	3-[(3aS,4S,7aS)-7a-methyl-1,5-dioxo-octahydro-1H-inden-4-yl]propanoyl:CoA ligase
SAMN04901664_02046	CDS	fadR	Fatty acid metabolism regulator protein	
SAMN04901664_02047	CDS	mngC_3	1.3.99.-	Acyl-CoA dehydrogenase
SAMN04901664_02048	CDS	2.1.3.1	carboxyltransferase 12S subunit	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02049	CDS	dpgD	4.2.1.17	Enoyl-CoA-hydratase
SAMN04901664_02050	CDS	accA1_1	Acetyl-/propionyl-coenzyme A carboxylase alpha chain	
SAMN04901664_02051	CDS	liuE	4.1.3.26	3-hydroxy-3-isohexenylglutaryl- CoA/hydroxy-methylglutaryl- CoA lyase
SAMN04901664_02052	CDS	dmlR_11	HTH-type transcriptional regulator DmIR	
SAMN04901664_02053	CDS	hypothetical protein		
SAMN04901664_02054	CDS	hypothetical protein		
SAMN04901664_02055	CDS	dmdC_1	1.3.8.-	3-methylmercaptopropionyl- CoA dehydrogenase
SAMN04901664_02056	CDS	hypothetical protein		
SAMN04901664_02057	CDS	putative transporter		
SAMN04901664_02058	CDS	hypothetical protein		
SAMN04901664_02059	CDS	pcaJ_1	2.8.3.6	3-oxoadipate CoA-transferase subunit B
SAMN04901664_02060	CDS	pcaI_1	2.8.3.6	3-oxoadipate CoA-transferase subunit A
SAMN04901664_02061	CDS	yjhB_2	Putative metabolite transport protein YjhB	
SAMN04901664_02062	CDS	mngC_4	1.3.99.-	Acyl-CoA dehydrogenase
SAMN04901664_02063	CDS	paaF_2	4.2.1.17	2,3-dehydroadipyl-CoA hydratase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02064	CDS	bacC_2	1.1.1.385	Dihydroantcapsin 7-dehydrogenase
SAMN04901664_02065	CDS	paaH_1	1.1.1.-	3-hydroxyadipyl-CoA dehydrogenase
SAMN04901664_02066	CDS	pcaF_1	2.3.1.174	Beta-ketoadipyl-CoA thiolase
SAMN04901664_02067	CDS	tsaQ1_1	HTH-type transcriptional regulator TsaQ1/TsaQ2	
SAMN04901664_02068	CDS	putative transporter		
SAMN04901664_02069	CDS	1.13.12.16	Nitronate monooxygenase	
SAMN04901664_02070	CDS	paaF_3	4.2.1.17	2,3-dehydroadipyl-CoA hydratase
SAMN04901664_02071	CDS	tsaQ1_2	HTH-type transcriptional regulator TsaQ1/TsaQ2	
SAMN04901664_02072	CDS	uctC_2	2.8.3.19	Acetyl-CoA:oxalate CoA-transferase
SAMN04901664_02073	CDS	carC_1	1.3.1.108	Caffeyl-CoA reductase-Eff complex subunit CarC
SAMN04901664_02074	CDS	yjhB_3	Putative metabolite transport protein YjhB	
SAMN04901664_02075	CDS	phnX	3.11.1.1	Phosphonoacetaldehyde hydrolase
SAMN04901664_02076	CDS	phnW	2.6.1.37	2-aminoethylphosphonate--pyruvate transaminase
SAMN04901664_02077	CDS	soxA	1.5.3.1	Monomeric sarcosine oxidase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02078	CDS	phnU	aminoethylphosphonate transport system permease protein PhnU	
SAMN04901664_02079	CDS	cysA_3	3.6.3.25	Sulfate/thiosulfate import ATP-binding protein CysA
SAMN04901664_02080	CDS	futA1	Iron uptake protein A1 regulator of 2-aminoethylphosphonate degradation operons	
SAMN04901664_02081	CDS	phnR		
SAMN04901664_02082	CDS	pobA	1.14.13.2 hydroxylase transcriptional activator	p-hydroxybenzoate hydroxylase
SAMN04901664_02083	CDS	pobR		
SAMN04901664_02084	CDS	azoR	1.7.-.-	FMN-dependent NADH-azoreductase
SAMN04901664_02085	CDS	pgrR_2	HTH-type transcriptional regulator PgrR	
SAMN04901664_02086	CDS	hypothetical protein		
SAMN04901664_02087	CDS	davD	1.2.1.20	Glutarate-semialdehyde dehydrogenase DavD
SAMN04901664_02088	CDS	hypothetical protein		
SAMN04901664_02089	CDS	hypothetical protein		
SAMN04901664_02090	CDS	betB_1	1.2.1.8	NAD/NADP-dependent betaine aldehyde dehydrogenase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02091	CDS	luxA	1.14.14.3	Alkanal monooxygenase alpha chain
SAMN04901664_02092	CDS	C1-hpah_2	1.5.1.36	p-hydroxyphenylacetate 3-hydroxylase, reductase component
SAMN04901664_02093	CDS	catD_1	3.1.1.24	3-oxoadipate enol-lactonase 2
SAMN04901664_02094	CDS	hypothetical protein		
SAMN04901664_02095	CDS	mcbR		HTH-type transcriptional regulator McbR
SAMN04901664_02096	CDS	hypothetical protein		
SAMN04901664_02097	CDS	yceJ_2	Cytochrome b561	
SAMN04901664_02098	CDS	srpA	1.11.1.-	Catalase-related peroxidase
SAMN04901664_02099	CDS	hypothetical protein		
SAMN04901664_02100	CDS	hypothetical protein		
SAMN04901664_02101	CDS	hypothetical protein		
SAMN04901664_02102	CDS	ltrA	protein LtrA	
SAMN04901664_02103	CDS	hypothetical protein		
SAMN04901664_02104	CDS	hypothetical protein		
SAMN04901664_02105	CDS	paaI	3.1.2.-	Acyl-coenzyme A thioesterase PaaI
SAMN04901664_02106	CDS	lacA	2.3.1.18	Galactoside O-acetyltransferase
SAMN04901664_02107	CDS	paaX	Transcriptional repressor PaaX	
SAMN04901664_02108	CDS	paaK	6.2.1.30	Phenylacetate-coenzyme A ligase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02109	CDS	paaJ	2.3.1.174	3-oxoadipyl-CoA/3-oxo-5,6-dehydrosuberyl-CoA thiolase
SAMN04901664_02110	CDS	paaH_2	1.1.1.-	3-hydroxyadipyl-CoA dehydrogenase
SAMN04901664_02111	CDS	paaG	5.3.3.18	1,2-epoxyphenylacetyl-CoA isomerase
SAMN04901664_02112	CDS	paaF_4	4.2.1.17	2,3-dehydroadipyl-CoA hydratase
SAMN04901664_02113	CDS	paaE	1.-.-.-	1,2-phenylacetyl-CoA epoxidase, subunit E
SAMN04901664_02114	CDS	paaD	Putative 1,2-phenylacetyl-CoA epoxidase, subunit D	
SAMN04901664_02115	CDS	paaC	1,2-phenylacetyl-CoA epoxidase, subunit C	
SAMN04901664_02116	CDS	paaB	1,2-phenylacetyl-CoA epoxidase, subunit B	
SAMN04901664_02117	CDS	paaA	1.14.13.149	1,2-phenylacetyl-CoA epoxidase, subunit A
SAMN04901664_02118	CDS	paaZ	Bifunctional protein PaaZ	
SAMN04901664_02119	CDS	sdaA	4.3.1.17	L-serine dehydratase 1
SAMN04901664_02120	CDS	yveA	Aspartate-proton symporter	
SAMN04901664_02121	CDS	1.2.1.26	Alpha-ketoglutaric semialdehyde dehydrogenase	
SAMN04901664_02122	CDS	proP_2	Proline/betaine transporter	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02123	CDS	btr_1	HTH-type transcriptional activator Btr	
SAMN04901664_02124	CDS	hcnB	1.4.99.5	Hydrogen cyanide synthase subunit HcnB
SAMN04901664_02125	CDS	hcnA	1.4.99.5	Hydrogen cyanide synthase subunit HcnA
SAMN04901664_02126	CDS	hcnC	1.4.99.5	Hydrogen cyanide synthase subunit HcnC
SAMN04901664_02127	CDS	5.1.1.8	4-hydroxyproline 2-epimerase	
SAMN04901664_02128	CDS	gntR_2	operon transcriptional repressor	
SAMN04901664_02129	CDS	hypothetical protein		
SAMN04901664_02130	CDS	dapA_2	4.3.3.7	4-hydroxy-tetrahydrodipicolinate synthase
SAMN04901664_02131	CDS	hypothetical protein		
SAMN04901664_02132	CDS	hypothetical protein		
SAMN04901664_02133	CDS	soxR	Redox-sensitive transcriptional activator SoxR	
SAMN04901664_02134	CDS	hypothetical protein		
SAMN04901664_02135	CDS	yciB_1	intracellular septation protein A	
SAMN04901664_02136	CDS	acpM	Meromycolate extension acyl carrier protein	
SAMN04901664_02137	CDS	acpP_2	Acyl carrier protein	
SAMN04901664_02138	CDS	hypothetical protein		
SAMN04901664_02139	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02140	CDS	der	GTPase Der	
SAMN04901664_02141	CDS	bamB	Outer membrane protein assembly factor BamB	
SAMN04901664_02142	CDS	hypothetical protein		
SAMN04901664_02143	CDS	hisS	6.1.1.21	Histidine--tRNA ligase 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin)
SAMN04901664_02144	CDS	ispG	1.17.7.3	
SAMN04901664_02145	CDS	rodZ	Cytoskeleton protein RodZ	
SAMN04901664_02146	CDS	lapB	Lipopolysaccharide assembly protein B	
SAMN04901664_02147	CDS	rlmN	2.1.1.192	Dual-specificity RNA methyltransferase RlmN
SAMN04901664_02148	CDS	ndk	2.7.4.6	Nucleoside diphosphate kinase
SAMN04901664_02149	CDS	hypothetical protein		
SAMN04901664_02150	CDS	bcrC	3.6.1.27	Undecaprenyl-diphosphatase BcrC
SAMN04901664_02151	CDS	mgta_1	2.4.1.-	GDP-mannose-dependent alpha-mannosyltransferase
SAMN04901664_02152	CDS	prc	3.4.21.102	Tail-specific protease
SAMN04901664_02153	CDS	nagZ	3.2.1.52	Beta-hexosaminidase
SAMN04901664_02154	CDS	hypothetical protein		
SAMN04901664_02155	CDS	menH_2	4.2.99.20	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02156	CDS	proA_1	1.2.1.41	Gamma-glutamyl phosphate reductase
SAMN04901664_02157	CDS	gapN	1.2.1.9	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
SAMN04901664_02158	CDS	gntK	2.7.1.12	Thermoresistant gluconokinase
SAMN04901664_02159	CDS	gntT	transporter	
SAMN04901664_02160	CDS	eda	KHG/KDPG aldolase	
SAMN04901664_02161	CDS	edd	4.2.1.12	Phosphogluconate dehydratase
SAMN04901664_02162	CDS	ackA	2.7.2.1	Acetate kinase
SAMN04901664_02163	CDS	pta	2.3.1.8	Phosphate acetyltransferase
SAMN04901664_02164	CDS	fumB	4.2.1.2	Fumarate hydratase class I, anaerobic
SAMN04901664_02165	CDS	hypothetical protein		
SAMN04901664_02166	CDS	hypothetical protein		
SAMN04901664_02167	CDS	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX	
SAMN04901664_02168	CDS	clpP	3.4.21.92	ATP-dependent Clp protease proteolytic subunit
SAMN04901664_02169	CDS	tig	5.2.1.8	Trigger factor
SAMN04901664_02170	CDS	bfrD_2	putative TonB-dependent receptor BfrD	
SAMN04901664_02171	CDS	1.14.11.-	PKHD-type hydroxylase	
SAMN04901664_02172	CDS	leuA	2.3.3.13	2-isopropylmalate synthase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02173	CDS	metX	2.3.1.31	Homoserine O-acetyltransferase
SAMN04901664_02174	CDS	ubiE_1	2.1.1.163	Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE
SAMN04901664_02175	CDS	esiB_2	Secretory immunoglobulin A-binding protein EsiB	
SAMN04901664_02176	CDS	3.6.1.9	Non-canonical purine NTP pyrophosphatase	
SAMN04901664_02177	CDS	hypothetical protein		
SAMN04901664_02178	CDS	tatA	Sec-independent protein translocase protein TatA	
SAMN04901664_02179	CDS	tatB	Sec-independent protein translocase protein TatB	
SAMN04901664_02180	CDS	tatC	Sec-independent protein translocase protein TatC	
SAMN04901664_02181	CDS	hypothetical protein		
SAMN04901664_02182	CDS	hypothetical protein		
SAMN04901664_02183	CDS	hypothetical protein		
SAMN04901664_02184	CDS	lgt	2.4.99.-	Prolipoprotein diacylglycerol transferase
SAMN04901664_02185	CDS	hypothetical protein		
SAMN04901664_02186	CDS	hypothetical protein		
SAMN04901664_02187	CDS	thyA	2.1.1.45	Thymidylate synthase
SAMN04901664_02188	CDS	dhfrIII	1.5.1.3	Dihydrofolate reductase type 3

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02189	CDS	hypothetical protein		
SAMN04901664_02190	CDS	msrA	1.8.4.11	Peptide methionine sulfoxide reductase MsrA
SAMN04901664_02191	CDS	exbD_4	ExbD	
SAMN04901664_02192	CDS	exbB_4	ExbB	
SAMN04901664_02193	CDS	hypothetical protein		
SAMN04901664_02194	CDS	purU	3.5.1.10	Formyltetrahydrofolate deformylase
SAMN04901664_02195	CDS	kstR2_1	HTH-type transcriptional repressor KstR2	
SAMN04901664_02196	CDS	calB_1	1.2.1.68	Coniferyl aldehyde dehydrogenase
SAMN04901664_02197	CDS	rpmB	50S ribosomal protein L28	
SAMN04901664_02198	CDS	rpmG	50S ribosomal protein L33	
SAMN04901664_02199	CDS	ybaL	Inner membrane protein YbaL	
SAMN04901664_02200	CDS	hypothetical protein		
SAMN04901664_02201	CDS	hypothetical protein		
SAMN04901664_02202	CDS	hypothetical protein		
SAMN04901664_02203	CDS	hypothetical protein		
SAMN04901664_02204	CDS	pcrA	3.6.4.12	ATP-dependent DNA helicase PcrA
SAMN04901664_02205	CDS	hypothetical protein		
SAMN04901664_02206	CDS	hypothetical protein		
SAMN04901664_02207	CDS	topA	5.99.1.2	DNA topoisomerase 1
SAMN04901664_02208	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02209	CDS	yybR_2	putative HTH-type transcriptional regulator YyBR	
		Zinc-type alcohol		
SAMN04901664_02210	CDS	dehydrogenase-like protein		
SAMN04901664_02211	CDS	slyX	Protein SlyX	
SAMN04901664_02212	CDS	uup	ABC transporter ATP-binding protein uup	
SAMN04901664_02213	CDS	leuE_2	Leucine efflux protein	
SAMN04901664_02214	CDS	lpxL_2	2.3.1.241	Lipid A biosynthesis lauroyltransferase
SAMN04901664_02215	CDS	bshA_1	2.4.1.-	N-acetyl-alpha-D-glucosaminyl L-malate synthase
SAMN04901664_02216	CDS	glpP_1	symporter	
SAMN04901664_02217	CDS	hypothetical protein		
SAMN04901664_02218	CDS	asd	1.2.1.11	Aspartate-semialdehyde dehydrogenase
SAMN04901664_02219	CDS	hypothetical protein		
SAMN04901664_02220	CDS	hypothetical protein		
SAMN04901664_02221	CDS	ansA	3.5.1.1	L-asparaginase 1
SAMN04901664_02222	CDS	truA	5.4.99.12	tRNA pseudouridine synthase A
		putative HTH-type		
SAMN04901664_02223	CDS	transcriptional regulator		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02224	CDS	infA	1	
SAMN04901664_02225	CDS	hypothetical protein		
SAMN04901664_02226	CDS	hypothetical protein		
SAMN04901664_02227	CDS	leuB	1.1.1.85	3-isopropylmalate dehydrogenase
SAMN04901664_02228	CDS	hypothetical protein		
SAMN04901664_02229	CDS	leuD	4.2.1.33	3-isopropylmalate dehydratase small subunit
SAMN04901664_02230	CDS	leuC	4.2.1.33	3-isopropylmalate dehydratase large subunit
SAMN04901664_02231	CDS	hypothetical protein		
SAMN04901664_02232	CDS	cmpR_3	HTH-type transcriptional activator CmpR	
SAMN04901664_02233	CDS	hypothetical protein		
SAMN04901664_02234	CDS	hypothetical protein		
SAMN04901664_02235	CDS	3.1.3.-	putative phosphatase	
SAMN04901664_02236	CDS	rppH	3.6.1.-	RNA pyrophosphohydrolase
SAMN04901664_02237	CDS	ptsP	2.7.3.9	Phosphoenolpyruvate-dependent phosphotransferase system
SAMN04901664_02238	CDS	katG	1.11.1.21	Catalase-peroxidase
SAMN04901664_02239	CDS	hypothetical protein		
SAMN04901664_02240	CDS	hcaR_2	Hca operon transcriptional activator HcaR	
SAMN04901664_02241	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02242	CDS	yfcG_1	1.8.4.-	Disulfide-bond oxidoreductase YfcG
SAMN04901664_02243	CDS	birA_2	6.3.4.15	Bifunctional ligase/repressor BirA
SAMN04901664_02244	CDS	3.1.3.5	5'-nucleotidase	
SAMN04901664_02245	CDS	rluC	5.4.99.24	Ribosomal large subunit pseudouridine synthase C
SAMN04901664_02246	CDS	rne	3.1.26.12	Ribonuclease E
SAMN04901664_02247	CDS	6.2.1.3	Long-chain-fatty-acid--CoA ligase FadD17	
SAMN04901664_02248	tRNA	tRNA-Lys(ttt)		
SAMN04901664_02249	tRNA	tRNA-Lys(ttt)		
SAMN04901664_02250	CDS	pgrR_3	HTH-type transcriptional regulator PgrR	
SAMN04901664_02251	CDS	fabG_4	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase FabG
SAMN04901664_02252	CDS	hemN	1.3.99.-	Oxygen-independent coproporphyrinogen-III oxidase- like protein
SAMN04901664_02253	CDS	hypothetical protein		
SAMN04901664_02254	CDS	norM_1	NorM	
SAMN04901664_02255	CDS	soxC_4	Dibenzothiophene desulfurization enzyme C	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02256	CDS	soxC_5	Dibenzothiophene desulfurization enzyme C	
SAMN04901664_02257	CDS	ubiB_2	2.7.-.- type B	putative protein kinase UbiB
SAMN04901664_02258	CDS	rpmE2		
SAMN04901664_02259	CDS	hypothetical protein		
SAMN04901664_02260	CDS	crcB	transporter CrcB	
SAMN04901664_02261	CDS	gfa_1	4.4.1.22	Glutathione-dependent formaldehyde-activating enzyme
SAMN04901664_02262	CDS	kmo_1	1.14.13.9	Kynurenine 3-monoxygenase
SAMN04901664_02263	CDS	trmB_1	2.1.1.33	tRNA (guanine-N(7)-) methyltransferase
SAMN04901664_02264	CDS	yacG	DNA gyrase inhibitor YacG	
SAMN04901664_02265	CDS	gloC	3.1.2.6	Hydroxyacylglutathione hydrolase GloC
SAMN04901664_02266	CDS	hemH	4.99.1.1	Ferrochelatase
SAMN04901664_02267	CDS	hypothetical protein		
SAMN04901664_02268	CDS	murI_2	5.1.1.3	Glutamate racemase
SAMN04901664_02269	CDS	hypothetical protein		
SAMN04901664_02270	CDS	1.5.5.1	Electron transfer flavoprotein-ubiquinone oxidoreductase	
SAMN04901664_02271	CDS	tusA_1	2.8.1.-	Sulfurtransferase TusA
SAMN04901664_02272	CDS	corC_2	Magnesium and cobalt efflux protein CorC	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02273	CDS	Int	2.3.1.-	Apolipoprotein N-acyltransferase
SAMN04901664_02274	CDS	csaA	putative chaperone CsaA	
SAMN04901664_02275	CDS	hypothetical protein		
SAMN04901664_02276	CDS	xcpT_1	protein G	
SAMN04901664_02277	CDS	epsF_1	protein F	
SAMN04901664_02278	CDS	priA	3.6.4.-	Primosomal protein N'
SAMN04901664_02279	CDS	kefC_1	potassium-efflux system protein KefC	
SAMN04901664_02280	CDS	hsiO	33 kDa chaperonin	
SAMN04901664_02281	CDS	leuE_3	Leucine efflux protein	
SAMN04901664_02282	CDS	cbpA	Curved DNA-binding protein CbpM	
SAMN04901664_02283	CDS	cbpM	CbpM	
SAMN04901664_02284	CDS	corA_1	Cobalt/magnesium transport protein CorA	
SAMN04901664_02285	CDS	pnp	2.7.7.8	Polyribonucleotide nucleotidyltransferase
SAMN04901664_02286	CDS	rpsO	30S ribosomal protein S15	
SAMN04901664_02287	CDS	estB	3.1.1.-	Esterase EstB
SAMN04901664_02288	CDS	recD	3.1.11.5	RecBCD enzyme subunit RecD
SAMN04901664_02289	CDS	recB	3.1.11.5	RecBCD enzyme subunit RecB
SAMN04901664_02290	CDS	recC	3.1.11.5	RecBCD enzyme subunit RecC

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02291	CDS	hypothetical protein		
SAMN04901664_02292	CDS	trnk_2	2.7.4.9	Thymidylate kinase
SAMN04901664_02293	CDS	hypothetical protein		
SAMN04901664_02294	CDS	ubiE_2	2.1.1.163	Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE
SAMN04901664_02295	CDS	hypothetical protein		
SAMN04901664_02296	CDS	ubiB_3	2.7.-.-	putative protein kinase UbiB
SAMN04901664_02297	CDS	hpxO_1	1.14.13.113	FAD-dependent urate hydroxylase
SAMN04901664_02298	CDS	hisI	3.5.4.19	Phosphoribosyl-AMP cyclohydrolase
SAMN04901664_02299	CDS	rep_2	3.6.4.12	ATP-dependent DNA helicase Rep
SAMN04901664_02300	CDS	hypothetical protein		
SAMN04901664_02301	CDS	mrpA	A	
SAMN04901664_02302	CDS	mnhC1	C1	
SAMN04901664_02303	CDS	mrpD	D	
SAMN04901664_02304	CDS	mnhE1	E1	
SAMN04901664_02305	CDS	mrpF	F	
SAMN04901664_02306	CDS	mrpG	G	
SAMN04901664_02307	CDS	rbfA	30S ribosome-binding factor	
SAMN04901664_02308	CDS	infB	2	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02309	CDS	nusA	Transcription termination/antitermination protein NusA	
SAMN04901664_02310	CDS	rimP	RimP	
SAMN04901664_02311	tRNA	tRNA-Met(cat)		
SAMN04901664_02312	tRNA	tRNA-Met(cat)		
SAMN04901664_02313	tRNA	tRNA-Leu(gag)		
SAMN04901664_02314	CDS	secG	Protein-export membrane protein SecG	
SAMN04901664_02315	CDS	tpiA	5.3.1.1	Triosephosphate isomerase
SAMN04901664_02316	CDS	epsE_1	protein E	
SAMN04901664_02317	CDS	epsF_2	protein F	
SAMN04901664_02318	CDS	outO	leader peptide-processing enzyme	
SAMN04901664_02319	CDS	coaE	2.7.1.24	Dephospho-CoA kinase
SAMN04901664_02320	CDS	hypothetical protein		
SAMN04901664_02321	CDS	rimB_2	2.1.1.185	23S rRNA (guanosine-2'-O-)- methyltransferase RimB
SAMN04901664_02322	CDS	hypothetical protein		
SAMN04901664_02323	CDS	hypothetical protein		
SAMN04901664_02324	CDS	recN	DNA repair protein RecN	
SAMN04901664_02325	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02326	CDS	yqgF	3.1.-.-	Putative pre-16S rRNA nuclease
SAMN04901664_02327	CDS	aaeA	p-hydroxybenzoic acid efflux pump subunit AaeA	
SAMN04901664_02328	CDS	hypothetical protein	p-hydroxybenzoic acid efflux pump subunit AaeB	
SAMN04901664_02329	CDS	aaeB	Pca operon regulatory protein	
SAMN04901664_02330	CDS	pcaU_1	activator/DNA repair enzyme	
SAMN04901664_02331	CDS	hypothetical protein	Ada	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
SAMN04901664_02332	CDS	ada_2	2.7.8.5	
SAMN04901664_02333	CDS	pgsA	UvrABC system protein C	
SAMN04901664_02334	CDS	hypothetical protein		
SAMN04901664_02335	CDS	uvrC		
SAMN04901664_02336	CDS	hypothetical protein		
SAMN04901664_02337	CDS	hypothetical protein		
SAMN04901664_02338	CDS	hypothetical protein		
SAMN04901664_02339	CDS	hypothetical protein		
SAMN04901664_02340	CDS	fadB	Fatty acid oxidation complex subunit alpha	
SAMN04901664_02341	CDS	fadA_1	2.3.1.16	3-ketoacyl-CoA thiolase
SAMN04901664_02342	CDS	hypothetical protein		
SAMN04901664_02343	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02344	CDS	ydeN	3.-.-.-	Putative hydrolase YdeN
SAMN04901664_02345	CDS	hmrR_1	HTH-type transcriptional regulator HmrR	
SAMN04901664_02346	CDS	hypothetical protein		
SAMN04901664_02347	CDS	hypothetical protein		
SAMN04901664_02348	CDS	hypothetical protein		
SAMN04901664_02349	CDS	hypothetical protein		
SAMN04901664_02350	CDS	htpG	Chaperone protein HtpG	
SAMN04901664_02351	CDS	hypothetical protein		
SAMN04901664_02352	CDS	ompW	Outer membrane protein W	
SAMN04901664_02353	CDS	hypothetical protein		
SAMN04901664_02354	CDS	ephD_2	1.-.-.-	putative oxidoreductase EphD
SAMN04901664_02355	CDS	hypothetical protein		
SAMN04901664_02356	CDS	hypothetical protein		
SAMN04901664_02357	CDS	hypothetical protein		
SAMN04901664_02358	CDS	hypothetical protein		
SAMN04901664_02359	CDS	hypothetical protein		
SAMN04901664_02360	CDS	putative HTH-type transcriptional regulator		
SAMN04901664_02361	CDS	keff_1	1.6.5.2	Glutathione-regulated potassium-efflux system ancillary protein Keff
SAMN04901664_02362	CDS	hypothetical protein		
SAMN04901664_02363	CDS	thrH	3.1.3.3	Phosphoserine phosphatase ThrH

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02364	CDS	cysH	1.8.4.8	Phosphoadenosine phosphosulfate reductase
SAMN04901664_02365	CDS	wax-dgaT	2.3.1.20	O-acyltransferase WSD
SAMN04901664_02366	CDS	hypothetical protein		
SAMN04901664_02367	CDS	rng	3.1.26.-	Ribonuclease G
SAMN04901664_02368	CDS	yhdE	Maf-like protein YhdE	
SAMN04901664_02369	CDS	hypothetical protein		
SAMN04901664_02370	CDS	mreC	MreC	
SAMN04901664_02371	CDS	mreB	MreB	
SAMN04901664_02372	CDS	gatC	6.3.5.-	Glutamyl-tRNA(Gln) amidotransferase subunit C
SAMN04901664_02373	CDS	gatA_1	6.3.5.7	Glutamyl-tRNA(Gln) amidotransferase subunit A
SAMN04901664_02374	CDS	gatB	6.3.5.-	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
SAMN04901664_02375	CDS	hypothetical protein		
SAMN04901664_02376	CDS	yraA	3.2.-.-	Putative cysteine protease YraA
SAMN04901664_02377	CDS	hypothetical protein		
SAMN04901664_02378	CDS	hypothetical protein		
SAMN04901664_02379	CDS	hypothetical protein		
SAMN04901664_02380	CDS	sbmA	SbmA	
SAMN04901664_02381	CDS	tdcB_2	4.3.1.19	L-threonine ammonia-lyase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02382	CDS	putative NTE family protein		
SAMN04901664_02383	CDS	alsT	AlsT	
SAMN04901664_02384	CDS	hypothetical protein		
SAMN04901664_02385	CDS	nfnB	1.-.-.- protein	Nitroreductase NfnB
SAMN04901664_02386	CDS	bcr_2		
SAMN04901664_02387	CDS	yccS_1	Inner membrane protein YccS	
SAMN04901664_02388	CDS	hypothetical protein		
SAMN04901664_02389	CDS	cysJ	1.8.1.2	Sulfite reductase [NADPH] flavoprotein alpha-component
SAMN04901664_02390	CDS	hypothetical protein		
SAMN04901664_02391	tRNA	tRNA-Val(tac)		
SAMN04901664_02392	tRNA	tRNA-Asp(gtc)		
SAMN04901664_02393	tRNA	tRNA-Val(tac)		
SAMN04901664_02394	tRNA	tRNA-Asp(gtc)		
SAMN04901664_02395	tRNA	tRNA-Asp(gtc)		
SAMN04901664_02396	tRNA	tRNA-Val(tac)		
SAMN04901664_02397	CDS	hypothetical protein		
SAMN04901664_02398	CDS	ybaN	Inner membrane protein YbaN	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02399	CDS	hypothetical protein		
SAMN04901664_02400	CDS	hypothetical protein		Succinyl-diaminopimelate desuccinylase
SAMN04901664_02401	CDS	dapE	3.5.1.18	
SAMN04901664_02402	CDS	hypothetical protein		
SAMN04901664_02403	CDS	cheA	2.7.13.3	Chemotaxis protein CheA
SAMN04901664_02404	CDS	mcpQ	Methyl-accepting chemotaxis protein M _{cp} Q	
SAMN04901664_02405	CDS	cheW	Chemotaxis protein CheW	
SAMN04901664_02406	CDS	pleD_3	Response regulator PleD	
SAMN04901664_02407	CDS	phoP	Alkaline phosphatase synthesis transcriptional regulatory protein PhoP	
SAMN04901664_02408	CDS	hypothetical protein		
SAMN04901664_02409	CDS	cnrB	Nickel and cobalt resistance protein CnrB	
SAMN04901664_02410	CDS	mdtC	MdtC	
SAMN04901664_02411	CDS	proS	6.1.1.15	Proline--tRNA ligase
SAMN04901664_02412	CDS	hypothetical protein		
SAMN04901664_02413	CDS	hypothetical protein		
SAMN04901664_02414	CDS	hypothetical protein		
SAMN04901664_02415	CDS	hypothetical protein		
SAMN04901664_02416	CDS	ygfZ	tRNA-modifying protein YgfZ	
SAMN04901664_02417	CDS	dsbC_3	putative thiol:disulfide interchange protein DsbC	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02418	CDS	esiB_3	Secretory immunoglobulin A-binding protein EsiB	
SAMN04901664_02419	CDS	hypothetical protein		
SAMN04901664_02420	CDS	namA	1.6.99.1	NADPH dehydrogenase
SAMN04901664_02421	CDS	iutA_2	Ferric aerobactin receptor	
SAMN04901664_02422	CDS	3.2.2.-	Putative 3-methyladenine DNA glycosylase	
SAMN04901664_02423	CDS	mutM	3.2.2.23	Formamidopyrimidine-DNA glycosylase
SAMN04901664_02424	CDS	ppiC	5.2.1.8	Peptidyl-prolyl cis-trans isomerase C
SAMN04901664_02425	CDS	hypothetical protein		
SAMN04901664_02426	CDS	mscL	Large-conductance	
SAMN04901664_02427	CDS	typA	mechanosensitive channel TypA/BipA	
SAMN04901664_02428	CDS	xanP	Xanthine permease XanP	
SAMN04901664_02429	CDS	rsmC	2.1.1.172	Ribosomal RNA small subunit methyltransferase C
SAMN04901664_02430	CDS	lysP	Lysine-specific permease	
SAMN04901664_02431	CDS	rtcB	6.5.1.-	RNA-splicing ligase RtcB
SAMN04901664_02432	CDS	hypothetical protein		
SAMN04901664_02433	CDS	Outer membrane protein Omp38		
SAMN04901664_02434	CDS	hypothetical protein		
SAMN04901664_02435	CDS	thlA_2	2.3.1.9	Acetyl-CoA acetyltransferase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02436	CDS	hypothetical protein		
SAMN04901664_02437	CDS	Multidrug transporter		
SAMN04901664_02438	CDS	hypothetical protein		
SAMN04901664_02439	CDS	sir	1.8.7.1	Sulfite reductase [ferredoxin]
SAMN04901664_02440	CDS	gcd	1.1.5.2	Quinoprotein glucose dehydrogenase
SAMN04901664_02441	CDS	oprB_1	Porin B	
SAMN04901664_02442	CDS	yfdE	2.8.3.19	Acetyl-CoA:oxalate CoA-transferase
SAMN04901664_02443	CDS	putative HTH-type transcriptional regulator		
SAMN04901664_02444	CDS	fadA_2	2.3.1.-	Putative acyltransferase
SAMN04901664_02445	CDS	fadJ	Fatty acid oxidation complex subunit alpha	
SAMN04901664_02446	CDS	hypothetical protein		
SAMN04901664_02447	CDS	hypothetical protein		
SAMN04901664_02448	CDS	2.3.1.-	Acetyltransferase	
SAMN04901664_02449	CDS	hypothetical protein		
SAMN04901664_02450	CDS	hypothetical protein		
SAMN04901664_02451	CDS	hypothetical protein		
SAMN04901664_02452	CDS	yhjE_2	Inner membrane metabolite transport protein YhjE	
SAMN04901664_02453	CDS	hypothetical protein		
SAMN04901664_02454	CDS	secA	SecA	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02455	CDS	ahpC_1	1.11.1.15	Alkyl hydroperoxide reductase subunit C
SAMN04901664_02456	CDS	3.-.-.-	putative metallo-hydrolase	
SAMN04901664_02457	CDS	hypothetical protein		
SAMN04901664_02458	CDS	ftsN_2	Cell division protein FtsN	
SAMN04901664_02459	CDS	folC	6.3.2.12	Dihydrofolate synthase/folypolyglutamate synthase
SAMN04901664_02460	CDS	accD	6.4.1.2	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
SAMN04901664_02461	CDS	trpA	4.2.1.20	Tryptophan synthase alpha chain
SAMN04901664_02462	CDS	hypothetical protein		
SAMN04901664_02463	CDS	hypothetical protein		
SAMN04901664_02464	CDS	hypothetical protein		
SAMN04901664_02465	CDS	hypothetical protein		
SAMN04901664_02466	CDS	trpB_2	4.2.1.20	Tryptophan synthase beta chain
SAMN04901664_02467	CDS	trpF	5.3.1.24	N-(5'-phosphoribosyl)anthranilate isomerase
SAMN04901664_02468	CDS	btuB_2	Vitamin B12 transporter BtuB	
SAMN04901664_02469	CDS	yvqK	2.5.1.17	Cob(I)yrinic acid a,c-diamide adenosyltransferase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02470	CDS	ugpQ	3.1.4.46	Glycerophosphodiester phosphodiesterase, cytoplasmic
SAMN04901664_02471	CDS	hypothetical protein		
SAMN04901664_02472	CDS	hypothetical protein		
SAMN04901664_02473	CDS	hypothetical protein		
SAMN04901664_02474	CDS	baeR	Transcriptional regulatory protein BaeR	
SAMN04901664_02475	CDS	baeS_2	2.7.13.3	Signal transduction histidine-protein kinase BaeS
SAMN04901664_02476	CDS	hypothetical protein		
SAMN04901664_02477	CDS	dmdC_2	1.3.8.-	3-methylmercaptopropionyl-CoA dehydrogenase
SAMN04901664_02478	CDS	dmdC_3	1.3.8.-	3-methylmercaptopropionyl-CoA dehydrogenase
SAMN04901664_02479	CDS	dmlR_12	HTH-type transcriptional regulator DmlR	
SAMN04901664_02480	CDS	gst	2.5.1.18	Glutathione S-transferase GST-4.5
SAMN04901664_02481	CDS	psiE	Protein PsiE	
SAMN04901664_02482	CDS	hypothetical protein		
SAMN04901664_02483	CDS	hypothetical protein		
SAMN04901664_02484	CDS	clsA	2.7.8.-	Cardiolipin synthase A
SAMN04901664_02485	CDS	putative TonB-dependent receptor		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02486	CDS	hypothetical protein		Aspartate--tRNA(Asp/Asn) ligase
SAMN04901664_02487	CDS	aspS	6.1.1.23	
SAMN04901664_02488	CDS	2.7.-.-	Capsular polysaccharide phosphotransferase cps12A	
SAMN04901664_02489	CDS	hypothetical protein		
SAMN04901664_02490	CDS	hypothetical protein		
SAMN04901664_02491	CDS	hypothetical protein		
SAMN04901664_02492	CDS	hypothetical protein		
SAMN04901664_02493	CDS	bshA_2	2.4.1.-	N-acetyl-alpha-D-glucosaminyl L-malate synthase
SAMN04901664_02494	CDS	sunS	2.4.1.-	SPBc2 prophage-derived glycosyltransferase SunS
SAMN04901664_02495	CDS	icaB	3.5.1.-	Poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase
SAMN04901664_02496	CDS	hypothetical protein		
SAMN04901664_02497	CDS	hypothetical protein		
SAMN04901664_02498	CDS	ilvE	2.6.1.42	Branched-chain-amino-acid aminotransferase
SAMN04901664_02499	CDS	glnE	synthetase	
SAMN04901664_02500	CDS	bvgS	adenyltransferase/adenyl-removing enzyme	
SAMN04901664_02501	CDS	hypothetical protein	2.7.13.3	Virulence sensor protein BvgS

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02502	CDS	hypothetical protein		
SAMN04901664_02503	CDS	hypothetical protein		
SAMN04901664_02504	tRNA	tRNA-Leu(caa)		
SAMN04901664_02505	CDS	queA	2.4.99.17	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
SAMN04901664_02506	CDS	hypothetical protein		
SAMN04901664_02507	CDS	hypothetical protein		
SAMN04901664_02508	CDS	tgt	2.4.2.29	Queuine tRNA- ribosyltransferase
SAMN04901664_02509	CDS	hypothetical protein		
SAMN04901664_02510	CDS	mzrA	Modulator protein MzrA	
SAMN04901664_02511	CDS	hypothetical protein		
SAMN04901664_02512	CDS	coaBC	Coenzyme A biosynthesis bifunctional protein CoaBC	
SAMN04901664_02513	CDS	hypothetical protein		
SAMN04901664_02514	CDS	hypothetical protein		
SAMN04901664_02515	CDS	yciV	3.1.13.-	5'-3' exoribonuclease
SAMN04901664_02516	CDS	yciB_2	Intracellular septation protein	
SAMN04901664_02517	CDS	hypothetical protein		
SAMN04901664_02518	CDS	hypothetical protein		
SAMN04901664_02519	CDS	mmmC	tRNA 5-methylaminomethyl-2- thiouridine biosynthesis bifunctional protein MmmC	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02520	CDS	glpE_3	2.8.1.1	Thiosulfate sulfurtransferase GlpE
SAMN04901664_02521	CDS	hypothetical protein		
SAMN04901664_02522	CDS	hypothetical protein		
SAMN04901664_02523	CDS	3.1.2.-	hydrolase	
SAMN04901664_02524	CDS	trxC	1.8.1.8	Thioredoxin 2
SAMN04901664_02525	CDS	hypothetical protein		
SAMN04901664_02526	CDS	blh_3	3.-.-.-	Beta-lactamase hydrolase-like protein
SAMN04901664_02527	CDS	hypothetical protein		
SAMN04901664_02528	CDS	pdhD	1.8.1.4	Dihydrolipoyl dehydrogenase
SAMN04901664_02529	rRNA	5S ribosomal RNA		
SAMN04901664_02530	CDS	hypothetical protein		
SAMN04901664_02531	CDS	hypothetical protein		
SAMN04901664_02532	CDS	bluF	Blue light- and temperature- regulated antirepressor BluF	
SAMN04901664_02533	CDS	hypothetical protein		
SAMN04901664_02534	CDS	hypothetical protein		
SAMN04901664_02535	CDS	ubiG_2	2.1.1.222	Ubiquinone biosynthesis O- methyltransferase
SAMN04901664_02536	CDS	mshB	3.5.1.103	1D-myo-inositol 2-acetamido-2- deoxy-alpha-D- glucopyranoside deacetylase
SAMN04901664_02537	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02538	CDS	hypothetical protein		
SAMN04901664_02539	CDS	gabP_3	GABA permease	
SAMN04901664_02540	CDS	bauC_2	1.2.1.-	Putative 3-oxopropanoate dehydrogenase
SAMN04901664_02541	CDS	bauA	2.6.1.18	Beta-alanine--pyruvate aminotransferase
SAMN04901664_02542	CDS	gltC_6	HTH-type transcriptional regulator GltC	
SAMN04901664_02543	tRNA	tRNA-Trp(cca)		
SAMN04901664_02544	tRNA	tRNA-Leu(tag)		
SAMN04901664_02545	tRNA	tRNA-Trp(cca)		
SAMN04901664_02546	tRNA	tRNA-Leu(tag)		
SAMN04901664_02547	CDS	pkn5	2.7.11.1	Serine/threonine-protein kinase pkn5
SAMN04901664_02548	CDS	hypothetical protein		
SAMN04901664_02549	CDS	hypothetical protein		
SAMN04901664_02550	CDS	hypothetical protein		
SAMN04901664_02551	CDS	tsaD	2.3.1.234	tRNA N6-adenosine threonylcarbamoyltransferase
SAMN04901664_02552	CDS	rpsU	30S ribosomal protein S21	
SAMN04901664_02553	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02554	CDS	bepA_2	3.4.-.-	Beta-barrel assembly-enhancing protease
SAMN04901664_02555	CDS	ghrB	1.1.1.79	Glyoxylate/hydroxyypyruvate reductase B
SAMN04901664_02556	CDS	hypothetical protein		
SAMN04901664_02557	CDS	htpX_2	3.4.24.-	Protease HtpX
SAMN04901664_02558	CDS	purF	2.4.2.14	Amidophosphoribosyltransferase
SAMN04901664_02559	CDS	cvpA	Colicin V production protein	
SAMN04901664_02560	CDS	pyrD	1.3.5.2	Dihydroorotate dehydrogenase (quinone)
SAMN04901664_02561	CDS	hypothetical protein		
SAMN04901664_02562	CDS	hypothetical protein		
SAMN04901664_02563	CDS	sixA	3.1.3.-	Phosphohistidine phosphatase SixA
SAMN04901664_02564	CDS	gpsA	1.1.1.94	Glycerol-3-phosphate dehydrogenase [NAD(P)+]
SAMN04901664_02565	CDS	ydjA	1.-.-.-	Putative NAD(P)H nitroreductase YdjA
SAMN04901664_02566	CDS	hypothetical protein		
SAMN04901664_02567	CDS	rhIB	3.6.4.13	ATP-dependent RNA helicase RhIB
SAMN04901664_02568	CDS	espG	Cold shock-like protein CspG	
SAMN04901664_02569	CDS	tusA_2	2.8.1.-	Sulfurtransferase TusA
SAMN04901664_02570	CDS	rpoH	RpoH	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02571	CDS	hypothetical protein		
SAMN04901664_02572	CDS	hypothetical protein		
SAMN04901664_02573	CDS	thiG	2.8.1.10	Thiazole synthase
SAMN04901664_02574	CDS	hypothetical protein		
SAMN04901664_02575	CDS	hypothetical protein		
SAMN04901664_02576	CDS	hypothetical protein		
SAMN04901664_02577	CDS	rbn	3.1.-.-	Ribonuclease BN
SAMN04901664_02578	CDS	pepD	3.4.13.18	Cytosol non-specific dipeptidase
SAMN04901664_02579	CDS	hypothetical protein		
SAMN04901664_02580	CDS	aroA	2.5.1.19	3-phosphoshikimate 1-carboxyvinyltransferase
SAMN04901664_02581	CDS	pheA	P-protein	
SAMN04901664_02582	CDS	besA	3.1.-.-	Ferri-bacillibactin esterase BesA
SAMN04901664_02583	CDS	mmgC_5	1.3.99.-	Acyl-CoA dehydrogenase
SAMN04901664_02584	CDS	dctA_1	Aerobic C4-dicarboxylate transport protein	
SAMN04901664_02585	CDS	trpD_1	2.4.2.18	Anthranilate phosphoribosyltransferase
SAMN04901664_02586	CDS	hypothetical protein		
SAMN04901664_02587	CDS	nadK	2.7.1.23	NAD kinase
SAMN04901664_02588	CDS	mrcB	Penicillin-binding protein 1B	
SAMN04901664_02589	CDS	hypothetical protein		
SAMN04901664_02590	CDS	mutT_1	3.6.1.55	8-oxo-dGTP diphosphatase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02591	CDS	hypothetical protein		
SAMN04901664_02592	CDS	qseC_2	2.7.13.3	Sensor protein QseC
SAMN04901664_02593	CDS	qseB_2	Transcriptional regulatory protein QseB	
SAMN04901664_02594	CDS	hypothetical protein		
SAMN04901664_02595	CDS	epsE_2	protein E	
SAMN04901664_02596	CDS	hypothetical protein		
SAMN04901664_02597	CDS	trmO	2.1.1.-	tRNA (adenine(37)-N6)-methyltransferase
SAMN04901664_02598	CDS	fpr_2	1.18.1.2	Ferredoxin--NADP reductase
SAMN04901664_02599	CDS	yddE_3	5.1.-.-	putative isomerase YddE
SAMN04901664_02600	CDS	norG_3	HTH-type transcriptional regulator NorG	
SAMN04901664_02601	CDS	ydcP	3.4.-.-	putative protease YdcP
SAMN04901664_02602	CDS	protein		
SAMN04901664_02603	CDS	emrE_2	Multidrug transporter EmrE	
SAMN04901664_02604	CDS	hisP	Histidine transport ATP-binding protein HisP	
SAMN04901664_02605	CDS	hisM	Histidine transport system permease protein HisM	
SAMN04901664_02606	CDS	hisQ	Histidine transport system permease protein HisQ	
SAMN04901664_02607	CDS	argT	Lysine/arginine/ornithine-binding periplasmic protein	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02608	CDS	dmlR_13	HTH-type transcriptional regulator DmlR	
SAMN04901664_02609	CDS	mdtE	MdtE	
SAMN04901664_02610	CDS	bepE	Efflux pump membrane transporter BepE	
SAMN04901664_02611	CDS	mepC	Multidrug/solvent efflux pump outer membrane protein MepC	
SAMN04901664_02612	CDS	glyA	2.1.2.1	Serine hydroxymethyltransferase
SAMN04901664_02613	CDS	rraB_2	activity B	
SAMN04901664_02614	CDS	hypothetical protein	3.1.11.-	Exodeoxyribonuclease 10
SAMN04901664_02615	CDS	exoX		
SAMN04901664_02616	CDS	hypothetical protein		
SAMN04901664_02617	tRNA	tRNA-Arg(ccg)		
SAMN04901664_02618	CDS	dirrA	3.6.3.-	Daunorubicin/doxorubicin resistance A TP-binding protein DrrA
SAMN04901664_02619	CDS	yadH	Inner membrane transport permease Y adH	
SAMN04901664_02620	CDS	queF	1.7.1.13	NADPH-dependent 7-cyano-7-deazaguanine reductase
SAMN04901664_02621	CDS	hypothetical protein		
SAMN04901664_02622	CDS	mrdB	2.4.1.129	Peptidoglycan glycosyltransferase MrdB

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02623	CDS	mltB_2	4.2.2.-	Membrane-bound lytic murein transglycosylase B
SAMN04901664_02624	CDS	rlpA	4.2.2.-	Endolytic peptidoglycan transglycosylase RlpA
SAMN04901664_02625	CDS	hypothetical protein		
SAMN04901664_02626	CDS	hypothetical protein		
SAMN04901664_02627	CDS	ygaZ_2	Inner membrane protein YgaZ	
SAMN04901664_02628	CDS	btr_2	HTH-type transcriptional activator Btr	
SAMN04901664_02629	CDS	hypothetical protein		
SAMN04901664_02630	CDS	tsf	Elongation factor Ts	
SAMN04901664_02631	CDS	rpsB	30S ribosomal protein S2	
SAMN04901664_02632	CDS	map_2	3.4.11.18	Methionine aminopeptidase
SAMN04901664_02633	CDS	hypothetical protein		
SAMN04901664_02634	CDS	narT	NarT	
SAMN04901664_02635	CDS	yhjX	YhjX	
SAMN04901664_02636	CDS	hypothetical protein		
SAMN04901664_02637	CDS	sthA	1.6.1.1	Soluble pyridine nucleotide transhydrogenase
SAMN04901664_02638	CDS	lipA_2	2.8.1.8	Lipoyl synthase
SAMN04901664_02639	CDS	fadE	1.3.99.-	Acyl-coenzyme A dehydrogenase
SAMN04901664_02640	CDS	hypothetical protein		
SAMN04901664_02641	CDS	hypothetical protein		
SAMN04901664_02642	CDS	ahcY	3.3.1.1	Adenosylhomocysteinase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02643	CDS	metF	1.5.1.20	5,10-methylenetetrahydrofolate reductase
SAMN04901664_02644	CDS	rsmE_1	2.1.1.193	Ribosomal RNA small subunit methyltransferase E
SAMN04901664_02645	CDS	putative signaling protein		NADP-dependent malic enzyme
SAMN04901664_02646	CDS	maeB	1.1.1.40	
SAMN04901664_02647	CDS	cca	Multifunctional CCA protein	
SAMN04901664_02648	CDS	degS	3.4.21.107	Serine endoprotease DegS
SAMN04901664_02649	CDS	GTP cyclohydrolase 1 type 2		
SAMN04901664_02650	CDS	sodB	1.15.1.1	Superoxide dismutase [Fe]
SAMN04901664_02651	tRNA	tRNA-Asn(gtt)		
SAMN04901664_02652	tRNA	tRNA-Asn(gtt)		
SAMN04901664_02653	tRNA	tRNA-Asn(gtt)		
SAMN04901664_02654	CDS	hypothetical protein		
SAMN04901664_02655	CDS	hypothetical protein		
SAMN04901664_02656	CDS	hypothetical protein		
SAMN04901664_02657	CDS	ubiA	2.5.1.-	4-hydroxybenzoate octaprenyltransferase
SAMN04901664_02658	CDS	ubiC	4.1.3.40	Chorismate pyruvate-lyase
SAMN04901664_02659	CDS	5.4.4.3	mutase	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02660	CDS	ntpT		
SAMN04901664_02661	CDS	3.4.11.-	Di-/tripeptide transporter Aminopeptidase	
SAMN04901664_02662	CDS	trpG	4.1.3.27	Anthranilate synthase component 2
SAMN04901664_02663	CDS	pepN_1	3.4.11.2	Aminopeptidase N
SAMN04901664_02664	CDS	cirA_2	Colicin I receptor	
SAMN04901664_02665	CDS	trpD_2	2.4.2.18	Anthranilate phosphoribosyltransferase
SAMN04901664_02666	CDS	trpC	4.1.1.48	Indole-3-glycerol phosphate synthase
SAMN04901664_02667	CDS	smrA	3.1.-.-	putative DNA endonuclease SmrA
SAMN04901664_02668	CDS	hypothetical protein		
SAMN04901664_02669	CDS	pucD	1.17.1.4	putative xanthine dehydrogenase subunit D
SAMN04901664_02670	CDS	kdhB	1.5.99.14	6-hydroxypseudooxynicotine dehydrogenase complex subunit beta
SAMN04901664_02671	CDS	folE	3.5.4.16	GTP cyclohydrolase 1
SAMN04901664_02672	CDS	hypothetical protein		
SAMN04901664_02673	CDS	hypothetical protein		
SAMN04901664_02674	CDS	hypothetical protein		
SAMN04901664_02675	CDS	pilA	Fimbrial protein	
SAMN04901664_02676	CDS	hypothetical protein		
SAMN04901664_02677	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02678	CDS	bfr_2	1.16.3.1	Bacterioferritin
SAMN04901664_02679	CDS	bfd	ferredoxin	
SAMN04901664_02680	CDS	yabJ	3.5.99.10	2-iminobutanoate/2-iminopropanoate deaminase
SAMN04901664_02681	CDS	spoT_2	Bifunctional (p)ppGpp synthase/hydrolase SpoT	
SAMN04901664_02682	CDS	rpoZ	2.7.7.6	DNA-directed RNA polymerase subunit omega
SAMN04901664_02683	CDS	gmk_1	2.7.4.8	Guanylate kinase
SAMN04901664_02684	CDS	ispH	1.17.7.4	4-hydroxy-3-methylbut-2-enyl diphosphate reductase
SAMN04901664_02685	CDS	hypothetical protein		
SAMN04901664_02686	CDS	hypothetical protein		
SAMN04901664_02687	CDS	hypothetical protein		
SAMN04901664_02688	CDS	hypothetical protein		
SAMN04901664_02689	CDS	pilY1_1	Type IV pilus biogenesis factor PilY1	
SAMN04901664_02690	CDS	xcpT_2	protein G	
SAMN04901664_02691	CDS	pilE	Fimbrial protein	
SAMN04901664_02692	CDS	rpsP	30S ribosomal protein S16	
SAMN04901664_02693	CDS	rimM	RimM	
SAMN04901664_02694	CDS	trmD	2.1.1.228	tRNA (guanine-N(1)-)-methyltransferase
SAMN04901664_02695	CDS	rplS	50S ribosomal protein L19	
SAMN04901664_02696	CDS	lip	3.1.1.3	Lactonizing lipase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02697	CDS	lifO	Lipase chaperone	
SAMN04901664_02698	CDS	truB	5.4.99.25	tRNA pseudouridine synthase B
SAMN04901664_02699	CDS	hypothetical protein		
SAMN04901664_02700	CDS	DNA nickase		
SAMN04901664_02701	CDS	rhtA_1	RhtA	
SAMN04901664_02702	CDS	rhtA_2	RhtA	
SAMN04901664_02703	CDS	serA	1.1.1.95	D-3-phosphoglycerate dehydrogenase
SAMN04901664_02704	CDS	1.-.-.-	oxidoreductase	
SAMN04901664_02705	CDS	hypothetical protein		
SAMN04901664_02706	CDS	ygiN	1.-.-.-	putative quinol monooxygenase YgiN
SAMN04901664_02707	CDS	mdaB	Modulator of drug activity B	
SAMN04901664_02708	CDS	hypothetical protein		
SAMN04901664_02709	CDS	mdfA	Multidrug transporter MdfA	
SAMN04901664_02710	CDS	yccS_2	Inner membrane protein YccS	
SAMN04901664_02711	CDS	sodC	1.15.1.1	Superoxide dismutase [Cu-Zn]
SAMN04901664_02712	CDS	hypothetical protein		
SAMN04901664_02713	CDS	hypothetical protein		
SAMN04901664_02714	CDS	hypothetical protein		
SAMN04901664_02715	CDS	hypothetical protein		
SAMN04901664_02716	CDS	hypothetical protein		
SAMN04901664_02717	CDS	2.1.1.-	putative methyltransferase	
SAMN04901664_02718	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02719	CDS	rocC_2	Amino-acid permease RocC	
SAMN04901664_02720	CDS	gdhA_1	1.4.1.3	Glutamate dehydrogenase
SAMN04901664_02721	CDS	astC_1	2.6.1.81	Succinylornithine transaminase
SAMN04901664_02722	CDS	astA_1	2.3.1.109	Arginine N-succinyltransferase
SAMN04901664_02723	CDS	astD	1.2.1.71	N-succinylglutamate 5-semialdehyde dehydrogenase
SAMN04901664_02724	CDS	astB	3.5.3.23	N-succinylarginine dihydrolase
SAMN04901664_02725	CDS	astE	3.5.1.96	Succinylglutamate desuccinylase
SAMN04901664_02726	CDS	hypothetical protein		
SAMN04901664_02727	CDS	hypothetical protein		
SAMN04901664_02728	CDS	aprE	3.4.21.62	Subtilisin E
SAMN04901664_02729	CDS	hypothetical protein		
SAMN04901664_02730	CDS	hypothetical protein		
SAMN04901664_02731	CDS	gltR_3	HTH-type transcriptional regulator GltR	
SAMN04901664_02732	CDS	yhbE	putative inner membrane transporter YhbE	
SAMN04901664_02733	CDS	hypothetical protein		
SAMN04901664_02734	CDS	glyS	6.1.1.14	Glycine--tRNA ligase beta subunit
SAMN04901664_02735	CDS	glyQ	6.1.1.14	Glycine--tRNA ligase alpha subunit

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02736	CDS	hypothetical protein		
SAMN04901664_02737	CDS	hypothetical protein		
SAMN04901664_02738	CDS	hypothetical protein		
SAMN04901664_02739	CDS	hypothetical protein		
SAMN04901664_02740	CDS	hrp1		
SAMN04901664_02741	CDS	hypothetical protein		
SAMN04901664_02742	CDS	hypothetical protein		
				Hypoxic response protein 1
SAMN04901664_02743	CDS	dmdC_4	1.3.8.-	3-methylmercaptopyruvyl-CoA dehydrogenase
SAMN04901664_02744	CDS	hypothetical protein		
SAMN04901664_02745	CDS	aroE	1.1.1.25	Shikimate dehydrogenase (NADP(+))
				Oxygen-dependent coproporphyrinogen-III oxidase
SAMN04901664_02746	CDS	hemF	1.3.3.3	GTP cyclohydrolase-2
SAMN04901664_02747	CDS	ribA	3.5.4.25	1-deoxy-D-xylulose-5-phosphate synthase
SAMN04901664_02748	CDS	dxs_1	2.2.1.7	Inositol-1-monophosphatase
SAMN04901664_02749	CDS	subB	3.1.3.25	ATP-dependent RNA helicase
SAMN04901664_02750	CDS	deaD	3.6.4.13	DeaD
SAMN04901664_02751	CDS	m1aF	3.6.3.-	putative phospholipid import ATP-binding protein M1aF
SAMN04901664_02752	CDS	m1aE		transporter permease protein M1aE

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02753	CDS	mlaD	transporter-binding protein MlaD	
SAMN04901664_02754	CDS	mlaC	putative phospholipid-binding protein MlaC	
SAMN04901664_02755	CDS	hypothetical protein		
SAMN04901664_02756	CDS	corA_2	CorA	
SAMN04901664_02757	CDS	yvdD_2	LOG family protein YvdD	
SAMN04901664_02758	CDS	mutT_2	3.6.1.55	8-oxo-dGTP diphosphatase
SAMN04901664_02759	CDS	pyrE_1	2.4.2.10	Orotate phosphoribosyltransferase
SAMN04901664_02760	CDS	recG	3.6.4.12	ATP-dependent DNA helicase RecG
SAMN04901664_02761	CDS	hypothetical protein		
SAMN04901664_02762	CDS	hypothetical protein		
SAMN04901664_02763	CDS	plsB	2.3.1.15	Glycerol-3-phosphate acyltransferase
SAMN04901664_02764	CDS	tesB	3.1.2.-	Acyl-CoA thioesterase 2
SAMN04901664_02765	CDS	glp_2	symporter	
SAMN04901664_02766	CDS	hypothetical protein		
SAMN04901664_02767	CDS	engB	EngB	
SAMN04901664_02768	CDS	nsrR	HTH-type transcriptional repressor NsrR	
SAMN04901664_02769	CDS	hmp	1.14.12.17	Flavoheмоprotein
SAMN04901664_02770	CDS	hypothetical protein		
SAMN04901664_02771	CDS	metC	4.4.1.8	Cystathionine beta-lyase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02772	CDS	<i>guaA_2</i>	6.3.5.2	GMP synthase [glutamine-hydrolyzing]
SAMN04901664_02773	CDS	<i>rpsJ</i>	30S ribosomal protein S10	
SAMN04901664_02774	CDS	<i>rplC</i>	50S ribosomal protein L3	
SAMN04901664_02775	CDS	<i>rplD</i>	50S ribosomal protein L4	
SAMN04901664_02776	CDS	<i>rplW</i>	50S ribosomal protein L23	
SAMN04901664_02777	CDS	<i>rplB</i>	50S ribosomal protein L2	
SAMN04901664_02778	CDS	<i>rpsS</i>	30S ribosomal protein S19	
SAMN04901664_02779	CDS	<i>rplV</i>	50S ribosomal protein L22	
SAMN04901664_02780	CDS	<i>rpsC</i>	30S ribosomal protein S3	
SAMN04901664_02781	CDS	<i>rplP</i>	50S ribosomal protein L16	
SAMN04901664_02782	CDS	<i>rpmC</i>	50S ribosomal protein L29	
SAMN04901664_02783	CDS	<i>rpsQ</i>	30S ribosomal protein S17	
SAMN04901664_02784	CDS	<i>rplN</i>	50S ribosomal protein L14	
SAMN04901664_02785	CDS	<i>rplX</i>	50S ribosomal protein L24	
SAMN04901664_02786	CDS	<i>rplE</i>	50S ribosomal protein L5	
SAMN04901664_02787	CDS	<i>rpsN</i>	30S ribosomal protein S14	
SAMN04901664_02788	CDS	<i>rpsH</i>	30S ribosomal protein S8	
SAMN04901664_02789	CDS	<i>rplF</i>	50S ribosomal protein L6	
SAMN04901664_02790	CDS	<i>rplR</i>	50S ribosomal protein L18	
SAMN04901664_02791	CDS	<i>rpsE</i>	30S ribosomal protein S5	
SAMN04901664_02792	CDS	<i>rpmD</i>	50S ribosomal protein L30	
SAMN04901664_02793	CDS	<i>rplO</i>	50S ribosomal protein L15	
SAMN04901664_02794	CDS	<i>secY</i>	SecY	
SAMN04901664_02795	CDS	<i>rpmJ</i>	50S ribosomal protein L36	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02796	CDS	rpsM	30S ribosomal protein S13	
SAMN04901664_02797	CDS	rpsK	30S ribosomal protein S11	
SAMN04901664_02798	CDS	rpsD	30S ribosomal protein S4	
SAMN04901664_02799	CDS	rpoA	2.7.7.6	DNA-directed RNA polymerase subunit alpha
SAMN04901664_02800	CDS	rplQ	50S ribosomal protein L17	
SAMN04901664_02801	CDS	mymA	1.14.13.-	Putative FAD-containing monooxygenase MymA
SAMN04901664_02802	CDS	mngC_6	1.3.99.-	Acyl-CoA dehydrogenase
SAMN04901664_02803	CDS	sdhE	FAD assembly factor SdhE	
SAMN04901664_02804	CDS	hypothetical protein		
SAMN04901664_02805	CDS	hypothetical protein		
SAMN04901664_02806	CDS	hypothetical protein		
SAMN04901664_02807	CDS	hypothetical protein		
SAMN04901664_02808	CDS	hypothetical protein		
SAMN04901664_02809	CDS	hypothetical protein		
SAMN04901664_02810	CDS	hypothetical protein		
SAMN04901664_02811	CDS	prlC_2	3.4.24.70	Oligopeptidase A
SAMN04901664_02812	CDS	rnr	3.1.13.1	Ribonuclease R
SAMN04901664_02813	tRNA	tRNA-Ser(gct)		
SAMN04901664_02814	tRNA	tRNA-Arg(acg)		
SAMN04901664_02815	tRNA	tRNA-Arg(acg)		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02816	CDS	hypothetical protein		
SAMN04901664_02817	CDS	hypothetical protein		
SAMN04901664_02818	CDS	recF_2		DNA replication and repair protein RecF
SAMN04901664_02819	CDS	hypothetical protein		
SAMN04901664_02820	CDS	hypothetical protein		
SAMN04901664_02821	CDS	hypothetical protein		
SAMN04901664_02822	CDS	hypothetical protein		
SAMN04901664_02823	CDS	hypothetical protein		
SAMN04901664_02824	CDS	naiP_2		Putative niacin/nicotinamide transporter NaiP
SAMN04901664_02825	CDS	dapA_3	4.3.3.7	4-hydroxy-tetrahydrodipicolinate synthase
SAMN04901664_02826	CDS	cynR_2		
SAMN04901664_02827	CDS	hypothetical protein		
SAMN04901664_02828	CDS	hypothetical protein		
SAMN04901664_02829	CDS	hypothetical protein		
SAMN04901664_02830	CDS	ydgl		antiporter
SAMN04901664_02831	CDS	mmuM	2.1.1.10	Homocysteine S-methyltransferase
SAMN04901664_02832	CDS	hypothetical protein		
SAMN04901664_02833	CDS	mqq	1.1.5.4	Malate:quinone oxidoreductase
SAMN04901664_02834	CDS	betA	1.1.99.1	Oxygen-dependent choline dehydrogenase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02835	CDS	betB_2	1.2.1.8	NAD/NADP-dependent betaine aldehyde dehydrogenase
SAMN04901664_02836	CDS	betI_4	HTH-type transcriptional regulator BetI	
SAMN04901664_02837	CDS	betT1	Osmo-independent choline transporter BetT1	
SAMN04901664_02838	CDS	betT2	Osmo-dependent choline transporter BetT2	
SAMN04901664_02839	CDS	hypothetical protein	hydrolase	
SAMN04901664_02840	CDS	3.1.2.-		
SAMN04901664_02841	CDS	hypothetical protein		
SAMN04901664_02842	CDS	yeiR	3.6.-.-	Zinc-binding GTPase YeiR
SAMN04901664_02843	CDS	dctA_2	Aerobic C4-dicarboxylate transport protein	
SAMN04901664_02844	CDS	hypothetical protein		
SAMN04901664_02845	CDS	fbp_2	5.2.1.8	FK506-binding protein
SAMN04901664_02846	CDS	pgaB_1	3.5.1.-	Poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase
SAMN04901664_02847	CDS	pgaC_1	2.4.1.-	Poly-beta-1,6-N-acetyl-D-glucosamine synthase
SAMN04901664_02848	CDS	hypothetical protein		
SAMN04901664_02849	CDS	paaF_5	4.2.1.17	2,3-dehydroadipyl-CoA hydratase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02850	CDS	pnuC		Nicotinamide riboside transporter PnuC
SAMN04901664_02851	CDS	hypothetical protein		
SAMN04901664_02852	CDS	kdgR		Transcriptional regulator KdgR
SAMN04901664_02853	CDS	ndoA		Naphthalene 1,2-dioxygenase system ferredoxin subunit
SAMN04901664_02854	CDS	hypothetical protein		
SAMN04901664_02855	CDS	tsaM1	1.14.14.-	Toluene-4-sulfonate monooxygenase system iron-sulfur subunit TsaM1
SAMN04901664_02856	CDS	cpnA	1.1.1.163	Cyclopentanol dehydrogenase
SAMN04901664_02857	CDS	hypothetical protein		
SAMN04901664_02858	CDS	thcD	1.18.1.-	Rhodocoxin reductase
SAMN04901664_02859	CDS	gudP		putative glucarate transporter
SAMN04901664_02860	CDS	hypothetical protein		
SAMN04901664_02861	CDS	catD_2	3.1.1.24	3-oxoadipate enol-lactonase 2
SAMN04901664_02862	CDS	fabG_5	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase FabG
SAMN04901664_02863	CDS	nadX	1.4.1.21	L-aspartate dehydrogenase
SAMN04901664_02864	CDS	betB_3	1.2.1.8	NAD/NADP-dependent betaine aldehyde dehydrogenase
SAMN04901664_02865	CDS	ilvB	2.2.1.6	Acetolactate synthase isozyme 1 large subunit
SAMN04901664_02866	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02867	CDS	proP_3	Proline/betaine transporter	
SAMN04901664_02868	CDS	hypothetical protein		
SAMN04901664_02869	CDS	def_2	3.5.1.88	Peptide deformylase
SAMN04901664_02870	CDS	glsA	3.5.1.2	Glutaminase
SAMN04901664_02871	CDS	nimR_4	HTH-type transcriptional regulator NimR	
SAMN04901664_02872	CDS	fsr	protein	
SAMN04901664_02873	CDS	mro	5.1.3.3	Aldose 1-epimerase
SAMN04901664_02874	CDS	hypothetical protein		
SAMN04901664_02875	CDS	perR	HTH-type transcriptional regulator PerR	
SAMN04901664_02876	CDS	fabG_6	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase FabG
SAMN04901664_02877	CDS	nicT	Putative metabolite transport protein NicT	
SAMN04901664_02878	CDS	tktB	2.2.1.1	Transketolase 2
SAMN04901664_02879	CDS	dxs_2	2.2.1.7	1-deoxy-D-xylulose-5-phosphate synthase
SAMN04901664_02880	CDS	metH	2.1.1.13	Methionine synthase
SAMN04901664_02881	CDS	pitA	Low-affinity inorganic phosphate transporter 1	
SAMN04901664_02882	CDS	dsdA	4.3.1.18	D-serine dehydratase
SAMN04901664_02883	CDS	hypothetical protein		
SAMN04901664_02884	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02885	CDS	pkn1	2.7.11.1	Serine/threonine-protein kinase pkn1
SAMN04901664_02886	CDS	atsA	3.1.6.1	Arylsulfatase
SAMN04901664_02887	CDS	glpG	3.4.21.105	Rhomboid protease GlpG
SAMN04901664_02888	CDS	nfuA	Fe/S biogenesis protein NfuA	
SAMN04901664_02889	CDS	pfeA	Ferric enterobactin receptor	
SAMN04901664_02890	CDS	hypothetical protein		
SAMN04901664_02891	CDS	lip1	3.1.1.3	Lipase 1
SAMN04901664_02892	CDS	mtcA2	4.2.1.1	Carbonic anhydrase 2
SAMN04901664_02893	CDS	tesA	3.1.1.1	Esterase TesA
SAMN04901664_02894	CDS	lolD_2	3.6.3.-	Lipoprotein-releasing system A ATP-binding protein LolD
SAMN04901664_02895	CDS	hypothetical protein		
SAMN04901664_02896	CDS	aarA	3.4.21.105	Rhomboid protease AarA
SAMN04901664_02897	CDS	mtgA	2.4.1.129	Biosynthetic peptidoglycan transglycosylase
SAMN04901664_02898	CDS	ppk_2	2.7.4.1	Polyphosphate kinase
SAMN04901664_02899	CDS	hypothetical protein		
SAMN04901664_02900	CDS	oxyR	Hydrogen peroxide-inducible genes activator	
SAMN04901664_02901	CDS	rdmC	3.1.1.95	Acilacinomycin methyltransferase RdmC
SAMN04901664_02902	CDS	rubB_2	1.18.1.1	Rubredoxin-NAD(+) reductase
SAMN04901664_02903	CDS	rubA	Rubredoxin	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02904	CDS	hypothetical protein		
SAMN04901664_02905	CDS	hypothetical protein		
SAMN04901664_02906	CDS	lysS	6.1.1.6	Lysine--tRNA ligase
SAMN04901664_02907	CDS	hypothetical protein		
SAMN04901664_02908	CDS	hypothetical protein		
SAMN04901664_02909	CDS	cysD	2.7.7.4	Sulfate adenylyltransferase subunit 2
SAMN04901664_02910	CDS	cysN	2.7.7.4	Sulfate adenylyltransferase subunit 1
SAMN04901664_02911	CDS	hypothetical protein		
SAMN04901664_02912	CDS	hypothetical protein		
SAMN04901664_02913	CDS	citN		Citrate transporter
SAMN04901664_02914	CDS	corC_3		Magnesium and cobalt efflux protein CorC
SAMN04901664_02915	CDS	syrM1		HTH-type transcriptional regulator SyrM 1
SAMN04901664_02916	CDS	4.1.3.1		Isocitrate lyase
SAMN04901664_02917	CDS	nlpE		Lipoprotein NlpE
SAMN04901664_02918	CDS	hypothetical protein		
SAMN04901664_02919	CDS	ureD		Urease accessory protein UreD
SAMN04901664_02920	CDS	ureA	3.5.1.5	Urease subunit gamma
SAMN04901664_02921	CDS	ureB	3.5.1.5	Urease subunit beta
SAMN04901664_02922	CDS	ureC_1	3.5.1.5	Urease subunit alpha
SAMN04901664_02923	CDS	ureC_2	3.5.1.5	Urease subunit alpha
SAMN04901664_02924	CDS	ureE		Urease accessory protein UreE

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02925	CDS	ureF	Urease accessory protein UreF	
SAMN04901664_02926	CDS	ureG	Urease accessory protein UreG	
SAMN04901664_02927	CDS	hypothetical protein		
SAMN04901664_02928	CDS	rsmD	2.1.1.171	Ribosomal RNA small subunit methyltransferase D
SAMN04901664_02929	CDS	mrdA	3.4.16.4	Peptidoglycan D,D-transpeptidase MrdA
SAMN04901664_02930	CDS	hypothetical protein		
SAMN04901664_02931	CDS	hypothetical protein		
SAMN04901664_02932	CDS	adk	2.7.4.3	Adenylate kinase
SAMN04901664_02933	CDS	nth	4.2.99.18	Endonuclease III
SAMN04901664_02934	CDS	rsxB	Electron transport complex subunit RsxB	
SAMN04901664_02935	CDS	gdhA_2	1.4.1.4	NADP-specific glutamate dehydrogenase
SAMN04901664_02936	CDS	hypothetical protein		
SAMN04901664_02937	CDS	ygiD	1.13.11.29	4,5-DOPA dioxygenase extradiol
SAMN04901664_02938	CDS	rlmH	2.1.1.177	Ribosomal RNA large subunit methyltransferase H
SAMN04901664_02939	CDS	hypothetical protein		
SAMN04901664_02940	CDS	hypothetical protein		
SAMN04901664_02941	CDS	ssuC_3	transport permease protein SsuC	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02942	CDS	ssuB_2	3.6.3.-	Aliphatic sulfonates import ATP-binding protein SsuB
SAMN04901664_02943	CDS	ssuA_4	Putative aliphatic sulfonates- binding protein	
SAMN04901664_02944	CDS	atzF	3.5.1.54	Allophanate hydrolase
SAMN04901664_02945	CDS	Putative nickel-responsive regulator		
SAMN04901664_02946	CDS	hypothetical protein		
SAMN04901664_02947	CDS	hypothetical protein		
SAMN04901664_02948	CDS	yybR_3	putative HTH-type transcriptional regulator YybR	
SAMN04901664_02949	CDS	keff_2	1.6.5.2	Glutathione-regulated potassium-efflux system ancillary protein Keff
SAMN04901664_02950	CDS	accA1_2	Acetyl-/propionyl-coenzyme A carboxylase alpha chain	
SAMN04901664_02951	CDS	hypothetical protein		
SAMN04901664_02952	CDS	hypothetical protein		
SAMN04901664_02953	CDS	1.1.1.1	putative zinc-binding alcohol dehydrogenase	
SAMN04901664_02954	CDS	hypothetical protein		
SAMN04901664_02955	CDS	hypothetical protein		
SAMN04901664_02956	CDS	hypothetical protein		
SAMN04901664_02957	CDS	hypothetical protein		
SAMN04901664_02958	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02959	CDS	esiB_4	Secretory immunoglobulin A-binding protein	
SAMN04901664_02960	CDS	eriC	protein	
SAMN04901664_02961	CDS	accC_2	6.3.4.14	Biotin carboxylase
SAMN04901664_02962	CDS	kipA	KipI antagonist	
SAMN04901664_02963	CDS	hypothetical protein		
SAMN04901664_02964	CDS	hypothetical protein		
SAMN04901664_02965	CDS	hypothetical protein		
SAMN04901664_02966	CDS	gltR_4	HTH-type transcriptional regulator	GltR
SAMN04901664_02967	CDS	hypothetical protein		
SAMN04901664_02968	CDS	hypothetical protein		
SAMN04901664_02969	CDS	rhsC_1	3.1.-.-	Putative deoxyribonuclease RhsC
SAMN04901664_02970	CDS	vgrG1_1		Actin cross-linking toxin
SAMN04901664_02971	CDS	hypothetical protein	6.3.2.-	VgrG1
SAMN04901664_02972	CDS	gph_3	3.1.3.18	Phosphoglycolate phosphatase
SAMN04901664_02973	CDS	hypothetical protein		
SAMN04901664_02974	CDS	hypothetical protein		
SAMN04901664_02975	CDS	lcdH	1.1.1.108	L-carnitine dehydrogenase
SAMN04901664_02976	CDS	hypothetical protein		
SAMN04901664_02977	CDS	tipA	HTH-type transcriptional activator	TipA
SAMN04901664_02978	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02979	CDS	pcaK_2	PcaK	
SAMN04901664_02980	CDS	yxaf_4	putative HTH-type transcriptional regulator YxaF	
SAMN04901664_02981	CDS	lpxP	2.3.1.242	Lipid A biosynthesis palmitoleoyltransferase
SAMN04901664_02982	CDS	cph2_2	Phytochrome-like protein cph2	
SAMN04901664_02983	CDS	rhtA_3	RhtA	
SAMN04901664_02984	CDS	lrp_5	protein	
SAMN04901664_02985	CDS	mutS	MutS	
SAMN04901664_02986	CDS	hypothetical protein		
SAMN04901664_02987	CDS	Ferredoxin 1		
SAMN04901664_02988	CDS	hypothetical protein		
SAMN04901664_02989	CDS	2.1.1.-	methyltransferase/MSMEI_49 47	
SAMN04901664_02990	CDS	hypothetical protein		
SAMN04901664_02991	CDS	2.3.1.-	Putative acetyltransferase	
SAMN04901664_02992	CDS	yigZ	IMPACT family member YigZ	
SAMN04901664_02993	CDS	prsE	Type I secretion system membrane fusion protein PrsE	
SAMN04901664_02994	CDS	ltxB	3.6.3.43	Leukotoxin export ATP- binding protein LtxB
SAMN04901664_02995	CDS	tolC_2	Outer membrane protein TolC	
SAMN04901664_02996	CDS	lptB	3.6.3.-	Lipopolysaccharide export system ATP-binding protein LptB

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_02997	CDS	lptA	Lipopolysaccharide export system protein LptA	
SAMN04901664_02998	CDS	lptC	Lipopolysaccharide export system protein LptC	
SAMN04901664_02999	CDS	kdsC	3.1.3.45	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase KdsC
SAMN04901664_03000	CDS	kdsD	5.3.1.13	Arabinose 5-phosphate isomerase KdsD
SAMN04901664_03001	CDS	cysS	6.1.1.16	Cysteine--tRNA ligase
SAMN04901664_03002	tRNA	tRNA-Gly(gcc)		
SAMN04901664_03003	CDS	hypothetical protein		
SAMN04901664_03004	CDS	hypothetical protein		
SAMN04901664_03005	CDS	hypothetical protein		
SAMN04901664_03006	CDS	hypothetical protein		
SAMN04901664_03007	CDS	putative HTH-type transcriptional regulator		
SAMN04901664_03008	CDS	putative transporter		
SAMN04901664_03009	CDS	hypothetical protein		
SAMN04901664_03010	CDS	hypothetical protein		
SAMN04901664_03011	CDS	hypothetical protein		
SAMN04901664_03012	CDS	hypothetical protein		
SAMN04901664_03013	CDS	proC_1	1.5.1.2	Pyrroline-5-carboxylate reductase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03014	CDS	hypothetical protein		
SAMN04901664_03015	CDS	ospV		Cold shock protein CspV
SAMN04901664_03016	CDS	rhtB_4		Homoserine/homoserine lactone efflux protein
SAMN04901664_03017	CDS	hypothetical protein		
SAMN04901664_03018	CDS	hypothetical protein		
SAMN04901664_03019	CDS	hypothetical protein		
SAMN04901664_03020	CDS	prtR		HTH-type transcriptional regulator PrtR
SAMN04901664_03021	CDS	hypothetical protein		
SAMN04901664_03022	tRNA	tRNA-Met(cat)		
SAMN04901664_03023	CDS	xseA	3.1.11.6	Exodeoxyribonuclease 7 large subunit
SAMN04901664_03024	CDS	hypothetical protein		
SAMN04901664_03025	CDS	hypothetical protein		
SAMN04901664_03026	CDS	hypothetical protein		
SAMN04901664_03027	CDS	hypothetical protein		
SAMN04901664_03028	CDS	yhjQ		YhjQ
SAMN04901664_03029	CDS	gfa_2	4.4.1.22	Glutathione-dependent formaldehyde-activating enzyme
SAMN04901664_03030	CDS	hmrR_2		HTH-type transcriptional regulator HmrR

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03031	CDS	actP_2	3.6.3.4	Copper-transporting P-type ATPase
SAMN04901664_03032	CDS	hypothetical protein	HTH-type transcriptional regulator BenM	
SAMN04901664_03033	CDS	benM_2	1.14.12.13	2-halobenzoate 1,2-dioxygenase large subunit
SAMN04901664_03034	CDS	cbdA	1.14.12.13	2-halobenzoate 1,2-dioxygenase small subunit
SAMN04901664_03035	CDS	cbdB_1	Benzoate 1,2-dioxygenase electron transfer component	
SAMN04901664_03036	CDS	benC	1.1.1.-	Levodione reductase
SAMN04901664_03037	CDS	lvr	Inner membrane protein YdcO	
SAMN04901664_03038	CDS	ycdO_1	PcaK	
SAMN04901664_03039	CDS	pcaK_3	Porin-like protein NicP	
SAMN04901664_03040	CDS	nicP_1	Beta-ketodecanoyl-[acyl-carrier-protein] synthase	
SAMN04901664_03041	CDS	2.3.1.207	1.11.1.15	Alkyl hydroperoxide reductase subunit C
SAMN04901664_03042	CDS	hypothetical protein		
SAMN04901664_03043	CDS	ahpC_2	2.1.1.77	Protein-L-isoaspartate O-methyltransferase
SAMN04901664_03044	CDS	hypothetical protein		
SAMN04901664_03045	CDS	pcm		
SAMN04901664_03046	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03047	CDS	ahpF_2	1.8.1.-	Alkyl hydroperoxide reductase subunit F
SAMN04901664_03048	CDS	hypothetical protein		
SAMN04901664_03049	CDS	gstB_1	2.5.1.18	Glutathione S-transferase GST-6.0
SAMN04901664_03050	CDS	hypothetical protein		
SAMN04901664_03051	CDS	trmB_2	2.1.1.33	tRNA (guanine-N(7)-)-methyltransferase
SAMN04901664_03052	CDS	gstB_2	2.5.1.18	Glutathione S-transferase GstB
SAMN04901664_03053	CDS	hypothetical protein		
SAMN04901664_03054	CDS	arfA	ArfA	
SAMN04901664_03055	CDS	pyrC_1	3.5.2.3	Dihydroorotase
SAMN04901664_03056	CDS	pyrB	2.1.3.2	Aspartate carbamoyltransferase
SAMN04901664_03057	CDS	hypothetical protein		
SAMN04901664_03058	CDS	rlmL	Ribosomal RNA large subunit methyltransferase K/L	
SAMN04901664_03059	CDS	hypothetical protein		
SAMN04901664_03060	CDS	pncC	3.5.1.42	Nicotinamide-nucleotide amidohydrolase PncC
SAMN04901664_03061	CDS	clpB_2	Chaperone protein ClpB	
SAMN04901664_03062	CDS	mepM_1	3.4.24.-	Murein DD-endopeptidase MepM

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03063	CDS	phnO	2.3.1.-	Aminoalkylphosphonate N-acetyltransferase
SAMN04901664_03064	CDS	hypothetical protein		
SAMN04901664_03065	CDS	vfr	protein	
SAMN04901664_03066	tRNA	tRNA-Ile(gat)		
SAMN04901664_03067	rRNA	16S ribosomal RNA		
SAMN04901664_03068	CDS	mIaA	putative phospholipid-binding lipoprotein MlaA	
SAMN04901664_03069	CDS	rsbP	3.1.3.3	Phosphoserine phosphatase RsbP
SAMN04901664_03070	CDS	hypothetical protein		
SAMN04901664_03071	CDS	3.5.-.-	Hydrolase	
SAMN04901664_03072	CDS	hypothetical protein	resistance transcriptional regulator	
SAMN04901664_03073	CDS	ohrR_1	Organic hydroperoxide resistance protein OhrB	
SAMN04901664_03074	CDS	ohrB	protein E	
SAMN04901664_03075	CDS	epsE_3	Small-conductance mechanosensitive channel	
SAMN04901664_03076	CDS	hypothetical protein		
SAMN04901664_03077	CDS	mScS_1		
SAMN04901664_03078	CDS	hypothetical protein		
SAMN04901664_03079	CDS	poIa_1	2.7.7.7	DNA polymerase I

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03080	CDS	hypothetical protein		
SAMN04901664_03081	CDS	proC_2	1.5.1.2	Pyrroline-5-carboxylate reductase
SAMN04901664_03082	CDS	tlfS	6.3.4.19	tRNA(Ile)-lysidine synthase
SAMN04901664_03083	CDS	accA	6.4.1.2	Acetyl-coenzyme A carboxylase
SAMN04901664_03084	CDS	ppx	3.6.1.11	transferase subunit alpha
SAMN04901664_03085	CDS	Thioredoxin C-2		Exopolyphosphatase
SAMN04901664_03086	CDS	rho	3.6.4.-	Transcription termination factor
SAMN04901664_03087	CDS	hypothetical protein		Rho
SAMN04901664_03088	CDS	ihfA	alpha	
SAMN04901664_03089	CDS	pheT	6.1.1.20	Phenylalanine--tRNA ligase
SAMN04901664_03090	CDS	pheS		beta subunit
SAMN04901664_03091	CDS	hypothetical protein		Phenylalanine--tRNA ligase
SAMN04901664_03092	CDS	hypothetical protein		alpha subunit
SAMN04901664_03093	CDS	3.2.2.-		
SAMN04901664_03094	CDS	rplT		
SAMN04901664_03095	CDS	rplM		
SAMN04901664_03096	CDS	entS		
SAMN04901664_03097	CDS	yqaA		
			N-glycosidase	
			50S ribosomal protein L20	
			50S ribosomal protein L35	
			Enterobactin exporter EntS	
			Inner membrane protein YqaA	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03098	CDS	yfcG_2	1.8.4.-	Disulfide-bond oxidoreductase
SAMN04901664_03099	CDS	infC	3	YfcG
SAMN04901664_03100	CDS	thrS	6.1.1.3	Threonine--tRNA ligase
SAMN04901664_03101	CDS	6.2.1.3	ligase	
SAMN04901664_03102	CDS	hypothetical protein		
SAMN04901664_03103	CDS	ptsO	2.7.11.-	Phosphocarrier protein NPr
SAMN04901664_03104	CDS	rapZ	RNase adapter protein RapZ	
SAMN04901664_03105	CDS	panC	6.3.2.1	Pantothenate synthetase
SAMN04901664_03106	CDS	panB	2.1.2.11	3-methyl-2-oxobutanoate hydroxymethyltransferase
SAMN04901664_03107	CDS	folK	2.7.6.3	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase
SAMN04901664_03108	CDS	pcnB	2.7.7.19	Poly(A) polymerase I
SAMN04901664_03109	CDS	comEA	ComE operon protein 1	
SAMN04901664_03110	CDS	mazG	3.6.1.8	Nucleoside triphosphate pyrophosphohydrolase
SAMN04901664_03111	CDS	1.1.1.51	dehydrogenase	
SAMN04901664_03112	CDS	relA	2.7.6.5	GTP pyrophosphokinase
SAMN04901664_03113	CDS	rlmD	2.1.1.190	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD
SAMN04901664_03114	CDS	hypothetical protein		
SAMN04901664_03115	CDS	cysM	2.5.1.47	Cysteine synthase B

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03116	CDS	barA	2.7.13.3	Signal transduction histidine-protein kinase BarA
SAMN04901664_03117	CDS	crt_3	4.2.1.150	Short-chain-enoyl-CoA hydratase
SAMN04901664_03118	CDS	glxR_2	1.1.1.60	2-hydroxy-3-oxopropionate reductase
SAMN04901664_03119	CDS	hyi	5.3.1.22	Hydroxypyruvate isomerase
SAMN04901664_03120	CDS	rsfS	RsfS	(S)-1-Phenylethanol dehydrogenase
SAMN04901664_03121	CDS	ped	1.1.1.311	NAD(P) transhydrogenase subunit beta
SAMN04901664_03122	CDS	pntB	1.6.1.2	NAD(P) transhydrogenase subunit alpha
SAMN04901664_03123	CDS	pntA	1.6.1.2	NAD(P) transhydrogenase subunit alpha part 1
SAMN04901664_03124	CDS	pntAA	1.6.1.2	tRNA-dihydrouridine(20/20a) synthase
SAMN04901664_03125	CDS	hypothetical protein		
SAMN04901664_03126	CDS	hypothetical protein		
SAMN04901664_03127	CDS	putative transporter		
SAMN04901664_03128	CDS	dusA	1.3.1.-	
SAMN04901664_03129	CDS	hypothetical protein		
SAMN04901664_03130	CDS	benM_3		HTH-type transcriptional regulator BenM

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03131	CDS	tecA	6.1.-.-	tRNA threonylcarbamoyladenosine dehydratase
SAMN04901664_03132	CDS	hypothetical protein		
SAMN04901664_03133	CDS	acnA	4.2.1.3	Aconitate hydratase A
SAMN04901664_03134	CDS	yjv	3.1.-.-	putative metal-dependent hydrolase Yjv
SAMN04901664_03135	CDS	pdaC	3.5.1.-	Peptidoglycan-N-acetylmutamic acid deacetylase PdaC
SAMN04901664_03136	CDS	hypothetical protein		
SAMN04901664_03137	CDS	prfC	RF3	
SAMN04901664_03138	CDS	hypothetical protein		
SAMN04901664_03139	CDS	nemR_2	HTH-type transcriptional repressor NemR	
SAMN04901664_03140	CDS	hypothetical protein		
SAMN04901664_03141	CDS	putative signaling protein		
SAMN04901664_03142	CDS	ilvC	1.1.1.86	Keto1-acid reductoisomerase (NADP(+))
SAMN04901664_03143	CDS	ilvH	2.2.1.6	Acetolactate synthase isozyme 3 small subunit
SAMN04901664_03144	CDS	ilvI	2.2.1.6	Acetolactate synthase isozyme 3 large subunit
SAMN04901664_03145	CDS	hypothetical protein		
SAMN04901664_03146	CDS	leuS	6.1.1.4	Leucine--tRNA ligase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03147	CDS	lptE	LPS-assembly lipoprotein LptE	
SAMN04901664_03148	CDS	hoIA	2.7.7.7	DNA polymerase III subunit delta
SAMN04901664_03149	CDS	macA_1	MacA	
SAMN04901664_03150	CDS	macB	3.6.3.-	Macrolide export ATP-binding/permease protein MacB
SAMN04901664_03151	CDS	tdeA	A	
SAMN04901664_03152	CDS	fabI	1.3.1.9	Enoyl-[acyl-carrier-protein] reductase [NADH] FabI
SAMN04901664_03153	CDS	hypothetical protein	3.1.-.-	Oligoribonuclease
SAMN04901664_03154	CDS	orn		Small ribosomal subunit biogenesis GTPase RsgA
SAMN04901664_03155	CDS	rsgA	3.6.1.-	Thiosulfate sulfurtransferase GlpE
SAMN04901664_03156	CDS	glpE_4	2.8.1.1	
SAMN04901664_03157	CDS	grxC	Glutaredoxin 3	
SAMN04901664_03158	CDS	secB	Protein-export protein SecB	
SAMN04901664_03159	CDS	sfp_2	2.7.8.-	4'-phosphopantetheinyl transferase sfp
SAMN04901664_03160	CDS	hypothetical protein		
SAMN04901664_03161	CDS	fabB_3	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase 1
SAMN04901664_03162	CDS	fabG_7	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase FabG

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03163	CDS	hypothetical protein		
SAMN04901664_03164	CDS	fabF	2.3.1.179	3-oxoacyl-[acyl-carrier-protein] synthase 2
SAMN04901664_03165	CDS	hypothetical protein		
SAMN04901664_03166	CDS	kmo_2	1.14.13.9	Kynurenine 3-monoxygenase
SAMN04901664_03167	CDS	hypothetical protein		
SAMN04901664_03168	CDS	lolA_2		Outer-membrane lipoprotein carrier protein
SAMN04901664_03169	CDS	3.1.2.28		1,4-dihydroxy-2-naphthoyl-CoA hydrolase
SAMN04901664_03170	CDS	hutH_1	4.3.1.3	Histidine ammonia-lyase
SAMN04901664_03171	CDS	lpxL_3	2.3.1.241	Lipid A biosynthesis lauroyltransferase
SAMN04901664_03172	CDS	2.4.1.54		Undecaprenyl-phosphate mannosyltransferase
SAMN04901664_03173	CDS	dltA	6.1.1.13	D-alanine--poly(phosphoribitol) ligase subunit 1
SAMN04901664_03174	CDS	hypothetical protein		
SAMN04901664_03175	CDS	hypothetical protein		
SAMN04901664_03176	CDS	hypothetical protein		
SAMN04901664_03177	CDS	hypothetical protein		
SAMN04901664_03178	CDS	cafIa		F1 capsule-anchoring protein
SAMN04901664_03179	CDS	hypothetical protein		
SAMN04901664_03180	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03181	CDS	proP_4	Proline/betaine transporter	
SAMN04901664_03182	CDS	hypothetical protein		
SAMN04901664_03183	CDS	hypothetical protein		
SAMN04901664_03184	CDS	asD	2.6.1.1	Bifunctional aspartate aminotransferase and L-aspartate beta-decarboxylase
SAMN04901664_03185	CDS	aspT	Aspartate/alanine antiporter	
SAMN04901664_03186	CDS	pqiA_1	Paraquat-inducible protein A	
SAMN04901664_03187	CDS	pqiA_2	Paraquat-inducible protein A	
SAMN04901664_03188	CDS	pqiB	Paraquat-inducible protein B	
SAMN04901664_03189	CDS	hypothetical protein		
SAMN04901664_03190	CDS	racX	5.1.1.-	putative amino-acid racemase
SAMN04901664_03191	CDS	yddG_2	YddG	
SAMN04901664_03192	CDS	yliI_1	1.1.5.-	Aldose sugar dehydrogenase YliI
SAMN04901664_03193	CDS	hypothetical protein		
SAMN04901664_03194	CDS	hypothetical protein		
SAMN04901664_03195	CDS	hypothetical protein		
SAMN04901664_03196	CDS	dctA_3	protein	
SAMN04901664_03197	CDS	hypothetical protein		
SAMN04901664_03198	CDS	gloB	3.1.2.6	Hydroxyacylglutathione hydrolase GloB
SAMN04901664_03199	CDS	metI_2	D-methionine transport system permease protein MetI	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03200	CDS	metN_2	3.6.3.-	Methionine import ATP-binding protein MetN
SAMN04901664_03201	CDS	metQ_3	MetQ	Phosphoribosylamine--glycine ligase
SAMN04901664_03202	CDS	purD	6.3.4.13	
SAMN04901664_03203	CDS	purH	Bifunctional purine biosynthesis protein PurH	
SAMN04901664_03204	CDS	fis	DNA-binding protein Fis	
SAMN04901664_03205	CDS	hypothetical protein		
SAMN04901664_03206	CDS	prmA_2	2.1.1.-	Ribosomal protein L11 methyltransferase
SAMN04901664_03207	CDS	hypothetical protein		
SAMN04901664_03208	CDS	mmmG	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MmmG	
SAMN04901664_03209	CDS	hypothetical protein		
SAMN04901664_03210	CDS	hypothetical protein		
SAMN04901664_03211	CDS	hypothetical protein		
SAMN04901664_03212	CDS	hypothetical protein		
SAMN04901664_03213	CDS	hypothetical protein		
SAMN04901664_03214	CDS	dadX_2	5.1.1.1	Alanine racemase, catabolic
SAMN04901664_03215	CDS	dnaB_2	3.6.4.12	Replicative DNA helicase
SAMN04901664_03216	CDS	rplI	50S ribosomal protein L9	
SAMN04901664_03217	CDS	rpsR	30S ribosomal protein S18	
SAMN04901664_03218	CDS	rpsF	30S ribosomal protein S6	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03219	CDS	cyoE	2.5.1.-	Protoheme IX farnesyltransferase
SAMN04901664_03220	CDS	cyoD	Cytochrome bo(3) ubiquinol oxidase subunit 4	
SAMN04901664_03221	CDS	cyoC	Cytochrome bo(3) ubiquinol oxidase subunit 3	
SAMN04901664_03222	CDS	cyoB	1.10.3.10	Cytochrome bo(3) ubiquinol oxidase subunit 1
SAMN04901664_03223	CDS	cyoA	Cytochrome bo(3) ubiquinol oxidase subunit 2	
SAMN04901664_03224	CDS	hypothetical protein		
SAMN04901664_03225	CDS	ppsA	2.7.9.2	Phosphoenolpyruvate synthase
SAMN04901664_03226	CDS	ppsR	2.7.11.33	Phosphoenolpyruvate synthase regulatory protein
SAMN04901664_03227	CDS	pgaA	Poly-beta-1,6-N-acetyl-D- glucosamine export protein	
SAMN04901664_03228	CDS	pgaB_2	3.5.1.-	Poly-beta-1,6-N-acetyl-D- glucosamine N-deacetylase
SAMN04901664_03229	CDS	pgaC_2	2.4.1.-	Poly-beta-1,6-N-acetyl-D- glucosamine synthase
SAMN04901664_03230	CDS	pgaD	PgaD	
SAMN04901664_03231	CDS	1.14.13.-	monooxygenase	
SAMN04901664_03232	CDS	limB	1.14.13.107	Limonene 1,2-monooxygenase
SAMN04901664_03233	CDS	hypothetical protein		
SAMN04901664_03234	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03235	CDS	pgrR_4	HTH-type transcriptional regulator PgrR	
SAMN04901664_03236	CDS	hchA_2	4.2.1.130	Molecular chaperone Hsp31 and glyoxalase 3
SAMN04901664_03237	CDS	prfA	RF1	
SAMN04901664_03238	CDS	prmC	2.1.1.297	Release factor glutamine methyltransferase
SAMN04901664_03239	CDS	ssuC_4	transport permease protein SsuC	
SAMN04901664_03240	CDS	ssuA_5	Putative aliphatic sulfonates-binding protein	
SAMN04901664_03241	CDS	putative HTH-type transcriptional regulator		
SAMN04901664_03242	CDS	1.-.-	putative oxidoreductase	
SAMN04901664_03243	CDS	mmgC_7	1.3.99.-	Acyl-CoA dehydrogenase
SAMN04901664_03244	CDS	acsA_3	6.2.1.1	Acetyl-coenzyme A synthetase
SAMN04901664_03245	CDS	flr	Flavoredoxin	
SAMN04901664_03246	CDS	moeB	2.7.7.80	Molybdopterin-synthase
SAMN04901664_03247	CDS	ubiB_4	2.7.-.-	adenylyltransferase
SAMN04901664_03248	CDS	folB	4.1.2.25	putative protein kinase UbiB
SAMN04901664_03249	CDS	hypothetical protein		Dihydroneopterin aldolase
SAMN04901664_03250	CDS	kdpA	ATPase potassium-binding subunit	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03251	CDS	kdpB	3.6.3.12	Potassium-transporting ATPase ATP-binding subunit
SAMN04901664_03252	CDS	kdpC	Potassium-transporting ATPase KdpC subunit	
SAMN04901664_03253	CDS	kdpD	2.7.13.3	Sensor protein KdpD
SAMN04901664_03254	CDS	kdpE	KDP operon transcriptional regulatory protein KdpE	
SAMN04901664_03255	CDS	puuA	6.3.1.11	Gamma-glutamylputrescine synthetase PuuA
SAMN04901664_03256	CDS	hypothetical protein		
SAMN04901664_03257	CDS	coq7	1.14.13.-	2-nonaprenyl-3-methyl-6- methoxy-1,4-benzoquinol hydroxylase
SAMN04901664_03258	CDS	lpIT	LpIT	
SAMN04901664_03259	CDS	tamA	Translocation and assembly module TamA	
SAMN04901664_03260	CDS	tamB	Translocation and assembly module TamB	
SAMN04901664_03261	CDS	hypothetical protein		
SAMN04901664_03262	CDS	acnB	4.2.1.3	Aconitate hydratase B
SAMN04901664_03263	CDS	hypothetical protein		
SAMN04901664_03264	CDS	hypothetical protein		
SAMN04901664_03265	CDS	hypothetical protein		
SAMN04901664_03266	CDS	fmdA	3.5.1.49	Formamidase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03267	CDS	psd	4.1.1.65	Phosphatidylserine decarboxylase proenzyme
SAMN04901664_03268	CDS	rhda	2.8.1.1	Thiosulfate sulfurtransferase
SAMN04901664_03269	CDS	pncB2	6.3.4.21	Nicotinate phosphoribosyltransferase 2
SAMN04901664_03270	CDS	dtd	3.1.1.96	D-aminoacyl-tRNA deacylase
SAMN04901664_03271	CDS	hypothetical protein		
SAMN04901664_03272	CDS	hypothetical protein		
SAMN04901664_03273	CDS	serB2	3.1.3.3	Phosphoserine phosphatase
SAMN04901664_03274	CDS	hypothetical protein		SerB2
SAMN04901664_03275	CDS	ribBA		Riboflavin biosynthesis protein RibBA
SAMN04901664_03276	CDS	ribH	2.5.1.78	6,7-dimethyl-8-ribityllumazine synthase
SAMN04901664_03277	CDS	nusB	B	
SAMN04901664_03278	CDS	thiL	2.7.4.16	Thiamine-monophosphate kinase
SAMN04901664_03279	CDS	pgpA	3.1.3.27	Phosphatidylglycerophosphatase A
SAMN04901664_03280	CDS	glmU	Bifunctional protein GlmU	
SAMN04901664_03281	CDS	glmS	2.6.1.16	Glutamine--fructose-6-phosphate aminotransferase [isomerizing]
SAMN04901664_03282	CDS	racE	5.1.1.3	Glutamate racemase 1

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03283	CDS	3.1.3.5	5'-nucleotidase	
SAMN04901664_03284	CDS	hypothetical protein		
SAMN04901664_03285	CDS	hutG	3.5.3.8	Formimidoylglutamase
SAMN04901664_03286	CDS	hutI	3.5.2.7	Imidazolonepropionase
SAMN04901664_03287	CDS	proY	ProY	
SAMN04901664_03288	CDS	hutH_2	4.3.1.3	Histidine ammonia-lyase
SAMN04901664_03289	CDS	hutU	4.2.1.49	Urocanate hydratase
SAMN04901664_03290	CDS	ves	Protein Ves	
SAMN04901664_03291	CDS	yvoA_2	HTH-type transcriptional repressor YvoA	
SAMN04901664_03292	CDS	oatA	2.3.1.-	O-acetyltransferase OatA
SAMN04901664_03293	CDS	yciC	Putative metal chaperone YciC	
SAMN04901664_03294	CDS	hypothetical protein		
SAMN04901664_03295	CDS	aroP_3	Aromatic amino acid transport protein AroP	
SAMN04901664_03296	CDS	hypothetical protein		
SAMN04901664_03297	CDS	nagL	5.2.1.4	Maleylpyruvate isomerase
SAMN04901664_03298	CDS	fosB	2.5.1.-	Metallothiol transferase FosB
SAMN04901664_03299	CDS	icIR	Transcriptional repressor IcIR	
SAMN04901664_03300	CDS	hpd	1.13.11.27	4-hydroxyphenylpyruvate dioxygenase
SAMN04901664_03301	CDS	hypothetical protein		
SAMN04901664_03302	CDS	norM_2	NorM	
SAMN04901664_03303	CDS	panS	Pantothenate precursors transporter PanS	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03304	CDS	pncA	3.5.1.19	Nicotinamidase
SAMN04901664_03305	CDS	dapA_4	4.3.3.7	4-hydroxy-tetrahydrodipicolinate synthase
SAMN04901664_03306	CDS	hypothetical protein		
SAMN04901664_03307	CDS	purC	6.3.2.6	Phosphoribosylaminoimidazole-succinocarboxamide synthase
SAMN04901664_03308	CDS	hypothetical protein		
SAMN04901664_03309	CDS	yfdC	Inner membrane protein YfdC	
SAMN04901664_03310	CDS	rarA	Replication-associated recombination protein A	
SAMN04901664_03311	CDS	yliI_2	1.1.5.-	Aldose sugar dehydrogenase YliI
SAMN04901664_03312	CDS	hypothetical protein		
SAMN04901664_03313	CDS	hypothetical protein		
SAMN04901664_03314	CDS	clcD_2	3.1.1.45	Carboxymethylenebutenolidase
SAMN04901664_03315	CDS	2.7.7.53	AP-4-A phosphorylase	
SAMN04901664_03316	CDS	mutY	3.2.2.-	Adenine DNA glycosylase
SAMN04901664_03317	CDS	lytH	3.4.-.-	L-Ala--D-Glu endopeptidase
SAMN04901664_03318	CDS	hypothetical protein		
SAMN04901664_03319	CDS	tag	3.2.2.20	DNA-3-methyladenine glycosylase I
SAMN04901664_03320	CDS	ahr	1.1.1.2	Aldehyde reductase Ahr

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03321	CDS	norG_4	HTH-type transcriptional regulator NorG	
SAMN04901664_03322	CDS	hypothetical protein	HTH-type transcriptional regulator DmlR	
SAMN04901664_03323	CDS	dmlR_14	1.1.1.346	2,5-diketo-D-gluconic acid reductase B
SAMN04901664_03324	CDS	dkgB	Inner membrane transport protein YdhP	
SAMN04901664_03325	CDS	ydhP_1		
SAMN04901664_03326	CDS	hypothetical protein		
SAMN04901664_03327	CDS	dapB	1.1.7.1.8	4-hydroxy-tetrahydrodipicolinate reductase
SAMN04901664_03328	CDS	hypothetical protein	Chaperone protein DnaJ	
SAMN04901664_03329	CDS	dnaJ		
SAMN04901664_03330	CDS	hypothetical protein	Cobalt-zinc-cadmium resistance protein CzcA	
SAMN04901664_03331	CDS	czcA_2	MacA	
SAMN04901664_03332	CDS	macA_2	HTH-type transcriptional regulator AcrR	
SAMN04901664_03333	CDS	acrR		
SAMN04901664_03334	CDS	ppc	4.1.1.31	Phosphoenolpyruvate carboxylase
SAMN04901664_03335	CDS	rutG	RutG	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03336	CDS	cysL	HTH-type transcriptional regulator CysL	
SAMN04901664_03337	CDS	hypothetical protein		
SAMN04901664_03338	CDS	hypothetical protein		
SAMN04901664_03339	CDS	ilvD	4.2.1.9	Dihydroxy-acid dehydratase
SAMN04901664_03340	CDS	fmt	2.1.2.9	Methionyl-tRNA formyltransferase
SAMN04901664_03341	CDS	rsmB	2.1.1.176	Ribosomal RNA small subunit methyltransferase B
SAMN04901664_03342	CDS	hypothetical protein		
SAMN04901664_03343	CDS	hypothetical protein		
SAMN04901664_03344	CDS	hypothetical protein		
SAMN04901664_03345	CDS	yfcG_3	1.8.4.-	Disulfide-bond oxidoreductase YfcG
SAMN04901664_03346	rRNA	5S ribosomal RNA		
SAMN04901664_03347	CDS	hypothetical protein		
SAMN04901664_03348	CDS	cycA_4	D-serine/D-alanine/glycine transporter	
SAMN04901664_03349	CDS	astA_2	2.3.1.109	Arginine N-succinyltransferase
SAMN04901664_03350	CDS	astC_2	2.6.1.81	Succinylornithine transaminase
SAMN04901664_03351	CDS	asnC	Regulatory protein AsnC	
SAMN04901664_03352	CDS	prf	1.2.1.19	Gamma-aminobutyraldehyde dehydrogenase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03353	CDS	hypothetical protein		
SAMN04901664_03354	CDS	pdhR_1		Pyruvate dehydrogenase complex repressor
SAMN04901664_03355	CDS	hypothetical protein		
SAMN04901664_03356	CDS	puuP		Putrescine importer PuuP
SAMN04901664_03357	CDS	puuB_4	1.4.3.-	Gamma-glutamylputrescine oxidoreductase
SAMN04901664_03358	CDS	aroP_4		Aromatic amino acid transport protein AroP
SAMN04901664_03359	CDS	hypothetical protein		
SAMN04901664_03360	CDS	hypothetical protein		
SAMN04901664_03361	CDS	hypothetical protein		
SAMN04901664_03362	CDS	hypothetical protein		
SAMN04901664_03363	CDS	esiB_5		Secretory immunoglobulin A-binding protein EsiB
SAMN04901664_03364	CDS	esiB_6		Secretory immunoglobulin A-binding protein EsiB
SAMN04901664_03365	CDS	esiB_7		Secretory immunoglobulin A-binding protein EsiB
SAMN04901664_03366	CDS	rhsC_2	3.1.-	Putative deoxyribonuclease RhsC
SAMN04901664_03367	CDS	vgrG1_2	6.3.2.-	Actin cross-linking toxin VgrG1
SAMN04901664_03368	CDS	hypothetical protein		
SAMN04901664_03369	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03370	CDS	Membrane lipoprotein TpN32		
SAMN04901664_03371	CDS	yjgN	Inner membrane protein YjgN	
SAMN04901664_03372	CDS	bepA_3	3.4.-.-	Beta-barrel assembly-enhancing protease
SAMN04901664_03373	tRNA	tRNA-Ser(iga)		
SAMN04901664_03374	CDS	fadH_1	1.3.1.34	2,4-dienoyl-CoA reductase [NADPH]
SAMN04901664_03375	CDS	argG	6.3.4.5	Argininosuccinate synthase
SAMN04901664_03376	CDS	cph2_3	Phytochrome-like protein cph2	
SAMN04901664_03377	CDS	pyrC_2	3.5.2.3	Dihydroorotase
SAMN04901664_03378	CDS	rnt	3.1.13.-	Ribonuclease T
SAMN04901664_03379	tRNA	tRNA-Glu(ttc)		
SAMN04901664_03380	CDS	fhuA_2	Ferrichrome-iron receptor	
SAMN04901664_03381	CDS	1.-.-	NADH oxidase	
SAMN04901664_03382	CDS	gsiA_2	3.6.3.-	Glutathione import ATP-binding protein GsiA
SAMN04901664_03383	CDS	yejE	transporter permease protein YejE	
SAMN04901664_03384	CDS	yejB	transporter permease protein YejB	
SAMN04901664_03385	CDS	oppA_2	OppA	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03386	CDS	mltD	4.2.2.-	Membrane-bound lytic murein transglycosylase D
SAMN04901664_03387	CDS	dnaQ_1	2.7.7.7	DNA polymerase III subunit epsilon
SAMN04901664_03388	CDS	hypothetical protein		
SAMN04901664_03389	CDS	nudC_2	3.6.1.22	NADH pyrophosphatase
SAMN04901664_03390	CDS	mlhB	3.1.1.83	Monoterpene epsilon-lactone hydrolase
SAMN04901664_03391	CDS	hypothetical protein		
SAMN04901664_03392	CDS	hypothetical protein		
SAMN04901664_03393	CDS	rsmI	2.1.1.198	Ribosomal RNA small subunit methyltransferase I
SAMN04901664_03394	CDS	hypothetical protein		
SAMN04901664_03395	CDS	putative HTH-type transcriptional regulator		
SAMN04901664_03396	CDS	argO	ArgO	
SAMN04901664_03397	CDS	czcD_3	Cadmium, cobalt and zinc/H(+)-K(+) antiporter	
SAMN04901664_03398	CDS	zntR	HTH-type transcriptional regulator ZntR	
SAMN04901664_03399	CDS	hypothetical protein		
SAMN04901664_03400	CDS	ubiI	1.14.13.-	2-octaprenylphenol hydroxylase
SAMN04901664_03401	CDS	ubiH	1.14.13.-	2-octaprenyl-6-methoxyphenol hydroxylase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03402	CDS	pepP	3.4.11.9	Xaa-Pro aminopeptidase
SAMN04901664_03403	CDS	hypothetical protein		
SAMN04901664_03404	CDS	smc_2	Smc	
SAMN04901664_03405	CDS	hypothetical protein		
SAMN04901664_03406	CDS	hypothetical protein		
SAMN04901664_03407	CDS	hypothetical protein		
SAMN04901664_03408	CDS	hypothetical protein		
SAMN04901664_03409	CDS	eptA_2	2.7.-.-	Phosphoethanolamine transferase EptA
SAMN04901664_03410	CDS	putative TonB-dependent receptor		
SAMN04901664_03411	CDS	hypothetical protein		
SAMN04901664_03412	CDS	hypothetical protein		
SAMN04901664_03413	CDS	hypothetical protein		
SAMN04901664_03414	CDS	hypothetical protein		
SAMN04901664_03415	CDS	hypothetical protein		
SAMN04901664_03416	CDS	hypothetical protein		
SAMN04901664_03417	CDS	hypothetical protein		
SAMN04901664_03418	CDS	hypothetical protein		
SAMN04901664_03419	CDS	hypothetical protein		
SAMN04901664_03420	CDS	phoR	2.7.13.3	Phosphate regulon sensor protein PhoR
SAMN04901664_03421	CDS	phoB	transcriptional regulatory protein PhoB	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03422	CDS	betl_5	HTH-type transcriptional regulator BetI	
SAMN04901664_03423	CDS	sadh	1.-.-.-	Putative oxidoreductase SadH
SAMN04901664_03424	CDS	mepA	MepA	
SAMN04901664_03425	CDS	ybdL	2.6.1.88	Methionine aminotransferase
SAMN04901664_03426	CDS	hypothetical protein		
SAMN04901664_03427	CDS	hypothetical protein		
SAMN04901664_03428	CDS	hypothetical protein		
SAMN04901664_03429	CDS	gshA	6.3.2.2	Glutamate--cysteine ligase
SAMN04901664_03430	CDS	dsbB	protein B	
SAMN04901664_03431	CDS	vgrG1_3	6.3.2.-	Actin cross-linking toxin VgrG1
SAMN04901664_03432	CDS	hypothetical protein		
SAMN04901664_03433	CDS	hypothetical protein		
SAMN04901664_03434	CDS	hypothetical protein		
SAMN04901664_03435	CDS	hypothetical protein		
SAMN04901664_03436	CDS	parE	5.99.1.3	DNA topoisomerase 4 subunit B
SAMN04901664_03437	CDS	fabG_8	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase FabG
SAMN04901664_03438	CDS	allA	4.3.2.3	Ureidoglycolate lyase
SAMN04901664_03439	CDS	alc	3.5.3.4	allantoicase
SAMN04901664_03440	CDS	hpxO_2	1.14.13.113	FAD-dependent urate hydroxylase
SAMN04901664_03441	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03442	CDS	pucK	Uric acid permease PucK	
SAMN04901664_03443	CDS	hiuH	3.5.2.17	5-hydroxyisourate hydrolase
SAMN04901664_03444	CDS	uao	Uric acid degradation bifunctional protein	
SAMN04901664_03445	CDS	hypothetical protein		
SAMN04901664_03446	CDS	hypothetical protein		
SAMN04901664_03447	CDS	hypothetical protein		
SAMN04901664_03448	CDS	hypothetical protein		
SAMN04901664_03449	CDS	dsbD	1.8.1.8	Thiol:disulfide interchange protein DsbD
SAMN04901664_03450	CDS	ycdT	2.7.7.65	putative diguanylate cyclase YcdT
SAMN04901664_03451	CDS	lipR	3.1.1.-	Putative acetyl-hydrolase LipR
SAMN04901664_03452	CDS	hypothetical protein		
SAMN04901664_03453	CDS	spxA	Regulatory protein Spx	
SAMN04901664_03454	CDS	exoA	3.1.11.2	Exodeoxyribonuclease Orotate
SAMN04901664_03455	CDS	pyrE_2	2.4.2.10	phosphoribosyltransferase
SAMN04901664_03456	CDS	fhuA_3	Ferrichrome-iron receptor	
SAMN04901664_03457	CDS	hypothetical protein		
SAMN04901664_03458	CDS	gshB	6.3.2.3	Glutathione synthetase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03459	CDS	murG	2.4.1.227	UDP-N-acetylglucosamine--N-acetylmutaroyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
SAMN04901664_03460	CDS	murC	6.3.2.8	UDP-N-acetylmutaroyl-L-alanine ligase
SAMN04901664_03461	CDS	ddl	6.3.2.4	D-alanine--D-alanine ligase
SAMN04901664_03462	CDS	ftsQ	Cell division protein FtsQ	
SAMN04901664_03463	CDS	ftsA_2	Cell division protein FtsA	
SAMN04901664_03464	CDS	ftsZ	Cell division protein FtsZ	
SAMN04901664_03465	CDS	lpxC	3.5.1.108	UDP-3-O-acyl-N-acetylglucosamine deacetylase
SAMN04901664_03466	CDS	hypothetical protein		
SAMN04901664_03467	CDS	mepM_2	3.4.24.-	Murein DD-endopeptidase MepM
SAMN04901664_03468	CDS	aceE	1.2.4.1	Pyruvate dehydrogenase E1 component
SAMN04901664_03469	CDS	2.3.1.12	acetyltransferase component of pyruvate dehydrogenase complex	
SAMN04901664_03470	CDS	hypothetical protein		
SAMN04901664_03471	CDS	hypothetical protein		
SAMN04901664_03472	CDS	fluA_4	Ferrichrome-iron receptor	
SAMN04901664_03473	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03474	CDS	hypothetical protein		
SAMN04901664_03475	CDS	guaB_2	1.1.1.205	Inosine-5'-monophosphate dehydrogenase
SAMN04901664_03476	CDS	glmM_2	5.4.2.10	Phosphoglucosamine mutase
SAMN04901664_03477	CDS	pdxH	1.4.3.5	Pyridoxine/pyridoxamine 5'-phosphate oxidase
SAMN04901664_03478	CDS	recJ	3.1.-.-	Single-stranded-DNA-specific exonuclease RecJ
SAMN04901664_03479	CDS	hypothetical protein		
SAMN04901664_03480	CDS	prfB	RF2	
SAMN04901664_03481	CDS	hypothetical protein		
SAMN04901664_03482	CDS	sdpR	Transcriptional repressor SdpR	
SAMN04901664_03483	CDS	nema_1	1.-.-.-	N-ethylmaleimide reductase
SAMN04901664_03484	CDS	waaA	2.4.99.12	3-deoxy-D-manno-octulosonic acid transferase
SAMN04901664_03485	CDS	rsmE_2	2.1.1.193	Ribosomal RNA small subunit methyltransferase E
SAMN04901664_03486	CDS	mcsS_2	Small-conductance mechanosensitive channel	
SAMN04901664_03487	CDS	clpA	ATP-dependent Clp protease	
SAMN04901664_03488	CDS	hypothetical protein	ATP-binding subunit ClpA	
SAMN04901664_03489	CDS	aroF_2	2.5.1.54	Phospho-2-dehydro-3-deoxyheptonate aldolase, Tyr-sensitive

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03490	CDS	ydjP	3.-.-.-	AB hydrolase superfamily protein YdjP
SAMN04901664_03491	CDS	hypothetical protein		
SAMN04901664_03492	CDS	fadH_2	1.3.1.34	2,4-dienoyl-CoA reductase [NADPH]
SAMN04901664_03493	CDS	hypothetical protein		
SAMN04901664_03494	CDS	hypothetical protein		
SAMN04901664_03495	CDS	hypothetical protein		
SAMN04901664_03496	CDS	hypothetical protein		
SAMN04901664_03497	CDS	hypothetical protein		
SAMN04901664_03498	CDS	pyrG	6.3.4.2	CTP synthase
SAMN04901664_03499	CDS	kdsA	2.5.1.55	2-dehydro-3-deoxyphosphooctonate aldolase
SAMN04901664_03500	CDS	eno	4.2.1.11	Enolase
SAMN04901664_03501	CDS	hypothetical protein		
SAMN04901664_03502	CDS	ftsB	Cell division protein FtsB	
SAMN04901664_03503	CDS	ispD	2.7.7.60	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase
SAMN04901664_03504	CDS	pcaI_2	2.8.3.6	3-oxoadipate CoA-transferase subunit A
SAMN04901664_03505	CDS	pcaJ_2	2.8.3.6	3-oxoadipate CoA-transferase subunit B
SAMN04901664_03506	CDS	pcaF_2	2.3.1.174	Beta-ketoadipyl-CoA thiolase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03507	CDS	pcaB	5.5.1.2	3-carboxy-cis,cis-muconate cycloisomerase
SAMN04901664_03508	CDS	catD_3	3.1.1.24	3-oxoadipate enol-lactonase 2
SAMN04901664_03509	CDS	pcaK_4	PcaK	
SAMN04901664_03510	CDS	hypothetical protein		
SAMN04901664_03511	CDS	pcaH	1.13.11.3	Protocatechuate 3,4- dioxygenase beta chain
SAMN04901664_03512	CDS	pcaG	1.13.11.3	Protocatechuate 3,4- dioxygenase alpha chain
SAMN04901664_03513	CDS	quiB	4.2.1.10	Catabolic 3-dehydroquininate dehydratase
SAMN04901664_03514	CDS	quiC	4.2.1.118	3-dehydroshikimate dehydratase
SAMN04901664_03515	CDS	oprB_2	Porin B	Quinate/shikimate dehydrogenase (quinone)
SAMN04901664_03516	CDS	quiA_2	1.1.5.8	
SAMN04901664_03517	CDS	hypothetical protein		
SAMN04901664_03518	CDS	hypothetical protein		
SAMN04901664_03519	CDS	hypothetical protein		
SAMN04901664_03520	CDS	3.-.-.-	putative metallo-hydrolase	
SAMN04901664_03521	CDS	pcaU_2	Pca operon regulatory protein	
SAMN04901664_03522	CDS	leuO	HTH-type transcriptional regulator LeuO	
SAMN04901664_03523	CDS	bbsG	1.3.8.3	(R)-benzylsuccinyl-CoA dehydrogenase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03524	CDS	hypothetical protein		
SAMN04901664_03525	CDS	hypothetical protein		
SAMN04901664_03526	CDS	1.-.-	putative oxidoreductase	
SAMN04901664_03527	CDS	nicP_2	Porin-like protein NicP	
SAMN04901664_03528	CDS	lgoT	transporter	
SAMN04901664_03529	CDS	marR	Multiple antibiotic resistance protein MarR	
SAMN04901664_03530	CDS	gata_2	6.3.5.7	Glutamyl-tRNA(Gln) amidotransferase subunit A
SAMN04901664_03531	CDS	hsaA	1.14.14.12	Flavin-dependent monooxygenase, oxygenase subunit HsaA
SAMN04901664_03532	CDS	hypothetical protein		
SAMN04901664_03533	CDS	hypothetical protein		
SAMN04901664_03534	CDS	antA_3	1.14.12.1	Anthranilate 1,2-dioxygenase large subunit
SAMN04901664_03535	CDS	cbdB_2	1.14.12.13	2-halobenzoate 1,2-dioxygenase small subunit
SAMN04901664_03536	CDS	fabG_9	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase FabG
SAMN04901664_03537	CDS	ophA1	1.-.-	Phthalate dioxygenase reductase p-hydroxyphenylacetate 3-hydroxylase, reductase component
SAMN04901664_03538	CDS	C1-hpah_3	1.5.1.36	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03539	CDS	feaR	Transcriptional activator FeaR	
SAMN04901664_03540	CDS	tynA	1.4.3.21	Primary amine oxidase
SAMN04901664_03541	CDS	hypothetical protein		
SAMN04901664_03542	CDS	feaB	1.2.1.39	Phenylacetaldehyde dehydrogenase
SAMN04901664_03543	CDS	pac	3.5.1.11	Penicillin G acylase
SAMN04901664_03544	CDS	catD_4	3.1.1.24	3-oxoadipate enol-lactonase 2
SAMN04901664_03545	CDS	pcaF_3	2.3.1.174	Beta-ketoadipyl-CoA thiolase
SAMN04901664_03546	CDS	pcaJ_3	2.8.3.6	3-oxoadipate CoA-transferase subunit B
SAMN04901664_03547	CDS	pcaI_3	2.8.3.6	3-oxoadipate CoA-transferase subunit A
SAMN04901664_03548	CDS	catA	1.13.11.1	Catechol 1,2-dioxygenase
SAMN04901664_03549	CDS	catC	5.3.3.4	Muconolactone Delta-isomerase
SAMN04901664_03550	CDS	catB	5.5.1.1	Muconate cycloisomerase 1
SAMN04901664_03551	CDS	catM	HTH-type transcriptional regulator CatM	
SAMN04901664_03552	CDS	hypothetical protein		
SAMN04901664_03553	CDS	pdhR_2	Pyruvate dehydrogenase complex repressor	
SAMN04901664_03554	CDS	araC_2	4.2.1.25	L-arabonate dehydratase
SAMN04901664_03555	CDS	ttuB_2	Putative tartrate transporter	
SAMN04901664_03556	CDS	hypothetical protein		
SAMN04901664_03557	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03558	CDS	Cyclic nucleotide-gated potassium channel		
SAMN04901664_03559	CDS	ydhP_2		Inner membrane transport protein YdhP
SAMN04901664_03560	CDS	hypothetical protein		
SAMN04901664_03561	CDS	hypothetical protein		
SAMN04901664_03562	CDS	metR		HTH-type transcriptional regulator MetR
SAMN04901664_03563	CDS	hypothetical protein		
SAMN04901664_03564	CDS	hypothetical protein		
SAMN04901664_03565	CDS	rsuA	5.4.99.19	Ribosomal small subunit pseudouridine synthase A
SAMN04901664_03566	CDS	hypothetical protein		
SAMN04901664_03567	CDS	hypothetical protein		
SAMN04901664_03568	CDS	5.4.99.-		putative RNA pseudouridine synthase
SAMN04901664_03569	CDS	tsaE		threonylcarbamoyladenine biosynthesis protein TsaE
SAMN04901664_03570	CDS	mutL		MutL
SAMN04901664_03571	CDS	miaA	2.5.1.75	tRNA dimethylallyltransferase
SAMN04901664_03572	CDS	hfq		RNA-binding protein Hfq
SAMN04901664_03573	CDS	hypothetical protein		
SAMN04901664_03574	CDS	nfsB		Oxygen-insensitive NAD(P)H nitroreductase
SAMN04901664_03575	CDS	hypothetical protein	1.-.-.-	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03576	CDS	lpxH	3.6.1.54	UDP-2,3-diacetylglucosamine hydrolase
SAMN04901664_03577	CDS	5.2.1.8	Peptidyl-prolyl cis-trans isomerase cyp18	
SAMN04901664_03578	CDS	glnS	6.1.1.18	Glutamine--tRNA ligase
SAMN04901664_03579	CDS	guaA_3	6.3.5.2	GMP synthase [glutamine-hydrolyzing]
SAMN04901664_03580	CDS	eutC	4.3.1.7	Ethanolamine ammonia-lyase light chain
SAMN04901664_03581	CDS	eutB	4.3.1.7	Ethanolamine ammonia-lyase heavy chain
SAMN04901664_03582	CDS	yhdG	YhdG	
SAMN04901664_03583	CDS	ald1	1.2.1.48	Long-chain-aldehyde dehydrogenase
SAMN04901664_03584	CDS	acoR_2	Acetoin dehydrogenase operon transcriptional activator AcoR	
SAMN04901664_03585	CDS	menH_3	4.2.99.20	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase
SAMN04901664_03586	CDS	dhaT_2	1.1.1.202	1,3-propanediol dehydrogenase
SAMN04901664_03587	CDS	recD2	3.6.4.12	ATP-dependent RecD-like DNA helicase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03588	CDS	hpcD	5.3.3.10	5-carboxymethyl-2-hydroxymuconate Delta-isomerase
SAMN04901664_03589	CDS	rob	Right origin-binding protein	
SAMN04901664_03590	CDS	thiM	2.7.1.50	Hydroxyethylthiazole kinase
SAMN04901664_03591	CDS	hypothetical protein		
SAMN04901664_03592	CDS	hypothetical protein		
SAMN04901664_03593	CDS	pepN_2	3.4.11.2	Aminopeptidase N
SAMN04901664_03594	CDS	ligE	Beta-etherase	
SAMN04901664_03595	CDS	fabG_10	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase
SAMN04901664_03596	CDS	hypothetical protein		
SAMN04901664_03597	CDS	pheA2	5.4.99.5	Secreted chorismate mutase
SAMN04901664_03598	CDS	lrp_6	protein	
SAMN04901664_03599	CDS	hypothetical protein		
SAMN04901664_03600	CDS	hypothetical protein		
SAMN04901664_03601	CDS	iutA_3	Ferric aerobactin receptor	
SAMN04901664_03602	CDS	ybdG	mechanosensitive channel	
SAMN04901664_03603	CDS	hypothetical protein	YbdG	
SAMN04901664_03604	CDS	hypothetical protein		
SAMN04901664_03605	CDS	hypothetical protein		
SAMN04901664_03606	CDS	hypothetical protein		
SAMN04901664_03607	CDS	hypothetical protein		
SAMN04901664_03608	CDS	fhuE_2	FhuE receptor	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03609	CDS	hypothetical protein		
SAMN04901664_03610	CDS	hypothetical protein		
SAMN04901664_03611	CDS	pliG		Inhibitor of g-type lysozyme
SAMN04901664_03612	CDS	yheS_2		putative ABC transporter ATP-binding protein YheS
SAMN04901664_03613	CDS	Putative universal stress protein		
SAMN04901664_03614	CDS	hypothetical protein		
SAMN04901664_03615	CDS	hypothetical protein		
SAMN04901664_03616	CDS	hypothetical protein		
SAMN04901664_03617	CDS	hypothetical protein		
SAMN04901664_03618	CDS	mgfA_2	3.6.3.2	Magnesium-transporting ATPase, P-type 1
SAMN04901664_03619	CDS	hypothetical protein		
SAMN04901664_03620	CDS	ycdO_2		Inner membrane protein YdcO protein
SAMN04901664_03621	CDS	lrp_7		Leucine efflux protein
SAMN04901664_03622	CDS	leuE_4	2.2.1.2	Transaldolase
SAMN04901664_03623	CDS	tal		
SAMN04901664_03624	CDS	yahB		putative HTH-type transcriptional regulator YahB
SAMN04901664_03625	CDS	hypothetical protein		
SAMN04901664_03626	CDS	fadI	2.3.1.16	3-ketoacyl-CoA thiolase
SAMN04901664_03627	CDS	fabG_11	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase FabG
SAMN04901664_03628	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03629	CDS	3.4.16.4	carboxypeptidase	
SAMN04901664_03630	CDS	betl_6	HTH-type transcriptional regulator BetI	
SAMN04901664_03631	CDS	smvA	Methyl viologen resistance protein SmvA	
SAMN04901664_03632	CDS	dnaX_2	2.7.7.7	DNA polymerase III subunit tau
SAMN04901664_03633	CDS	hypothetical protein		Non-hemolytic phospholipase C
SAMN04901664_03634	CDS	plcN_3	3.1.4.3	Long-chain-alcohol dehydrogenase 1
SAMN04901664_03635	CDS	hypothetical protein		6-phosphogluconolactonase
SAMN04901664_03636	CDS	adh1	1.1.1.192	Low molecular weight protein-tyrosine-phosphatase YfkJ
SAMN04901664_03637	CDS	pgl	3.1.1.31	UDP-N-acetylerythroglucosamine reductase
SAMN04901664_03638	CDS	yfkJ	3.1.3.48	Phospholipase YtpA
SAMN04901664_03639	CDS	murB	1.3.1.98	Glutamate synthase [NADPH] large chain
SAMN04901664_03640	CDS	hypothetical protein		
SAMN04901664_03641	CDS	ytpA	3.1.1.-	
SAMN04901664_03642	CDS	gltA_2	1.4.1.13	
SAMN04901664_03643	CDS	hypothetical protein		
SAMN04901664_03644	CDS	tetC	Transposon Tn10 TetC protein	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03645	CDS	hypothetical protein		
SAMN04901664_03646	CDS	hypothetical protein		
SAMN04901664_03647	CDS	hypothetical protein		
SAMN04901664_03648	CDS	hypothetical protein		
SAMN04901664_03649	CDS	hypothetical protein		
SAMN04901664_03650	CDS	hypothetical protein		
SAMN04901664_03651	CDS	hypothetical protein		
SAMN04901664_03652	CDS	hypothetical protein		
SAMN04901664_03653	CDS	hypothetical protein		
SAMN04901664_03654	CDS	hypothetical protein		
SAMN04901664_03655	CDS	hypothetical protein		
SAMN04901664_03656	CDS	hypothetical protein		
SAMN04901664_03657	CDS	hypothetical protein		
SAMN04901664_03658	CDS	hypothetical protein		
SAMN04901664_03659	CDS	hypothetical protein		
SAMN04901664_03660	CDS	hypothetical protein		
SAMN04901664_03661	CDS	hypothetical protein		
SAMN04901664_03662	CDS	hypothetical protein		
SAMN04901664_03663	CDS	hypothetical protein		
SAMN04901664_03664	CDS	hypothetical protein		
SAMN04901664_03665	CDS	hypothetical protein		
SAMN04901664_03666	rRNA	5S ribosomal RNA		
SAMN04901664_03667	CDS	hypothetical protein		
SAMN04901664_03668	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03669	CDS	mmgC_8	1.3.99.-	Acyl-CoA dehydrogenase
SAMN04901664_03670	CDS	kstR2_2	HTH-type transcriptional repressor KstR2	
SAMN04901664_03671	CDS	hypothetical protein		
SAMN04901664_03672	CDS	fadH_3	1.3.1.34	putative 2,4-dienoyl-CoA reductase
SAMN04901664_03673	CDS	pccB	6.4.1.3	Propionyl-CoA carboxylase beta chain
SAMN04901664_03674	CDS	mmgC_9	1.3.99.-	Acyl-CoA dehydrogenase
SAMN04901664_03675	CDS	echA8_2	4.2.1.17	putative enoyl-CoA hydratase echA8
SAMN04901664_03676	CDS	accA1_3	Acetyl-/propionyl-coenzyme A carboxylase alpha chain	
SAMN04901664_03677	CDS	hypothetical protein		
SAMN04901664_03678	CDS	sspB	Stringent starvation protein B	
SAMN04901664_03679	CDS	sspA	Stringent starvation protein A	
SAMN04901664_03680	CDS	rpsI	30S ribosomal protein S9	
SAMN04901664_03681	CDS	rplM	50S ribosomal protein L13	
SAMN04901664_03682	CDS	pdxA1	1.1.1.262	4-hydroxythreonine-4-phosphate dehydrogenase 1
SAMN04901664_03683	CDS	rsmA	2.1.1.182	Ribosomal RNA small subunit methyltransferase A
SAMN04901664_03684	CDS	apaH	3.6.1.41	Bis(5'-nucleosyl)-tetraphosphatase, symmetrical
SAMN04901664_03685	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03686	CDS	cidB_2	Holin-like protein CidB	
SAMN04901664_03687	CDS	hypothetical protein		
SAMN04901664_03688	CDS	hflX	GTPase HflX	
SAMN04901664_03689	CDS	hypothetical protein		
SAMN04901664_03690	CDS	clsC_2	2.7.8.-	Cardiolipin synthase C 3',5'-cyclic adenosine monophosphate
SAMN04901664_03691	CDS	cpdA_3	3.1.4.53	phosphodiesterase CpdA
SAMN04901664_03692	CDS	psaB	1.97.1.12	Photosystem I P700 chlorophyll a apoprotein A2
SAMN04901664_03693	CDS	yfiN	2.7.7.65	putative diguanylate cyclase YfiN
SAMN04901664_03694	CDS	hypothetical protein		
SAMN04901664_03695	rRNA	16S ribosomal RNA		
SAMN04901664_03696	tRNA	tRNA-Ile(gat)		
SAMN04901664_03697	CDS	lon	3.4.21.53	Lon protease
SAMN04901664_03698	rRNA	16S ribosomal RNA		
SAMN04901664_03699	tRNA	tRNA-Ile(gat)		
SAMN04901664_03700	CDS	hypothetical protein		
SAMN04901664_03701	CDS	hypothetical protein		
SAMN04901664_03702	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03703	CDS	hypothetical protein		
SAMN04901664_03704	CDS	hypothetical protein		
SAMN04901664_03705	CDS	hypothetical protein		
SAMN04901664_03706	CDS	trxA	Thioredoxin	
SAMN04901664_03707	CDS	ssuB_3	3.6.3.-	Aliphatic sulfonates import A ATP-binding protein SsuB
SAMN04901664_03708	CDS	hypothetical protein		
SAMN04901664_03709	CDS	hypothetical protein		
SAMN04901664_03710	CDS	noc		
SAMN04901664_03711	CDS	uvrB_2	Nucleoid occlusion protein UvrABC system protein B	
SAMN04901664_03712	CDS	hypothetical protein		
SAMN04901664_03713	CDS	hypothetical protein		
SAMN04901664_03714	CDS	spa		
SAMN04901664_03715	CDS	hypothetical protein		protein A
SAMN04901664_03716	CDS	hypothetical protein		
SAMN04901664_03717	CDS	hypothetical protein		
SAMN04901664_03718	CDS	hypothetical protein		
SAMN04901664_03719	CDS	hypothetical protein		
SAMN04901664_03720	CDS	hypothetical protein		
SAMN04901664_03721	CDS	hypothetical protein		
SAMN04901664_03722	CDS	hypothetical protein		
SAMN04901664_03723	CDS	hypothetical protein		
SAMN04901664_03724	CDS	hypothetical protein		
SAMN04901664_03725	tRNA	tRNA tRNA-Asn(gtt)		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03726	CDS	hypothetical protein		
SAMN04901664_03727	CDS	hypothetical protein		putative zinc-binding alcohol dehydrogenase
SAMN04901664_03728	CDS	1.1.1.1		
SAMN04901664_03729	CDS	hypothetical protein		
SAMN04901664_03730	CDS	hypothetical protein		
SAMN04901664_03731	CDS	hypothetical protein		
SAMN04901664_03732	CDS	frmR		Transcriptional repressor FrmR
SAMN04901664_03733	CDS	frmA_2	1.1.1.284	S-(hydroxymethyl)glutathione dehydrogenase
SAMN04901664_03734	CDS	frmB	3.1.2.12	S-formylglutathione hydrolase FrmB
SAMN04901664_03735	CDS	hypothetical protein		
SAMN04901664_03736	CDS	yqhD	1.1.1.-	Alcohol dehydrogenase YqhD
SAMN04901664_03737	CDS	hchA_3	4.2.1.130	Molecular chaperone Hsp31 and glyoxalase 3
SAMN04901664_03738	CDS	nemA_2	1.-.-	N-ethylmaleimide reductase
SAMN04901664_03739	CDS	hypothetical protein		
SAMN04901664_03740	CDS	nemR_3		HTH-type transcriptional repressor NemR
SAMN04901664_03741	CDS	curA	1.3.1.-	NADPH-dependent curcumin reductase
SAMN04901664_03742	CDS	hypothetical protein		
SAMN04901664_03743	CDS	hypothetical protein		
SAMN04901664_03744	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03745	CDS	hypothetical protein		
SAMN04901664_03746	CDS	hypothetical protein		
SAMN04901664_03747	CDS	hypothetical protein		
SAMN04901664_03748	CDS	hypothetical protein		
SAMN04901664_03749	CDS	dnaQ_2	2.7.7.7	DNA polymerase III subunit epsilon
SAMN04901664_03750	CDS	hypothetical protein		
SAMN04901664_03751	CDS	hypothetical protein		
SAMN04901664_03752	CDS	hypothetical protein		
SAMN04901664_03753	CDS	hypothetical protein		
SAMN04901664_03754	CDS	hypothetical protein		
SAMN04901664_03755	CDS	hypothetical protein		
SAMN04901664_03756	CDS	hypothetical protein		
SAMN04901664_03757	CDS	hypothetical protein		
SAMN04901664_03758	CDS	nrdB_2	1.17.4.1	Ribonucleoside-diphosphate reductase subunit beta
SAMN04901664_03759	CDS	nrdA_2	1.17.4.1	Ribonucleoside-diphosphate reductase 1 subunit alpha
SAMN04901664_03760	CDS	hypothetical protein		
SAMN04901664_03761	CDS	ruvC_2	3.1.22.4	Crossover junction endodeoxyribonuclease RuvC
SAMN04901664_03762	CDS	hypothetical protein putative DNA double-strand break repair Rad50 ATPase		
SAMN04901664_03763	CDS	ATPase		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03764	CDS	hypothetical protein		
SAMN04901664_03765	CDS	hypothetical protein		
SAMN04901664_03766	CDS	hypothetical protein		
SAMN04901664_03767	CDS	hypothetical protein		
SAMN04901664_03768	CDS	hypothetical protein		
SAMN04901664_03769	CDS	recA_2	Protein RecA	
SAMN04901664_03770	CDS	poIA_2	2.7.7.7	DNA polymerase I
SAMN04901664_03771	CDS	hypothetical protein		
SAMN04901664_03772	CDS	hypothetical protein		
SAMN04901664_03773	CDS	dnaE_2	2.7.7.7	DNA polymerase III subunit alpha
SAMN04901664_03774	CDS	hypothetical protein		
SAMN04901664_03775	CDS	dnaE_3	2.7.7.7	DNA polymerase III subunit alpha
SAMN04901664_03776	CDS	hypothetical protein		
SAMN04901664_03777	CDS	hypothetical protein		
SAMN04901664_03778	CDS	cobS_2	6.6.1.2	Aerobic cobaltochelatase subunit CobS
SAMN04901664_03779	CDS	cobT_2	6.6.1.2	Aerobic cobaltochelatase subunit CobT
SAMN04901664_03780	CDS	hypothetical protein		
SAMN04901664_03781	CDS	hypothetical protein		
SAMN04901664_03782	CDS	xerD_3	Tyrosine recombinase XerD	
SAMN04901664_03783	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03784	CDS	soj_2	3.6.-.-	Chromosome-partitioning ATPase Soj
SAMN04901664_03785	CDS	hypothetical protein		
SAMN04901664_03786	CDS	hypothetical protein		
SAMN04901664_03787	CDS	gmk_2	2.7.4.8	Guanylate kinase
SAMN04901664_03788	CDS	hypothetical protein		
SAMN04901664_03789	CDS	hypothetical protein		
SAMN04901664_03790	CDS	hypothetical protein		
SAMN04901664_03791	CDS	hypothetical protein		
SAMN04901664_03792	CDS	hypothetical protein		
SAMN04901664_03793	CDS	dnaG_2	2.7.7.-	DNA primase
SAMN04901664_03794	CDS	hypothetical protein		
SAMN04901664_03795	CDS	hypothetical protein		
SAMN04901664_03796	CDS	hypothetical protein		
SAMN04901664_03797	CDS	repE		Replication initiation protein
SAMN04901664_03798	CDS	rrrD	3.2.1.17	Lysozyme RrrD
SAMN04901664_03799	CDS	hypothetical protein		
SAMN04901664_03800	CDS	hypothetical protein		
SAMN04901664_03801	CDS	hypothetical protein		
SAMN04901664_03802	CDS	hypothetical protein		
SAMN04901664_03803	CDS	hypothetical protein		
SAMN04901664_03804	CDS	smc_3		Smc
SAMN04901664_03805	CDS	hypothetical protein		
SAMN04901664_03806	CDS	hypothetical protein		
SAMN04901664_03807	CDS	hypothetical protein		

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03808	CDS	hypothetical protein		
SAMN04901664_03809	CDS	hypothetical protein		
SAMN04901664_03810	CDS	hypothetical protein		
SAMN04901664_03811	CDS	hypothetical protein		
SAMN04901664_03812	CDS	hypothetical protein		
SAMN04901664_03813	CDS	hypothetical protein		
SAMN04901664_03814	CDS	hypothetical protein		
SAMN04901664_03815	CDS	hypothetical protein		
SAMN04901664_03816	CDS	hypothetical protein		
SAMN04901664_03817	CDS	hypothetical protein		
SAMN04901664_03818	CDS	hypothetical protein		
SAMN04901664_03819	CDS	hypothetical protein		
SAMN04901664_03820	CDS	hypothetical protein		
SAMN04901664_03821	CDS	hypothetical protein		
SAMN04901664_03822	CDS	hypothetical protein		
SAMN04901664_03823	CDS	hypothetical protein		
SAMN04901664_03824	CDS	hypothetical protein		
SAMN04901664_03825	CDS	hypothetical protein		
SAMN04901664_03826	CDS	hypothetical protein		
SAMN04901664_03827	CDS	proA_2	4.1.3.16	4-hydroxy-4-methyl-2-oxoglutarate aldolase/4-carboxy-4-hydroxy-2-oxoadipate aldolase
SAMN04901664_03828	CDS	1.1.1.81	Hydroxypyruvate reductase	
SAMN04901664_03829	CDS	ttuB_3	Putative tartrate transporter	

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03830	CDS	kipR	HTH-type transcriptional regulator KipR	
SAMN04901664_03831	CDS	hypothetical protein		
SAMN04901664_03832	CDS	hypothetical protein		
SAMN04901664_03833	CDS	dmlR_15	HTH-type transcriptional regulator DmlR	
SAMN04901664_03834	CDS	sauU	SauU	
SAMN04901664_03835	CDS	3.1.1.99	sulfogluconolactonase	
SAMN04901664_03836	CDS	yvoA_3	HTH-type transcriptional repressor YvoA	
SAMN04901664_03837	CDS	hypothetical protein		
SAMN04901664_03838	CDS	3.1.1.92	hydrolase	
SAMN04901664_03839	CDS	ttuB_4	Putative tartrate transporter	
SAMN04901664_03840	CDS	hypothetical protein		
SAMN04901664_03841	CDS	hypothetical protein		
SAMN04901664_03842	CDS	cdiA2		tRNA nuclease CdiA-2
SAMN04901664_03843	CDS	shlB	3.1.-.- ShlB	
SAMN04901664_03844	CDS	betl_7	HTH-type transcriptional regulator Betl	
SAMN04901664_03845	CDS	yxep_3	3.-.-.-	putative hydrolase YxeP
SAMN04901664_03846	CDS	hypothetical protein		
SAMN04901664_03847	CDS	kefC_2	potassium-efflux system protein KefC	
SAMN04901664_03848	CDS	gdhB_2	1.1.5.2	Quinoprotein glucose dehydrogenase B

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03849	CDS	dmlR_16	HTH-type transcriptional regulator DmlR	
SAMN04901664_03850	CDS	hypothetical protein		
SAMN04901664_03851	CDS	hypothetical protein		
SAMN04901664_03852	CDS	bm3R1_3	HTH-type transcriptional repressor Bm3R1	
SAMN04901664_03853	CDS	hypothetical protein		
SAMN04901664_03854	CDS	iscR_2	HTH-type transcriptional regulator IscR	
SAMN04901664_03855	CDS	1.6.-.-	protein	Molecular chaperone Hsp31 and glyoxalase 3
SAMN04901664_03856	CDS	hchA_4	4.2.1.130	
SAMN04901664_03857	CDS	hmrR_3	HTH-type transcriptional regulator HmrR	
SAMN04901664_03858	CDS	hypothetical protein		
SAMN04901664_03859	CDS	1.3.1.-	Trans-acting enoyl reductase	
SAMN04901664_03860	CDS	1.-.-.-	NADH oxidase	
SAMN04901664_03861	CDS	ohrR_2	resistance transcriptional regulator	
SAMN04901664_03862	CDS	nlhH_3	3.1.1.1	Carboxylesterase NlhH
SAMN04901664_03863	CDS	hchA_5	4.2.1.130	Molecular chaperone Hsp31 and glyoxalase 3
SAMN04901664_03864	CDS	hypothetical protein		
SAMN04901664_03865	CDS	kata	1.11.1.6	Catalase
SAMN04901664_03866	CDS	cpo	1.11.1.10	Non-heme chloroperoxidase

AR_0274 locus_tag	type	gene	EC_number	product
SAMN04901664_03867	CDS	hypothetical protein		
SAMN04901664_03868	CDS	calB_2	1.2.1.68	Coniferyl aldehyde dehydrogenase
SAMN04901664_03869	CDS	1.3.1.103	2-haloacrylate reductase	
SAMN04901664_03870	CDS	actP_3	Cation/acetate symporter ActP	
SAMN04901664_03871	CDS	yjch_2	Inner membrane protein Yjch	
SAMN04901664_03872	CDS	dmdB	6.2.1.44	3-methylmercaptopropionyl-CoA ligase
SAMN04901664_03873	CDS	prpR	Propionate catabolism operon regulatory protein	
SAMN04901664_03874	CDS	gno	1.1.1.69	Gluconate 5-dehydrogenase
SAMN04901664_03875	CDS	carC_2	1.3.1.108	Caffeyl-CoA reductase-Eff complex subunit CarC
SAMN04901664_03876	CDS	gpmA	5.4.2.11	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
SAMN04901664_03877	CDS	hypothetical protein		
SAMN04901664_03878	CDS	2.7.1.-	Putative aminoglycoside phosphotransferase	
SAMN04901664_03879	CDS	1.2.1.26	Alpha-ketoglutaric semialdehyde dehydrogenase	

APPENDIX F: CDC FDA gene glossary

Allele	Variant	Antibiotic Class	Accession	Product Annotation
aac(2')-Ia	aac(2')-Ia_1	Aminoglycoside resistance	L06156	aminoglycoside 2'-N- acetyltransferase
aac(3)-Ia	aac(3)-Ia_1	Aminoglycoside resistance	X15852	unnamed protein product; aacC1 product acetyltransferase (AA 1-177)"
aac(3)-Ib	aac(3)-Ib_1	Aminoglycoside resistance	L06157	aminoglycoside 3'-N- acetyltransferase
aac(3)-Ic	aac(3)-Ic_1	Aminoglycoside resistance	AJ511268	aminoglycoside acetyltransferase
aac(3)-Id	aac(3)-Id_1	Aminoglycoside resistance	AB114632	aminoglycoside acetyltransferase
aac(3)-IIa	aac(3)-IIa_1	Aminoglycoside resistance	X51534	unnamed protein product; AAC(3)-II (AA 1-286)
aac(3)-IIc	aac(3)-IIc_1	Aminoglycoside resistance	EU022314	aminoglycoside-(3)-N- acetyl-transferase
aac(6')-33	aac(6')-33_1	Aminoglycoside resistance	GQ337064	aminoglycoside acetyltransferase
aac(6')-aph(2'')	aac(6')-aph(2'')_1	Aminoglycoside resistance	M13771	AAC(6')-APH(2') bifunctional resistance protein
aac(6')-Ib	aac(6')-Ib_1	Aminoglycoside resistance	M21682	aminoglycoside 6'-N- acetyltransferase
aac(6')Ib-cr	aac(6')Ib- cr_1	Fluoroquinolone and aminoglycoside resistance	DQ303918	fluroquinolone acetylating aminoglycoside acetyltransferase

Allele	Variant	Antibiotic Class	Accession	Product Annotation
aac(6')-Ic	aac(6')-Ic_1	Aminoglycoside resistance	M94066	aminoglycoside acetyltransferase
aac(6')-If	aac(6')-If_1	Aminoglycoside resistance	X55353	AG-6'-acetyltransferase
aac(6')-IIa	aac(6')-IIa_1	Aminoglycoside resistance	M29695	6'-N-acetyltransferase
aac(6')-IIc	aac(6')-IIc_1	Aminoglycoside resistance	AF162771	aminoglycoside 6'-N- acetyltransferase
aadA1	aadA1_4	Aminoglycoside resistance	M95287	aminoglycoside (3'') adenylyltransferase
aadA1	aadA1_5	Aminoglycoside resistance	JQ480156	aminoglycoside- adenylyltransferase
aadA11	aadA11_1	Aminoglycoside resistance	AY144590	aminoglycoside adenylyltransferase
aadA2	aadA2_2	Aminoglycoside resistance	JQ364967	aminoglycosides adenylyltransferase
aadA5	aadA5_1	Aminoglycoside resistance	AF137361	streptomycin and spectinomycin resistance aminoglycoside adenylyltransferase
aadA6	aadA6_1	Aminoglycoside resistance	AF140629	aminoglycoside adenylyltransferase AADA6
aadA7	aadA7_1	Aminoglycoside resistance	AF224733	aminoglycoside adenylyltransferase
aadB	aadB_1	Aminoglycoside resistance	JN119852	aminoglycoside-2'' - adenylyltransferase"

Allele	Variant	Antibiotic Class	Accession	Product Annotation
aadD	aadD_1	Aminoglycoside resistance	AF181950	kanamycin resistance protein
ACT-15	ACT-15_1	Beta-lactam resistance:AmpC- type	JX440356	AmpC beta-lactamase ACT- 15
ACT-16	ACT-16_1	Beta-lactam resistance:AmpC- type	AB737978	beta lactamase ACT-16
ACT-5	ACT-5_1	Beta-lactam resistance:AmpC- type	FJ237369	beta-lactamase ACT-5
ACT-7	ACT-7_1	Beta-lactam resistance:AmpC- type	FJ237368	beta-lactamase EBC-1464
ADC-25	ADC-25_1	Beta-lactam resistance	EF016355	AmpC cephalosporinase
aph(3')-Ia	aph(3')-Ia_1	Aminoglycoside resistance	V00359	AmpC cephalosporinase
aph(3')-Ic	aph(3')-Ic_1	Aminoglycoside resistance	X62115	neomycin phosphotransferase
aph(3')-IIb	aph(3')-IIb_1	Aminoglycoside resistance	X90856	aminoglycoside phosphotransferase (3')IIps
aph(3')-III	aph(3')-III_1	Aminoglycoside resistance	M26832	kanamycin resistance protein
aph(3')-VIa	aph(3')-VIa_1	Aminoglycoside resistance	X07753	kanamycin resistance protein

Allele	Variant	Antibiotic Class	Accession	Product Annotation
aph(3')-XV	aph(3')-XV_1	Aminoglycoside resistance	Y18050	aminoglycoside phosphotransferase
aph(4)-Ia	aph(4)-Ia_1	Aminoglycoside resistance	V01499	unnamed protein product; aph(4)
armA	armA_1	Aminoglycoside resistance	AY220558	16S rRNA methylase
ARR-3	ARR-3_4	Rifampicin resistance	FM207631	rifampicin ADP-ribosylating transferase
blaZ	blaZ_34	Beta-lactam resistance	AP003139	beta-lactamase
blaZ	blaZ_35	Beta-lactam resistance	AJ302698	beta-lactamase
blaZ	blaZ_36	Beta-lactam resistance	AJ400722	beta-lactamase
catA1	catA1_1	Phenicol resistance	V00622	
catA3	catA3_1	Phenicol resistance	X07848	
catB2	catB2_1	Phenicol resistance	AF047479	chloramphenicol acetyltransferase
catB3	catB3_1	Phenicol resistance	AJ009818	Chloramphenicol acetyltransferase
catB7	catB7_1	Phenicol resistance	AF036933	chloramphenicol acetyltransferase
catB8	catB8_1	Phenicol resistance	AF227506	chloramphenicol acetyltransferase
cmlA1	cmlA1_1	Phenicol resistance	M64556	nonenzymatic chloramphenicol- resistance protein
cmlA1	cmlA1_2	Phenicol resistance	AB212941	chloramphenicol resistance
cmx	cmx_1	Phenicol resistance	U85507	chloramphenicol resistance protein
CMY-2	CMY-2_1	Beta-lactam resistance	X91840	extended spectrum beta- lactamase
CMY-4	CMY-4_1	Beta-lactam resistance	AF420597	cephamycinase
CMY-42	CMY-42_1	Beta-lactam resistance	HM146927	AmpC beta-lactamase
CMY-6	CMY-6_1	Beta-lactam resistance	AJ011293	beta-lactamase
CMY-76	CMY-76_1	Beta-lactam resistance	JQ733573	AmpC beta-lactamase CMY-76

Allele	Variant	Antibiotic Class	Accession	Product Annotation
CMY-79	CMY-79_1	Beta-lactam resistance	JQ733576	AmpC beta-lactamase CMY-79
CMY-80	CMY-80_1	Beta-lactam resistance	JQ733577	AmpC beta-lactamase CMY-80
CMY-84	CMY-84_1	Beta-lactam resistance	JQ733579	AmpC beta-lactamase CMY-84
CMY-94	CMY-94_1	Beta-lactam resistance	JX514368	CMY-like beta-lactamase
CTX-M-124	CTX-M-124_1	Beta-lactam resistance	JQ429324	extended-spectrum beta- lactamase CTX-M-124
CTX-M-14	CTX-M-14_1	Beta-lactam resistance	AF252622	beta-lactamase CTX-M-14
CTX-M-15	CTX-M-15_23	Beta-lactam resistance	DQ302097	extended-spectrum beta- lactamase CTX-M-15
CTX-M-2	CTX-M-2_1	Beta-lactam resistance	EU622041	resistance to beta-lactams including extended-spectrum cephalosporins
CTX-M-55	CTX-M-55_2	Beta-lactam resistance	GQ456159	extended-spectrum beta- lactamase CTX-M-55
dfrA1	dfrA1_1	Trimethoprim resistance	X00926	dihydrofolate reductase (DHFR)
dfrA1	dfrA1_30	Trimethoprim resistance	JQ690541	dihydrofolate reductase type I
dfrA12	dfrA12_1	Trimethoprim resistance	AB571791	dihydrofolate reductase
dfrA14	dfrA14_1	Trimethoprim resistance	DQ388123	dihydrofolate reductase
dfrA15	dfrA15_1	Trimethoprim resistance	HM449019	dihydrofolate reductase
dfrA17	dfrA17_1	Trimethoprim resistance	FJ460238	dihydrofolate reductase; trimethoprim resistance

Allele	Variant	Antibiotic Class	Accession	Product Annotation
dfrA18	dfrA18_1	Trimethoprim resistance	AJ310778	dihydrofolate reductase
dfrA29	dfrA29_1	Trimethoprim resistance	AM237806	dihydrofolate reductase type VII
dfrA30	dfrA30_1	Trimethoprim resistance	AM997279	dihydrofolate reductase
dfrA3b	dfrA3b_1	Trimethoprim resistance	AY878717	dihydrofolate reductase type IIIb
dfrA5	dfrA5_1	Trimethoprim resistance	X12868	
dfrA8	dfrA8_1	Trimethoprim resistance	U10186	dihydrofolate reductase type VIII
dfrB1	dfrB1_2	Trimethoprim resistance	U36276	dihydrofolate reductase
dfrB5	dfrB5_1	Trimethoprim resistance	AY943084	dihydrofolate reductase
dfrG	dfrG_1	Trimethoprim resistance	AB205645	dihydrofolate reductase
DHA-1	DHA-1_1	Beta-lactam resistance:AmpC- type	Y16410	beta-lactamase class C
ere(A)	ere(A)_2	Macrolide resistance	AF099140	erythromycin esterase
erm(42)	erm(42)_2	Macrolide resistance	AB601890	erythromycin resistance protein
erm(A)	erm(A)_1	Macrolide resistance	X03216	
erm(B)	erm(B)_1	Macrolide resistance	JN899585	rRNA methylase

Allele	Variant	Antibiotic Class	Accession	Product Annotation
fosA	fosA_10	Fosfomycin resistance	EU195449	putative fosfomycin- resistance protein
fosA	fosA_13	Fosfomycin resistance	EU487198	fosfomycin-resistance protein
fosA	fosA_14	Fosfomycin resistance	AB522970 NZ_ACWO	fosfomycin resistance protein FosA3
fosA	fosA_3	Fosfomycin resistance	01000079 NZ_AFBO0	
fosA	fosA_7	Fosfomycin resistance	1000747	
GES-1	GES-1_1	Beta-lactam resistance	HQ170511	extended-spectrum beta- lactamase GES-7
IMP-1	IMP-1_1	Beta-lactam resistance	DQ522237	metallo-beta-lactamase IMP-1-like
IMP-14	IMP-14_1	Beta-lactam resistance	AY553332	metallo-beta-lactamase; carbapenemase IMP-14
IMP-4	IMP-4_1	Beta-lactam resistance	AF244145	carbapenem-hydrolysing beta-lactamase
KPC-2	KPC-2_1	Beta-lactam resistance	AY034847	carbapenemase
KPC-3	KPC-3_1	Beta-lactam resistance	HM769262	beta-lactamase KPC-3
KPC-4	KPC-4_1	Beta-lactam resistance	FJ473382	beta-lactamase KPC-4
KPC-5	KPC-5_1	Beta-lactam resistance	EU400222	beta-lactamase KPC-5
KPC-6	KPC-6_1	Beta-lactam resistance	EU555534	beta-lactamase KPC-6
LEN16	LEN16_1	Beta-lactam resistance	AY743416	LEN-type penicillinase
MAL-1	MAL-1_1	Beta-lactam resistance	AJ277209	beta-lactamase MAL-1
MAL-1	MAL-1_2	Beta-lactam resistance	AJ609506	class A beta-lactamase
mcr-1	mcr-1_1	Colistin resistance	KP347127	phosphoethanolamine transferase
mecA	mecA_14	Beta-lactam resistance	AB505630	penicillin-binding protein 2'

Allele	Variant	Antibiotic Class	Accession	Product Annotation
mecA	mecA_15	Beta-lactam resistance	AB505628	penicillin-binding protein 2' beta-lactam-inducible penicillin-binding protein
mecA	mecA_6	Beta-lactam resistance	FR821779	
mph(A)	mph(A)_1	Macrolide resistance	D16251	macrolide 2'-phosphotransferase I
mph(C)	mph(C)_2	Macrolide resistance	AF167161	
mph(E)	mph(E)_3	Macrolide resistance	EU294228	macrolide 2'-phosphotransferase
		Macrolide, Lincosamide and Streptogramin B		
msr(A)	msr(A)_3	resistance	M81802	21kDa product of the C- terminal of MsrB
		Macrolide, Lincosamide and Streptogramin B		
msr(E)	msr(E)_4	resistance	EU294228	
NDM-1	NDM-1_1	Beta-lactam resistance	FN396876	metallo-beta-lactamase
NDM-5	NDM-5_1	Beta-lactam resistance	JN104597	NDM-5 metallo-beta- lactamase
NDM-6	NDM-6_1	Beta-lactam resistance	JN967644	NDM carbenemase
NDM-7	NDM-7_1	Beta-lactam resistance	JX262694	NDM-7 metallo-beta- lactamase
NMC-A	NMC-A_1	Beta-lactam resistance	AJ536087	class A nonmetallocarbenemase
OKP-B-2	OKP-B-2_1	Beta-lactam resistance	AM051151	OKP-B beta-lactamase
oqxA	oqxA_1	Quinolone resistance	EU370913	component of RND-type multidrug efflux pump that confers resistance to olaquinox
oqxB	oqxB_1	Quinolone resistance	EU370913	component of RND-type multidrug efflux pump that confers resistance to olaquinox
OXA-1	OXA-1_1	Beta-lactam resistance	J02967	OXA-1 beta-lactamase

Allele	Variant	Antibiotic Class	Accession	Product Annotation
OXA-10	OXA-10_2	Beta-lactam resistance	EU886981	Beta-lactamase
OXA-100	OXA-100_1	Beta-lactam resistance	AM231720	blaOXA-100 class D beta-lactamase
OXA-181	OXA-181_1	Beta-lactam resistance	HM992946	carbapenemase OXA-181
OXA-2	OXA-2_1	Beta-lactam resistance	DQ310703	oxacillinase type 2
OXA-203	OXA-203_1	Beta-lactam resistance	HQ998857	beta-lactamase OXA-203
OXA-223	OXA-223_1	Beta-lactam resistance	JN248564	beta-lactamase OXA-223
OXA-23	OXA-23_1	Beta-lactam resistance	HQ700358	beta-lactamase OXA-23
OXA-232	OXA-232_1	Beta-lactam resistance	JX423831	class D beta-lactamase
OXA-237	OXA-237_1	Beta-lactam resistance	JQ820241	beta-lactamase OXA-237
OXA-24	OXA-24_1	Beta-lactam resistance	AJ239129	Beta-lactamase
OXA-4	OXA-4_1	Beta-lactam resistance	AY162283	beta-lactamase OXA-4
OXA-48	OXA-48_2	Beta-lactam resistance	AY236073	class D carbapenem- hydrolyzing beta-lactamase
OXA-50	OXA-50_1	Beta-lactam resistance	AY306135	oxacillinase
OXA-50	OXA-50_2	Beta-lactam resistance	AY306133	oxacillinase
OXA-50	OXA-50_3	Beta-lactam resistance	AY306130	oxacillinase
OXA-50	OXA-50_3	Beta-lactam resistance	AY306132	oxacillinase
OXA-56	OXA-56_1	Beta-lactam resistance	AY660529	restricted spectrum class D beta-lactamase
OXA-58	OXA-58_1	Beta-lactam resistance	AY665723	carbapenem-hydrolyzing oxacillinase
OXA-64	OXA-64_1	Beta-lactam resistance	AY750907	beta-lactamase OXA-64
OXA-65	OXA-65_1	Beta-lactam resistance	AY750908	beta-lactamase OXA-65
OXA-66	OXA-66_4	Beta-lactam resistance	FJ360530	OXA carbapenemase; class D oxacillinase
OXA-69	OXA-69_1	Beta-lactam resistance	HM564339	carbapenem-hydrolyzing oxacillinase OXA-69

Allele	Variant	Antibiotic Class	Accession	Product Annotation
OXA-71	OXA-71_1	Beta-lactam resistance	AY859528	carbapenem-hydrolyzing oxacillinase OXA-71
OXA-72	OXA-72_1	Beta-lactam resistance	GU199039	class D beta-lactamase OXA-72
OXA-82	OXA-82_1	Beta-lactam resistance	GQ352402	beta-lactamase OXA-82 protein
OXA-9	OXA-9_2	Beta-lactam resistance	JF703130	oxacillinase- carbenicillinase
OXA-94	OXA-94_1	Beta-lactam resistance	DQ519088	beta-lactamase OXA-94
OXY-1-4	OXY-1-4_4	Beta-lactam resistance	AY077483	K1 beta-lactamase
OXY-1-7	OXY-1-7_7	Beta-lactam resistance	M27459	beta-lactamase
OXY-2-8	OXY-2-8_8	Beta-lactam resistance	AY055205	K1 beta-lactamase OXY-2
PAO	PAO_1	Beta-lactam resistance	AY083595	beta-lactamase precursor
PAO	PAO_2	Beta-lactam resistance	FJ666065	class C beta-lactamase PDC-1
PAO	PAO_3	Beta-lactam resistance	FJ666073	class C beta-lactamase PDC-10
PAO	PAO_4	Beta-lactam resistance	AY083592	beta-lactamase precursor
PER-7	PER-7_1	Beta-lactam resistance	HQ713678	extended spectrum beta- lactamase
QnrB13	QnrB13_1	Quinolone resistance	EU273755	quinolone resistance protein; pentapeptide repeat protein
QnrB2	QnrB2_1	Quinolone resistance	HM125698	fluoroquinolone resistance protein
QnrB34	QnrB34_1	Quinolone resistance	JN173056	quinolone resistance protein QnrB34
QnrB38	QnrB38_1	Quinolone resistance	JN173060	QnrB38
QnrB4	QnrB4_1	Quinolone resistance	DQ303921	contains pentapeptide repeat
QnrB5	QnrB5_1	Quinolone resistance	DQ303919	contains pentapeptide repeat
QnrB6	QnrB6_3	Quinolone resistance	EF523819	QnrB6
QnrB7	QnrB7_1	Quinolone resistance	EU043311	QnrB7
QnrS1	QnrS1_1	Quinolone resistance	AB187515	Qnr

Allele	Variant	Antibiotic Class	Accession	Product Annotation
rmtB	rmtB_1	Aminoglycoside resistance	AB103506	16S rRNA methylase
rmtC	rmtC_1	Aminoglycoside resistance	AB194779	16S rRNA methylase
rmtf	rmtf_1	Aminoglycoside resistance	JQ808129	aminoglycoside 16s rRNA methyltransferase
rmtG	rmtG_1	Aminoglycoside resistance	KJ004567	16S rRNA methyltransferase
SFO-1	SFO-1_1	Beta-lactam resistance	AB003148	class A beta-lactamase SFO-1
SHV-1	SHV-1_11	Beta-lactam resistance	EF035565	extended spectrum beta lactamase
SHV-1	SHV-1_13	Beta-lactam resistance	AF462396	extended-spectrum beta- lactamase SHV-1
SHV-1	SHV-1_18	Beta-lactam resistance	FJ668818	beta-lactamase SHV-1
SHV-1	SHV-1_9	Beta-lactam resistance	HM751102	SHV-1 beta-lactamase
SHV-11	SHV-11_10	Beta-lactam resistance	EF035557	extended spectrum beta lactamase
SHV-11	SHV-11_15	Beta-lactam resistance	DQ219473	extended-spectrum beta- lactamase SHV-11
SHV-11	SHV-11_1	Beta-lactam resistance	AY528717	beta-lactamase
SHV-11	SHV-11_2	Beta-lactam resistance	HM751098	SHV-11 beta-lactamase
SHV-11	SHV-11_5	Beta-lactam resistance	GQ407117	beta-lactamase blaSHV-11
SHV-11	SHV-11_8	Beta-lactam resistance	GQ387358	beta-lactamase SHV-11
SHV-11	SHV-11_9	Beta-lactam resistance	FJ483937	beta-lactamase SHV-11
SHV-12	SHV-12_1	Beta-lactam resistance	AF462395	extended-spectrum beta- lactamase SHV-12
SHV-26	SHV-26_1	Beta-lactam resistance	AF227204	beta-lactamase
SHV-30	SHV-30_1	Beta-lactam resistance	AY661885	beta-lactamase SHV-30
SHV-5	SHV-5_6	Beta-lactam resistance	EF653399	beta-lactamase SHV-5
SHV-83	SHV-83_1	Beta-lactam resistance	AM176558	beta-lactamase

Allele	Variant	Antibiotic Class	Accession	Product Annotation
SME-3	SME-3_1	Beta-lactam resistance	AY584237	carbapenem-hydrolyzing beta-lactamase SME-3
spc	spc_1	Aminoglycoside resistance	X02588	
SPM-1	SPM-1_1	Beta-lactam resistance	AY341249	carbapenemase
strA	strA_1	Aminoglycoside resistance	M96392	
strA	strA_4	Aminoglycoside resistance	AF321551	aminoglycoside 3" - phosphotransferase
strB	strB_1	Aminoglycoside resistance	M96392	streptomycin phosphotransferase
sul1	sul1_11	Sulphonamide resistance	DQ914960	dihydropteroate synthase
sul1	sul1_2	Sulphonamide resistance	CP002151	dihydropteroate synthase protein Sul1
sul2	sul2_2	Sulphonamide resistance	GQ421466	dihydropteroate synthase
sul2	sul2_3	Sulphonamide resistance	HQ840942	sulfonamide-insensitive dihydropteroate synthetase
sul3	sul3_2	Sulphonamide resistance	AJ459418	dihydropteroate synthase
TEM-1A	TEM-1A_4	Beta-lactam resistance	HM749966	TEM-1 beta-lactamase
TEM-1B	TEM-1B_1	Beta-lactam resistance	JF910132	beta-lactamase
TEM-1D	TEM-1D_83	Beta-lactam resistance	AF188200	beta-lactamase variant TEM-1D
TEM-52B	TEM-52B_1	Beta-lactam resistance	AF027199	extended spectrum beta- lactamase

Allele	Variant	Antibiotic Class	Accession	Product Annotation
tet(A)	tet(A)_3	Tetracycline resistance	AY196695	tetracycline resistance efflux pump
tet(A)	tet(A)_4	Tetracycline resistance	AJ517790	tetracycline resistance protein
tet(B)	tet(B)_3	Tetracycline resistance	AP000342	tetracycline resistance protein
tet(B)	tet(B)_4	Tetracycline resistance	AF326777	tetracycline resistance protein TetA(B)
tet(C)	tet(C)_5	Tetracycline resistance	NC_003213	TetA(C) protein
tet(D)	tet(D)_1	Tetracycline resistance	AF467077	TetA(D); class D; efflux pump
tet(G)	tet(G)_4	Tetracycline resistance	AF133140 ACLE01000	tetracycline resistance protein
tet(J)	tet(J)_1	Tetracycline resistance	065	transporter, major facilitator family protein
tet(K)	tet(K)_4	Tetracycline resistance	U38428	tetracycline resistance protein
tet(M)	tet(M)_7	Tetracycline resistance	FN433596	tetracycline resistance protein
VEB-1	VEB-1_1	Beta-lactam resistance	HM370393	extended-spectrum beta- lactamase
VIM-1	VIM-1_1	Beta-lactam resistance	Y18050	beta-lactamase VIM-1
VIM-11	VIM-11_1	Beta-lactam resistance	AY605049	VIM-11
VIM-2	VIM-2_1	Beta-lactam resistance	AF302086	metallo-beta-lactamase
VIM-27	VIM-27_1	Beta-lactam resistance	HQ858608	metallo-beta-lactamase VIM-27

Allele	Variant	Antibiotic Class	Accession	Product Annotation
VIM-4	VIM-4_1	Beta-lactam resistance	EU581706	metallo-beta-lactamase

APPENDIX G: *A. baumannii* genomes used for pangenome analysis

	NCBI Reference Sequence ID#	Strain	
1	NZ_JSAO01000001.1	<i>Acinetobacter baumannii</i>	1
2	NZ_NKKO01000103.1	<i>Acinetobacter baumannii</i>	13
3	NZ_NKKP01000243.1	<i>Acinetobacter baumannii</i>	15
4	NZ_MAF01000001.1	<i>Acinetobacter baumannii</i>	28
5	NZ_MACA01000001.1	<i>Acinetobacter baumannii</i>	65
6	NZ_MEDG01000049.1	<i>Acinetobacter baumannii</i>	71
7	NZ_MDTR01000001.1	<i>Acinetobacter baumannii</i>	80
8	NZ_NXHM01000094.1	<i>Acinetobacter baumannii</i>	151
9	NZ_NSJA01000001.1	<i>Acinetobacter baumannii</i>	247
10	NZ_QNV01000001.1	<i>Acinetobacter baumannii</i>	269
11	NZ_MDTT01000001.1	<i>Acinetobacter baumannii</i>	314
12	NZ_JQSD01000001.1	<i>Acinetobacter baumannii</i>	341
13	NZ_MDTS01000001.1	<i>Acinetobacter baumannii</i>	428
14	NZ_MEDH01000051.1	<i>Acinetobacter baumannii</i>	440
15	NZ_NRSX01000001.1	<i>Acinetobacter baumannii</i>	460
16	NZ_LCTE01000001.1	<i>Acinetobacter baumannii</i>	461
17	NZ_MWPK01000077.1	<i>Acinetobacter baumannii</i>	499
18	NZ_MWPL01000090.1	<i>Acinetobacter baumannii</i>	502
19	NZ_LZTF01000001.1	<i>Acinetobacter baumannii</i>	863
20	NZ_MWPM01000084.1	<i>Acinetobacter baumannii</i>	891
21	NZ_MWPN01000086.1	<i>Acinetobacter baumannii</i>	895
22	NZ_MWPO01000076.1	<i>Acinetobacter baumannii</i>	923
23	NZ_MWPP01000078.1	<i>Acinetobacter baumannii</i>	991
24	NZ_JEZ01000001.1	<i>Acinetobacter baumannii</i>	1297
25	NZ_AUWL01000001.1	<i>Acinetobacter baumannii</i>	1605

	NCBI Reference Sequence ID#	Strain	
26	NZ_JFEP01000001.1	<i>Acinetobacter baumannii</i>	2887
27	NZ_CP015364.1	<i>Acinetobacter baumannii</i>	3207
28	NZ_JFER01000001.1	<i>Acinetobacter baumannii</i>	3390
29	NZ_AEOZ01000236.1	<i>Acinetobacter baumannii</i>	3909
30	NZ_AEOY01000095.1	<i>Acinetobacter baumannii</i>	3990
31	NZ_MSDA01000001.1	<i>Acinetobacter baumannii</i>	4113
32	NZ_JZBY01000001.1	<i>Acinetobacter baumannii</i>	4390
33	NZ_JEXC01000001.1	<i>Acinetobacter baumannii</i>	4749
34	NZ_JMNY01000001.1	<i>Acinetobacter baumannii</i>	6112
35	NZ_CP010397.1	<i>Acinetobacter baumannii</i>	6200
36	NZ_JFDK01000001.1	<i>Acinetobacter baumannii</i>	7893
37	NZ_JFFF01000001.1	<i>Acinetobacter baumannii</i>	10519
38	NZ_JFWS01000001.1	<i>Acinetobacter baumannii</i>	11126
39	NZ_MSCX01000012.1	<i>Acinetobacter baumannii</i>	11502
40	NZ_CP018861.2	<i>Acinetobacter baumannii</i>	11510
41	NZ_MSCY01000036.1	<i>Acinetobacter baumannii</i>	11536
42	NZ_MSDB01000037.1	<i>Acinetobacter baumannii</i>	11547
43	NZ_MSDC01000029.1	<i>Acinetobacter baumannii</i>	11551
44	NZ_MSCZ01000021.1	<i>Acinetobacter baumannii</i>	11598
45	NZ_MSDD01000040.1	<i>Acinetobacter baumannii</i>	11606
46	NZ_JFXN01000001.1	<i>Acinetobacter baumannii</i>	14216
47	NZ_FUEN01000177.1	<i>Acinetobacter baumannii</i>	14336
48	NZ_JEYQ01000001.1	<i>Acinetobacter baumannii</i>	17534
49	NZ_JMNI01000001.1	<i>Acinetobacter baumannii</i>	18689
50	NZ_JMOD01000001.1	<i>Acinetobacter baumannii</i>	21072
51	NZ_JMOC01000001.1	<i>Acinetobacter baumannii</i>	23037
52	NZ_JFEN01000001.1	<i>Acinetobacter baumannii</i>	23671

	NCBI Reference Sequence ID#	Strain	
53	NZ_JEZI01000001.1	<i>Acinetobacter baumannii</i>	29280
54	NZ_JEJK01000001.1	<i>Acinetobacter baumannii</i>	34001
55	NZ_JEZO01000001.1	<i>Acinetobacter baumannii</i>	34654
56	NZ_JEYG01000001.1	<i>Acinetobacter baumannii</i>	42887
57	NZ_JEXW01000001.1	<i>Acinetobacter baumannii</i>	43926
58	NZ_AOSP01000001.1	<i>Acinetobacter baumannii</i>	48055
59	NZ_JEXP01000001.1	<i>Acinetobacter baumannii</i>	50595
60	NZ_ALPW01000001.1	<i>Acinetobacter baumannii</i>	53264
61	NZ_JEZV01000001.1	<i>Acinetobacter baumannii</i>	58452
62	NZ_JFYK01000001.1	<i>Acinetobacter baumannii</i>	70136
63	NZ_JFFE01000001.1	<i>Acinetobacter baumannii</i>	73736
64	NZ_JEYC01000001.1	<i>Acinetobacter baumannii</i>	83444
65	NZ_JMKN01000001.1	<i>Acinetobacter baumannii</i>	96512
66	NZ_JFYJ01000001.1	<i>Acinetobacter baumannii</i>	98826
67	NZ_JEXJ01000001.1	<i>Acinetobacter baumannii</i>	99063
68	NZ_JEVZ02000001.1	<i>Acinetobacter baumannii</i>	110912
69	NZ_JEWB01000001.1	<i>Acinetobacter baumannii</i>	118362
70	NZ_JFDB01000001.1	<i>Acinetobacter baumannii</i>	121738
71	NZ_JEZH01000001.1	<i>Acinetobacter baumannii</i>	136706
72	NZ_JEYE01000001.1	<i>Acinetobacter baumannii</i>	144107
73	NZ_JFXU01000001.1	<i>Acinetobacter baumannii</i>	145660
74	NZ_JEWS01000001.1	<i>Acinetobacter baumannii</i>	146457
75	NZ_JFYE01000001.1	<i>Acinetobacter baumannii</i>	213697
76	NZ_JFXR01000001.1	<i>Acinetobacter baumannii</i>	214216
77	NZ_JEYI01000001.1	<i>Acinetobacter baumannii</i>	232184
78	NZ_JMOG01000001.1	<i>Acinetobacter baumannii</i>	233846
79	NZ_JEYN01000001.1	<i>Acinetobacter baumannii</i>	268680

	NCBI Reference Sequence ID#	Strain	
80	NZ_JFEO1000001.1	<i>Acinetobacter baumannii</i>	273929
81	NZ_JFXS01000001.1	<i>Acinetobacter baumannii</i>	277047
82	NZ_JEWY01000001.1	<i>Acinetobacter baumannii</i>	299505
83	NZ_JFXW01000001.1	<i>Acinetobacter baumannii</i>	303002
84	NZ_JFEQ01000001.1	<i>Acinetobacter baumannii</i>	318814
85	NZ_JFCZ01000001.1	<i>Acinetobacter baumannii</i>	323408
86	NZ_JFXO01000001.1	<i>Acinetobacter baumannii</i>	339786
87	NZ_JEWZ01000001.1	<i>Acinetobacter baumannii</i>	342950
88	NZ_JEVW01000001.1	<i>Acinetobacter baumannii</i>	348935
89	NZ_JEYD01000001.1	<i>Acinetobacter baumannii</i>	397971
90	NZ_JEXA01000001.1	<i>Acinetobacter baumannii</i>	400834
91	NZ_JFYF01000001.1	<i>Acinetobacter baumannii</i>	426863
92	NZ_JFET01000001.1	<i>Acinetobacter baumannii</i>	457946
93	NZ_JFCY01000001.1	<i>Acinetobacter baumannii</i>	458282
94	NZ_JFXP01000001.1	<i>Acinetobacter baumannii</i>	466215
95	NZ_JEXB01000001.1	<i>Acinetobacter baumannii</i>	466760
96	NZ_JFCX01000001.1	<i>Acinetobacter baumannii</i>	470922
97	NZ_JFEU01000001.1	<i>Acinetobacter baumannii</i>	480175
98	NZ_JMNR01000001.1	<i>Acinetobacter baumannii</i>	496487
99	NZ_JEYH01000001.1	<i>Acinetobacter baumannii</i>	532279
100	NZ_JEZO01000001.1	<i>Acinetobacter baumannii</i>	532413
101	NZ_JFXQ01000001.1	<i>Acinetobacter baumannii</i>	541915
102	NZ_JEXT01000001.1	<i>Acinetobacter baumannii</i>	554515
103	NZ_JEZO01000001.1	<i>Acinetobacter baumannii</i>	562700
104	NZ_JEZQ01000001.1	<i>Acinetobacter baumannii</i>	564012
105	NZ_JFYA01000001.1	<i>Acinetobacter baumannii</i>	573719
106	NZ_JFES01000001.1	<i>Acinetobacter baumannii</i>	607805

	NCBI Reference Sequence ID#	Strain	
107	NZ_JEXD01000001.1	<i>Acinetobacter baumannii</i>	625974
108	NZ_JFXX01000001.1	<i>Acinetobacter baumannii</i>	628418
109	NZ_JEXE01000001.1	<i>Acinetobacter baumannii</i>	647609
110	NZ_JEZU01000001.1	<i>Acinetobacter baumannii</i>	653020
111	NZ_JFCE02000001.1	<i>Acinetobacter baumannii</i>	655378
112	NZ_JFEW01000001.1	<i>Acinetobacter baumannii</i>	655555
113	NZ_JFCV01000001.1	<i>Acinetobacter baumannii</i>	722310
114	NZ_JEXF01000001.1	<i>Acinetobacter baumannii</i>	724909
115	NZ_JFYB01000001.1	<i>Acinetobacter baumannii</i>	730795
116	NZ_JFEY01000001.1	<i>Acinetobacter baumannii</i>	737393
117	NZ_JZBZ01000006.1	<i>Acinetobacter baumannii</i>	741019
118	NZ_JMNU01000001.1	<i>Acinetobacter baumannii</i>	754286
119	NZ_JFXY01000001.1	<i>Acinetobacter baumannii</i>	755829
120	NZ_JMOR01000001.1	<i>Acinetobacter baumannii</i>	756476
121	NZ_JEZO01000001.1	<i>Acinetobacter baumannii</i>	781407
122	NZ_JFEZ01000001.1	<i>Acinetobacter baumannii</i>	825610
123	NZ_JEYO01000001.1	<i>Acinetobacter baumannii</i>	831240
124	NZ_JFFA01000001.1	<i>Acinetobacter baumannii</i>	836190
125	NZ_JFFD01000001.1	<i>Acinetobacter baumannii</i>	846928
126	NZ_JMNT01000001.1	<i>Acinetobacter baumannii</i>	855125
127	NZ_JMNI01000001.1	<i>Acinetobacter baumannii</i>	916567
128	NZ_JFFB01000001.1	<i>Acinetobacter baumannii</i>	923118
129	NZ_JMNV01000001.1	<i>Acinetobacter baumannii</i>	940793
130	NZ_JEZX01000001.1	<i>Acinetobacter baumannii</i>	942133
131	NZ_JFAC01000001.1	<i>Acinetobacter baumannii</i>	942194
132	NZ_JEZY01000001.1	<i>Acinetobacter baumannii</i>	947299
133	NZ_JEXI01000001.1	<i>Acinetobacter baumannii</i>	951631

	NCBI Reference Sequence ID#	Strain	
134	NZ_JEZZ01000001.1	<i>Acinetobacter baumannii</i>	959073
135	NZ_JFAA01000001.1	<i>Acinetobacter baumannii</i>	972082
136	NZ_JFYH01000001.1	<i>Acinetobacter baumannii</i>	981176
137	NZ_JEVX01000001.1	<i>Acinetobacter baumannii</i>	984213
138	NZ_JMNL01000001.1	<i>Acinetobacter baumannii</i>	987421
139	NZ_JFAB01000001.1	<i>Acinetobacter baumannii</i>	993520
140	NZ_JFWQ01000001.1	<i>Acinetobacter baumannii</i>	1007214
141	NZ_JFDQ01000001.1	<i>Acinetobacter baumannii</i>	1022959
142	NZ_JEYR01000001.1	<i>Acinetobacter baumannii</i>	1031433
143	NZ_JEYS01000001.1	<i>Acinetobacter baumannii</i>	1032241
144	NZ_JEYV01000001.1	<i>Acinetobacter baumannii</i>	1035119
145	NZ_JEYT01000001.1	<i>Acinetobacter baumannii</i>	1036938
146	NZ_JEYU02000001.1	<i>Acinetobacter baumannii</i>	1039621
147	NZ_JEYV01000001.1	<i>Acinetobacter baumannii</i>	1040094
148	NZ_JEYX01000001.1	<i>Acinetobacter baumannii</i>	1043794
149	NZ_JEYY01000001.1	<i>Acinetobacter baumannii</i>	1043903
150	NZ_JJFC01000001.1	<i>Acinetobacter baumannii</i>	1045092
151	NZ_JEYZ01000001.1	<i>Acinetobacter baumannii</i>	1046051
152	NZ_JEZA01000001.1	<i>Acinetobacter baumannii</i>	1046674
153	NZ_JEZO01000001.1	<i>Acinetobacter baumannii</i>	1051176
154	NZ_JEZA01000001.1	<i>Acinetobacter baumannii</i>	1051830
155	NZ_JFWR01000001.1	<i>Acinetobacter baumannii</i>	1058283
156	NZ_JFDR01000001.1	<i>Acinetobacter baumannii</i>	1062314
157	NZ_JEZO01000001.1	<i>Acinetobacter baumannii</i>	1075025
158	NZ_JFDT01000001.1	<i>Acinetobacter baumannii</i>	1095464
159	NZ_JEXM01000001.1	<i>Acinetobacter baumannii</i>	1096934
160	NZ_JEXN01000001.1	<i>Acinetobacter baumannii</i>	1106579

	NCBI Reference Sequence ID#	Strain	
161	NZ_JFWW01000001.1	<i>Acinetobacter baumannii</i>	1117819
162	NZ_JEZE02000001.1	<i>Acinetobacter baumannii</i>	1121032
163	NZ_JMNS01000001.1	<i>Acinetobacter baumannii</i>	1146103
164	NZ_JEWA01000001.1	<i>Acinetobacter baumannii</i>	1159076
165	NZ_JFWT01000001.1	<i>Acinetobacter baumannii</i>	1170863
166	NZ_JFDU01000001.1	<i>Acinetobacter baumannii</i>	1178044
167	NZ_JFDV01000001.1	<i>Acinetobacter baumannii</i>	1188188
168	NZ_JEWC01000001.1	<i>Acinetobacter baumannii</i>	1202252
169	NZ_JFEC01000001.1	<i>Acinetobacter baumannii</i>	1207552
170	NZ_JFWY01000001.1	<i>Acinetobacter baumannii</i>	1232509
171	NZ_JFWU01000001.1	<i>Acinetobacter baumannii</i>	1237202
172	NZ_JFEA01000001.1	<i>Acinetobacter baumannii</i>	1237893
173	NZ_JEF01000001.1	<i>Acinetobacter baumannii</i>	1247182
174	NZ_JFED01000001.1	<i>Acinetobacter baumannii</i>	1264936
175	NZ_JFXA01000001.1	<i>Acinetobacter baumannii</i>	1266220
176	NZ_JEWD01000001.1	<i>Acinetobacter baumannii</i>	1267820
177	NZ_JFDX01000001.1	<i>Acinetobacter baumannii</i>	1271213
178	NZ_JFDZ01000001.1	<i>Acinetobacter baumannii</i>	1271651
179	NZ_JEXL01000001.1	<i>Acinetobacter baumannii</i>	1277411
180	NZ_JMOB01000001.1	<i>Acinetobacter baumannii</i>	1284800
181	NZ_JFFG01000001.1	<i>Acinetobacter baumannii</i>	1287985
182	NZ_JEZG01000001.1	<i>Acinetobacter baumannii</i>	1289546
183	NZ_JEXK01000001.1	<i>Acinetobacter baumannii</i>	1291820
184	NZ_JFEE01000001.1	<i>Acinetobacter baumannii</i>	1293320
185	NZ_JEWF01000001.1	<i>Acinetobacter baumannii</i>	1294217
186	NZ_JFXF01000001.1	<i>Acinetobacter baumannii</i>	1294222
187	NZ_JFXB01000001.1	<i>Acinetobacter baumannii</i>	1295549

	NCBI Reference Sequence ID#	Strain	
188	NZ_JEWH01000001.1	<i>Acinetobacter baumannii</i>	1295743
189	NZ_JFFU01000001.1	<i>Acinetobacter baumannii</i>	1296252
190	NZ_JEVV01000001.1	<i>Acinetobacter baumannii</i>	1297549
191	NZ_JFXH01000001.1	<i>Acinetobacter baumannii</i>	1391434
192	NZ_JFXJ01000001.1	<i>Acinetobacter baumannii</i>	1392509
193	NZ_JEWJ01000001.1	<i>Acinetobacter baumannii</i>	1397084
194	NZ_JFXI01000001.1	<i>Acinetobacter baumannii</i>	1397513
195	NZ_JFKK01000001.1	<i>Acinetobacter baumannii</i>	1406182
196	NZ_JFYI01000001.1	<i>Acinetobacter baumannii</i>	1406589
197	NZ_JEWK01000001.1	<i>Acinetobacter baumannii</i>	1406750
198	NZ_JFEF01000001.1	<i>Acinetobacter baumannii</i>	1412924
199	NZ_JFWZ01000001.1	<i>Acinetobacter baumannii</i>	1413735
200	NZ_JEYP01000001.1	<i>Acinetobacter baumannii</i>	1417041
201	NZ_JEWL01000001.1	<i>Acinetobacter baumannii</i>	1419130
202	NZ_JFCU01000001.1	<i>Acinetobacter baumannii</i>	1426993
203	NZ_JFXM02000001.1	<i>Acinetobacter baumannii</i>	1428368
204	NZ_JEWM01000001.1	<i>Acinetobacter baumannii</i>	1429530
205	NZ_JEWN01000001.1	<i>Acinetobacter baumannii</i>	1437282
206	NZ_JEWO01000001.1	<i>Acinetobacter baumannii</i>	1440422
207	NZ_JEXQ01000001.1	<i>Acinetobacter baumannii</i>	1440750
208	NZ_JMNQ01000001.1	<i>Acinetobacter baumannii</i>	1451147
209	NZ_JEWQ01000001.1	<i>Acinetobacter baumannii</i>	1461963
210	NZ_JEWR01000001.1	<i>Acinetobacter baumannii</i>	1462234
211	NZ_JEWT01000001.1	<i>Acinetobacter baumannii</i>	1465485
212	NZ_JFEH01000001.1	<i>Acinetobacter baumannii</i>	1471012
213	NZ_JFEJ01000001.1	<i>Acinetobacter baumannii</i>	1475764
214	NZ_JFEK01000001.1	<i>Acinetobacter baumannii</i>	1482820

	NCBI Reference Sequence ID#	Strain	
215	NZ_JFCT01000001.1	<i>Acinetobacter baumannii</i>	1488685
216	NZ_JFXT01000001.1	<i>Acinetobacter baumannii</i>	1494580
217	NZ_JMOA01000001.1	<i>Acinetobacter baumannii</i>	1499986
218	NZ_JMOL01000001.1	<i>Acinetobacter baumannii</i>	1505311
219	NZ_JEXR01000001.1	<i>Acinetobacter baumannii</i>	1525283
220	NZ_JEXV01000001.1	<i>Acinetobacter baumannii</i>	1526966
221	NZ_JFEI01000001.1	<i>Acinetobacter baumannii</i>	1533268
222	NZ_JMNH01000001.1	<i>Acinetobacter baumannii</i>	1539026
223	NZ_JEXU01000001.1	<i>Acinetobacter baumannii</i>	1546444
224	NZ_JFCS01000001.1	<i>Acinetobacter baumannii</i>	1552389
225	NZ_JFCD01000001.1	<i>Acinetobacter baumannii</i>	1552818
226	NZ_JEXY01000001.1	<i>Acinetobacter baumannii</i>	1552865
227	NZ_JMOM01000001.1	<i>Acinetobacter baumannii</i>	1571545
228	NZ_JEYM01000001.1	<i>Acinetobacter baumannii</i>	1575710
229	NZ_JEYL01000001.1	<i>Acinetobacter baumannii</i>	1593273
230	NZ_JMOE01000001.1	<i>Acinetobacter baumannii</i>	1598530
231	NZ_NDXK01000055.1	<i>Acinetobacter baumannii</i>	2012046
232	NZ_GL891496.1	<i>Acinetobacter baumannii</i>	6013113
233	NZ_GL891614.1	<i>Acinetobacter baumannii</i>	6013150
234	NZ_GL891816.1	<i>Acinetobacter baumannii</i>	6014059
235	NZ_FBWX01000001.1	<i>Acinetobacter baumannii</i>	6772166
236	NZ_JRWO01000006.1	<i>Acinetobacter baumannii</i>	6870155
237	NZ_JWGN01000026.1	<i>Acinetobacter baumannii</i>	1008_ABAU
238	NZ_JWFF01000001.1	<i>Acinetobacter baumannii</i>	1038_ABAU
239	NZ_JWFE01000001.1	<i>Acinetobacter baumannii</i>	1039_ABAU
240	NZ_FUEM01000146.1	<i>Acinetobacter baumannii</i>	103SM
241	NZ_JMOH01000001.1	<i>Acinetobacter baumannii</i>	1042969-1197

	NCBI Reference Sequence ID#	Strain
242	NZ_JEYW01000001.1	<i>Acinetobacter baumannii</i> 1042969-1265
243	NZ_LGYW01000001.1	<i>Acinetobacter baumannii</i> 10441_14
244	NZ_JWEQ01000037.1	<i>Acinetobacter baumannii</i> 1054_ABAU
245	NZ_JFDS01000001.1	<i>Acinetobacter baumannii</i> 1064293_45
246	NZ_JMHL01000001.1	<i>Acinetobacter baumannii</i> 1064293_46
247	NZ_CBSG010000001.1	<i>Acinetobacter baumannii</i> 107m
248	NZ_JWBD01000010.1	<i>Acinetobacter baumannii</i> 1153_ABAU
249	NZ_JWAN01000030.1	<i>Acinetobacter baumannii</i> 1168_ABAU
250	NZ_JFEB02000001.1	<i>Acinetobacter baumannii</i> 1195185_11
251	NZ_JMOI01000001.1	<i>Acinetobacter baumannii</i> 1195185_80
252	NZ_JMOJ01000001.1	<i>Acinetobacter baumannii</i> 1262761-105
253	NZ_JFWV01000001.1	<i>Acinetobacter baumannii</i> 1262761-97
254	NZ_JMOK01000001.1	<i>Acinetobacter baumannii</i> 1276470-132
255	NZ_JFXE01000001.1	<i>Acinetobacter baumannii</i> 1276470-86
256	NZ_NIWJ01000010.1	<i>Acinetobacter baumannii</i> 151/1C
257	NZ_CP020590.1	<i>Acinetobacter baumannii</i> 15A34
258	NZ_CP020574.1	<i>Acinetobacter baumannii</i> 15A5
259	NZ_JZCA01000008.1	<i>Acinetobacter baumannii</i> 161/07
260	NZ_JHPM01000001.1	<i>Acinetobacter baumannii</i> 16553_1
261	NZ_JHPF01000001.1	<i>Acinetobacter baumannii</i> 16553_10
262	NZ_JHPL01000001.1	<i>Acinetobacter baumannii</i> 16553_2
263	NZ_JHPK01000001.1	<i>Acinetobacter baumannii</i> 16553_3
264	NZ_JHPJ01000001.1	<i>Acinetobacter baumannii</i> 16553_4
265	NZ_JHPI01000001.1	<i>Acinetobacter baumannii</i> 16553_6
266	NZ_JHPH01000001.1	<i>Acinetobacter baumannii</i> 16553_8
267	NZ_JHPG01000001.1	<i>Acinetobacter baumannii</i> 16553_9
268	NC_017162.1	<i>Acinetobacter baumannii</i> 1656-2

	NCBI Reference Sequence ID#	Strain
269	NZ_MABY01000001.1	<i>Acinetobacter baumannii</i> 192/2C
270	NZ_JSDB01000001.1	<i>Acinetobacter baumannii</i> 1999BJAB11
271	NZ_JSCK01000001.1	<i>Acinetobacter baumannii</i> 2003BJAB12
272	NZ_JSCJ01000001.1	<i>Acinetobacter baumannii</i> 2004BJAB10
273	NZ_JSCL01000001.1	<i>Acinetobacter baumannii</i> 2004BJAB13
274	NZ_JSCM01000001.1	<i>Acinetobacter baumannii</i> 2004BJAB14
275	NZ_KN708298.1	<i>Acinetobacter baumannii</i> 2004ZJAB5
276	NZ_JSCX01000001.1	<i>Acinetobacter baumannii</i> 2004ZJAB6
277	NZ_JSCO01000001.1	<i>Acinetobacter baumannii</i> 2005JSAB1
278	NZ_KN708285.1	<i>Acinetobacter baumannii</i> 2005LNAB4
279	NZ_KN708622.1	<i>Acinetobacter baumannii</i> 2011BJAB1
280	NZ_JRHW01000001.1	<i>Acinetobacter baumannii</i> 2011BJAB2
281	NZ_JSCG01000001.1	<i>Acinetobacter baumannii</i> 2011BJAB3
282	NZ_JSCH01000001.1	<i>Acinetobacter baumannii</i> 2011BJAB4
283	NZ_JSCY01000001.1	<i>Acinetobacter baumannii</i> 2011BJAB5
284	NZ_JSDM01000001.1	<i>Acinetobacter baumannii</i> 2011BJAB6
285	NZ_JSCI01000001.1	<i>Acinetobacter baumannii</i> 2011BJAB7
286	NZ_JSCZ01000001.1	<i>Acinetobacter baumannii</i> 2011BJAB8
287	NZ_JSDA01000001.1	<i>Acinetobacter baumannii</i> 2011BJAB9
288	NZ_JSDC01000001.1	<i>Acinetobacter baumannii</i> 2011GDAB1
289	NZ_JSDD01000001.1	<i>Acinetobacter baumannii</i> 2011GDAB2
290	NZ_JSCN01000001.1	<i>Acinetobacter baumannii</i> 2011GDAB3
291	NZ_JSDE01000001.1	<i>Acinetobacter baumannii</i> 2011GDAB4
292	NZ_JSDF01000001.1	<i>Acinetobacter baumannii</i> 2011HNAB1
293	NZ_JSCT01000001.1	<i>Acinetobacter baumannii</i> 2011LNAB1
294	NZ_KN708450.1	<i>Acinetobacter baumannii</i> 2011LNAB2
295	NZ_JSDI01000001.1	<i>Acinetobacter baumannii</i> 2011LNAB3

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296	NZ_KN708155.1	<i>Acinetobacter baumannii</i> 2011SDAB1
297	NZ_KN708186.1	<i>Acinetobacter baumannii</i> 2011SDAB2
298	NZ_JSCS01000001.1	<i>Acinetobacter baumannii</i> 2011SDAB3
299	NZ_JSCP01000001.1	<i>Acinetobacter baumannii</i> 2011SHAB1
300	NZ_JSDG01000001.1	<i>Acinetobacter baumannii</i> 2011TJAB1
301	NZ_JSCV01000001.1	<i>Acinetobacter baumannii</i> 2011ZJAB1
302	NZ_JSDJ01000001.1	<i>Acinetobacter baumannii</i> 2011ZJAB2
303	NZ_JSDK01000001.1	<i>Acinetobacter baumannii</i> 2011ZJAB3
304	NZ_JSDL01000001.1	<i>Acinetobacter baumannii</i> 2011ZJAB4
305	NZ_LQCM01000033.1	<i>Acinetobacter baumannii</i> 2015ZJAB1
306	NZ_LQCN01000033.1	<i>Acinetobacter baumannii</i> 2015ZJAB2
307	NZ_LQCO01000023.1	<i>Acinetobacter baumannii</i> 2015ZJAB3
308	NZ_LQCP01000031.1	<i>Acinetobacter baumannii</i> 2015ZJAB4
309	NZ_LQCQ01000032.1	<i>Acinetobacter baumannii</i> 2015ZJAB7
310	NZ_LQCR01000038.1	<i>Acinetobacter baumannii</i> 2015ZJAB8
311	NZ_FUEQ01000240.1	20C15
312	NZ_JVFN01000009.1	219_ABAU
313	NZ_JFDJ01000001.1	24812_10
314	NZ_JMNN01000001.1	24812_2
315	NZ_JFDI01000001.1	24812_4
316	NZ_JFDH01000001.1	24812_6
317	NZ_JMOU01000001.1	24812_7
318	NZ_JMON01000001.1	24812_8
319	NZ_JFWM01000001.1	24845_1
320	NZ_JFWN01000001.1	24845_10
321	NZ_JFWL01000001.1	24845_3
322	NZ_JFWK01000001.1	24845_4

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323	NZ_JFWJ01000001.1	<i>Acinetobacter baumannii</i>	24845_5
324	NZ_JFWI01000001.1	<i>Acinetobacter baumannii</i>	24845_6
325	NZ_JFWH01000001.1	<i>Acinetobacter baumannii</i>	24845_7
326	NZ_JFWG01000001.1	<i>Acinetobacter baumannii</i>	24845_8
327	NZ_JFWF01000001.1	<i>Acinetobacter baumannii</i>	24845_9
328	NZ_JIDG01000001.1	<i>Acinetobacter baumannii</i>	24860_1
329	NZ_JFDG01000001.1	<i>Acinetobacter baumannii</i>	24860_10
330	NZ_JFDF01000001.1	<i>Acinetobacter baumannii</i>	24860_2
331	NZ_JMOO01000001.1	<i>Acinetobacter baumannii</i>	24860_3
332	NZ_JFDE01000001.1	<i>Acinetobacter baumannii</i>	24860_4
333	NZ_JMOP01000001.1	<i>Acinetobacter baumannii</i>	24860_5
334	NZ_JIDF01000001.1	<i>Acinetobacter baumannii</i>	24860_6
335	NZ_JFDD01000001.1	<i>Acinetobacter baumannii</i>	24860_7
336	NZ_JFDC01000001.1	<i>Acinetobacter baumannii</i>	24860_8
337	NZ_JMOQ01000001.1	<i>Acinetobacter baumannii</i>	24860_9
338	NZ_JGAI01000001.1	<i>Acinetobacter baumannii</i>	24975_1
339	NZ_JIDE01000001.1	<i>Acinetobacter baumannii</i>	24975_10
340	NZ_JGAH01000001.1	<i>Acinetobacter baumannii</i>	24975_4
341	NZ_JGAG01000001.1	<i>Acinetobacter baumannii</i>	24975_5
342	NZ_JGAF01000001.1	<i>Acinetobacter baumannii</i>	24975_7
343	NZ_JGAE01000001.1	<i>Acinetobacter baumannii</i>	24975_9
344	NZ_JFWD01000001.1	<i>Acinetobacter baumannii</i>	25253_1
345	NZ_JFWE01000001.1	<i>Acinetobacter baumannii</i>	25253_10
346	NZ_JFWC01000001.1	<i>Acinetobacter baumannii</i>	25253_3
347	NZ_JFWB01000001.1	<i>Acinetobacter baumannii</i>	25253_4
348	NZ_JFWA01000001.1	<i>Acinetobacter baumannii</i>	25253_5
349	NZ_JFVZ01000001.1	<i>Acinetobacter baumannii</i>	25253_6

	NCBI Reference Sequence ID#	Strain	
350	NZ_JFVY01000001.1	<i>Acinetobacter baumannii</i>	25253_7
351	NZ_JFVX01000001.1	<i>Acinetobacter baumannii</i>	25253_8
352	NZ_JFWO01000001.1	<i>Acinetobacter baumannii</i>	25307_1
353	NZ_JFVW01000001.1	<i>Acinetobacter baumannii</i>	25307_2
354	NZ_JFVV01000001.1	<i>Acinetobacter baumannii</i>	25307_3
355	NZ_JFVU01000001.1	<i>Acinetobacter baumannii</i>	25307_4
356	NZ_JFVT01000001.1	<i>Acinetobacter baumannii</i>	25307_5
357	NZ_JFVS01000001.1	<i>Acinetobacter baumannii</i>	25307_6
358	NZ_JFVR01000001.1	<i>Acinetobacter baumannii</i>	25307_8
359	NZ_JMHI01000001.1	<i>Acinetobacter baumannii</i>	25442_1
360	NZ_JICS01000001.1	<i>Acinetobacter baumannii</i>	25442_5
361	NZ_JICR01000001.1	<i>Acinetobacter baumannii</i>	25442_7
362	NZ_JICQ01000001.1	<i>Acinetobacter baumannii</i>	25442_9
363	NZ_JHDD01000001.1	<i>Acinetobacter baumannii</i>	25493_1
364	NZ_JHDE01000001.1	<i>Acinetobacter baumannii</i>	25493_10
365	NZ_JHDC01000001.1	<i>Acinetobacter baumannii</i>	25493_2
366	NZ_JHDB01000001.1	<i>Acinetobacter baumannii</i>	25493_3
367	NZ_JHDA01000001.1	<i>Acinetobacter baumannii</i>	25493_4
368	NZ_JHCZ01000001.1	<i>Acinetobacter baumannii</i>	25493_5
369	NZ_JHCY01000001.1	<i>Acinetobacter baumannii</i>	25493_6
370	NZ_JHCX01000001.1	<i>Acinetobacter baumannii</i>	25493_8
371	NZ_JHCW01000001.1	<i>Acinetobacter baumannii</i>	25493_9
372	NZ_JGAD01000001.1	<i>Acinetobacter baumannii</i>	25561_1
373	NZ_JGBG01000001.1	<i>Acinetobacter baumannii</i>	25561_10
374	NZ_JGAC01000001.1	<i>Acinetobacter baumannii</i>	25561_2
375	NZ_JGAB01000001.1	<i>Acinetobacter baumannii</i>	25561_7
376	NZ_JHPE01000001.1	<i>Acinetobacter baumannii</i>	25569_1

	NCBI Reference Sequence ID#	Strain
377	NZ_JMNO01000001.1	<i>Acinetobacter baumannii</i> 25569_10
378	NZ_JHPD01000001.1	<i>Acinetobacter baumannii</i> 25569_2
379	NZ_JHOW01000001.1	<i>Acinetobacter baumannii</i> 25569_3
380	NZ_JHPC01000001.1	<i>Acinetobacter baumannii</i> 25569_4
381	NZ_JHOR01000001.1	<i>Acinetobacter baumannii</i> 25569_5
382	NZ_JHOT01000001.1	<i>Acinetobacter baumannii</i> 25569_6
383	NZ_JHOV01000001.1	<i>Acinetobacter baumannii</i> 25569_7
384	NZ_JICU01000001.1	<i>Acinetobacter baumannii</i> 25569_8
385	NZ_JICT01000001.1	<i>Acinetobacter baumannii</i> 25569_9
386	NZ_JGCI01000001.1	<i>Acinetobacter baumannii</i> 25681_2
387	NZ_JGCH01000001.1	<i>Acinetobacter baumannii</i> 25681_3
388	NZ_JGCG01000001.1	<i>Acinetobacter baumannii</i> 25681_5
389	NZ_JGCF01000001.1	<i>Acinetobacter baumannii</i> 25681_6
390	NZ_JGCE01000001.1	<i>Acinetobacter baumannii</i> 25681_8
391	NZ_JGCD01000001.1	<i>Acinetobacter baumannii</i> 25681_9
392	NZ_JGAW01000001.1	<i>Acinetobacter baumannii</i> 25691_1
393	NZ_JGAS01000001.1	<i>Acinetobacter baumannii</i> 25691_10
394	NZ_JGAV01000001.1	<i>Acinetobacter baumannii</i> 25691_2
395	NZ_JMOV01000001.1	<i>Acinetobacter baumannii</i> 25691_5
396	NZ_JGAU01000001.1	<i>Acinetobacter baumannii</i> 25691_6
397	NZ_JMPH01000001.1	<i>Acinetobacter baumannii</i> 25691_7
398	NZ_JMOW01000001.1	<i>Acinetobacter baumannii</i> 25691_8
399	NZ_JGAT01000001.1	<i>Acinetobacter baumannii</i> 25691_9
400	NZ_JMOX01000001.1	<i>Acinetobacter baumannii</i> 25750_1
401	NZ_JGCC01000001.1	<i>Acinetobacter baumannii</i> 25750_6
402	NZ_JGCB01000001.1	<i>Acinetobacter baumannii</i> 25750_7
403	NZ_JGCA01000001.1	<i>Acinetobacter baumannii</i> 25750_8

	NCBI Reference Sequence ID#	Strain	
404	NZ_JGBF01000001.1	<i>Acinetobacter baumannii</i>	25766_1
405	NZ_JGAX01000001.1	<i>Acinetobacter baumannii</i>	25766_10
406	NZ_JGBE01000001.1	<i>Acinetobacter baumannii</i>	25766_2
407	NZ_JGBD01000001.1	<i>Acinetobacter baumannii</i>	25766_3
408	NZ_JGBC01000001.1	<i>Acinetobacter baumannii</i>	25766_4
409	NZ_JGBB01000001.1	<i>Acinetobacter baumannii</i>	25766_5
410	NZ_JGBA01000001.1	<i>Acinetobacter baumannii</i>	25766_6
411	NZ_JGAZ01000001.1	<i>Acinetobacter baumannii</i>	25766_7
412	NZ_JGAY01000001.1	<i>Acinetobacter baumannii</i>	25766_9
413	NZ_JHCV01000001.1	<i>Acinetobacter baumannii</i>	25878_1
414	NZ_JHCU01000001.1	<i>Acinetobacter baumannii</i>	25878_2
415	NZ_JHCT01000001.1	<i>Acinetobacter baumannii</i>	25878_3
416	NZ_JGAR01000001.1	<i>Acinetobacter baumannii</i>	25935_1
417	NZ_JGAJ01000001.1	<i>Acinetobacter baumannii</i>	25935_10
418	NZ_JGAQ01000001.1	<i>Acinetobacter baumannii</i>	25935_2
419	NZ_JGAP01000001.1	<i>Acinetobacter baumannii</i>	25935_4
420	NZ_JGAA01000001.1	<i>Acinetobacter baumannii</i>	25935_5
421	NZ_JGAN01000001.1	<i>Acinetobacter baumannii</i>	25935_6
422	NZ_JGAM01000001.1	<i>Acinetobacter baumannii</i>	25935_7
423	NZ_JGAL01000001.1	<i>Acinetobacter baumannii</i>	25935_8
424	NZ_JGAK01000001.1	<i>Acinetobacter baumannii</i>	25935_9
425	NZ_JMPF01000001.1	<i>Acinetobacter baumannii</i>	25977_9
426	NZ_FUER01000153.1	<i>Acinetobacter baumannii</i>	25C30
427	NZ_JHOY01000001.1	<i>Acinetobacter baumannii</i>	26016_1
428	NZ_JHOU01000001.1	<i>Acinetobacter baumannii</i>	26016_10
429	NZ_JMOY01000001.1	<i>Acinetobacter baumannii</i>	26016_2
430	NZ_JMOZ01000001.1	<i>Acinetobacter baumannii</i>	26016_3

	NCBI Reference Sequence ID#	Strain	
431	NZ_JHPB01000001.1	<i>Acinetobacter baumannii</i>	26016_4
432	NZ_JHOS01000001.1	<i>Acinetobacter baumannii</i>	26016_5
433	NZ_JHOX01000001.1	<i>Acinetobacter baumannii</i>	26016_6
434	NZ_JMPA01000001.1	<i>Acinetobacter baumannii</i>	26016_7
435	NZ_JHOO01000001.1	<i>Acinetobacter baumannii</i>	26016_8
436	NZ_JIDC01000001.1	<i>Acinetobacter baumannii</i>	26016_9
437	NZ_MACB01000001.1	<i>Acinetobacter baumannii</i>	280/1C
438	NZ_MABW01000001.1	<i>Acinetobacter baumannii</i>	29D2
439	NZ_NIWK01000010.1	<i>Acinetobacter baumannii</i>	29R1
440	NZ_FUEX01000121.1	<i>Acinetobacter baumannii</i>	2MG
441	NZ_FUEU01000116.1	<i>Acinetobacter baumannii</i>	2RED09
442	NZ_MABZ01000001.1	<i>Acinetobacter baumannii</i>	3.5D
443	NZ_MABX01000001.1	<i>Acinetobacter baumannii</i>	31D1
444	NZ_JICP01000001.1	<i>Acinetobacter baumannii</i>	42057_2
445	NZ_JMPB01000001.1	<i>Acinetobacter baumannii</i>	42057_3
446	NZ_JMHJ01000001.1	<i>Acinetobacter baumannii</i>	42057_4
447	NZ_JMPC01000001.1	<i>Acinetobacter baumannii</i>	42057_5
448	NZ_JICO01000001.1	<i>Acinetobacter baumannii</i>	42057_6
449	NZ_MACC01000001.1	<i>Acinetobacter baumannii</i>	42R3
450	NZ_JHCS01000001.1	<i>Acinetobacter baumannii</i>	43557_1
451	NZ_JIDB01000001.1	<i>Acinetobacter baumannii</i>	44298_1
452	NZ_JICV01000001.1	<i>Acinetobacter baumannii</i>	44298_10
453	NZ_JIDA01000001.1	<i>Acinetobacter baumannii</i>	44298_2
454	NZ_JMHA01000001.1	<i>Acinetobacter baumannii</i>	44298_3
455	NZ_JICZ01000001.1	<i>Acinetobacter baumannii</i>	44298_4
456	NZ_JMHB01000001.1	<i>Acinetobacter baumannii</i>	44298_5
457	NZ_JICY01000001.1	<i>Acinetobacter baumannii</i>	44298_6

	NCBI Reference Sequence ID#	Strain	
458	NZ_JICX01000001.1	<i>Acinetobacter baumannii</i>	44298_7
459	NZ_JMHC01000001.1	<i>Acinetobacter baumannii</i>	44298_8
460	NZ_JICW01000001.1	<i>Acinetobacter baumannii</i>	44298_9
461	NZ_JGBZ01000001.1	<i>Acinetobacter baumannii</i>	44327_1
462	NZ_JGBY01000001.1	<i>Acinetobacter baumannii</i>	44327_2
463	NZ_JGBX01000001.1	<i>Acinetobacter baumannii</i>	44327_4
464	NZ_JGBW01000001.1	<i>Acinetobacter baumannii</i>	44327_5
465	NZ_JGBH01000001.1	<i>Acinetobacter baumannii</i>	44327_6
466	NZ_JGBV01000001.1	<i>Acinetobacter baumannii</i>	44327_7
467	NZ_JGBU01000001.1	<i>Acinetobacter baumannii</i>	44327_8
468	NZ_JHCQ01000001.1	<i>Acinetobacter baumannii</i>	44362_1
469	NZ_JHCR01000001.1	<i>Acinetobacter baumannii</i>	44362_10
470	NZ_JHCP01000001.1	<i>Acinetobacter baumannii</i>	44362_2
471	NZ_JHCO01000001.1	<i>Acinetobacter baumannii</i>	44362_3
472	NZ_JHCN01000001.1	<i>Acinetobacter baumannii</i>	44362_4
473	NZ_JHCM01000001.1	<i>Acinetobacter baumannii</i>	44362_5
474	NZ_JHCL01000001.1	<i>Acinetobacter baumannii</i>	44362_6
475	NZ_JHCK01000001.1	<i>Acinetobacter baumannii</i>	44362_7
476	NZ_JHCJ01000001.1	<i>Acinetobacter baumannii</i>	44362_8
477	NZ_JHCI01000001.1	<i>Acinetobacter baumannii</i>	44362_9
478	NZ_JHCH01000001.1	<i>Acinetobacter baumannii</i>	44437_3
479	NZ_JHCG01000001.1	<i>Acinetobacter baumannii</i>	44437_4
480	NZ_JHCF01000001.1	<i>Acinetobacter baumannii</i>	44437_5
481	NZ_JHCE01000001.1	<i>Acinetobacter baumannii</i>	44437_7
482	NZ_JHCD01000001.1	<i>Acinetobacter baumannii</i>	44437_8
483	NZ_JHCC01000001.1	<i>Acinetobacter baumannii</i>	44437_9
484	NZ_JGBS01000001.1	<i>Acinetobacter baumannii</i>	44467_1

	NCBI Reference Sequence ID#	Strain	
485	NZ_JGBT01000001.1	<i>Acinetobacter baumannii</i>	44467_10
486	NZ_JGBR01000001.1	<i>Acinetobacter baumannii</i>	44467_2
487	NZ_JGBQ01000001.1	<i>Acinetobacter baumannii</i>	44467_3
488	NZ_JGBP01000001.1	<i>Acinetobacter baumannii</i>	44467_4
489	NZ_JGBO01000001.1	<i>Acinetobacter baumannii</i>	44467_5
490	NZ_JGBN01000001.1	<i>Acinetobacter baumannii</i>	44467_6
491	NZ_JGBM01000001.1	<i>Acinetobacter baumannii</i>	44467_7
492	NZ_JGBL01000001.1	<i>Acinetobacter baumannii</i>	44467_8
493	NZ_JGBK01000001.1	<i>Acinetobacter baumannii</i>	44467_9
494	NZ_JIDD01000001.1	<i>Acinetobacter baumannii</i>	44839_10
495	NZ_JMHD01000001.1	<i>Acinetobacter baumannii</i>	44839_8
496	NZ_JMHE01000001.1	<i>Acinetobacter baumannii</i>	44839_9
497	NZ_JGBJ01000001.1	<i>Acinetobacter baumannii</i>	44857_10
498	NZ_JGBI01000001.1	<i>Acinetobacter baumannii</i>	44857_9
499	NZ_JFVH01000001.1	<i>Acinetobacter baumannii</i>	44895_1
500	NZ_JFVI01000001.1	<i>Acinetobacter baumannii</i>	44895_10
501	NZ_JFVG01000001.1	<i>Acinetobacter baumannii</i>	44895_2
502	NZ_JFVF01000001.1	<i>Acinetobacter baumannii</i>	44895_3
503	NZ_JFVE01000001.1	<i>Acinetobacter baumannii</i>	44895_4
504	NZ_JFVD01000001.1	<i>Acinetobacter baumannii</i>	44895_5
505	NZ_JFVC01000001.1	<i>Acinetobacter baumannii</i>	44895_6
506	NZ_JFVB01000001.1	<i>Acinetobacter baumannii</i>	44895_8
507	NZ_JFVA01000001.1	<i>Acinetobacter baumannii</i>	44895_9
508	NZ_JFUZ01000001.1	<i>Acinetobacter baumannii</i>	45002_10
509	NZ_JFUY01000001.1	<i>Acinetobacter baumannii</i>	45002_3
510	NZ_JFUX01000001.1	<i>Acinetobacter baumannii</i>	45002_4
511	NZ_JFUW01000001.1	<i>Acinetobacter baumannii</i>	45002_5

	NCBI Reference Sequence ID#	Strain	
512	NZ_JFUV01000001.1	<i>Acinetobacter baumannii</i>	45002_6
513	NZ_JFUU01000001.1	<i>Acinetobacter baumannii</i>	45002_7
514	NZ_JFUT01000001.1	<i>Acinetobacter baumannii</i>	45002_8
515	NZ_JMPG01000001.1	<i>Acinetobacter baumannii</i>	45002_9
516	NZ_JHOQ01000001.1	<i>Acinetobacter baumannii</i>	45052_1
517	NZ_JMPD01000001.1	<i>Acinetobacter baumannii</i>	45052_2
518	NZ_JHPA01000001.1	<i>Acinetobacter baumannii</i>	45052_3
519	NZ_JICN01000001.1	<i>Acinetobacter baumannii</i>	45052_4
520	NZ_JHOZ01000001.1	<i>Acinetobacter baumannii</i>	45052_5
521	NZ_JMPE01000001.1	<i>Acinetobacter baumannii</i>	45057_1
522	NZ_JHOP01000001.1	<i>Acinetobacter baumannii</i>	45057_4
523	NZ_JMHF01000001.1	<i>Acinetobacter baumannii</i>	45075_1
524	NZ_JMNV01000001.1	<i>Acinetobacter baumannii</i>	45075_10
525	NZ_JMHG01000001.1	<i>Acinetobacter baumannii</i>	45075_2
526	NZ_JMHH01000001.1	<i>Acinetobacter baumannii</i>	45075_3
527	NZ_JMND01000001.1	<i>Acinetobacter baumannii</i>	45075_4
528	NZ_JMHN01000001.1	<i>Acinetobacter baumannii</i>	45075_5
529	NZ_JMHO01000001.1	<i>Acinetobacter baumannii</i>	45075_6
530	NZ_JMNE01000001.1	<i>Acinetobacter baumannii</i>	45075_8
531	NZ_JMNF01000001.1	<i>Acinetobacter baumannii</i>	45075_9
532	NZ_JEZM01000001.1	<i>Acinetobacter baumannii</i>	472237-1196
533	NZ_JFCW01000001.1	<i>Acinetobacter baumannii</i>	472237-120
534	NZ_LGYV01000001.1	<i>Acinetobacter baumannii</i>	5021_13
535	NZ_NKXQ01000001.1	<i>Acinetobacter baumannii</i>	554L
536	NZ_NKXP01000001.1	<i>Acinetobacter baumannii</i>	554S
537	NZ_FUEY01000159.1	<i>Acinetobacter baumannii</i>	5MO
538	NZ_PUEI01000001.1	<i>Acinetobacter baumannii</i>	6009-2

	NCBI Reference Sequence ID#	Strain	
539	NZ_FUEL01000121.1	<i>Acinetobacter baumannii</i>	61SM01
540	NZ_FUEV01000138.1	<i>Acinetobacter baumannii</i>	65SM01
541	NZ_JEZR01000001.1	<i>Acinetobacter baumannii</i>	662545-1347
542	NZ_FUEK01000091.1	<i>Acinetobacter baumannii</i>	68SM01
543	NZ_FUEW01000168.1	<i>Acinetobacter baumannii</i>	72SM01
544	NZ_FUES01000153.1	<i>Acinetobacter baumannii</i>	74SM01
545	NZ_JEZO01000001.1	<i>Acinetobacter baumannii</i>	796380-2102
546	NZ_NIWI01000093.1	<i>Acinetobacter baumannii</i>	86II/2C
547	NZ_MABV01000001.1	<i>Acinetobacter baumannii</i>	8D1
548	NZ_JEZW01000001.1	<i>Acinetobacter baumannii</i>	929679-2095
549	NZ_FUEP01000119.1	<i>Acinetobacter baumannii</i>	96SM
550	NZ_JUKM01000026.1	<i>Acinetobacter baumannii</i>	996_ABAU
551	NZ_CP010781.1	<i>Acinetobacter baumannii</i>	A1
552	NZ_CP018332.1	<i>Acinetobacter baumannii</i>	A1296
553	NZ_AVPO01000001.1	<i>Acinetobacter baumannii</i>	A13
554	NZ_JQSF01000001.1	<i>Acinetobacter baumannii</i>	A144
555	NZ_JXSV01000001.1	<i>Acinetobacter baumannii</i>	A155
556	NZ_LKAH01000001.1	<i>Acinetobacter baumannii</i>	A186
557	NZ_FBWR01000001.1	<i>Acinetobacter baumannii</i>	A297
558	NZ_JPZZ01000001.1	<i>Acinetobacter baumannii</i>	A33405
559	NZ_FBXE01000001.1	<i>Acinetobacter baumannii</i>	A388
560	NZ_CP024418.1	<i>Acinetobacter baumannii</i>	A388
561	NZ_LTCY01000001.1	<i>Acinetobacter baumannii</i>	A457
562	NZ_FBWU01000001.1	<i>Acinetobacter baumannii</i>	A83
563	NZ_CP021782.1	<i>Acinetobacter baumannii</i>	A85
564	NZ_FBXA01000001.1	<i>Acinetobacter baumannii</i>	A85
565	NZ_FBWV01000001.1	<i>Acinetobacter baumannii</i>	A92

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566	NZ_AMGA01000001.1	<i>Acinetobacter baumannii</i> AA-014
567	NZ_LKAG01000001.1	<i>Acinetobacter baumannii</i> Ab
568	NZ_NJIB01000001.1	<i>Acinetobacter baumannii</i> Ab_12
569	NZ_AMHA01000001.1	<i>Acinetobacter baumannii</i> AB_1536-8
570	NZ_AMHB01000001.1	<i>Acinetobacter baumannii</i> AB_1582-8
571	NZ_AMHC01000001.1	<i>Acinetobacter baumannii</i> AB_1583-8
572	NZ_AMHD01000001.1	<i>Acinetobacter baumannii</i> AB_1594-8
573	NZ_AMHE01000001.1	<i>Acinetobacter baumannii</i> AB_1595-8
574	NZ_AMHF01000001.1	<i>Acinetobacter baumannii</i> AB_1649-8
575	NZ_AMHG01000001.1	<i>Acinetobacter baumannii</i> AB_1650-8
576	NZ_AMJO01000001.1	<i>Acinetobacter baumannii</i> AB_1766_8
577	NZ_AMHH01000001.1	<i>Acinetobacter baumannii</i> AB_2007-09-110-01-7
578	NZ_AMHI01000001.1	<i>Acinetobacter baumannii</i> AB_2007-16-25-01-7
579	NZ_AMHJ01000001.1	<i>Acinetobacter baumannii</i> AB_2007-16-27-01
580	NZ_AMHK01000001.1	<i>Acinetobacter baumannii</i> AB_2008-15-34-7
581	NZ_AMHL01000001.1	<i>Acinetobacter baumannii</i> AB_2008-15-45
582	NZ_AMHM01000001.1	<i>Acinetobacter baumannii</i> AB_2008-15-52
583	NZ_AMHN01000001.1	<i>Acinetobacter baumannii</i> AB_2008-15-69
584	NZ_AMHO01000001.1	<i>Acinetobacter baumannii</i> AB_2008-15-70
585	NZ_AMHP01000001.1	<i>Acinetobacter baumannii</i> AB_2008-15-71
586	NZ_AMHQ01000001.1	<i>Acinetobacter baumannii</i> AB_2008-23-01-01-7
587	NZ_AMHR01000242.1	<i>Acinetobacter baumannii</i> AB_2008-23-07-01-7
588	NZ_AMHS01000001.1	<i>Acinetobacter baumannii</i> AB_2009-04-01-7
589	NZ_AMHT01000001.1	<i>Acinetobacter baumannii</i> AB_2009-04-02-7
590	NZ_AMHU01000001.1	<i>Acinetobacter baumannii</i> AB_515-8
591	NZ_AMHV01000001.1	<i>Acinetobacter baumannii</i> AB_908-12
592	NZ_AMHW01000001.1	<i>Acinetobacter baumannii</i> AB_908-13

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593	NZ_AMHX01000001.1	<i>Acinetobacter baumannii</i> AB_908-14-7
594	NZ_AMHY01000001.1	<i>Acinetobacter baumannii</i> AB_909-01-7
595	NZ_AMHZ01000001.1	<i>Acinetobacter baumannii</i> AB_909-02-7
596	NZ_AMIA01000001.1	<i>Acinetobacter baumannii</i> AB_909-05
597	NZ_AMIB01000001.1	<i>Acinetobacter baumannii</i> AB_909-14-7
598	NZ_AMID01000001.1	<i>Acinetobacter baumannii</i> AB_TG19617
599	NZ_AMIE01000001.1	<i>Acinetobacter baumannii</i> AB_TG2018
600	NZ_AMIF01000001.1	<i>Acinetobacter baumannii</i> AB_TG2022
601	NZ_AMIG01000001.1	<i>Acinetobacter baumannii</i> AB_TG2023
602	NZ_AMIH01000001.1	<i>Acinetobacter baumannii</i> AB_TG2026
603	NZ_AMII01000001.1	<i>Acinetobacter baumannii</i> AB_TG2028
604	NZ_AMIJ01000001.1	<i>Acinetobacter baumannii</i> AB_TG2030
605	NZ_AMIK01000001.1	<i>Acinetobacter baumannii</i> AB_TG2031
606	NZ_AMIL01000001.1	<i>Acinetobacter baumannii</i> AB_TG2032
607	NZ_AMIM01000001.1	<i>Acinetobacter baumannii</i> AB_TG2631
608	NZ_AMIN01000001.1	<i>Acinetobacter baumannii</i> AB_TG27323
609	NZ_AMIO01000001.1	<i>Acinetobacter baumannii</i> AB_TG27327
610	NZ_AMIP01000001.1	<i>Acinetobacter baumannii</i> AB_TG27331
611	NZ_AMIQ01000001.1	<i>Acinetobacter baumannii</i> AB_TG27335
612	NZ_AMIR01000001.1	<i>Acinetobacter baumannii</i> AB_TG27339
613	NZ_AMIS01000001.1	<i>Acinetobacter baumannii</i> AB_TG27343
614	NZ_AMIU01000001.1	<i>Acinetobacter baumannii</i> AB_TG5064
615	NZ_LWSM01000001.1	<i>Acinetobacter baumannii</i> AB-A
616	NZ_LWSN01000001.1	<i>Acinetobacter baumannii</i> AB-B
617	NZ_LWSO01000001.1	<i>Acinetobacter baumannii</i> AB-C
618	NZ_ATHY01000001.1	<i>Acinetobacter baumannii</i> AB-HKU3-08
619	NZ_ATHZ01000001.1	<i>Acinetobacter baumannii</i> AB-HKU3-10

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620	NZ_LMZH01000001.1	<i>Acinetobacter baumannii</i>	Ab03
621	NZ_CP009257.1	<i>Acinetobacter baumannii</i>	AB030
622	NZ_CP009256.1	<i>Acinetobacter baumannii</i>	AB031
623	NZ_CP012006.1	<i>Acinetobacter baumannii</i>	Ab04-mff
624	NZ_CP019034.1	<i>Acinetobacter baumannii</i>	AB042
625	NZ_ADGZ01000959.1	<i>Acinetobacter baumannii</i>	AB056
626	NZ_ADHA01001040.1	<i>Acinetobacter baumannii</i>	AB058
627	NZ_ADHB01001062.1	<i>Acinetobacter baumannii</i>	AB059
628	NZ_LZOC01000001.1	<i>Acinetobacter baumannii</i>	AB067
629	NZ_FPEM01000074.1	<i>Acinetobacter baumannii</i>	Ab1
630	NZ_PXNJ01000001.1	<i>Acinetobacter baumannii</i>	AB1
631	NZ_LAVJ01000126.1	<i>Acinetobacter baumannii</i>	Ab1
632	NZ_PXNA01000001.1	<i>Acinetobacter baumannii</i>	AB10
633	NZ_FPGB01000063.1	<i>Acinetobacter baumannii</i>	Ab10
634	NZ_NKJY01000001.1	<i>Acinetobacter baumannii</i>	AB100
635	NZ_NKJX01000001.1	<i>Acinetobacter baumannii</i>	AB101
636	NZ_FPGW01000083.1	<i>Acinetobacter baumannii</i>	Ab101
637	NZ_FPGV01000078.1	<i>Acinetobacter baumannii</i>	Ab102
638	NZ_MSLX01000001.1	<i>Acinetobacter baumannii</i>	Ab103_GEIH-2010
639	NZ_MSMA01000001.1	<i>Acinetobacter baumannii</i>	Ab104_GEIH-2010
640	NZ_NKJW01000001.1	<i>Acinetobacter baumannii</i>	AB108
641	NZ_FPFN01000077.1	<i>Acinetobacter baumannii</i>	Ab11
642	NZ_JH815553.1	<i>Acinetobacter baumannii</i>	Ab11111
643	NZ_NKJV01000001.1	<i>Acinetobacter baumannii</i>	AB112
644	NZ_FPGY01000072.1	<i>Acinetobacter baumannii</i>	Ab113
645	NZ_FPHA01000081.1	<i>Acinetobacter baumannii</i>	Ab114
646	NZ_FPGP01000087.1	<i>Acinetobacter baumannii</i>	Ab116

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647	NZ_NKJU01000001.1	<i>Acinetobacter baumannii</i> AB118
648	NZ_PXMY01000001.1	<i>Acinetobacter baumannii</i> AB12
649	NZ_FPEW01000080.1	<i>Acinetobacter baumannii</i> Ab12
650	NZ_MSLZ01000001.1	<i>Acinetobacter baumannii</i> Ab121_GEIH-2010
651	NZ_MSMD01000487.1	<i>Acinetobacter baumannii</i> Ab122_GEIH-2010
652	NZ_FPGA01000081.1	<i>Acinetobacter baumannii</i> Ab13
653	NZ_PXMX01000001.1	<i>Acinetobacter baumannii</i> AB13
654	NZ_NKJT01000001.1	<i>Acinetobacter baumannii</i> AB134
655	NZ_FPDF01000078.1	<i>Acinetobacter baumannii</i> Ab14
656	NZ_NKJS01000001.1	<i>Acinetobacter baumannii</i> AB147
657	NZ_FPFG01000081.1	<i>Acinetobacter baumannii</i> Ab15
658	NZ_PXMV01000001.1	<i>Acinetobacter baumannii</i> AB15
659	NZ_NKJR01000001.1	<i>Acinetobacter baumannii</i> AB156
660	NZ_MSMMC01000001.1	<i>Acinetobacter baumannii</i> Ab158_GEIH-2000
661	NZ_FPFV01000078.1	<i>Acinetobacter baumannii</i> Ab16
662	NZ_PXMU01000001.1	<i>Acinetobacter baumannii</i> AB16
663	NZ_NKJQ01000001.1	<i>Acinetobacter baumannii</i> AB161
664	NZ_MSMB01000006.1	<i>Acinetobacter baumannii</i> Ab161_GEIH-2000
665	NZ_NKJP01000001.1	<i>Acinetobacter baumannii</i> AB162
666	NZ_NKJO01000001.1	<i>Acinetobacter baumannii</i> AB165
667	NZ_NKJN01000001.1	<i>Acinetobacter baumannii</i> AB166
668	NZ_MSMT01000001.1	<i>Acinetobacter baumannii</i> Ab166_GEIH-2000
669	NZ_MSMT01000001.1	<i>Acinetobacter baumannii</i> Ab169_GEIH-2000
670	NZ_FPFK01000099.1	<i>Acinetobacter baumannii</i> Ab17
671	NZ_PXMT01000001.1	<i>Acinetobacter baumannii</i> AB17
672	NZ_NKJM01000001.1	<i>Acinetobacter baumannii</i> AB172
673	NZ_NKJL01000001.1	<i>Acinetobacter baumannii</i> AB173

	NCBI Reference Sequence ID#	Strain
674	NZ_NKJK01000001.1	<i>Acinetobacter baumannii</i> AB174
675	NZ_MSMI01000001.1	<i>Acinetobacter baumannii</i> Ab175_GEIH-2000
676	NZ_MSME01000001.1	<i>Acinetobacter baumannii</i> Ab177_GEIH-2000
677	NZ_FPF01000076.1	<i>Acinetobacter baumannii</i> Ab18
678	NZ_PXMS01000001.1	<i>Acinetobacter baumannii</i> AB18
679	NZ_MSJM01000001.1	<i>Acinetobacter baumannii</i> Ab183_GEIH-2000
680	NZ_LVYA01000001.1	<i>Acinetobacter baumannii</i> AB1845
681	NZ_PXMR01000001.1	<i>Acinetobacter baumannii</i> AB19
682	NZ_FPFZ01000074.1	<i>Acinetobacter baumannii</i> Ab19
683	NZ_MSMM01000001.1	<i>Acinetobacter baumannii</i> Ab192_GEIH-2000
684	NZ_ANNC01000001.1	<i>Acinetobacter baumannii</i> AB1H8
685	NZ_PXNI01000001.1	<i>Acinetobacter baumannii</i> AB2
686	NZ_FPEL01000074.1	<i>Acinetobacter baumannii</i> AB2
687	NZ_QCYE01000100.1	<i>Acinetobacter baumannii</i> AB2
688	NZ_PXMQ01000001.1	<i>Acinetobacter baumannii</i> AB20
689	NZ_FPEK01000063.1	<i>Acinetobacter baumannii</i> AB20
690	NZ_PXMP01000001.1	<i>Acinetobacter baumannii</i> AB21
691	NZ_FPET01000070.1	<i>Acinetobacter baumannii</i> AB21
692	NZ_AEOX01000106.1	<i>Acinetobacter baumannii</i> AB210
693	NZ_CM003909.1	<i>Acinetobacter baumannii</i> AB210M
694	NZ_LXJV01000001.1	<i>Acinetobacter baumannii</i> AB217
695	NZ_PXMO01000001.1	<i>Acinetobacter baumannii</i> AB22
696	NZ_FPF01000070.1	<i>Acinetobacter baumannii</i> Ab22
697	NZ_PXMN01000001.1	<i>Acinetobacter baumannii</i> AB23
698	NZ_FPFU01000068.1	<i>Acinetobacter baumannii</i> Ab23
699	NZ_PXMM01000001.1	<i>Acinetobacter baumannii</i> AB24
700	NZ_FPEN01000070.1	<i>Acinetobacter baumannii</i> Ab24

	NCBI Reference Sequence ID#	Strain	
701	NZ_PXML01000001.1	<i>Acinetobacter baumannii</i>	AB25
702	NZ_FPF01000065.1	<i>Acinetobacter baumannii</i>	Ab25
703	NZ_LXJW01000001.1	<i>Acinetobacter baumannii</i>	AB250
704	NZ_LXNE01000001.1	<i>Acinetobacter baumannii</i>	AB252
705	NZ_LXNF01000001.1	<i>Acinetobacter baumannii</i>	AB254
706	NZ_FPFY01000069.1	<i>Acinetobacter baumannii</i>	Ab26
707	NZ_PXMK01000001.1	<i>Acinetobacter baumannii</i>	AB26
708	NZ_LYNI01000001.1	<i>Acinetobacter baumannii</i>	AB263
709	NZ_PXMJ01000001.1	<i>Acinetobacter baumannii</i>	AB27
710	NZ_FPFO01000070.1	<i>Acinetobacter baumannii</i>	Ab27
711	NZ_PXMI01000001.1	<i>Acinetobacter baumannii</i>	AB28
712	NZ_FPFH01000088.1	<i>Acinetobacter baumannii</i>	Ab28
713	NZ_LRDT01000001.1	<i>Acinetobacter baumannii</i>	AB2828
714	NZ_FPFJ01000070.1	<i>Acinetobacter baumannii</i>	Ab29
715	NZ_PXMH01000001.1	<i>Acinetobacter baumannii</i>	AB29
716	NZ_PXNH01000001.1	<i>Acinetobacter baumannii</i>	AB3
717	NZ_FPGC01000074.1	<i>Acinetobacter baumannii</i>	Ab3
718	NZ_FPEX01000081.1	<i>Acinetobacter baumannii</i>	Ab30
719	NZ_PXMG01000001.1	<i>Acinetobacter baumannii</i>	AB30
720	NZ_CP024911.1	<i>Acinetobacter baumannii</i>	AB307-0294
721	NZ_LXTY01000001.1	<i>Acinetobacter baumannii</i>	AB309
722	NZ_PXMF01000001.1	<i>Acinetobacter baumannii</i>	AB31
723	NZ_FPER01000075.1	<i>Acinetobacter baumannii</i>	Ab31
724	NZ_FPFM01000070.1	<i>Acinetobacter baumannii</i>	Ab32
725	NZ_LYNK01000001.1	<i>Acinetobacter baumannii</i>	AB321
726	NZ_FPFS01000074.1	<i>Acinetobacter baumannii</i>	Ab33
727	NZ_MSMMK01000018.1	<i>Acinetobacter baumannii</i>	Ab33_GEIH-2010

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728	NZ_JH815563.1	<i>Acinetobacter baumannii</i>	Ab33333
729	NZ_LRDU01000001.1	<i>Acinetobacter baumannii</i>	AB3340
730	NZ_FPFE01000084.1	<i>Acinetobacter baumannii</i>	Ab34
731	NZ_PXMC01000001.1	<i>Acinetobacter baumannii</i>	AB34
732	NZ_PXMB01000001.1	<i>Acinetobacter baumannii</i>	AB35
733	NZ_FPFW01000091.1	<i>Acinetobacter baumannii</i>	Ab35
734	NZ_LYNL01000001.1	<i>Acinetobacter baumannii</i>	AB354
735	NZ_LRDV01000001.1	<i>Acinetobacter baumannii</i>	AB3560
736	NZ_LYOG01000001.1	<i>Acinetobacter baumannii</i>	AB357
737	NZ_PXMA01000001.1	<i>Acinetobacter baumannii</i>	AB36
738	NZ_FPEV01000086.1	<i>Acinetobacter baumannii</i>	Ab36
739	NZ_NGKM01000100.1	<i>Acinetobacter baumannii</i>	AB360
740	NZ_LYNM01000001.1	<i>Acinetobacter baumannii</i>	AB363
741	NZ_LRDW01000001.1	<i>Acinetobacter baumannii</i>	AB3638
742	NZ_FPES01000085.1	<i>Acinetobacter baumannii</i>	Ab37
743	NZ_PXLZ01000001.1	<i>Acinetobacter baumannii</i>	AB37
744	NZ_LRDX01000001.1	<i>Acinetobacter baumannii</i>	AB3785
745	NZ_PXLY01000001.1	<i>Acinetobacter baumannii</i>	AB38
746	NZ_FPEQ01000089.1	<i>Acinetobacter baumannii</i>	Ab38
747	NZ_LRDY01000001.1	<i>Acinetobacter baumannii</i>	AB3806
748	NZ_LYNN01000001.1	<i>Acinetobacter baumannii</i>	AB388
749	NZ_PXLX01000001.1	<i>Acinetobacter baumannii</i>	AB39
750	NZ_FPGD01000068.1	<i>Acinetobacter baumannii</i>	Ab39
751	NZ_LRZD01000001.1	<i>Acinetobacter baumannii</i>	AB3927
752	NZ_LYNO01000001.1	<i>Acinetobacter baumannii</i>	AB393
753	NZ_PXNG01000001.1	<i>Acinetobacter baumannii</i>	AB4
754	NZ_FPFA01000075.1	<i>Acinetobacter baumannii</i>	Ab4

	NCBI Reference Sequence ID#	Strain	
755	NZ_PXLW01000001.1	<i>Acinetobacter baumannii</i>	AB40
756	NZ_FFFF01000084.1	<i>Acinetobacter baumannii</i>	Ab40
757	NZ_LREA01000001.1	<i>Acinetobacter baumannii</i>	AB4025
758	NZ_LREB01000001.1	<i>Acinetobacter baumannii</i>	AB4026
759	NZ_LREC01000001.1	<i>Acinetobacter baumannii</i>	AB4027
760	NZ_LRED01000001.1	<i>Acinetobacter baumannii</i>	AB4052
761	NZ_ANND01000001.1	<i>Acinetobacter baumannii</i>	AB405E4
762	NZ_FPEP01000079.1	<i>Acinetobacter baumannii</i>	Ab41
763	NZ_PXLV01000001.1	<i>Acinetobacter baumannii</i>	AB41
764	NZ_LXTZ01000001.1	<i>Acinetobacter baumannii</i>	AB417
765	NZ_FPFR01000071.1	<i>Acinetobacter baumannii</i>	Ab42
766	NZ_PXLU01000001.1	<i>Acinetobacter baumannii</i>	AB42
767	NZ_FPEO01000068.1	<i>Acinetobacter baumannii</i>	Ab43
768	NZ_LYNP01000001.1	<i>Acinetobacter baumannii</i>	AB432
769	NZ_FPGF01000070.1	<i>Acinetobacter baumannii</i>	Ab44
770	NZ_JH815574.1	<i>Acinetobacter baumannii</i>	Ab444444
771	NZ_LREE01000001.1	<i>Acinetobacter baumannii</i>	AB4448
772	NZ_LREF01000001.1	<i>Acinetobacter baumannii</i>	AB4456
773	NZ_LREG01000001.1	<i>Acinetobacter baumannii</i>	AB4490
774	NZ_LREH01000001.1	<i>Acinetobacter baumannii</i>	AB4498
775	NZ_CP024613.1	<i>Acinetobacter baumannii</i>	Ab4568
776	NZ_FPEZ01000044.1	<i>Acinetobacter baumannii</i>	Ab46
777	NZ_NKKN01000001.1	<i>Acinetobacter baumannii</i>	AB46
778	NZ_LXUA01000001.1	<i>Acinetobacter baumannii</i>	AB462
779	NZ_CP024612.1	<i>Acinetobacter baumannii</i>	Ab4653
780	NZ_LYNQ01000001.1	<i>Acinetobacter baumannii</i>	AB466
781	NZ_LYNR01000001.1	<i>Acinetobacter baumannii</i>	AB469

	NCBI Reference Sequence ID#	Strain	
782	NZ_FPEY01000083.1	<i>Acinetobacter baumannii</i>	Ab47
783	NZ_LREJ01000001.1	<i>Acinetobacter baumannii</i>	AB4795
784	NZ_FPFQ01000086.1	<i>Acinetobacter baumannii</i>	Ab48
785	NZ_LYNS01000001.1	<i>Acinetobacter baumannii</i>	AB487
786	NZ_LREJ01000001.1	<i>Acinetobacter baumannii</i>	AB4878
787	NZ_MSMM01000003.1	<i>Acinetobacter baumannii</i>	Ab49_GEIH-2010
788	NZ_LYNT01000001.1	<i>Acinetobacter baumannii</i>	AB492
789	NZ_LREK01000001.1	<i>Acinetobacter baumannii</i>	AB4932
790	NZ_LREL01000001.1	<i>Acinetobacter baumannii</i>	AB4957
791	NZ_CP024611.1	<i>Acinetobacter baumannii</i>	Ab4977
792	NZ_LREM01000001.1	<i>Acinetobacter baumannii</i>	AB4991
793	NZ_AOLU01000001.1	<i>Acinetobacter baumannii</i>	AB4A3
794	NZ_FPEU01000074.1	<i>Acinetobacter baumannii</i>	Ab5
795	NZ_LANH01000001.1	<i>Acinetobacter baumannii</i>	Ab5
796	NZ_PXNF01000001.1	<i>Acinetobacter baumannii</i>	AB5
797	NZ_LREN01000001.1	<i>Acinetobacter baumannii</i>	AB5001
798	NZ_JHUI01000005.1	<i>Acinetobacter baumannii</i>	AB5075
799	NZ_CP008706.1	<i>Acinetobacter baumannii</i>	AB5075-UW
800	NZ_LREO01000001.1	<i>Acinetobacter baumannii</i>	AB5197
801	NZ_NKKM01000001.1	<i>Acinetobacter baumannii</i>	AB52
802	NZ_AHAJ01000050.1	<i>Acinetobacter baumannii</i>	AB5256
803	NZ_NKKL01000001.1	<i>Acinetobacter baumannii</i>	AB54
804	NZ_MSML01000001.1	<i>Acinetobacter baumannii</i>	Ab54_GEIH-2010
805	NZ_LYNU01000001.1	<i>Acinetobacter baumannii</i>	AB543
806	NZ_LXUE01000001.1	<i>Acinetobacter baumannii</i>	AB552
807	NZ_LXUB01000001.1	<i>Acinetobacter baumannii</i>	AB558
808	NZ_LYNV01000001.1	<i>Acinetobacter baumannii</i>	AB559

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809	NZ_NKKG01000001.1	<i>Acinetobacter baumannii</i>	AB56
810	NZ_LREP01000001.1	<i>Acinetobacter baumannii</i>	AB5674
811	NZ_AHAJ01000045.1	<i>Acinetobacter baumannii</i>	AB5711
812	NZ_LYNW01000001.1	<i>Acinetobacter baumannii</i>	AB576
813	NZ_LYNX01000001.1	<i>Acinetobacter baumannii</i>	AB578
814	NZ_LYNZ01000001.1	<i>Acinetobacter baumannii</i>	AB596
815	NZ_FPFT01000073.1	<i>Acinetobacter baumannii</i>	Ab6
816	NZ_LYOA01000001.1	<i>Acinetobacter baumannii</i>	AB601
817	NZ_NKKJ01000001.1	<i>Acinetobacter baumannii</i>	AB72
818	NZ_NKKI01000001.1	<i>Acinetobacter baumannii</i>	AB73
819	NZ_FFP01000069.1	<i>Acinetobacter baumannii</i>	Ab73
820	NZ_CP015121.1	<i>Acinetobacter baumannii</i>	ab736
821	NZ_NKKG01000001.1	<i>Acinetobacter baumannii</i>	AB74
822	NZ_MSLY01000001.1	<i>Acinetobacter baumannii</i>	Ab76_GEIH-2010
823	NZ_FPGG01000040.1	<i>Acinetobacter baumannii</i>	Ab77
824	NZ_NKKF01000001.1	<i>Acinetobacter baumannii</i>	AB79
825	NZ_FPFC01000074.1	<i>Acinetobacter baumannii</i>	Ab8
826	NZ_PXNC01000001.1	<i>Acinetobacter baumannii</i>	AB8
827	NZ_FPGI01000089.1	<i>Acinetobacter baumannii</i>	Ab80
828	NZ_PQVM01000010.1	<i>Acinetobacter baumannii</i>	Ab804
829	NZ_NKKE01000001.1	<i>Acinetobacter baumannii</i>	AB81
830	NZ_FPGH01000085.1	<i>Acinetobacter baumannii</i>	Ab85
831	NZ_FPGK01000081.1	<i>Acinetobacter baumannii</i>	Ab86
832	NZ_FPGT01000093.1	<i>Acinetobacter baumannii</i>	Ab87
833	NZ_NKGD01000001.1	<i>Acinetobacter baumannii</i>	AB88
834	NZ_FPGL01000081.1	<i>Acinetobacter baumannii</i>	Ab89
835	NZ_NKGC01000001.1	<i>Acinetobacter baumannii</i>	AB89

	NCBI Reference Sequence ID#	Strain	
836	NZ_FPGE01000065.1	<i>Acinetobacter baumannii</i>	Ab9
837	NZ_PXNB01000001.1	<i>Acinetobacter baumannii</i>	AB9
838	NZ_FPGJ01000069.1	<i>Acinetobacter baumannii</i>	Ab90
839	NZ_ABXK01000068.1	<i>Acinetobacter baumannii</i>	AB900
840	NZ_NKKB01000001.1	<i>Acinetobacter baumannii</i>	AB91
841	NZ_FPGN01000081.1	<i>Acinetobacter baumannii</i>	Ab94
842	NZ_FPGQ01000086.1	<i>Acinetobacter baumannii</i>	Ab96
843	NZ_NKKA01000001.1	<i>Acinetobacter baumannii</i>	AB96
844	NZ_LRDS01000001.1	<i>Acinetobacter baumannii</i>	AB967
845	NZ_NKJZ01000001.1	<i>Acinetobacter baumannii</i>	AB99
846	NZ_NNSJ01000001.1	<i>Acinetobacter baumannii</i>	ABA1614
847	NZ_NNSI01000001.1	<i>Acinetobacter baumannii</i>	ABA2114
848	NZ_NXGU01000001.1	<i>Acinetobacter baumannii</i>	Abau471
849	NZ_LLCI01000001.1	<i>Acinetobacter baumannii</i>	ABBL001
850	NZ_LLCJ01000001.1	<i>Acinetobacter baumannii</i>	ABBL003
851	NZ_LLC01000001.1	<i>Acinetobacter baumannii</i>	ABBL004
852	NZ_LLCM01000001.1	<i>Acinetobacter baumannii</i>	ABBL006
853	NZ_LLCN01000001.1	<i>Acinetobacter baumannii</i>	ABBL007
854	NZ_LLCO01000001.1	<i>Acinetobacter baumannii</i>	ABBL008
855	NZ_LLC01000001.1	<i>Acinetobacter baumannii</i>	ABBL009
856	NZ_LLCR01000001.1	<i>Acinetobacter baumannii</i>	ABBL011
857	NZ_LLCS01000001.1	<i>Acinetobacter baumannii</i>	ABBL012
858	NZ_LLCT01000001.1	<i>Acinetobacter baumannii</i>	ABBL013
859	NZ_LLCU01000001.1	<i>Acinetobacter baumannii</i>	ABBL014
860	NZ_LLCX01000001.1	<i>Acinetobacter baumannii</i>	ABBL017
861	NZ_LLCY01000001.1	<i>Acinetobacter baumannii</i>	ABBL018
862	NZ_LLDA01000001.1	<i>Acinetobacter baumannii</i>	ABBL020

	NCBI Reference Sequence ID#	Strain	
863	NZ_LLDB01000001.1	<i>Acinetobacter baumannii</i>	ABBL021
864	NZ_LLDC01000001.1	<i>Acinetobacter baumannii</i>	ABBL022
865	NZ_LLDD01000001.1	<i>Acinetobacter baumannii</i>	ABBL023
866	NZ_LLDF01000001.1	<i>Acinetobacter baumannii</i>	ABBL025
867	NZ_LLDDG01000001.1	<i>Acinetobacter baumannii</i>	ABBL026
868	NZ_LLDDI01000001.1	<i>Acinetobacter baumannii</i>	ABBL028
869	NZ_LLDDJ01000001.1	<i>Acinetobacter baumannii</i>	ABBL029
870	NZ_LLDDK01000001.1	<i>Acinetobacter baumannii</i>	ABBL030
871	NZ_LLDDO01000001.1	<i>Acinetobacter baumannii</i>	ABBL034
872	NZ_LLDDP01000001.1	<i>Acinetobacter baumannii</i>	ABBL035
873	NZ_LLDDQ01000001.1	<i>Acinetobacter baumannii</i>	ABBL036
874	NZ_LLDR01000001.1	<i>Acinetobacter baumannii</i>	ABBL037
875	NZ_LLDS01000001.1	<i>Acinetobacter baumannii</i>	ABBL038
876	NZ_LLDT01000001.1	<i>Acinetobacter baumannii</i>	ABBL039
877	NZ_LLDU01000001.1	<i>Acinetobacter baumannii</i>	ABBL040
878	NZ_LLDDV01000001.1	<i>Acinetobacter baumannii</i>	ABBL041
879	NZ_LLDDX01000001.1	<i>Acinetobacter baumannii</i>	ABBL043
880	NZ_LLDDY01000001.1	<i>Acinetobacter baumannii</i>	ABBL044
881	NZ_LLDDZ01000001.1	<i>Acinetobacter baumannii</i>	ABBL045
882	NZ_LLED01000001.1	<i>Acinetobacter baumannii</i>	ABBL049
883	NZ_LLEE01000001.1	<i>Acinetobacter baumannii</i>	ABBL050
884	NZ_LLEF01000001.1	<i>Acinetobacter baumannii</i>	ABBL051
885	NZ_LLEG01000001.1	<i>Acinetobacter baumannii</i>	ABBL052
886	NZ_LLEH01000001.1	<i>Acinetobacter baumannii</i>	ABBL053
887	NZ_LLFA01000001.1	<i>Acinetobacter baumannii</i>	ABBL055
888	NZ_LLFB01000001.1	<i>Acinetobacter baumannii</i>	ABBL056
889	NZ_LLFC01000001.1	<i>Acinetobacter baumannii</i>	ABBL057

	NCBI Reference Sequence ID#	Strain	
890	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL058
891	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL059
892	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL060
893	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL061
894	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL062
895	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL063
896	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL066
897	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL067
898	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL067a
899	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL067b
900	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL067c
901	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL067e
902	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL067f
903	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL067g
904	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL067h
905	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL067i
906	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL067j
907	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL067k
908	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL067l
909	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL068
910	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL069
911	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL070
912	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL071
913	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL072
914	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL073
915	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL076
916	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	ABBL079

	NCBI Reference Sequence ID#	Strain	
917	NZ_LLG01000001.1	<i>Acinetobacter baumannii</i>	ABBL082
918	NZ_LLG01000001.1	<i>Acinetobacter baumannii</i>	ABBL083
919	NZ_LLG01000001.1	<i>Acinetobacter baumannii</i>	ABBL085
920	NZ_LLG01000001.1	<i>Acinetobacter baumannii</i>	ABBL088
921	NZ_LLG01000001.1	<i>Acinetobacter baumannii</i>	ABBL089
922	NZ_LLG01000001.1	<i>Acinetobacter baumannii</i>	ABBL091
923	NZ_LLG01000001.1	<i>Acinetobacter baumannii</i>	ABBL092
924	NZ_LLG01000001.1	<i>Acinetobacter baumannii</i>	ABBL093
925	NZ_LLG01000001.1	<i>Acinetobacter baumannii</i>	ABBL094
926	NZ_LLG01000001.1	<i>Acinetobacter baumannii</i>	ABBL095
927	NZ_LLG01000001.1	<i>Acinetobacter baumannii</i>	ABBL097
928	NZ_JPDG01000001.1	<i>Acinetobacter baumannii</i>	ABBL099
929	NZ_LLHA01000001.1	<i>Acinetobacter baumannii</i>	ABBL100
930	NZ_LLHB01000001.1	<i>Acinetobacter baumannii</i>	ABBL101
931	NZ_LLHC01000001.1	<i>Acinetobacter baumannii</i>	ABBL102
932	NZ_LLHE01000001.1	<i>Acinetobacter baumannii</i>	ABBL105
933	NZ_LLHF01000001.1	<i>Acinetobacter baumannii</i>	ABBL106
934	NZ_LLHG01000001.1	<i>Acinetobacter baumannii</i>	ABBL107
935	NZ_LLHH01000001.1	<i>Acinetobacter baumannii</i>	ABBL109
936	NZ_LLHI01000001.1	<i>Acinetobacter baumannii</i>	ABBL110
937	NZ_LLHK01000001.1	<i>Acinetobacter baumannii</i>	ABBL113
938	NZ_LLHL01000001.1	<i>Acinetobacter baumannii</i>	ABBL114
939	NZ_LLHM01000001.1	<i>Acinetobacter baumannii</i>	ABBL115
940	NZ_LLHN01000001.1	<i>Acinetobacter baumannii</i>	ABBL116
941	NZ_LLHO01000001.1	<i>Acinetobacter baumannii</i>	ABBL117
942	NZ_LLHP01000001.1	<i>Acinetobacter baumannii</i>	ABBL118
943	NZ_LLHR01000001.1	<i>Acinetobacter baumannii</i>	ABBL121

	NCBI Reference Sequence ID#	Strain	
944	NZ_LLHS01000001.1	<i>Acinetobacter baumannii</i>	ABBL122
945	NZ_LLHT01000001.1	<i>Acinetobacter baumannii</i>	ABBL123
946	NZ_LLHU01000001.1	<i>Acinetobacter baumannii</i>	ABBL124
947	NZ_LLV01000001.1	<i>Acinetobacter baumannii</i>	ABBL125
948	NZ_LLHX01000001.1	<i>Acinetobacter baumannii</i>	ABBL127
949	NZ_LLHZ01000001.1	<i>Acinetobacter baumannii</i>	ABBL129
950	NZ_LLIA01000001.1	<i>Acinetobacter baumannii</i>	ABBL130
951	NZ_LLJB01000001.1	<i>Acinetobacter baumannii</i>	ABBL131
952	NZ_LLIC01000001.1	<i>Acinetobacter baumannii</i>	ABBL132
953	NZ_LLID01000001.1	<i>Acinetobacter baumannii</i>	ABBL133
954	NZ_LLIE01000001.1	<i>Acinetobacter baumannii</i>	ABBL134
955	NZ_LLIG01000001.1	<i>Acinetobacter baumannii</i>	ABBL137
956	NZ_LLIH01000001.1	<i>Acinetobacter baumannii</i>	ABBL138
957	NZ_LLII01000001.1	<i>Acinetobacter baumannii</i>	ABBL140
958	NZ_LLJJ01000001.1	<i>Acinetobacter baumannii</i>	ABBL141
959	NZ_LLIK01000001.1	<i>Acinetobacter baumannii</i>	ABBL142
960	NZ_LLIL01000001.1	<i>Acinetobacter baumannii</i>	ABBL143
961	NZ_LLIM01000001.1	<i>Acinetobacter baumannii</i>	ABBL144
962	NZ_LLIN01000001.1	<i>Acinetobacter baumannii</i>	ABBL147
963	NZ_LLIP01000001.1	<i>Acinetobacter baumannii</i>	ABBL149
964	NZ_NQEQ01000036.1	<i>Acinetobacter baumannii</i>	ABCRPSTH03
965	NZ_NQER01000066.1	<i>Acinetobacter baumannii</i>	ABCRPSTH04
966	NZ_NQES01000079.1	<i>Acinetobacter baumannii</i>	ABCRPSTH05
967	NZ_NQET01000014.1	<i>Acinetobacter baumannii</i>	ABCRPSTH06
968	NZ_NQEU01000075.1	<i>Acinetobacter baumannii</i>	ABCRPSTH07
969	NZ_NQEV01000020.1	<i>Acinetobacter baumannii</i>	ABCRPSTH08
970	NZ_NQEW01000047.1	<i>Acinetobacter baumannii</i>	ABCRPSTH09

	NCBI Reference Sequence ID#	Strain
971	NZ_NQEX01000080.1	<i>Acinetobacter baumannii</i> ABCRPSTH10
972	NZ_NQEY01000069.1	<i>Acinetobacter baumannii</i> ABCRPSTH11
973	NZ_NQEZ01000072.1	<i>Acinetobacter baumannii</i> ABCRPSTH12
974	NZ_NQFA01000065.1	<i>Acinetobacter baumannii</i> ABCRPUTH04
975	NZ_NQFB01000032.1	<i>Acinetobacter baumannii</i> ABCRPUTH05
976	NZ_NQFC01000076.1	<i>Acinetobacter baumannii</i> ABCRPUTH06
977	NZ_NQFD01000036.1	<i>Acinetobacter baumannii</i> ABCRPUTH07
978	NZ_NQFE01000028.1	<i>Acinetobacter baumannii</i> ABCRPUTH08
979	NZ_NQFF01000052.1	<i>Acinetobacter baumannii</i> ABCRPUTH09
980	NZ_NQFG01000061.1	<i>Acinetobacter baumannii</i> ABCRPUTH10
981	NZ_NQFH01000001.1	<i>Acinetobacter baumannii</i> ABCRPUTH11
982	NZ_NQFI01000073.1	<i>Acinetobacter baumannii</i> ABCRPUTH12
983	NZ_NQFJ01000030.1	<i>Acinetobacter baumannii</i> ABCRPUTH13
984	NZ_NQFK01000069.1	<i>Acinetobacter baumannii</i> ABCRPUTH14
985	NZ_NQFL01000074.1	<i>Acinetobacter baumannii</i> ABCRPUTH15
986	NZ_FPEF01000194.1	ABE12_M
987	NZ_FWWP01000191.1	ABE21_M
988	NZ_FWWO01000203.1	ABE27_M
989	NZ_FPKN01000185.1	ABE8_07
990	NZ_CP009534.1	AbH12O-A2
991	NZ_CAKB01000108.1	ABIsac_ColiR
992	NZ_CAKA01000275.1	ABIsac_ColiS
993	NZ_LIWE01000001.1	AbMDR-GLH1
994	NZ_LJAH01000001.1	AbMDR-GLH10
995	NZ_LJAI01000001.1	AbMDR-GLH11
996	NZ_LIZZ01000001.1	AbMDR-GLH2
997	NZ_LJAA01000001.1	AbMDR-GLH3

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998	NZ_LJAB01000001.1	<i>Acinetobacter baumannii</i> AbMDR-GLH4
999	NZ_LJAC01000001.1	<i>Acinetobacter baumannii</i> AbMDR-GLH5
1000	NZ_LJAD01000001.1	<i>Acinetobacter baumannii</i> AbMDR-GLH6
1001	NZ_LJAE01000001.1	<i>Acinetobacter baumannii</i> AbMDR-GLH7
1002	NZ_LJAF01000001.1	<i>Acinetobacter baumannii</i> AbMDR-GLH8
1003	NZ_LJAG01000001.1	<i>Acinetobacter baumannii</i> AbMDR-GLH9
1004	NZ_LYOB01000001.1	<i>Acinetobacter baumannii</i> ABNH1
1005	NZ_LYOC01000001.1	<i>Acinetobacter baumannii</i> ABNH2
1006	NZ_LYOD01000001.1	<i>Acinetobacter baumannii</i> ABNH4
1007	NZ_LXUD01000001.1	<i>Acinetobacter baumannii</i> ABNH7
1008	NZ_LYOF01000001.1	<i>Acinetobacter baumannii</i> ABNH8
1009	NZ_AFSZ01000103.1	<i>Acinetobacter baumannii</i> ABNIH1
1010	NZ_APBA01000001.1	<i>Acinetobacter baumannii</i> ABNIH11
1011	NZ_APB01000245.1	<i>Acinetobacter baumannii</i> ABNIH13
1012	NZ_APC01000001.1	<i>Acinetobacter baumannii</i> ABNIH14
1013	NZ_APB01000001.1	<i>Acinetobacter baumannii</i> ABNIH15
1014	NZ_APE01000001.1	<i>Acinetobacter baumannii</i> ABNIH16
1015	NZ_APF01000001.1	<i>Acinetobacter baumannii</i> ABNIH17
1016	NZ_APG01000001.1	<i>Acinetobacter baumannii</i> ABNIH18
1017	NZ_APH01000001.1	<i>Acinetobacter baumannii</i> ABNIH19
1018	NZ_AFTA01000125.1	<i>Acinetobacter baumannii</i> ABNIH2
1019	NZ_APB01000001.1	<i>Acinetobacter baumannii</i> ABNIH20
1020	NZ_APB01000001.1	<i>Acinetobacter baumannii</i> ABNIH22
1021	NZ_APB01000001.1	<i>Acinetobacter baumannii</i> ABNIH23
1022	NZ_APL01000001.1	<i>Acinetobacter baumannii</i> ABNIH24
1023	NZ_APM01000001.1	<i>Acinetobacter baumannii</i> ABNIH25
1024	NZ_AOG01000001.1	<i>Acinetobacter baumannii</i> ABNIH26

	NCBI Reference Sequence ID#	Strain	
1025	NZ_CP026125.1	<i>Acinetobacter baumannii</i>	ABNIH28
1026	NZ_AFTB01000285.1	<i>Acinetobacter baumannii</i>	ABNIH3
1027	NZ_AFTC01000184.1	<i>Acinetobacter baumannii</i>	ABNIH4
1028	NZ_APAY01000001.1	<i>Acinetobacter baumannii</i>	ABNIH7
1029	NZ_LLIQ01000001.1	<i>Acinetobacter baumannii</i>	ABOB01
1030	NZ_LLIR01000001.1	<i>Acinetobacter baumannii</i>	ABOB02
1031	NZ_LLIS01000001.1	<i>Acinetobacter baumannii</i>	ABOB03
1032	NZ_LLIT01000001.1	<i>Acinetobacter baumannii</i>	ABOB04
1033	NZ_LLIU01000001.1	<i>Acinetobacter baumannii</i>	ABOB04_a
1034	NZ_LLIV01000001.1	<i>Acinetobacter baumannii</i>	ABOB04_b
1035	NZ_LLIW01000001.1	<i>Acinetobacter baumannii</i>	ABOB06
1036	NZ_LLIX01000001.1	<i>Acinetobacter baumannii</i>	ABOB06_a
1037	NZ_LLIY01000001.1	<i>Acinetobacter baumannii</i>	ABOB07
1038	NZ_LLJZ01000001.1	<i>Acinetobacter baumannii</i>	ABOB08
1039	NZ_LLJA01000001.1	<i>Acinetobacter baumannii</i>	ABOB09
1040	NZ_LLJB01000001.1	<i>Acinetobacter baumannii</i>	ABOB10
1041	NZ_LLJC01000001.1	<i>Acinetobacter baumannii</i>	ABOB11
1042	NZ_LLJD01000001.1	<i>Acinetobacter baumannii</i>	ABOB12
1043	NZ_LLJE01000001.1	<i>Acinetobacter baumannii</i>	ABOB15
1044	NZ_LLJF01000001.1	<i>Acinetobacter baumannii</i>	ABOB16
1045	NZ_LLJG01000001.1	<i>Acinetobacter baumannii</i>	ABOBEN
1046	NZ_CP024576.1	<i>Acinetobacter baumannii</i>	AbPK1
1047	NZ_MTQI01000001.1	<i>Acinetobacter baumannii</i>	AbS1
1048	NZ_MTQH01000001.1	<i>Acinetobacter baumannii</i>	AbS2
1049	NZ_JWSF03000001.1	<i>Acinetobacter baumannii</i>	ABUH304350
1050	NZ_JWSH03000001.1	<i>Acinetobacter baumannii</i>	ABUH304352
1051	NZ_JWRW03000001.1	<i>Acinetobacter baumannii</i>	ABUH319118

	NCBI Reference Sequence ID#	Strain	
1052	NZ_MWVN01000032.1	<i>Acinetobacter baumannii</i>	ABUH337
1053	NZ_MWVO01000049.1	<i>Acinetobacter baumannii</i>	ABUH339
1054	NZ_MWVP01000053.1	<i>Acinetobacter baumannii</i>	ABUH341
1055	NZ_MWVQ01000042.1	<i>Acinetobacter baumannii</i>	ABUH343
1056	NZ_NCZL01000006.1	<i>Acinetobacter baumannii</i>	ABUH345
1057	NZ_NCZM01000018.1	<i>Acinetobacter baumannii</i>	ABUH347
1058	NZ_NCZN01000025.1	<i>Acinetobacter baumannii</i>	ABUH353
1059	NZ_NCZO01000050.1	<i>Acinetobacter baumannii</i>	ABUH356
1060	NZ_NCZP01000071.1	<i>Acinetobacter baumannii</i>	ABUH358
1061	NZ_NCZQ01000003.1	<i>Acinetobacter baumannii</i>	ABUH360
1062	NZ_NCZR01000086.1	<i>Acinetobacter baumannii</i>	ABUH363
1063	NZ_NCZS01000006.1	<i>Acinetobacter baumannii</i>	ABUH367
1064	NZ_NCZT01000021.1	<i>Acinetobacter baumannii</i>	ABUH371
1065	NZ_NCZU01000053.1	<i>Acinetobacter baumannii</i>	ABUH374
1066	NZ_NCYJ01000020.1	<i>Acinetobacter baumannii</i>	ABUH375
1067	NZ_NCYK01000033.1	<i>Acinetobacter baumannii</i>	ABUH379
1068	NZ_NCYL01000063.1	<i>Acinetobacter baumannii</i>	ABUH383
1069	NZ_NCYM01000026.1	<i>Acinetobacter baumannii</i>	ABUH388
1070	NZ_MSMMR01000001.1	<i>Acinetobacter baumannii</i>	ABUH390
1071	NZ_MSMS01000001.1	<i>Acinetobacter baumannii</i>	ABUH393
1072	NZ_NCYN01000024.1	<i>Acinetobacter baumannii</i>	ABUH394
1073	NZ_MSMT01000001.1	<i>Acinetobacter baumannii</i>	ABUH396
1074	NZ_NCYO01000022.1	<i>Acinetobacter baumannii</i>	ABUH397
1075	NZ_MSMTU01000001.1	<i>Acinetobacter baumannii</i>	ABUH399
1076	NZ_NCYP01000037.1	<i>Acinetobacter baumannii</i>	ABUH400
1077	NZ_MSMTV01000001.1	<i>Acinetobacter baumannii</i>	ABUH402
1078	NZ_JWSJ03000001.1	<i>Acinetobacter baumannii</i>	ABUH404571

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1079	NZ_MSMW01000001.1	<i>Acinetobacter baumannii</i>	ABUH405
1080	NZ_NCYQ01000041.1	<i>Acinetobacter baumannii</i>	ABUH407
1081	NZ_NCYR01000042.1	<i>Acinetobacter baumannii</i>	ABUH413
1082	NZ_MSMY01000001.1	<i>Acinetobacter baumannii</i>	ABUH414
1083	NZ_MSMZ01000001.1	<i>Acinetobacter baumannii</i>	ABUH417
1084	NZ_MSNA01000001.1	<i>Acinetobacter baumannii</i>	ABUH420
1085	NZ_NCY01000033.1	<i>Acinetobacter baumannii</i>	ABUH421
1086	NZ_NCYT01000055.1	<i>Acinetobacter baumannii</i>	ABUH424
1087	NZ_NCYU01000047.1	<i>Acinetobacter baumannii</i>	ABUH425
1088	NZ_MSNA01000001.1	<i>Acinetobacter baumannii</i>	ABUH426
1089	NZ_JWRU03000001.1	<i>Acinetobacter baumannii</i>	ABUH42783
1090	NZ_NCYV01000082.1	<i>Acinetobacter baumannii</i>	ABUH428
1091	NZ_NCYW01000048.1	<i>Acinetobacter baumannii</i>	ABUH431
1092	NZ_MSNC01000001.1	<i>Acinetobacter baumannii</i>	ABUH432
1093	NZ_NCYX01000058.1	<i>Acinetobacter baumannii</i>	ABUH434
1094	NZ_MSND01000001.1	<i>Acinetobacter baumannii</i>	ABUH435
1095	NZ_NCY01000031.1	<i>Acinetobacter baumannii</i>	ABUH437
1096	NZ_MSNE01000001.1	<i>Acinetobacter baumannii</i>	ABUH438
1097	NZ_MSNE01000001.1	<i>Acinetobacter baumannii</i>	ABUH441
1098	NZ_NCYZ01000043.1	<i>Acinetobacter baumannii</i>	ABUH442
1099	NZ_NCZA01000077.1	<i>Acinetobacter baumannii</i>	ABUH446
1100	NZ_NCB01000045.1	<i>Acinetobacter baumannii</i>	ABUH449
1101	NZ_MSPB01000001.1	<i>Acinetobacter baumannii</i>	ABUH453
1102	NZ_NCZC01000093.1	<i>Acinetobacter baumannii</i>	ABUH454
1103	NZ_NCZD01000116.1	<i>Acinetobacter baumannii</i>	ABUH457
1104	NZ_NCZE01000100.1	<i>Acinetobacter baumannii</i>	ABUH458
1105	NZ_MSPC01000001.1	<i>Acinetobacter baumannii</i>	ABUH462

	NCBI Reference Sequence ID#	Strain	
1106	NZ_JWSE0300001.1	<i>Acinetobacter baumannii</i>	ABUH463346
1107	NZ_NCZF01000040.1	<i>Acinetobacter baumannii</i>	ABUH464
1108	NZ_MSPD01000001.1	<i>Acinetobacter baumannii</i>	ABUH468
1109	NZ_MSPE01000001.1	<i>Acinetobacter baumannii</i>	ABUH471
1110	NZ_NCZG01000110.1	<i>Acinetobacter baumannii</i>	ABUH473
1111	NZ_MSPF01000001.1	<i>Acinetobacter baumannii</i>	ABUH474
1112	NZ_NCZH01000004.1	<i>Acinetobacter baumannii</i>	ABUH475
1113	NZ_MSPG01000001.1	<i>Acinetobacter baumannii</i>	ABUH477
1114	NZ_NCZI01000104.1	<i>Acinetobacter baumannii</i>	ABUH479
1115	NZ_MSPH01000001.1	<i>Acinetobacter baumannii</i>	ABUH480
1116	NZ_MSPI01000001.1	<i>Acinetobacter baumannii</i>	ABUH483
1117	NZ_JWRT03000001.1	<i>Acinetobacter baumannii</i>	ABUH4837
1118	NZ_NCZJ01000027.1	<i>Acinetobacter baumannii</i>	ABUH485
1119	NZ_NCZK01000046.1	<i>Acinetobacter baumannii</i>	ABUH496
1120	NZ_JWRY03000001.1	<i>Acinetobacter baumannii</i>	ABUH497144
1121	NZ_NCXT01000021.1	<i>Acinetobacter baumannii</i>	ABUH499
1122	NZ_MSPJ01000001.1	<i>Acinetobacter baumannii</i>	ABUH501
1123	NZ_NCXU01000130.1	<i>Acinetobacter baumannii</i>	ABUH502
1124	NZ_MSPK01000001.1	<i>Acinetobacter baumannii</i>	ABUH504
1125	NZ_JWRZ03000001.1	<i>Acinetobacter baumannii</i>	ABUH504227
1126	NZ_JWSA03000001.1	<i>Acinetobacter baumannii</i>	ABUH504238
1127	NZ_NCXV01000135.1	<i>Acinetobacter baumannii</i>	ABUH505
1128	NZ_NCXW01000071.1	<i>Acinetobacter baumannii</i>	ABUH508
1129	NZ_NCXX01000085.1	<i>Acinetobacter baumannii</i>	ABUH511
1130	NZ_MSPL01000001.1	<i>Acinetobacter baumannii</i>	ABUH513
1131	NZ_MSPM01000001.1	<i>Acinetobacter baumannii</i>	ABUH516
1132	NZ_NCXY01000042.1	<i>Acinetobacter baumannii</i>	ABUH518

	NCBI Reference Sequence ID#	Strain
1133	NZ_JWSC03000001.1	<i>Acinetobacter baumannii</i> ABUH518307
1134	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i> ABUH519
1135	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i> ABUH522
1136	NZ_JWSI03000001.1	<i>Acinetobacter baumannii</i> ABUH524354
1137	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i> ABUH525
1138	NZ_NCXX01000051.1	<i>Acinetobacter baumannii</i> ABUH526
1139	NZ_NCYA01000016.1	<i>Acinetobacter baumannii</i> ABUH529
1140	NZ_NCYB01000070.1	<i>Acinetobacter baumannii</i> ABUH532
1141	NZ_NCYC01000068.1	<i>Acinetobacter baumannii</i> ABUH533
1142	NZ_MSOA01000001.1	<i>Acinetobacter baumannii</i> ABUH534
1143	NZ_MSOB01000001.1	<i>Acinetobacter baumannii</i> ABUH537
1144	NZ_NCYD01000048.1	<i>Acinetobacter baumannii</i> ABUH542
1145	NZ_MSOD01000001.1	<i>Acinetobacter baumannii</i> ABUH546
1146	NZ_NCYE01000010.1	<i>Acinetobacter baumannii</i> ABUH547
1147	NZ_MSOF01000001.1	<i>Acinetobacter baumannii</i> ABUH549
1148	NZ_NCYF01000016.1	<i>Acinetobacter baumannii</i> ABUH550
1149	NZ_MSOG01000001.1	<i>Acinetobacter baumannii</i> ABUH552
1150	NZ_NCYG01000069.1	<i>Acinetobacter baumannii</i> ABUH553
1151	NZ_MSOG01000001.1	<i>Acinetobacter baumannii</i> ABUH555
1152	NZ_NCYH01000005.1	<i>Acinetobacter baumannii</i> ABUH557
1153	NZ_MSOH01000001.1	<i>Acinetobacter baumannii</i> ABUH561
1154	NZ_NCYI01000023.1	<i>Acinetobacter baumannii</i> ABUH562
1155	NZ_MSOI01000001.1	<i>Acinetobacter baumannii</i> ABUH564
1156	NZ_MSOJ01000001.1	<i>Acinetobacter baumannii</i> ABUH567
1157	NZ_MSOK01000001.1	<i>Acinetobacter baumannii</i> ABUH570
1158	NZ_NDAN01000096.1	<i>Acinetobacter baumannii</i> ABUH572
1159	NZ_NDAO01000051.1	<i>Acinetobacter baumannii</i> ABUH575

	NCBI Reference Sequence ID#	Strain	
1160	NZ_MSOL01000001.1	<i>Acinetobacter baumannii</i>	ABUH576
1161	NZ_NDAP01000083.1	<i>Acinetobacter baumannii</i>	ABUH578
1162	NZ_MSOM01000001.1	<i>Acinetobacter baumannii</i>	ABUH579
1163	NZ_NDAQ01000059.1	<i>Acinetobacter baumannii</i>	ABUH580
1164	NZ_MSON01000001.1	<i>Acinetobacter baumannii</i>	ABUH582
1165	NZ_MSOO01000001.1	<i>Acinetobacter baumannii</i>	ABUH585
1166	NZ_NDAR01000040.1	<i>Acinetobacter baumannii</i>	ABUH586
1167	NZ_MSOP01000001.1	<i>Acinetobacter baumannii</i>	ABUH588
1168	NZ_NDAS01000028.1	<i>Acinetobacter baumannii</i>	ABUH589
1169	NZ_MSOQ01000001.1	<i>Acinetobacter baumannii</i>	ABUH591
1170	NZ_NDAT01000083.1	<i>Acinetobacter baumannii</i>	ABUH592
1171	NZ_MSOR01000001.1	<i>Acinetobacter baumannii</i>	ABUH594
1172	NZ_NDAU01000029.1	<i>Acinetobacter baumannii</i>	ABUH596
1173	NZ_MSOS01000001.1	<i>Acinetobacter baumannii</i>	ABUH597
1174	NZ_MSOT01000001.1	<i>Acinetobacter baumannii</i>	ABUH603
1175	NZ_NDAV01000069.1	<i>Acinetobacter baumannii</i>	ABUH604
1176	NZ_JWRV03000001.1	<i>Acinetobacter baumannii</i>	ABUH60486
1177	NZ_MSOU01000001.1	<i>Acinetobacter baumannii</i>	ABUH606
1178	NZ_NDAW01000023.1	<i>Acinetobacter baumannii</i>	ABUH608
1179	NZ_NDAX01000055.1	<i>Acinetobacter baumannii</i>	ABUH610
1180	NZ_MSOV01000001.1	<i>Acinetobacter baumannii</i>	ABUH612
1181	NZ_MSOW01000001.1	<i>Acinetobacter baumannii</i>	ABUH615
1182	NZ_MSOX01000001.1	<i>Acinetobacter baumannii</i>	ABUH618
1183	NZ_NDAY01000029.1	<i>Acinetobacter baumannii</i>	ABUH619
1184	NZ_MSOU01000001.1	<i>Acinetobacter baumannii</i>	ABUH621
1185	NZ_NDAZ01000021.1	<i>Acinetobacter baumannii</i>	ABUH622
1186	NZ_NDBA01000019.1	<i>Acinetobacter baumannii</i>	ABUH625

	NCBI Reference Sequence ID#	Strain	
1187	NZ_MSOZ01000001.1	<i>Acinetobacter baumannii</i>	ABUH627
1188	NZ_NCZV01000106.1	<i>Acinetobacter baumannii</i>	ABUH628
1189	NZ_MSPA01000001.1	<i>Acinetobacter baumannii</i>	ABUH630
1190	NZ_NCZW01000027.1	<i>Acinetobacter baumannii</i>	ABUH631
1191	NZ_NCZX01000039.1	<i>Acinetobacter baumannii</i>	ABUH632
1192	NZ_MSNG01000001.1	<i>Acinetobacter baumannii</i>	ABUH633
1193	NZ_NCZY01000057.1	<i>Acinetobacter baumannii</i>	ABUH634
1194	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i>	ABUH636
1195	NZ_NCZZ01000026.1	<i>Acinetobacter baumannii</i>	ABUH638
1196	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i>	ABUH639
1197	NZ_NDAA01000142.1	<i>Acinetobacter baumannii</i>	ABUH641
1198	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i>	ABUH642
1199	NZ_NDAB01000148.1	<i>Acinetobacter baumannii</i>	ABUH644
1200	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i>	ABUH645
1201	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i>	ABUH648
1202	NZ_NDAC01000110.1	<i>Acinetobacter baumannii</i>	ABUH649
1203	NZ_NDAD01000029.1	<i>Acinetobacter baumannii</i>	ABUH650
1204	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i>	ABUH651
1205	NZ_NDAE01000015.1	<i>Acinetobacter baumannii</i>	ABUH653
1206	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i>	ABUH654
1207	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i>	ABUH657
1208	NZ_NDAF01000038.1	<i>Acinetobacter baumannii</i>	ABUH658
1209	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i>	ABUH660
1210	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i>	ABUH669
1211	NZ_NDAG01000021.1	<i>Acinetobacter baumannii</i>	ABUH670
1212	NZ_MSNI01000001.1	<i>Acinetobacter baumannii</i>	ABUH672
1213	NZ_NDAH01000088.1	<i>Acinetobacter baumannii</i>	ABUH673

	NCBI Reference Sequence ID#	Strain	
1214	NZ_MSNS01000001.1	<i>Acinetobacter baumannii</i>	ABUH675
1215	NZ_NDAI01000089.1	<i>Acinetobacter baumannii</i>	ABUH678
1216	NZ_NDAJ01000018.1	<i>Acinetobacter baumannii</i>	ABUH680
1217	NZ_MSNT01000001.1	<i>Acinetobacter baumannii</i>	ABUH681
1218	NZ_MSNU01000001.1	<i>Acinetobacter baumannii</i>	ABUH687
1219	NZ_NDAK01000054.1	<i>Acinetobacter baumannii</i>	ABUH688
1220	NZ_MSNU01000001.1	<i>Acinetobacter baumannii</i>	ABUH690
1221	NZ_NDAL01000066.1	<i>Acinetobacter baumannii</i>	ABUH691
1222	NZ_NDAM01000088.1	<i>Acinetobacter baumannii</i>	ABUH692
1223	NZ_MSNU01000001.1	<i>Acinetobacter baumannii</i>	ABUH693
1224	NZ_LZVK01000001.1	<i>Acinetobacter baumannii</i>	ABUH695
1225	NZ_LZTR01000001.1	<i>Acinetobacter baumannii</i>	ABUH696
1226	NZ_LZVL01000001.1	<i>Acinetobacter baumannii</i>	ABUH698
1227	NZ_LZTV01000001.1	<i>Acinetobacter baumannii</i>	ABUH699
1228	NZ_LZTW01000001.1	<i>Acinetobacter baumannii</i>	ABUH702
1229	NZ_LZXK01000001.1	<i>Acinetobacter baumannii</i>	ABUH703
1230	NZ_LZVM01000001.1	<i>Acinetobacter baumannii</i>	ABUH704
1231	NZ_LZWB01000001.1	<i>Acinetobacter baumannii</i>	ABUH705
1232	NZ_LZTS01000001.1	<i>Acinetobacter baumannii</i>	ABUH706
1233	NZ_LZWC01000001.1	<i>Acinetobacter baumannii</i>	ABUH707
1234	NZ_LZXL01000001.1	<i>Acinetobacter baumannii</i>	ABUH708
1235	NZ_LZVN01000001.1	<i>Acinetobacter baumannii</i>	ABUH709
1236	NZ_LZWD01000001.1	<i>Acinetobacter baumannii</i>	ABUH710
1237	NZ_LZUN01000001.1	<i>Acinetobacter baumannii</i>	ABUH712
1238	NZ_LZTX01000001.1	<i>Acinetobacter baumannii</i>	ABUH713
1239	NZ_LZUO01000001.1	<i>Acinetobacter baumannii</i>	ABUH714
1240	NZ_LZXM01000001.1	<i>Acinetobacter baumannii</i>	ABUH715

	NCBI Reference Sequence ID#	Strain	
1241	NZ_LZWE01000001.1	<i>Acinetobacter baumannii</i>	ABUH716
1242	NZ_LZXN01000001.1	<i>Acinetobacter baumannii</i>	ABUH717
1243	NZ_LZWF01000001.1	<i>Acinetobacter baumannii</i>	ABUH718
1244	NZ_LZWG01000001.1	<i>Acinetobacter baumannii</i>	ABUH719
1245	NZ_LZTT01000001.1	<i>Acinetobacter baumannii</i>	ABUH720
1246	NZ_LZWH01000001.1	<i>Acinetobacter baumannii</i>	ABUH721
1247	NZ_LZTY01000001.1	<i>Acinetobacter baumannii</i>	ABUH722
1248	NZ_LZTZ01000001.1	<i>Acinetobacter baumannii</i>	ABUH723
1249	NZ_LZXO01000001.1	<i>Acinetobacter baumannii</i>	ABUH724
1250	NZ_LZVO01000001.1	<i>Acinetobacter baumannii</i>	ABUH725
1251	NZ_LZWI01000001.1	<i>Acinetobacter baumannii</i>	ABUH726
1252	NZ_LZVP01000001.1	<i>Acinetobacter baumannii</i>	ABUH728
1253	NZ_LZUA01000001.1	<i>Acinetobacter baumannii</i>	ABUH729
1254	NZ_LZWJ01000001.1	<i>Acinetobacter baumannii</i>	ABUH730
1255	NZ_LZVH01000001.1	<i>Acinetobacter baumannii</i>	ABUH731
1256	NZ_LZWK01000001.1	<i>Acinetobacter baumannii</i>	ABUH733
1257	NZ_LZWL01000001.1	<i>Acinetobacter baumannii</i>	ABUH734
1258	NZ_LZVQ01000001.1	<i>Acinetobacter baumannii</i>	ABUH735
1259	NZ_LZUY01000001.1	<i>Acinetobacter baumannii</i>	ABUH736
1260	NZ_LZUH01000001.1	<i>Acinetobacter baumannii</i>	ABUH737
1261	NZ_LZXW01000001.1	<i>Acinetobacter baumannii</i>	ABUH738
1262	NZ_LZUP01000001.1	<i>Acinetobacter baumannii</i>	ABUH739
1263	NZ_LZXP01000001.1	<i>Acinetobacter baumannii</i>	ABUH740
1264	NZ_LZXQ01000001.1	<i>Acinetobacter baumannii</i>	ABUH741
1265	NZ_LZVR01000001.1	<i>Acinetobacter baumannii</i>	ABUH743
1266	NZ_LZXR01000001.1	<i>Acinetobacter baumannii</i>	ABUH744
1267	NZ_LZVS01000001.1	<i>Acinetobacter baumannii</i>	ABUH745

	NCBI Reference Sequence ID#	Strain	
1268	NZ_LZUZ01000001.1	<i>Acinetobacter baumannii</i>	ABUH746
1269	NZ_LZXS01000001.1	<i>Acinetobacter baumannii</i>	ABUH747
1270	NZ_LZVA01000001.1	<i>Acinetobacter baumannii</i>	ABUH748
1271	NZ_LZUK01000001.1	<i>Acinetobacter baumannii</i>	ABUH749
1272	NZ_LZVB01000001.1	<i>Acinetobacter baumannii</i>	ABUH750
1273	NZ_LZTU01000001.1	<i>Acinetobacter baumannii</i>	ABUH751
1274	NZ_LZVC01000001.1	<i>Acinetobacter baumannii</i>	ABUH752
1275	NZ_LZVD01000001.1	<i>Acinetobacter baumannii</i>	ABUH753
1276	NZ_LZVZ01000001.1	<i>Acinetobacter baumannii</i>	ABUH754
1277	NZ_LZVT01000001.1	<i>Acinetobacter baumannii</i>	ABUH755
1278	NZ_LZXT01000001.1	<i>Acinetobacter baumannii</i>	ABUH756
1279	NZ_LZVJ01000001.1	<i>Acinetobacter baumannii</i>	ABUH758
1280	NZ_LZUB01000001.1	<i>Acinetobacter baumannii</i>	ABUH759
1281	NZ_LZVE01000001.1	<i>Acinetobacter baumannii</i>	ABUH760
1282	NZ_LZVF01000001.1	<i>Acinetobacter baumannii</i>	ABUH761
1283	NZ_LZVI01000001.1	<i>Acinetobacter baumannii</i>	ABUH762
1284	NZ_LZVU01000001.1	<i>Acinetobacter baumannii</i>	ABUH763
1285	NZ_LZUF01000001.1	<i>Acinetobacter baumannii</i>	ABUH764
1286	NZ_LZXU01000001.1	<i>Acinetobacter baumannii</i>	ABUH765
1287	NZ_LZVG01000001.1	<i>Acinetobacter baumannii</i>	ABUH766
1288	NZ_LZUQ01000001.1	<i>Acinetobacter baumannii</i>	ABUH767
1289	NZ_LZXC01000001.1	<i>Acinetobacter baumannii</i>	ABUH768
1290	NZ_LZWA01000001.1	<i>Acinetobacter baumannii</i>	ABUH769
1291	NZ_LZWM01000001.1	<i>Acinetobacter baumannii</i>	ABUH770
1292	NZ_LZWN01000001.1	<i>Acinetobacter baumannii</i>	ABUH771
1293	NZ_LZTQ01000001.1	<i>Acinetobacter baumannii</i>	ABUH772
1294	NZ_LZUR01000001.1	<i>Acinetobacter baumannii</i>	ABUH773

	NCBI Reference Sequence ID#	Strain	
1295	NZ_LZUC01000001.1	<i>Acinetobacter baumannii</i>	ABUH774
1296	NZ_LZUS01000001.1	<i>Acinetobacter baumannii</i>	ABUH775
1297	NZ_LZXV01000001.1	<i>Acinetobacter baumannii</i>	ABUH776
1298	NZ_LZUL01000001.1	<i>Acinetobacter baumannii</i>	ABUH777
1299	NZ_LZUM01000001.1	<i>Acinetobacter baumannii</i>	ABUH778
1300	NZ_LZW0010000001.1	<i>Acinetobacter baumannii</i>	ABUH779
1301	NZ_LZWP01000001.1	<i>Acinetobacter baumannii</i>	ABUH780
1302	NZ_LZWQ01000001.1	<i>Acinetobacter baumannii</i>	ABUH781
1303	NZ_LZTP01000001.1	<i>Acinetobacter baumannii</i>	ABUH782
1304	NZ_LZWR01000001.1	<i>Acinetobacter baumannii</i>	ABUH783
1305	NZ_LZWS01000001.1	<i>Acinetobacter baumannii</i>	ABUH784
1306	NZ_LZXD01000001.1	<i>Acinetobacter baumannii</i>	ABUH785
1307	NZ_LZUT01000001.1	<i>Acinetobacter baumannii</i>	ABUH786
1308	NZ_LZWT01000001.1	<i>Acinetobacter baumannii</i>	ABUH787
1309	NZ_LZUJ01000001.1	<i>Acinetobacter baumannii</i>	ABUH788
1310	NZ_LZUU01000001.1	<i>Acinetobacter baumannii</i>	ABUH789
1311	NZ_LZUD01000001.1	<i>Acinetobacter baumannii</i>	ABUH790
1312	NZ_LZVV01000001.1	<i>Acinetobacter baumannii</i>	ABUH791
1313	NZ_LZUG01000001.1	<i>Acinetobacter baumannii</i>	ABUH792
1314	NZ_LZWW01000001.1	<i>Acinetobacter baumannii</i>	ABUH793
1315	NZ_LZWX01000001.1	<i>Acinetobacter baumannii</i>	ABUH794
1316	NZ_LZVV01000001.1	<i>Acinetobacter baumannii</i>	ABUH795
1317	NZ_LZVW01000001.1	<i>Acinetobacter baumannii</i>	ABUH796
1318	NZ_LZUU01000001.1	<i>Acinetobacter baumannii</i>	ABUH797
1319	NZ_LZXE01000001.1	<i>Acinetobacter baumannii</i>	ABUH798
1320	NZ_LZXF01000001.1	<i>Acinetobacter baumannii</i>	ABUH799
1321	NZ_LZYG01000001.1	<i>Acinetobacter baumannii</i>	ABUH800

	NCBI Reference Sequence ID#	Strain	
1322	NZ_LZXH01000001.1	<i>Acinetobacter baumannii</i>	ABUH801
1323	NZ_LZXI01000001.1	<i>Acinetobacter baumannii</i>	ABUH802
1324	NZ_JWSB03000001.1	<i>Acinetobacter baumannii</i>	ABUH80286
1325	NZ_LZWY01000001.1	<i>Acinetobacter baumannii</i>	ABUH803
1326	NZ_LZWZ01000001.1	<i>Acinetobacter baumannii</i>	ABUH804
1327	NZ_LZXA01000001.1	<i>Acinetobacter baumannii</i>	ABUH805
1328	NZ_LZXB01000001.1	<i>Acinetobacter baumannii</i>	ABUH806
1329	NZ_LZVX01000001.1	<i>Acinetobacter baumannii</i>	ABUH807
1330	NZ_LZXJ01000001.1	<i>Acinetobacter baumannii</i>	ABUH808
1331	NZ_LZUI01000001.1	<i>Acinetobacter baumannii</i>	ABUH809
1332	NZ_LZUV01000001.1	<i>Acinetobacter baumannii</i>	ABUH810
1333	NZ_LZUW01000001.1	<i>Acinetobacter baumannii</i>	ABUH811
1334	NZ_LZUX01000001.1	<i>Acinetobacter baumannii</i>	ABUH812
1335	NZ_LZVY01000001.1	<i>Acinetobacter baumannii</i>	ABUH813
1336	NZ_LZUE01000001.1	<i>Acinetobacter baumannii</i>	ABUH814
1337	NZ_MJBA01000010.1	<i>Acinetobacter baumannii</i>	AC_2355
1338	NZ_MJAY01000100.1	<i>Acinetobacter baumannii</i>	AC_4160
1339	NZ_MJAZ01000010.1	<i>Acinetobacter baumannii</i>	AC_4820
1340	NZ_MJBB01000100.1	<i>Acinetobacter baumannii</i>	AC_5696
1341	NZ_MJBD01000100.1	<i>Acinetobacter baumannii</i>	AC_6031
1342	NZ_MJBC01000010.1	<i>Acinetobacter baumannii</i>	AC_6066
1343	NZ_MJBE01000100.1	<i>Acinetobacter baumannii</i>	AC_6321
1344	NZ_LNUY01000001.1	<i>Acinetobacter baumannii</i>	AC001
1345	NZ_LNVB01000001.1	<i>Acinetobacter baumannii</i>	AC001-8-R1
1346	NZ_LNVC01000001.1	<i>Acinetobacter baumannii</i>	AC001-8-R1-S1
1347	NZ_LNUZ01000001.1	<i>Acinetobacter baumannii</i>	AC002
1348	NZ_CM008330.1	<i>Acinetobacter baumannii</i>	AC002-1-R4

	NCBI Reference Sequence ID#	Strain
1349	NZ_LNVD01000001.1	<i>Acinetobacter baumannii</i> AC002-1-R4-S1
1350	NZ_LNUX01000001.1	<i>Acinetobacter baumannii</i> AC003
1351	NZ_LNVA01000001.1	<i>Acinetobacter baumannii</i> AC003-2-R1
1352	NZ_FWWQ01000174.1	<i>Acinetobacter baumannii</i> AC13_M
1353	NZ_FWYM01000084.1	<i>Acinetobacter baumannii</i> AC15_M
1354	NZ_CP007535.2	<i>Acinetobacter baumannii</i> AC29
1355	NZ_FWYN01000236.1	<i>Acinetobacter baumannii</i> AC40_M
1356	NZ_OEON01000118.1	<i>Acinetobacter baumannii</i> ACB5
1357	NZ_PXHY01000010.1	<i>Acinetobacter baumannii</i> ACM-1
1358	NZ_PYCW01000099.1	<i>Acinetobacter baumannii</i> ACM-11
1359	NZ_PYCY01000098.1	<i>Acinetobacter baumannii</i> ACM-12
1360	NZ_PYCZ01000099.1	<i>Acinetobacter baumannii</i> ACM-13
1361	NZ_PYDA01000100.1	<i>Acinetobacter baumannii</i> ACM-14
1362	NZ_PYDB01000099.1	<i>Acinetobacter baumannii</i> ACM-15
1363	NZ_PYDC01000100.1	<i>Acinetobacter baumannii</i> ACM-16
1364	NZ_PYDD01000100.1	<i>Acinetobacter baumannii</i> ACM-17
1365	NZ_PYDE01000098.1	<i>Acinetobacter baumannii</i> ACM-18
1366	NZ_PYDF01000095.1	<i>Acinetobacter baumannii</i> ACM-19
1367	NZ_PYDG01000100.1	<i>Acinetobacter baumannii</i> ACM-20
1368	NZ_PYDH01000099.1	<i>Acinetobacter baumannii</i> ACM-21
1369	NZ_PYDI01000099.1	<i>Acinetobacter baumannii</i> ACM-22
1370	NZ_PYDJ01000100.1	<i>Acinetobacter baumannii</i> ACM-23
1371	NZ_PYDK01000100.1	<i>Acinetobacter baumannii</i> ACM-24
1372	NZ_PXYP01000100.1	<i>Acinetobacter baumannii</i> ACM-25
1373	NZ_PYDM01000094.1	<i>Acinetobacter baumannii</i> ACM-27
1374	NZ_PYDN01000099.1	<i>Acinetobacter baumannii</i> ACM-28
1375	NZ_PYDO01000100.1	<i>Acinetobacter baumannii</i> ACM-29

	NCBI Reference Sequence ID#	Strain	
1376	NZ_PYPD01000098.1	<i>Acinetobacter baumannii</i>	ACM-30
1377	NZ_PYDQ01000100.1	<i>Acinetobacter baumannii</i>	ACM-31
1378	NZ_PYDR01000097.1	<i>Acinetobacter baumannii</i>	ACM-32
1379	NZ_PYDS01000100.1	<i>Acinetobacter baumannii</i>	ACM-33
1380	NZ_PYCX01000100.1	<i>Acinetobacter baumannii</i>	ACM-5
1381	NZ_PYCV01000100.1	<i>Acinetobacter baumannii</i>	ACM-9
1382	NZ_LKMA01000001.1	<i>Acinetobacter baumannii</i>	ACMH-6200
1383	NZ_LKMB01000001.1	<i>Acinetobacter baumannii</i>	ACMH-6201
1384	NZ_FWFB01000250.1	<i>Acinetobacter baumannii</i>	AE3M
1385	NZ_CP018254.1	<i>Acinetobacter baumannii</i>	AF-401
1386	NZ_CP018256.1	<i>Acinetobacter baumannii</i>	AF-673
1387	NZ_KB84951.1	<i>Acinetobacter baumannii</i>	ANC
1388	NZ_MSFY01000053.1	<i>Acinetobacter baumannii</i>	antalya35
1389	NZ_MPCA01000001.1	<i>Acinetobacter baumannii</i>	AR_0033
1390	NZ_MPZ01000001.1	<i>Acinetobacter baumannii</i>	AR_0035
1391	NZ_MPBY01000001.1	<i>Acinetobacter baumannii</i>	AR_0036
1392	NZ_MPBX01000001.1	<i>Acinetobacter baumannii</i>	AR_0037
1393	NZ_MPBW01000001.1	<i>Acinetobacter baumannii</i>	AR_0045
1394	NZ_CP026707.1	<i>Acinetobacter baumannii</i>	AR_0056
1395	NZ_CP027123.1	<i>Acinetobacter baumannii</i>	AR_0056
1396	NZ_CP026711.1	<i>Acinetobacter baumannii</i>	AR_0063
1397	NZ_CP026761.1	<i>Acinetobacter baumannii</i>	AR_0078
1398	NZ_CP027528.1	<i>Acinetobacter baumannii</i>	AR_0083
1399	NZ_CP027530.1	<i>Acinetobacter baumannii</i>	AR_0088
1400	NZ_CP027611.1	<i>Acinetobacter baumannii</i>	AR_0101
1401	NZ_CP027607.1	<i>Acinetobacter baumannii</i>	AR_0102
1402	NZ_NEQF01000075.1	<i>Acinetobacter baumannii</i>	ARLG-1775

	NCBI Reference Sequence ID#	Strain
1403	NZ_NEQH01000008.1	<i>Acinetobacter baumannii</i> ARLG-1777
1404	NZ_NEQG01000032.1	<i>Acinetobacter baumannii</i> ARLG-1788
1405	NZ_NEQE01000046.1	<i>Acinetobacter baumannii</i> ARLG-1818
1406	NZ_NEQI01000042.1	<i>Acinetobacter baumannii</i> ARLG-1854
1407	NZ_NEQK01000090.1	<i>Acinetobacter baumannii</i> ARLG-1860
1408	NZ_NEQL01000073.1	<i>Acinetobacter baumannii</i> ARLG-1894
1409	NZ_NEQM01000073.1	<i>Acinetobacter baumannii</i> ARLG-1912
1410	NZ_NEQJ01000126.1	<i>Acinetobacter baumannii</i> ARLG-1915
1411	NZ_NGHK01000055.1	<i>Acinetobacter baumannii</i> ARLG1275
1412	NZ_NGHL01000078.1	<i>Acinetobacter baumannii</i> ARLG1294
1413	NZ_NGHM01000021.1	<i>Acinetobacter baumannii</i> ARLG1306
1414	NZ_NGHN01000062.1	<i>Acinetobacter baumannii</i> ARLG1314
1415	NZ_NGHO01000003.1	<i>Acinetobacter baumannii</i> ARLG1317
1416	NZ_NGHP01000049.1	<i>Acinetobacter baumannii</i> ARLG1323
1417	NZ_NGHQ01000032.1	<i>Acinetobacter baumannii</i> ARLG1326
1418	NZ_NGHR01000009.1	<i>Acinetobacter baumannii</i> ARLG1327
1419	NZ_NGGJ01000021.1	<i>Acinetobacter baumannii</i> ARLG1786
1420	NZ_NGGK01000023.1	<i>Acinetobacter baumannii</i> ARLG1787
1421	NZ_NNGM01000041.1	<i>Acinetobacter baumannii</i> ARLG1790
1422	NZ_NNGN01000043.1	<i>Acinetobacter baumannii</i> ARLG1792
1423	NZ_NNGO01000025.1	<i>Acinetobacter baumannii</i> ARLG1793
1424	NZ_NNGP01000097.1	<i>Acinetobacter baumannii</i> ARLG1794
1425	NZ_NNGR01000056.1	<i>Acinetobacter baumannii</i> ARLG1800
1426	NZ_NNGS01000022.1	<i>Acinetobacter baumannii</i> ARLG1802
1427	NZ_NNGV01000024.1	<i>Acinetobacter baumannii</i> ARLG1806
1428	NZ_NNGX01000019.1	<i>Acinetobacter baumannii</i> ARLG1810
1429	NZ_NNGY01000046.1	<i>Acinetobacter baumannii</i> ARLG1814

	NCBI Reference Sequence ID#	Strain	
1430	NZ_NGGZ01000155.1	<i>Acinetobacter baumannii</i>	ARLG1816
1431	NZ_NGHA01000075.1	<i>Acinetobacter baumannii</i>	ARLG1819
1432	NZ_NGHB01000137.1	<i>Acinetobacter baumannii</i>	ARLG1821
1433	NZ_NGHC01000006.1	<i>Acinetobacter baumannii</i>	ARLG1824
1434	NZ_NGHD01000001.1	<i>Acinetobacter baumannii</i>	ARLG1827
1435	NZ_NGHE01000010.1	<i>Acinetobacter baumannii</i>	ARLG1830
1436	NZ_NGHF01000043.1	<i>Acinetobacter baumannii</i>	ARLG1833
1437	NZ_NGHG01000083.1	<i>Acinetobacter baumannii</i>	ARLG1835
1438	NZ_NGHH01000053.1	<i>Acinetobacter baumannii</i>	ARLG1836
1439	NZ_NGHI01000008.1	<i>Acinetobacter baumannii</i>	ARLG1838
1440	NZ_NGFQ01000028.1	<i>Acinetobacter baumannii</i>	ARLG1840
1441	NZ_NGFR01000081.1	<i>Acinetobacter baumannii</i>	ARLG1841
1442	NZ_NGFS01000007.1	<i>Acinetobacter baumannii</i>	ARLG1842
1443	NZ_NGFT01000094.1	<i>Acinetobacter baumannii</i>	ARLG1843
1444	NZ_NGFU01000023.1	<i>Acinetobacter baumannii</i>	ARLG1845
1445	NZ_NGFV01000063.1	<i>Acinetobacter baumannii</i>	ARLG1846
1446	NZ_NGFW01000068.1	<i>Acinetobacter baumannii</i>	ARLG1847
1447	NZ_NGFX01000019.1	<i>Acinetobacter baumannii</i>	ARLG1849
1448	NZ_NGFY01000033.1	<i>Acinetobacter baumannii</i>	ARLG1851
1449	NZ_NGFZ01000030.1	<i>Acinetobacter baumannii</i>	ARLG1853
1450	NZ_NGGA01000006.1	<i>Acinetobacter baumannii</i>	ARLG1855
1451	NZ_NGGB01000034.1	<i>Acinetobacter baumannii</i>	ARLG1856
1452	NZ_NGGC01000006.1	<i>Acinetobacter baumannii</i>	ARLG1857
1453	NZ_NGGD01000005.1	<i>Acinetobacter baumannii</i>	ARLG1858
1454	NZ_NGGE01000005.1	<i>Acinetobacter baumannii</i>	ARLG1859
1455	NZ_NGGF01000009.1	<i>Acinetobacter baumannii</i>	ARLG1862
1456	NZ_NGIV01000054.1	<i>Acinetobacter baumannii</i>	ARLG1864

	NCBI Reference Sequence ID#		Strain	
1457	NZ_NGIY01000013.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1871
1458	NZ_NGIZ01000021.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1872
1459	NZ_NGJA01000182.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1873
1460	NZ_NGJB01000106.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1874
1461	NZ_NGJD01000033.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1880
1462	NZ_NGJE01000034.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1881
1463	NZ_NGJF01000042.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1882
1464	NZ_NGJG01000052.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1885
1465	NZ_NGJH01000056.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1886
1466	NZ_NGJI01000008.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1891
1467	NZ_NGHU01000147.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1892
1468	NZ_NGHV01000010.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1893
1469	NZ_NGHW01000010.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1896
1470	NZ_NGHX01000052.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1898
1471	NZ_NGHY01000031.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1899
1472	NZ_NGHZ01000129.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1900
1473	NZ_NGIA01000011.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1901
1474	NZ_NGIB01000027.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1902
1475	NZ_NGIC01000074.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1904
1476	NZ_NGID01000020.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1906
1477	NZ_NGIE01000081.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1907
1478	NZ_NGIF01000023.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1914
1479	NZ_NGIG01000066.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1929
1480	NZ_NGII01000005.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1933
1481	NZ_NGIJ01000016.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1935
1482	NZ_NGIK01000023.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1936
1483	NZ_NGIM01000074.1	<i>Acinetobacter</i>	<i>baumannii</i>	ARLG1940

	NCBI Reference Sequence ID#	Strain	
1484	NZ_NGIN01000012.1	<i>Acinetobacter baumannii</i>	ARLG1941
1485	NZ_NGIP01000166.1	<i>Acinetobacter baumannii</i>	ARLG1946
1486	NZ_NGIU01000004.1	<i>Acinetobacter baumannii</i>	ARLG1962
1487	NZ_GG704593.1	<i>Acinetobacter baumannii</i>	ATCC
1488	NZ_KL810966.1	<i>Acinetobacter baumannii</i>	ATCC
1489	NZ_KB849970.1	<i>Acinetobacter baumannii</i>	ATCC
1490	NZ_CP012004.1	<i>Acinetobacter baumannii</i>	ATCC
1491	NZ_MJHA01000001.1	<i>Acinetobacter baumannii</i>	ATCC
1492	NZ_MTTGG01000001.1	<i>Acinetobacter baumannii</i>	ATCC
1493	NZ_CP018664.1	<i>Acinetobacter baumannii</i>	ATCC
1494	NZ_CZWC01000001.1	<i>Acinetobacter baumannii</i>	ATCC19606
1495	NZ_CP024124.1	<i>Acinetobacter baumannii</i>	AYP-A2
1496	NZ_FITR01000001.1	<i>Acinetobacter baumannii</i>	B
1497	NZ_CP021345.1	<i>Acinetobacter baumannii</i>	B11911
1498	NZ_CP021347.1	<i>Acinetobacter baumannii</i>	B8300
1499	NZ_CP021342.1	<i>Acinetobacter baumannii</i>	B8342
1500	NZ_CZWB01000001.1	<i>Acinetobacter baumannii</i>	BAL
1501	NZ_CZWD01000001.1	<i>Acinetobacter baumannii</i>	BAL
1502	NZ_CZWF01000001.1	<i>Acinetobacter baumannii</i>	BAL
1503	NZ_CZWE01000001.1	<i>Acinetobacter baumannii</i>	BAL
1504	NZ_CZWG01000001.1	<i>Acinetobacter baumannii</i>	BAL
1505	NZ_LT594095.1	<i>Acinetobacter baumannii</i>	BAL062
1506	NZ_NIWN01000100.1	<i>Acinetobacter baumannii</i>	BAuABod-3
1507	NZ_KK736155.1	<i>Acinetobacter baumannii</i>	BIDMC
1508	NZ_KK737786.1	<i>Acinetobacter baumannii</i>	BIDMC
1509	NZ_JPLF01000001.1	<i>Acinetobacter baumannii</i>	BJ1
1510	NZ_JPLG01000001.1	<i>Acinetobacter baumannii</i>	BJ2

	NCBI Reference Sequence ID#	Strain	
1511	NZ_JPLH01000001.1	<i>Acinetobacter baumannii</i>	BJ3
1512	NZ_JPLJ01000001.1	<i>Acinetobacter baumannii</i>	BJ4
1513	NZ_JPLJ01000001.1	<i>Acinetobacter baumannii</i>	BJ5
1514	NZ_JPLK01000001.1	<i>Acinetobacter baumannii</i>	BJ6
1515	NZ_JPLL01000001.1	<i>Acinetobacter baumannii</i>	BJ7
1516	NZ_JPLM01000001.1	<i>Acinetobacter baumannii</i>	BJ8
1517	NC_021726.1	<i>Acinetobacter baumannii</i>	BJAB07104
1518	NC_021733.1	<i>Acinetobacter baumannii</i>	BJAB0715
1519	NC_021729.1	<i>Acinetobacter baumannii</i>	BJAB0868
1520	NZ_JNOT01000001.1	<i>Acinetobacter baumannii</i>	BM4587
1521	NZ_JNFY01000001.1	<i>Acinetobacter baumannii</i>	BR097
1522	NZ_JNFZ01000001.1	<i>Acinetobacter baumannii</i>	BU310
1523	NZ_ALOH01000001.1	<i>Acinetobacter baumannii</i>	BZICU-2
1524	NZ_FCNC01000001.1	<i>Acinetobacter baumannii</i>	C
1525	NZ_AMSZ01000001.1	<i>Acinetobacter baumannii</i>	Canada
1526	NZ_AFDN01000003.1	<i>Acinetobacter baumannii</i>	Canada
1527	NZ_CP020586.1	<i>Acinetobacter baumannii</i>	CBA7
1528	NZ_NLCO01000001.1	<i>Acinetobacter baumannii</i>	CCBH15815
1529	NZ_LAXF01000002.1	<i>Acinetobacter baumannii</i>	CCBH5233
1530	NZ_LYZL01000001.1	<i>Acinetobacter baumannii</i>	CCF1
1531	NZ_LZAD01000001.1	<i>Acinetobacter baumannii</i>	CCF10
1532	NZ_LZAE01000001.1	<i>Acinetobacter baumannii</i>	CCF11
1533	NZ_LZAF01000001.1	<i>Acinetobacter baumannii</i>	CCF12
1534	NZ_LZAG01000001.1	<i>Acinetobacter baumannii</i>	CCF13
1535	NZ_LZAH01000001.1	<i>Acinetobacter baumannii</i>	CCF14
1536	NZ_LZAI01000001.1	<i>Acinetobacter baumannii</i>	CCF15
1537	NZ_LZAJ01000001.1	<i>Acinetobacter baumannii</i>	CCF16

	NCBI Reference Sequence ID#	Strain	
1538	NZ_LZAK01000001.1	<i>Acinetobacter baumannii</i>	CCF17
1539	NZ_LZAL01000001.1	<i>Acinetobacter baumannii</i>	CCF18
1540	NZ_LZAM01000001.1	<i>Acinetobacter baumannii</i>	CCF19
1541	NZ_LYZV01000001.1	<i>Acinetobacter baumannii</i>	CCF2
1542	NZ_LZAN01000001.1	<i>Acinetobacter baumannii</i>	CCF20
1543	NZ_LZAO01000001.1	<i>Acinetobacter baumannii</i>	CCF21
1544	NZ_LZAP01000001.1	<i>Acinetobacter baumannii</i>	CCF22
1545	NZ_LZAQ01000001.1	<i>Acinetobacter baumannii</i>	CCF23
1546	NZ_LZAR01000001.1	<i>Acinetobacter baumannii</i>	CCF24
1547	NZ_LZAS01000001.1	<i>Acinetobacter baumannii</i>	CCF25
1548	NZ_LZAT01000001.1	<i>Acinetobacter baumannii</i>	CCF26
1549	NZ_LZAU01000001.1	<i>Acinetobacter baumannii</i>	CCF28
1550	NZ_LZAV01000001.1	<i>Acinetobacter baumannii</i>	CCF29
1551	NZ_LYZW01000001.1	<i>Acinetobacter baumannii</i>	CCF3
1552	NZ_LZAW01000001.1	<i>Acinetobacter baumannii</i>	CCF30
1553	NZ_LZAX01000001.1	<i>Acinetobacter baumannii</i>	CCF31
1554	NZ_LZAY01000001.1	<i>Acinetobacter baumannii</i>	CCF32
1555	NZ_LYZM01000001.1	<i>Acinetobacter baumannii</i>	CCF33
1556	NZ_LYZN01000001.1	<i>Acinetobacter baumannii</i>	CCF34
1557	NZ_LYZO01000001.1	<i>Acinetobacter baumannii</i>	CCF35
1558	NZ_LYZP01000001.1	<i>Acinetobacter baumannii</i>	CCF36
1559	NZ_LYZQ01000001.1	<i>Acinetobacter baumannii</i>	CCF37
1560	NZ_LYZR01000001.1	<i>Acinetobacter baumannii</i>	CCF38
1561	NZ_LYZS01000001.1	<i>Acinetobacter baumannii</i>	CCF39
1562	NZ_LYZX01000001.1	<i>Acinetobacter baumannii</i>	CCF4
1563	NZ_LZEV01000001.1	<i>Acinetobacter baumannii</i>	CCF40
1564	NZ_LYZT01000001.1	<i>Acinetobacter baumannii</i>	CCF41

	NCBI Reference Sequence ID#	Strain	
1565	NZ_LYZU01000001.1	<i>Acinetobacter baumannii</i>	CCF42
1566	NZ_LZAZ01000001.1	<i>Acinetobacter baumannii</i>	CCF43
1567	NZ_LZBA01000001.1	<i>Acinetobacter baumannii</i>	CCF44
1568	NZ_LZBB01000001.1	<i>Acinetobacter baumannii</i>	CCF45
1569	NZ_LZBC01000001.1	<i>Acinetobacter baumannii</i>	CCF47
1570	NZ_LZBD01000001.1	<i>Acinetobacter baumannii</i>	CCF48
1571	NZ_LZBE01000001.1	<i>Acinetobacter baumannii</i>	CCF49
1572	NZ_LZFY01000001.1	<i>Acinetobacter baumannii</i>	CCF5
1573	NZ_LZBF01000001.1	<i>Acinetobacter baumannii</i>	CCF50
1574	NZ_LZBG01000001.1	<i>Acinetobacter baumannii</i>	CCF51
1575	NZ_LZBH01000001.1	<i>Acinetobacter baumannii</i>	CCF52
1576	NZ_LZBI01000001.1	<i>Acinetobacter baumannii</i>	CCF53
1577	NZ_LZBJ01000001.1	<i>Acinetobacter baumannii</i>	CCF54
1578	NZ_LZBK01000001.1	<i>Acinetobacter baumannii</i>	CCF55
1579	NZ_LZBL01000001.1	<i>Acinetobacter baumannii</i>	CCF57
1580	NZ_LZBM01000001.1	<i>Acinetobacter baumannii</i>	CCF58
1581	NZ_LZBN01000001.1	<i>Acinetobacter baumannii</i>	CCF59
1582	NZ_LZZZ01000001.1	<i>Acinetobacter baumannii</i>	CCF6
1583	NZ_LZBO01000001.1	<i>Acinetobacter baumannii</i>	CCF60
1584	NZ_LZBP01000001.1	<i>Acinetobacter baumannii</i>	CCF62
1585	NZ_LZBQ01000001.1	<i>Acinetobacter baumannii</i>	CCF63
1586	NZ_LZBR01000001.1	<i>Acinetobacter baumannii</i>	CCF64
1587	NZ_LZBS01000001.1	<i>Acinetobacter baumannii</i>	CCF65
1588	NZ_LZBT01000001.1	<i>Acinetobacter baumannii</i>	CCF66
1589	NZ_LZBU01000001.1	<i>Acinetobacter baumannii</i>	CCF67
1590	NZ_LZBV01000001.1	<i>Acinetobacter baumannii</i>	CCF68
1591	NZ_LZBW01000001.1	<i>Acinetobacter baumannii</i>	CCF69

	NCBI Reference Sequence ID#	Strain	
1592	NZ_LZAA01000001.1	<i>Acinetobacter baumannii</i>	CCF7
1593	NZ_LZBX01000001.1	<i>Acinetobacter baumannii</i>	CCF70
1594	NZ_LZBY01000001.1	<i>Acinetobacter baumannii</i>	CCF72
1595	NZ_LZBZ01000001.1	<i>Acinetobacter baumannii</i>	CCF73
1596	NZ_LZCA01000001.1	<i>Acinetobacter baumannii</i>	CCF74
1597	NZ_LZCB01000001.1	<i>Acinetobacter baumannii</i>	CCF75
1598	NZ_LZAB01000001.1	<i>Acinetobacter baumannii</i>	CCF8
1599	NZ_LZAC01000001.1	<i>Acinetobacter baumannii</i>	CCF9
1600	NZ_CVLD01000001.1	<i>Acinetobacter baumannii</i>	CHI-34
1601	NZ_CVLE01000001.1	<i>Acinetobacter baumannii</i>	CHI-45-1
1602	NZ_AVOC01000001.1	<i>Acinetobacter baumannii</i>	CI77
1603	NZ_AVOE01000001.1	<i>Acinetobacter baumannii</i>	CI78
1604	NZ_AVOD01000001.1	<i>Acinetobacter baumannii</i>	CI79
1605	NZ_AVOB01000001.1	<i>Acinetobacter baumannii</i>	CI86
1606	NZ_CP016295.1	<i>Acinetobacter baumannii</i>	CMC-CR-MDR-Ab4
1607	NZ_CP016300.1	<i>Acinetobacter baumannii</i>	CMC-CR-MDR-Ab66
1608	NZ_CP016298.1	<i>Acinetobacter baumannii</i>	CMC-MDR-Ab59
1609	NZ_HG977526.1	<i>Acinetobacter baumannii</i>	CR17
1610	NZ_LZYQ01000001.1	<i>Acinetobacter baumannii</i>	CRO1
1611	NZ_LZYR01000001.1	<i>Acinetobacter baumannii</i>	CRO2
1612	NZ_LZYS01000001.1	<i>Acinetobacter baumannii</i>	CRO3
1613	NZ_HG977522.1	<i>Acinetobacter baumannii</i>	CS01
1614	NZ_LXYW01000007.1	<i>Acinetobacter baumannii</i>	CU032113
1615	NZ_LXWY01000002.1	<i>Acinetobacter baumannii</i>	CU060707
1616	NZ_FCND01000001.1	<i>Acinetobacter baumannii</i>	D
1617	NC_020547.2	<i>Acinetobacter baumannii</i>	D1279779
1618	NZ_FBXI01000001.1	<i>Acinetobacter baumannii</i>	D13

	NCBI Reference Sequence ID#	Strain	
1619	NZ_FBWY01000001.1	<i>Acinetobacter baumannii</i>	D2
1620	NZ_FBXG01000001.1	<i>Acinetobacter baumannii</i>	D30
1621	NZ_FBWZ01000001.1	<i>Acinetobacter baumannii</i>	D3208
1622	NZ_CP012952.1	<i>Acinetobacter baumannii</i>	D36
1623	NZ_FBWW01000001.1	<i>Acinetobacter baumannii</i>	D62
1624	NZ_FBXH01000001.1	<i>Acinetobacter baumannii</i>	D78
1625	NZ_FBXC01000001.1	<i>Acinetobacter baumannii</i>	D81
1626	NZ_AP014649.1	<i>Acinetobacter baumannii</i>	DNA
1627	NZ_NOXP01000010.1	<i>Acinetobacter baumannii</i>	DR1
1628	NZ_NOXO01000010.1	<i>Acinetobacter baumannii</i>	DR2
1629	NZ_JJOC02000001.1	<i>Acinetobacter baumannii</i>	DSM
1630	NZ_CP017152.1	<i>Acinetobacter baumannii</i>	DU202
1631	NZ_FCNG01000001.1	<i>Acinetobacter baumannii</i>	E
1632	NZ_AVST01000001.1	<i>Acinetobacter baumannii</i>	EGD-HP18
1633	NZ_FCNI01000001.1	<i>Acinetobacter baumannii</i>	F
1634	NZ_LORJ02000002.1	<i>Acinetobacter baumannii</i>	FDAARGOS_123
1635	NZ_FCNI01000001.1	<i>Acinetobacter baumannii</i>	G
1636	NZ_FBXF01000001.1	<i>Acinetobacter baumannii</i>	G7
1637	NZ_NIWL01000010.1	<i>Acinetobacter baumannii</i>	GaenseEi-1
1638	NZ_NIWM01000098.1	<i>Acinetobacter baumannii</i>	Gaensemehl-2
1639	NZ_NIWO01000097.1	<i>Acinetobacter baumannii</i>	GB1-2
1640	NZ_LN868200.1	<i>Acinetobacter baumannii</i>	genome
1641	NZ_LN865143.1	<i>Acinetobacter baumannii</i>	genome
1642	NZ_LN997846.1	<i>Acinetobacter baumannii</i>	genome
1643	NZ_BBSP01000041.1	<i>Acinetobacter baumannii</i>	GTC
1644	NZ_BBNH01000037.1	<i>Acinetobacter baumannii</i>	GTC
1645	NZ_BBNG01000087.1	<i>Acinetobacter baumannii</i>	GTC

	NCBI Reference Sequence ID#	Strain	
1646	NZ_BBN10100092.1	<i>Acinetobacter baumannii</i>	GTC
1647	NZ_BBNF01000083.1	<i>Acinetobacter baumannii</i>	GTC
1648	NZ_BBNJ01000044.1	<i>Acinetobacter baumannii</i>	GTC
1649	NZ_PEIF01000001.1	<i>Acinetobacter baumannii</i>	GU71
1650	NZ_FTRW01000127.1	<i>Acinetobacter baumannii</i>	H31499
1651	NZ_FTRX01000225.1	<i>Acinetobacter baumannii</i>	H31506
1652	NZ_NQXM01000017.1	<i>Acinetobacter baumannii</i>	HC9436
1653	NZ_NQXU01000089.1	<i>Acinetobacter baumannii</i>	HEU2
1654	NZ_NQXQ01000015.1	<i>Acinetobacter baumannii</i>	HEU3
1655	NZ_NQXB01000095.1	<i>Acinetobacter baumannii</i>	HEU5
1656	NZ_NQXD01000027.1	<i>Acinetobacter baumannii</i>	HEU55808
1657	NZ_LYTI01000001.1	<i>Acinetobacter baumannii</i>	HJ01
1658	NZ_MACP01000001.1	<i>Acinetobacter baumannii</i>	HJ03
1659	NZ_MACQ01000001.1	<i>Acinetobacter baumannii</i>	HJ04
1660	NZ_MACR01000001.1	<i>Acinetobacter baumannii</i>	HJ05
1661	NZ_MACS01000001.1	<i>Acinetobacter baumannii</i>	HJ06
1662	NZ_MACT01000001.1	<i>Acinetobacter baumannii</i>	HJ07
1663	NZ_MACU01000001.1	<i>Acinetobacter baumannii</i>	HJ08
1664	NZ_MACV01000001.1	<i>Acinetobacter baumannii</i>	HJ10
1665	NZ_MACW01000001.1	<i>Acinetobacter baumannii</i>	HJ11
1666	NZ_MACX01000001.1	<i>Acinetobacter baumannii</i>	HJ12
1667	NZ_MACY01000001.1	<i>Acinetobacter baumannii</i>	HJ13
1668	NZ_MACZ01000001.1	<i>Acinetobacter baumannii</i>	HJ16
1669	NZ_MADA01000001.1	<i>Acinetobacter baumannii</i>	HJ16-2
1670	NZ_MADG01000001.1	<i>Acinetobacter baumannii</i>	HJ18
1671	NZ_MADB01000001.1	<i>Acinetobacter baumannii</i>	HJ18-2
1672	NZ_MADC01000001.1	<i>Acinetobacter baumannii</i>	HJ19

	NCBI Reference Sequence ID#	Strain
1673	NZ_MADD01000001.1	<i>Acinetobacter baumannii</i> HJ19-2
1674	NZ_MADE01000001.1	<i>Acinetobacter baumannii</i> HJ20
1675	NZ_CP018143.1	<i>Acinetobacter baumannii</i> HRAB-85
1676	NZ_LQRQ01000001.1	<i>Acinetobacter baumannii</i> HUMC1
1677	NZ_CP020597.1	<i>Acinetobacter baumannii</i> HWBA8
1678	NZ_FCNK01000001.1	<i>Acinetobacter baumannii</i> I
1679	NZ_CP027483.1	<i>Acinetobacter baumannii</i> I43
1680	NZ_MAKO01000001.1	<i>Acinetobacter baumannii</i> IHIT17886
1681	NZ_MAKP01000001.1	<i>Acinetobacter baumannii</i> IHIT17966
1682	NZ_MAKQ01000001.1	<i>Acinetobacter baumannii</i> IHIT25424
1683	NZ_MAKR01000001.1	<i>Acinetobacter baumannii</i> IHIT29106
1684	NZ_NWUK01000089.1	<i>Acinetobacter baumannii</i> IHIT32296
1685	NZ_LWTH01000001.1	<i>Acinetobacter baumannii</i> IHIT7853
1686	NZ_NQXR01000048.1	<i>Acinetobacter baumannii</i> IHSS3526
1687	NZ_FPGM01000063.1	<i>Acinetobacter baumannii</i> ILBAbau5423446
1688	NZ_FPGO01000066.1	<i>Acinetobacter baumannii</i> ILBAbau5423449
1689	NZ_FPGR01000066.1	<i>Acinetobacter baumannii</i> ILBAbau5423457
1690	NZ_FPGZ01000108.1	<i>Acinetobacter baumannii</i> ILBAbau5423458
1691	NZ_FPGS01000108.1	<i>Acinetobacter baumannii</i> ILBAbau5423462
1692	NZ_FPGX01000113.1	<i>Acinetobacter baumannii</i> ILBAbau5423469
1693	NZ_FPGU01000086.1	<i>Acinetobacter baumannii</i> ILBAbau5423495
1694	NZ_AMGF01000001.1	<i>Acinetobacter baumannii</i> IS-116
1695	NZ_ALII01000018.1	<i>Acinetobacter baumannii</i> IS-123
1696	NZ_AMGE01000001.1	<i>Acinetobacter baumannii</i> IS-143
1697	NZ_AMEI01000001.1	<i>Acinetobacter baumannii</i> IS-235
1698	NZ_AMEJ01000001.1	<i>Acinetobacter baumannii</i> IS-251
1699	NZ_AMGH01000001.1	<i>Acinetobacter baumannii</i> IS-58

	NCBI Reference Sequence ID#	Strain	
1700	NZ_FCNH01000001.1	<i>Acinetobacter baumannii</i>	J
1701	NZ_FBWQ01000001.1	<i>Acinetobacter baumannii</i>	J1
1702	NZ_FBWS01000001.1	<i>Acinetobacter baumannii</i>	J10
1703	NZ_LAKQ01000001.1	<i>Acinetobacter baumannii</i>	J133
1704	NZ_LAKR01000001.1	<i>Acinetobacter baumannii</i>	J2770
1705	NZ_FBWP01000001.1	<i>Acinetobacter baumannii</i>	J5
1706	NZ_LAKO01000001.1	<i>Acinetobacter baumannii</i>	J65
1707	NZ_FBWT01000001.1	<i>Acinetobacter baumannii</i>	J7
1708	NZ_CP020584.1	<i>Acinetobacter baumannii</i>	JBA13
1709	NZ_QCXU01000001.1	<i>Acinetobacter baumannii</i>	JX101
1710	NZ_FCNI01000001.1	<i>Acinetobacter baumannii</i>	K
1711	NZ_OHJL01000004.1	<i>Acinetobacter baumannii</i>	K50
1712	NZ_CP017642.1	<i>Acinetobacter baumannii</i>	KAB01
1713	NZ_CP017644.1	<i>Acinetobacter baumannii</i>	KAB02
1714	NZ_CP017646.1	<i>Acinetobacter baumannii</i>	KAB03
1715	NZ_CP017648.1	<i>Acinetobacter baumannii</i>	KAB04
1716	NZ_CP017650.1	<i>Acinetobacter baumannii</i>	KAB05
1717	NZ_CP017652.1	<i>Acinetobacter baumannii</i>	KAB06
1718	NZ_CP017654.1	<i>Acinetobacter baumannii</i>	KAB07
1719	NZ_CP017656.1	<i>Acinetobacter baumannii</i>	KAB08
1720	NZ_MSFZ01000030.1	<i>Acinetobacter baumannii</i>	kayseri102
1721	NZ_CP013924.1	<i>Acinetobacter baumannii</i>	KBN10P02143
1722	NZ_NEPK01000100.1	<i>Acinetobacter baumannii</i>	KUFAR39
1723	NZ_NEPJ01000010.1	<i>Acinetobacter baumannii</i>	KUFAR40
1724	NZ_NEPI01000010.1	<i>Acinetobacter baumannii</i>	KUFAR41
1725	NZ_NEPH01000010.1	<i>Acinetobacter baumannii</i>	KUFAR42
1726	NZ_NEPG01000010.1	<i>Acinetobacter baumannii</i>	KUFAR44

	NCBI Reference Sequence ID#	Strain	
1727	NZ_NEPF01000098.1	<i>Acinetobacter baumannii</i>	KUFAR50
1728	NZ_NEPE01000099.1	<i>Acinetobacter baumannii</i>	KUFAR51
1729	NZ_NEPD01000087.1	<i>Acinetobacter baumannii</i>	KUFAR53
1730	NZ_NEPC01000010.1	<i>Acinetobacter baumannii</i>	KUFAR56
1731	NZ_NEPB01000098.1	<i>Acinetobacter baumannii</i>	KUFAR57
1732	NZ_NEPA01000090.1	<i>Acinetobacter baumannii</i>	KUFAR60
1733	NZ_NEOZ01000010.1	<i>Acinetobacter baumannii</i>	KUFAR61
1734	NZ_NEOY01000100.1	<i>Acinetobacter baumannii</i>	KUFAR62
1735	NZ_NEOX01000010.1	<i>Acinetobacter baumannii</i>	KUFAR63
1736	NZ_NEOW01000010.1	<i>Acinetobacter baumannii</i>	KUFAR64
1737	NZ_NEOV01000010.1	<i>Acinetobacter baumannii</i>	KUFAR65
1738	NZ_NEOU01000100.1	<i>Acinetobacter baumannii</i>	KUFAR67
1739	NZ_NEQD01000010.1	<i>Acinetobacter baumannii</i>	KUSSH01
1740	NZ_NEQC01000100.1	<i>Acinetobacter baumannii</i>	KUSSH02
1741	NZ_NEQB01000100.1	<i>Acinetobacter baumannii</i>	KUSSH08
1742	NZ_NEQA01000098.1	<i>Acinetobacter baumannii</i>	KUSSH09
1743	NZ_NEPZ01000010.1	<i>Acinetobacter baumannii</i>	KUSSH10
1744	NZ_NEPY01000010.1	<i>Acinetobacter baumannii</i>	KUSSH13
1745	NZ_NEPX01000100.1	<i>Acinetobacter baumannii</i>	KUSSH14
1746	NZ_NEPW01000100.1	<i>Acinetobacter baumannii</i>	KUSSH15
1747	NZ_NEPV01000100.1	<i>Acinetobacter baumannii</i>	KUSSH16
1748	NZ_NEPU01000010.1	<i>Acinetobacter baumannii</i>	KUSSH18
1749	NZ_NEPT01000100.1	<i>Acinetobacter baumannii</i>	KUSSH20
1750	NZ_NEPS01000010.1	<i>Acinetobacter baumannii</i>	KUSSH25
1751	NZ_NEPR01000010.1	<i>Acinetobacter baumannii</i>	KUSSH26
1752	NZ_NEPQ01000100.1	<i>Acinetobacter baumannii</i>	KUSSH27
1753	NZ_NEPP01000097.1	<i>Acinetobacter baumannii</i>	KUSSH32

	NCBI Reference Sequence ID#	Strain	
1754	NZ_NEPO01000010.1	<i>Acinetobacter baumannii</i>	KUSSH33
1755	NZ_NEPN01000010.1	<i>Acinetobacter baumannii</i>	KUSSH35
1756	NZ_NEPM01000010.1	<i>Acinetobacter baumannii</i>	KUSSH36
1757	NZ_NEPL01000100.1	<i>Acinetobacter baumannii</i>	KUSSH37
1758	NZ_FCNE01000001.1	<i>Acinetobacter baumannii</i>	L
1759	NZ_KK211418.1	<i>Acinetobacter baumannii</i>	LAC-4
1760	NZ_CP007712.1	<i>Acinetobacter baumannii</i>	LAC-4
1761	NZ_CP018677.1	<i>Acinetobacter baumannii</i>	LAC4
1762	NZ_LUVK01000939.1	<i>Acinetobacter baumannii</i>	LIM1029
1763	NZ_LUVG01000075.1	<i>Acinetobacter baumannii</i>	LIM1049
1764	NZ_LUVI01000075.1	<i>Acinetobacter baumannii</i>	LIM1099
1765	NZ_LUVH01000081.1	<i>Acinetobacter baumannii</i>	LIM1126
1766	NZ_LUVL01000079.1	<i>Acinetobacter baumannii</i>	LIM1128
1767	NZ_LUVM01000083.1	<i>Acinetobacter baumannii</i>	LIM1132
1768	NZ_LUUX01000091.1	<i>Acinetobacter baumannii</i>	LIM1819
1769	NZ_LUUY01000096.1	<i>Acinetobacter baumannii</i>	LIM1820
1770	NZ_MANM01000001.1	<i>Acinetobacter baumannii</i>	LIM3689
1771	NZ_MANN01000001.1	<i>Acinetobacter baumannii</i>	LIM3695
1772	NZ_MANO01000001.1	<i>Acinetobacter baumannii</i>	LIM3705
1773	NZ_MANP01000001.1	<i>Acinetobacter baumannii</i>	LIM3732
1774	NZ_MANR01000001.1	<i>Acinetobacter baumannii</i>	LIM3756
1775	NZ_LUUV01000084.1	<i>Acinetobacter baumannii</i>	LIM552
1776	NZ_LUUVW01000088.1	<i>Acinetobacter baumannii</i>	LIM565
1777	NZ_LUUZ01000079.1	<i>Acinetobacter baumannii</i>	LIM891
1778	NZ_LUVB01000941.1	<i>Acinetobacter baumannii</i>	LIM929
1779	NZ_MANL01000001.1	<i>Acinetobacter baumannii</i>	LIM941
1780	NZ_LUVA01000082.1	<i>Acinetobacter baumannii</i>	LIM994

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1781	NZ_LUVC01000076.1	<i>Acinetobacter baumannii</i> LIM997
1782	NZ_NIWP01000085.1	<i>Acinetobacter baumannii</i> LoGelst3-1
1783	NZ_JZBW01000012.1	<i>Acinetobacter baumannii</i> LUH_6220
1784	NZ_JZBX01000001.1	<i>Acinetobacter baumannii</i> LUH_7841
1785	NZ_JDSV01000001.1	<i>Acinetobacter baumannii</i> LY1
1786	NZ_JDSW01000001.1	<i>Acinetobacter baumannii</i> LY2
1787	NZ_JDSX01000001.1	<i>Acinetobacter baumannii</i> LY3
1788	NZ_JDSY01000001.1	<i>Acinetobacter baumannii</i> LY4
1789	NZ_JDSZ01000001.1	<i>Acinetobacter baumannii</i> LY5
1790	NZ_JDTA01000001.1	<i>Acinetobacter baumannii</i> LY6
1791	NZ_JDTB01000001.1	<i>Acinetobacter baumannii</i> LY7
1792	NZ_JDTC01000001.1	<i>Acinetobacter baumannii</i> LY8
1793	NZ_JDTD01000001.1	<i>Acinetobacter baumannii</i> LY9
1794	NZ_FJMY01000001.1	<i>Acinetobacter baumannii</i> M
1795	NZ_LAIL01000001.1	<i>Acinetobacter baumannii</i> M1
1796	NZ_LAKP01000001.1	<i>Acinetobacter baumannii</i> M2
1797	NZ_CM004453.1	<i>Acinetobacter baumannii</i> M3AC14-8
1798	NZ_JTEC01000021.1	<i>Acinetobacter baumannii</i> M3AC9-7
1799	NZ_LKIB01000001.1	<i>Acinetobacter baumannii</i> MAL
1800	NZ_JRHB01000001.1	<i>Acinetobacter baumannii</i> MAR002
1801	NZ_MWTR01000001.1	<i>Acinetobacter baumannii</i> MBL_M1
1802	NZ_MWUA01000001.1	<i>Acinetobacter baumannii</i> MBL_M10
1803	NZ_MWUB01000001.1	<i>Acinetobacter baumannii</i> MBL_M11
1804	NZ_MWTS01000001.1	<i>Acinetobacter baumannii</i> MBL_M2
1805	NZ_MWTT01000001.1	<i>Acinetobacter baumannii</i> MBL_M3
1806	NZ_MWTU01000001.1	<i>Acinetobacter baumannii</i> MBL_M4
1807	NZ_MWTV01000001.1	<i>Acinetobacter baumannii</i> MBL_M5

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1808	NZ_MWTTW01000001.1	<i>Acinetobacter baumannii</i>	MBL_M6
1809	NZ_MWTTX01000001.1	<i>Acinetobacter baumannii</i>	MBL_M7
1810	NZ_MWTTY01000001.1	<i>Acinetobacter baumannii</i>	MBL_M8
1811	NZ_MWTTZ01000001.1	<i>Acinetobacter baumannii</i>	MBL_M9
1812	NZ_NQXI01000001.1	<i>Acinetobacter baumannii</i>	MCR10126
1813	NZ_NQXH01000055.1	<i>Acinetobacter baumannii</i>	MCR10172
1814	NZ_NQXG01000056.1	<i>Acinetobacter baumannii</i>	MCR10179
1815	NZ_NQXP01000007.1	<i>Acinetobacter baumannii</i>	MCR54
1816	NZ_NQXT01000097.1	<i>Acinetobacter baumannii</i>	MCR56
1817	NZ_NQXL01000106.1	<i>Acinetobacter baumannii</i>	MCR6056
1818	NZ_NQXO01000062.1	<i>Acinetobacter baumannii</i>	MCR6739
1819	NZ_NQXK01000071.1	<i>Acinetobacter baumannii</i>	MCR8676
1820	NZ_NQXS01000018.1	<i>Acinetobacter baumannii</i>	MCR8683
1821	NZ_NRSN01000002.1	<i>Acinetobacter baumannii</i>	MCR9238
1822	NC_017847.1	<i>Acinetobacter baumannii</i>	MDR-TJ
1823	NC_017171.1	<i>Acinetobacter baumannii</i>	MDR-ZJ06
1824	NZ_CM003741.1	<i>Acinetobacter baumannii</i>	MEX11594
1825	NZ_FUEO01000112.1	<i>Acinetobacter baumannii</i>	MGTN
1826	NZ_FUET01000115.1	<i>Acinetobacter baumannii</i>	MONUR
1827	NZ_JABT01000001.1	<i>Acinetobacter baumannii</i>	MRSN
1828	NZ_CM003320.1	<i>Acinetobacter baumannii</i>	MRSN
1829	NZ_CM003313.1	<i>Acinetobacter baumannii</i>	MRSN
1830	NZ_JNOU01000001.1	<i>Acinetobacter baumannii</i>	MRSN
1831	NZ_CM003318.1	<i>Acinetobacter baumannii</i>	MRSN
1832	NZ_CM003316.1	<i>Acinetobacter baumannii</i>	MRSN
1833	NZ_CM003315.1	<i>Acinetobacter baumannii</i>	MRSN
1834	NZ_CM003319.1	<i>Acinetobacter baumannii</i>	MRSN

	NCBI Reference Sequence ID#	Strain	MRSN
1835	NZ_JABU01000001.1	<i>Acinetobacter baumannii</i>	MRSN
1836	NZ_JPIB01000008.1	<i>Acinetobacter baumannii</i>	MRSN
1837	NZ_LMZX01000001.1	<i>Acinetobacter baumannii</i>	MRSN15038
1838	NZ_LMZW01000001.1	<i>Acinetobacter baumannii</i>	MRSN15084
1839	NZ_LNBD01000001.1	<i>Acinetobacter baumannii</i>	MRSN16874
1840	NZ_LAZK01000001.1	<i>Acinetobacter baumannii</i>	MRSN16875
1841	NZ_LMAN01000001.1	<i>Acinetobacter baumannii</i>	MRSN16881
1842	NZ_LMAL01000001.1	<i>Acinetobacter baumannii</i>	MRSN16882
1843	NZ_LMAM01000001.1	<i>Acinetobacter baumannii</i>	MRSN16896
1844	NZ_LAYM01000001.1	<i>Acinetobacter baumannii</i>	MRSN16897
1845	NZ_LMAO01000001.1	<i>Acinetobacter baumannii</i>	MRSN16898
1846	NZ_LLF01000001.1	<i>Acinetobacter baumannii</i>	MRSN16901
1847	NZ_LLZD01000001.1	<i>Acinetobacter baumannii</i>	MRSN17592
1848	NZ_LLZE01000001.1	<i>Acinetobacter baumannii</i>	MRSN17593
1849	NZ_LMZV01000001.1	<i>Acinetobacter baumannii</i>	MRSN20315
1850	NZ_LMYO01000001.1	<i>Acinetobacter baumannii</i>	MRSN20755
1851	NZ_LNCV01000001.1	<i>Acinetobacter baumannii</i>	MRSN3941
1852	NZ_LNBZ01000001.1	<i>Acinetobacter baumannii</i>	MRSN4119
1853	NZ_LNCW01000001.1	<i>Acinetobacter baumannii</i>	MRSN5540
1854	NZ_LNCX01000001.1	<i>Acinetobacter baumannii</i>	MRSN6269
1855	NZ_LNCY01000001.1	<i>Acinetobacter baumannii</i>	MRSN6273
1856	NZ_LMZY01000001.1	<i>Acinetobacter baumannii</i>	MRSN7081
1857	NZ_BASB01000077.1	<i>Acinetobacter baumannii</i>	MRY10-0558
1858	NZ_AODW01000001.1	<i>Acinetobacter baumannii</i>	MSP4-16
1859	NZ_QCXW01000001.1	<i>Acinetobacter baumannii</i>	N8
1860	NZ_AMZU01000001.1	<i>Acinetobacter baumannii</i>	Naval-113
1861	NZ_AMDR01000001.1	<i>Acinetobacter baumannii</i>	Naval-13

	NCBI Reference Sequence ID#	Strain	
1862	NZ_AFDO01000021.1	<i>Acinetobacter baumannii</i>	Naval-17
1863	NZ_AMSX01000001.1	<i>Acinetobacter baumannii</i>	Naval-2
1864	NZ_AMSY01000001.1	<i>Acinetobacter baumannii</i>	Naval-21
1865	NZ_AMFP01000001.1	<i>Acinetobacter baumannii</i>	Naval-57
1866	NZ_AMFI01000001.1	<i>Acinetobacter baumannii</i>	Naval-72
1867	NZ_AMFZ01000001.1	<i>Acinetobacter baumannii</i>	Naval-78
1868	NZ_AFDDB02000005.1	<i>Acinetobacter baumannii</i>	Naval-81
1869	NZ_AMSW01000001.1	<i>Acinetobacter baumannii</i>	Naval-82
1870	NZ_AMFK01000001.1	<i>Acinetobacter baumannii</i>	Naval-83
1871	NZ_BBSU01000087.1	<i>Acinetobacter baumannii</i>	NBRC
1872	NZ_BBOP01000095.1	<i>Acinetobacter baumannii</i>	NBRC
1873	NZ_BBOR01000042.1	<i>Acinetobacter baumannii</i>	NBRC
1874	NZ_BBOQ01000047.1	<i>Acinetobacter baumannii</i>	NBRC
1875	NZ_BBTC01000090.1	<i>Acinetobacter baumannii</i>	NBRC
1876	NZ_BBTD01000173.1	<i>Acinetobacter baumannii</i>	NBRC
1877	NZ_BBTN01000053.1	<i>Acinetobacter baumannii</i>	NBRC
1878	NZ_BBTE01000045.1	<i>Acinetobacter baumannii</i>	NBRC
1879	NZ_AP013357.1	<i>Acinetobacter baumannii</i>	NCGM
1880	NZ_LOHD01000001.1	<i>Acinetobacter baumannii</i>	NCTC
1881	NZ_KB849481.1	<i>Acinetobacter baumannii</i>	NIPH
1882	NZ_KB849942.1	<i>Acinetobacter baumannii</i>	NIPH
1883	NZ_KB849144.1	<i>Acinetobacter baumannii</i>	NIPH
1884	NZ_KB849309.1	<i>Acinetobacter baumannii</i>	NIPH
1885	NZ_KB849850.1	<i>Acinetobacter baumannii</i>	NIPH
1886	NZ_KB849248.1	<i>Acinetobacter baumannii</i>	NIPH
1887	NZ_KB849913.1	<i>Acinetobacter baumannii</i>	NIPH
1888	NZ_KB849240.1	<i>Acinetobacter baumannii</i>	NIPH

	NCBI Reference Sequence ID#	Strain	
1889	NZ_KB849868.1	<i>Acinetobacter baumannii</i>	NIPH
1890	NZ_KB849308.1	<i>Acinetobacter baumannii</i>	NIPH
1891	NZ_KB849891.1	<i>Acinetobacter baumannii</i>	NIPH
1892	NZ_KE340359.1	<i>Acinetobacter baumannii</i>	NIPH
1893	NZ_KB849876.1	<i>Acinetobacter baumannii</i>	NIPH
1894	NZ_KB849906.1	<i>Acinetobacter baumannii</i>	NIPH
1895	NZ_KB849841.1	<i>Acinetobacter baumannii</i>	NIPH
1896	NZ_KB849296.1	<i>Acinetobacter baumannii</i>	NIPH
1897	NZ_KB849470.1	<i>Acinetobacter baumannii</i>	NIPH
1898	NZ_KB849928.1	<i>Acinetobacter baumannii</i>	NIPH
1899	NZ_KB849901.1	<i>Acinetobacter baumannii</i>	NIPH
1900	NZ_KB849321.1	<i>Acinetobacter baumannii</i>	NIPH
1901	NZ_JZBV01000001.1	<i>Acinetobacter baumannii</i>	NM3
1902	NZ_NIWQ01000094.1	<i>Acinetobacter baumannii</i>	O1D3-2
1903	NZ_BDHK01000001.1	<i>Acinetobacter baumannii</i>	OCU_Ac16a
1904	NZ_AMFH01000055.1	<i>Acinetobacter baumannii</i>	OIFC0162
1905	NZ_AFCZ02000003.1	<i>Acinetobacter baumannii</i>	OIFC032
1906	NZ_AMTB01000001.1	<i>Acinetobacter baumannii</i>	OIFC035
1907	NZ_AMFW01000001.1	<i>Acinetobacter baumannii</i>	OIFC047
1908	NZ_AMFV01000001.1	<i>Acinetobacter baumannii</i>	OIFC065
1909	NZ_AMDE01000001.1	<i>Acinetobacter baumannii</i>	OIFC074
1910	NZ_AMFS01000001.1	<i>Acinetobacter baumannii</i>	OIFC087
1911	NZ_AMDF01000001.1	<i>Acinetobacter baumannii</i>	OIFC098
1912	NZ_AMFT01000001.1	<i>Acinetobacter baumannii</i>	OIFC099
1913	NZ_ALAL01000013.1	<i>Acinetobacter baumannii</i>	OIFC109
1914	NZ_AMFL01000001.1	<i>Acinetobacter baumannii</i>	OIFC110
1915	NZ_AMFY01000001.1	<i>Acinetobacter baumannii</i>	OIFC111

	NCBI Reference Sequence ID#	Strain	
1916	NZ_AFDK01000004.1	<i>Acinetobacter baumannii</i>	OIFC137
1917	NZ_AFDL01000008.1	<i>Acinetobacter baumannii</i>	OIFC143
1918	NZ_AMDQ01000001.1	<i>Acinetobacter baumannii</i>	OIFC180
1919	NZ_AFDM01000010.1	<i>Acinetobacter baumannii</i>	OIFC189
1920	NZ_AMFX01000001.1	<i>Acinetobacter baumannii</i>	OIFC338
1921	NZ_CP015483.1	<i>Acinetobacter baumannii</i>	ORAB01
1922	NZ_JZCO02000001.1	<i>Acinetobacter baumannii</i>	ORAB02
1923	NZ_JZCN02000001.1	<i>Acinetobacter baumannii</i>	ORAB03
1924	NZ_JZCM02000001.1	<i>Acinetobacter baumannii</i>	ORAB08
1925	NZ_JZCL02000001.1	<i>Acinetobacter baumannii</i>	ORAB09
1926	NZ_JZCK02000001.1	<i>Acinetobacter baumannii</i>	ORAB10
1927	NZ_JZCJ02000001.1	<i>Acinetobacter baumannii</i>	ORAB13
1928	NZ_JZCI02000001.1	<i>Acinetobacter baumannii</i>	ORAB14
1929	NZ_JZCH02000001.1	<i>Acinetobacter baumannii</i>	ORAB15
1930	NZ_JZCG02000001.1	<i>Acinetobacter baumannii</i>	ORAB16
1931	NZ_JZCF02000001.1	<i>Acinetobacter baumannii</i>	ORAB17
1932	NZ_JZCE02000001.1	<i>Acinetobacter baumannii</i>	ORAB18
1933	NZ_JZCD02000001.1	<i>Acinetobacter baumannii</i>	ORAB19
1934	NZ_LRME02000001.1	<i>Acinetobacter baumannii</i>	ORAB21
1935	NZ_LRMF02000001.1	<i>Acinetobacter baumannii</i>	ORAB23
1936	NZ_LRMJ02000001.1	<i>Acinetobacter baumannii</i>	ORAB6b
1937	NZ_LRMG01000001.1	<i>Acinetobacter baumannii</i>	ORABAshR
1938	NZ_LRMI02000001.1	<i>Acinetobacter baumannii</i>	ORABMayT
1939	NZ_LRMH02000001.1	<i>Acinetobacter baumannii</i>	ORABRicT
1940	NZ_LRMK02000001.1	<i>Acinetobacter baumannii</i>	ORABSC
1941	NZ_CBYG010000001.1	<i>Acinetobacter baumannii</i>	P630
1942	NZ_PXUK01000010.1	<i>Acinetobacter baumannii</i>	pet_ACB108

	NCBI Reference Sequence ID#	Strain
1943	NZ_PXUJ01000100.1	<i>Acinetobacter baumannii</i> pet_ACB115
1944	NZ_PXUI01000100.1	<i>Acinetobacter baumannii</i> pet_ACB213
1945	NZ_PXUM01000100.1	<i>Acinetobacter baumannii</i> pet_ACB87
1946	NZ_PXUL01000100.1	<i>Acinetobacter baumannii</i> pet_ACB92
1947	NZ_CP006963.1	<i>Acinetobacter baumannii</i> PKAB07
1948	NZ_NIWR01000010.1	<i>Acinetobacter baumannii</i> PLG9P835
1949	NZ_NGBU01000020.1	<i>Acinetobacter baumannii</i> PR304
1950	NZ_NGBV01000085.1	<i>Acinetobacter baumannii</i> PR305
1951	NZ_NGBW01000024.1	<i>Acinetobacter baumannii</i> PR306
1952	NZ_NGBX01000007.1	<i>Acinetobacter baumannii</i> PR307
1953	NZ_NGBY01000012.1	<i>Acinetobacter baumannii</i> PR308
1954	NZ_NGBZ01000002.1	<i>Acinetobacter baumannii</i> PR309
1955	NZ_NGCA01000009.1	<i>Acinetobacter baumannii</i> PR310
1956	NZ_NGCB01000030.1	<i>Acinetobacter baumannii</i> PR311
1957	NZ_NGCC01000040.1	<i>Acinetobacter baumannii</i> PR312
1958	NZ_NGEM01000010.1	<i>Acinetobacter baumannii</i> PR315
1959	NZ_NGEO01000064.1	<i>Acinetobacter baumannii</i> PR317
1960	NZ_NGDJ01000052.1	<i>Acinetobacter baumannii</i> PR319
1961	NZ_NGDL01000018.1	<i>Acinetobacter baumannii</i> PR321
1962	NZ_NGDM01000097.1	<i>Acinetobacter baumannii</i> PR322
1963	NZ_NGDN01000111.1	<i>Acinetobacter baumannii</i> PR323
1964	NZ_NGDP01000008.1	<i>Acinetobacter baumannii</i> PR325
1965	NZ_NGDQ01000074.1	<i>Acinetobacter baumannii</i> PR327
1966	NZ_NGDR01000034.1	<i>Acinetobacter baumannii</i> PR328
1967	NZ_NGDS01000139.1	<i>Acinetobacter baumannii</i> PR329
1968	NZ_NGDV01000037.1	<i>Acinetobacter baumannii</i> PR332
1969	NZ_NGDW01000012.1	<i>Acinetobacter baumannii</i> PR333

	NCBI Reference Sequence ID#	Strain	
1970	NZ_NGDXX01000011.1	<i>Acinetobacter baumannii</i>	PR334
1971	NZ_NGDY01000039.1	<i>Acinetobacter baumannii</i>	PR335
1972	NZ_NGDZ01000012.1	<i>Acinetobacter baumannii</i>	PR336
1973	NZ_NGEA01000014.1	<i>Acinetobacter baumannii</i>	PR337
1974	NZ_NGEC01000002.1	<i>Acinetobacter baumannii</i>	PR340
1975	NZ_NGED01000043.1	<i>Acinetobacter baumannii</i>	PR341
1976	NZ_NGEE01000017.1	<i>Acinetobacter baumannii</i>	PR343
1977	NZ_NGEG01000030.1	<i>Acinetobacter baumannii</i>	PR345
1978	NZ_NGEI01000087.1	<i>Acinetobacter baumannii</i>	PR347
1979	NZ_NGEK01000066.1	<i>Acinetobacter baumannii</i>	PR349
1980	NZ_NGEL01000189.1	<i>Acinetobacter baumannii</i>	PR350
1981	NZ_NGCE01000030.1	<i>Acinetobacter baumannii</i>	PR351
1982	NZ_NGCF01000068.1	<i>Acinetobacter baumannii</i>	PR352
1983	NZ_NGCG01000057.1	<i>Acinetobacter baumannii</i>	PR353
1984	NZ_NGCI01000010.1	<i>Acinetobacter baumannii</i>	PR355
1985	NZ_NGCJ01000033.1	<i>Acinetobacter baumannii</i>	PR356
1986	NZ_NGCK01000039.1	<i>Acinetobacter baumannii</i>	PR357
1987	NZ_NGCL01000016.1	<i>Acinetobacter baumannii</i>	PR358
1988	NZ_NGCM01000020.1	<i>Acinetobacter baumannii</i>	PR359
1989	NZ_NGCN01000015.1	<i>Acinetobacter baumannii</i>	PR360
1990	NZ_NGCO01000011.1	<i>Acinetobacter baumannii</i>	PR361
1991	NZ_NGCQ01000016.1	<i>Acinetobacter baumannii</i>	PR363
1992	NZ_NGCR01000042.1	<i>Acinetobacter baumannii</i>	PR364
1993	NZ_NGCY01000009.1	<i>Acinetobacter baumannii</i>	PR371
1994	NZ_NGCZ01000025.1	<i>Acinetobacter baumannii</i>	PR372
1995	NZ_NGDA01000008.1	<i>Acinetobacter baumannii</i>	PR373
1996	NZ_NGDB01000044.1	<i>Acinetobacter baumannii</i>	PR374

	NCBI Reference Sequence ID#	Strain	
1997	NZ_LGDC01000227.1	<i>Acinetobacter baumannii</i>	PR375
1998	NZ_LGDD01000064.1	<i>Acinetobacter baumannii</i>	PR376
1999	NZ_LGDE01000057.1	<i>Acinetobacter baumannii</i>	PR377
2000	NZ_LGDF01000070.1	<i>Acinetobacter baumannii</i>	PR379
2001	NZ_LGDG01000062.1	<i>Acinetobacter baumannii</i>	PR380
2002	NZ_LGDH01000022.1	<i>Acinetobacter baumannii</i>	PR381
2003	NZ_LGEP01000067.1	<i>Acinetobacter baumannii</i>	PR382
2004	NZ_LGEQ01000081.1	<i>Acinetobacter baumannii</i>	PR383
2005	NZ_LGER01000038.1	<i>Acinetobacter baumannii</i>	PR384
2006	NZ_LGES01000073.1	<i>Acinetobacter baumannii</i>	PR385
2007	NZ_LGEU01000008.1	<i>Acinetobacter baumannii</i>	PR387
2008	NZ_LGEV01000046.1	<i>Acinetobacter baumannii</i>	PR388
2009	NZ_LGEW01000029.1	<i>Acinetobacter baumannii</i>	PR389
2010	NZ_LGEX01000112.1	<i>Acinetobacter baumannii</i>	PR390
2011	NZ_LGEY01000028.1	<i>Acinetobacter baumannii</i>	PR391
2012	NZ_LGEZ01000017.1	<i>Acinetobacter baumannii</i>	PR392
2013	NZ_LGFB01000111.1	<i>Acinetobacter baumannii</i>	PR394
2014	NZ_LGFC01000081.1	<i>Acinetobacter baumannii</i>	PR395
2015	NZ_LGFD01000026.1	<i>Acinetobacter baumannii</i>	PR396
2016	NZ_LGFE01000055.1	<i>Acinetobacter baumannii</i>	PR398
2017	NZ_LGFF01000022.1	<i>Acinetobacter baumannii</i>	PR399
2018	NZ_LGFG01000053.1	<i>Acinetobacter baumannii</i>	PR400
2019	NZ_CBXD01000001.1	<i>Acinetobacter baumannii</i>	Pulsotype
2020	NZ_PUCB01000001.1	<i>Acinetobacter baumannii</i>	R1
2021	NZ_PUCT01000001.1	<i>Acinetobacter baumannii</i>	R10
2022	NZ_PUCV01000001.1	<i>Acinetobacter baumannii</i>	R11
2023	NZ_PUCX01000001.1	<i>Acinetobacter baumannii</i>	R12

	NCBI Reference Sequence ID#	Strain	
2024	NZ_PUCZ01000001.1	<i>Acinetobacter baumannii</i>	R13
2025	NZ_PUDB01000001.1	<i>Acinetobacter baumannii</i>	R14
2026	NZ_PUDD01000001.1	<i>Acinetobacter baumannii</i>	R15
2027	NZ_PUDF01000001.1	<i>Acinetobacter baumannii</i>	R16
2028	NZ_PUDH01000001.1	<i>Acinetobacter baumannii</i>	R17
2029	NZ_PUDJ01000001.1	<i>Acinetobacter baumannii</i>	R18
2030	NZ_PUDL01000001.1	<i>Acinetobacter baumannii</i>	R19
2031	NZ_KK211431.1	<i>Acinetobacter baumannii</i>	R1B
2032	NZ_PUCD01000001.1	<i>Acinetobacter baumannii</i>	R2
2033	NZ_PUDN01000001.1	<i>Acinetobacter baumannii</i>	R20
2034	NZ_PUDP01000001.1	<i>Acinetobacter baumannii</i>	R21
2035	NZ_PUCF01000001.1	<i>Acinetobacter baumannii</i>	R3
2036	NZ_PUCH01000001.1	<i>Acinetobacter baumannii</i>	R4
2037	NZ_PUCJ01000001.1	<i>Acinetobacter baumannii</i>	R5
2038	NZ_PUCL01000001.1	<i>Acinetobacter baumannii</i>	R6
2039	NZ_PUCN01000001.1	<i>Acinetobacter baumannii</i>	R7
2040	NZ_PUCP01000001.1	<i>Acinetobacter baumannii</i>	R8
2041	NZ_PUCR01000001.1	<i>Acinetobacter baumannii</i>	R9
2042	NZ_MPPK01000001.1	<i>Acinetobacter baumannii</i>	RB-1399
2043	NZ_FBXD01000001.1	<i>Acinetobacter baumannii</i>	RBH3
2044	NZ_JZBU01000030.1	<i>Acinetobacter baumannii</i>	RUH1486
2045	NZ_CP026943.1	<i>Acinetobacter baumannii</i>	S1
2046	NZ_PUCS01000001.1	<i>Acinetobacter baumannii</i>	S10
2047	NZ_LAIM01000001.1	<i>Acinetobacter baumannii</i>	S10
2048	NZ_PUCU01000001.1	<i>Acinetobacter baumannii</i>	S11
2049	NZ_LAIY01000009.1	<i>Acinetobacter baumannii</i>	S11
2050	NZ_PUCW01000001.1	<i>Acinetobacter baumannii</i>	S12

	NCBI Reference Sequence ID#	Strain	
2051	NZ_PUCY01000001.1	<i>Acinetobacter baumannii</i>	S13
2052	NZ_PUDA01000001.1	<i>Acinetobacter baumannii</i>	S14
2053	NZ_PUDC01000001.1	<i>Acinetobacter baumannii</i>	S15
2054	NZ_PUDE01000001.1	<i>Acinetobacter baumannii</i>	S16
2055	NZ_PUDG01000001.1	<i>Acinetobacter baumannii</i>	S17
2056	NZ_PUDI01000001.1	<i>Acinetobacter baumannii</i>	S18
2057	NZ_LAIN01000001.1	<i>Acinetobacter baumannii</i>	S19
2058	NZ_PUDK01000001.1	<i>Acinetobacter baumannii</i>	S19
2059	NZ_PUCC01000001.1	<i>Acinetobacter baumannii</i>	S2
2060	NZ_PUDM01000001.1	<i>Acinetobacter baumannii</i>	S20
2061	NZ_PUDO01000001.1	<i>Acinetobacter baumannii</i>	S21
2062	NZ_PUCE01000001.1	<i>Acinetobacter baumannii</i>	S3
2063	NZ_LAIO01000001.1	<i>Acinetobacter baumannii</i>	S36
2064	NZ_PUCG01000001.1	<i>Acinetobacter baumannii</i>	S4
2065	NZ_LAIZ01000001.1	<i>Acinetobacter baumannii</i>	S46
2066	NZ_PUCI01000001.1	<i>Acinetobacter baumannii</i>	S5
2067	NZ_PUCK01000001.1	<i>Acinetobacter baumannii</i>	S6
2068	NZ_PUCM01000001.1	<i>Acinetobacter baumannii</i>	S7
2069	NZ_PUCO01000001.1	<i>Acinetobacter baumannii</i>	S8
2070	NZ_PUCQ01000001.1	<i>Acinetobacter baumannii</i>	S9
2071	NZ_CP020579.1	<i>Acinetobacter baumannii</i>	SAA14
2072	NZ_PYEO01000010.1	<i>Acinetobacter baumannii</i>	SGH0402
2073	NZ_PYEN01000010.1	<i>Acinetobacter baumannii</i>	SGH0403
2074	NZ_PYEB01000010.1	<i>Acinetobacter baumannii</i>	SGH0410
2075	NZ_PYEA01000010.1	<i>Acinetobacter baumannii</i>	SGH0411
2076	NZ_PYEM01000010.1	<i>Acinetobacter baumannii</i>	SGH0602
2077	NZ_PYEL01000010.1	<i>Acinetobacter baumannii</i>	SGH0604

	NCBI Reference Sequence ID#	Strain	
2078	NZ_PYDZ01000100.1	<i>Acinetobacter baumannii</i>	SGH0606
2079	NZ_PYEK01000010.1	<i>Acinetobacter baumannii</i>	SGH0702
2080	NZ_PYDY01000010.1	<i>Acinetobacter baumannii</i>	SGH0805
2081	NZ_PYDX01000100.1	<i>Acinetobacter baumannii</i>	SGH0807
2082	NZ_PYEJ01000010.1	<i>Acinetobacter baumannii</i>	SGH0823
2083	NZ_PYEI01000010.1	<i>Acinetobacter baumannii</i>	SGH0825
2084	NZ_PYEH01000010.1	<i>Acinetobacter baumannii</i>	SGH0905
2085	NZ_PYEG01000010.1	<i>Acinetobacter baumannii</i>	SGH0907
2086	NZ_PYDW01000010.1	<i>Acinetobacter baumannii</i>	SGH0915
2087	NZ_PYEF01000010.1	<i>Acinetobacter baumannii</i>	SGH1010
2088	NZ_PYEE01000010.1	<i>Acinetobacter baumannii</i>	SGH1011
2089	NZ_PYED01000010.1	<i>Acinetobacter baumannii</i>	SGH1012
2090	NZ_PYDV01000100.1	<i>Acinetobacter baumannii</i>	SGH1101
2091	NZ_PYEC01000010.1	<i>Acinetobacter baumannii</i>	SGH1113
2092	NZ_QCXXV01000001.1	<i>Acinetobacter baumannii</i>	SH37
2093	NZ_NIUN01000004.1	<i>Acinetobacter baumannii</i>	SIPA14
2094	NZ_NIUM01000023.1	<i>Acinetobacter baumannii</i>	SIPA5
2095	NZ_NIUL01000002.1	<i>Acinetobacter baumannii</i>	SIUA14
2096	NZ_NIUK01000019.1	<i>Acinetobacter baumannii</i>	SIUA6
2097	NZ_CP025266.1	<i>Acinetobacter baumannii</i>	SMC_Paed_Ab_BL01
2098	NZ_NIBI01000001.1	<i>Acinetobacter baumannii</i>	SMGC-ABI
2099	NZ_NIBH01000001.1	<i>Acinetobacter baumannii</i>	SMGC-AB2
2100	NZ_LFYW01000001.1	<i>Acinetobacter baumannii</i>	SP1917
2101	NZ_CP020578.1	<i>Acinetobacter baumannii</i>	SSA12
2102	NZ_CP020591.1	<i>Acinetobacter baumannii</i>	SSA6
2103	NZ_CP020581.1	<i>Acinetobacter baumannii</i>	SSMA17
2104	NZ_NBNJ01000001.1	<i>Acinetobacter baumannii</i>	SSMA8

	NCBI Reference Sequence ID#	Strain	
2105	NZ_LJHA01000001.1	<i>Acinetobacter baumannii</i>	ST-2_clon_2000
2106	NZ_LJHB01000039.1	<i>Acinetobacter baumannii</i>	ST-2_clon_2010
2107	NC_010410.1	<i>Acinetobacter baumannii</i>	str.
2108	NZ_JRTX01000001.1	<i>Acinetobacter baumannii</i>	T122
2109	NZ_JRTY01000001.1	<i>Acinetobacter baumannii</i>	T173
2110	NZ_JRQU01000001.1	<i>Acinetobacter baumannii</i>	T185
2111	NZ_JRQV01000001.1	<i>Acinetobacter baumannii</i>	T188
2112	NZ_JRTZ01000001.1	<i>Acinetobacter baumannii</i>	T214
2113	NZ_JRQW01000001.1	<i>Acinetobacter baumannii</i>	T229
2114	NZ_JPKX01000001.1	<i>Acinetobacter baumannii</i>	T25
2115	NZ_JRQX01000001.1	<i>Acinetobacter baumannii</i>	T258
2116	NZ_JRQY01000001.1	<i>Acinetobacter baumannii</i>	T271
2117	NZ_JRQT01000001.1	<i>Acinetobacter baumannii</i>	T7
2118	NZ_JRQS01000001.1	<i>Acinetobacter baumannii</i>	T87
2119	NZ_JMRW01000001.1	<i>Acinetobacter baumannii</i>	TCM206
2120	NZ_LGHQ01000001.1	<i>Acinetobacter baumannii</i>	TCM331
2121	NZ_MSRV01000001.1	<i>Acinetobacter baumannii</i>	TDAB1
2122	NZ_ASER01000001.1	<i>Acinetobacter baumannii</i>	TG00314
2123	NZ_ASES01000001.1	<i>Acinetobacter baumannii</i>	TG02011
2124	NZ_ASET01000001.1	<i>Acinetobacter baumannii</i>	TG02017
2125	NZ_ASEU01000001.1	<i>Acinetobacter baumannii</i>	TG07725
2126	NZ_ASEV01000001.1	<i>Acinetobacter baumannii</i>	TG15233
2127	NZ_ASEW01000001.1	<i>Acinetobacter baumannii</i>	TG15234
2128	NZ_ASEX01000001.1	<i>Acinetobacter baumannii</i>	TG15236
2129	NZ_ASEY01000001.1	<i>Acinetobacter baumannii</i>	TG15237
2130	NZ_ASEZ01000001.1	<i>Acinetobacter baumannii</i>	TG15238
2131	NZ_ASFA01000001.1	<i>Acinetobacter baumannii</i>	TG15239

	NCBI Reference Sequence ID#	Strain	
2132	NZ_ASFB01000001.1	<i>Acinetobacter baumannii</i>	TG15240
2133	NZ_ASFC01000001.1	<i>Acinetobacter baumannii</i>	TG15241
2134	NZ_ASFD01000001.1	<i>Acinetobacter baumannii</i>	TG15242
2135	NZ_AMIV01000001.1	<i>Acinetobacter baumannii</i>	TG19582
2136	NZ_ASFE01000001.1	<i>Acinetobacter baumannii</i>	TG2012
2137	NZ_ASFF01000001.1	<i>Acinetobacter baumannii</i>	TG2013
2138	NZ_ASFG01000001.1	<i>Acinetobacter baumannii</i>	TG2014
2139	NZ_ASFH01000001.1	<i>Acinetobacter baumannii</i>	TG20277
2140	NZ_ASFI01000001.1	<i>Acinetobacter baumannii</i>	TG20546
2141	NZ_ASFJ01000001.1	<i>Acinetobacter baumannii</i>	TG22110
2142	NZ_ASFK01000001.1	<i>Acinetobacter baumannii</i>	TG22112
2143	NZ_ASFL01000001.1	<i>Acinetobacter baumannii</i>	TG22142
2144	NZ_ASFM01000001.1	<i>Acinetobacter baumannii</i>	TG22146
2145	NZ_ASFN01000001.1	<i>Acinetobacter baumannii</i>	TG22148
2146	NZ_ASFO01000001.1	<i>Acinetobacter baumannii</i>	TG22150
2147	NZ_ASFP01000001.1	<i>Acinetobacter baumannii</i>	TG22190
2148	NZ_ASFQ01000001.1	<i>Acinetobacter baumannii</i>	TG22192
2149	NZ_ASFR01000001.1	<i>Acinetobacter baumannii</i>	TG22194
2150	NZ_ASFS01000001.1	<i>Acinetobacter baumannii</i>	TG22196
2151	NZ_ASFT01000001.1	<i>Acinetobacter baumannii</i>	TG22198
2152	NZ_ASFU01000001.1	<i>Acinetobacter baumannii</i>	TG22202
2153	NZ_ASFV01000001.1	<i>Acinetobacter baumannii</i>	TG22204
2154	NZ_ASFW01000001.1	<i>Acinetobacter baumannii</i>	TG22212
2155	NZ_ASFX01000001.1	<i>Acinetobacter baumannii</i>	TG22214
2156	NZ_ASFY01000001.1	<i>Acinetobacter baumannii</i>	TG22332
2157	NZ_ASFZ01000001.1	<i>Acinetobacter baumannii</i>	TG22336
2158	NZ_ASFA01000001.1	<i>Acinetobacter baumannii</i>	TG27295

	NCBI Reference Sequence ID#	Strain	
2159	NZ_ASGB01000001.1	<i>Acinetobacter baumannii</i>	TG27299
2160	NZ_ASGC01000001.1	<i>Acinetobacter baumannii</i>	TG27307
2161	NZ_ASGD01000001.1	<i>Acinetobacter baumannii</i>	TG27311
2162	NZ_ASGE01000001.1	<i>Acinetobacter baumannii</i>	TG27315
2163	NZ_ASGF01000001.1	<i>Acinetobacter baumannii</i>	TG27319
2164	NZ_ASGG01000001.1	<i>Acinetobacter baumannii</i>	TG27371
2165	NZ_ASGH01000001.1	<i>Acinetobacter baumannii</i>	TG27379
2166	NZ_ASGI01000001.1	<i>Acinetobacter baumannii</i>	TG27383
2167	NZ_ASGJ01000001.1	<i>Acinetobacter baumannii</i>	TG27387
2168	NZ_AS GK01000001.1	<i>Acinetobacter baumannii</i>	TG27391
2169	NZ_ASGL01000001.1	<i>Acinetobacter baumannii</i>	TG27395
2170	NZ_AS GM01000001.1	<i>Acinetobacter baumannii</i>	TG27399
2171	NZ_AS GN01000001.1	<i>Acinetobacter baumannii</i>	TG27407
2172	NZ_AS GO01000001.1	<i>Acinetobacter baumannii</i>	TG27411
2173	NZ_LKJZ01000001.1	<i>Acinetobacter baumannii</i>	TTU2014-131AME
2174	NC_018706.1	<i>Acinetobacter baumannii</i>	TYTH-1
2175	NZ_AG SQ01000009.1	<i>Acinetobacter baumannii</i>	TYTH-2
2176	NZ_AG SR01000001.1	<i>Acinetobacter baumannii</i>	TYTH-3
2177	NZ_AG SS01000009.1	<i>Acinetobacter baumannii</i>	TYTH-4
2178	NZ_AG ST01000001.1	<i>Acinetobacter baumannii</i>	TYTH-5
2179	NZ_AG SU01000009.1	<i>Acinetobacter baumannii</i>	TYTH-6
2180	NZ_AG SV01000009.1	<i>Acinetobacter baumannii</i>	TYTH-7
2181	NZ_AG YG01000001.1	<i>Acinetobacter baumannii</i>	UH0207
2182	NZ_AG YG R01000001.1	<i>Acinetobacter baumannii</i>	UH0707
2183	NZ_AG YG Q01000001.1	<i>Acinetobacter baumannii</i>	UH0807
2184	NZ_AG YG O01000001.1	<i>Acinetobacter baumannii</i>	UH10007
2185	NZ_AG YG P01000001.1	<i>Acinetobacter baumannii</i>	UH1007

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2186	NZ_AYGN01000001.1	<i>Acinetobacter baumannii</i>	UH10107
2187	NZ_JWVB03000001.1	<i>Acinetobacter baumannii</i>	UH106_429
2188	NZ_JWUZ03000001.1	<i>Acinetobacter baumannii</i>	UH106_440
2189	NZ_JWUW03000001.1	<i>Acinetobacter baumannii</i>	UH106_447
2190	NZ_AYOI01000002.1	<i>Acinetobacter baumannii</i>	UH10707
2191	NZ_AYGM01000001.1	<i>Acinetobacter baumannii</i>	UH10707
2192	NZ_AYGL01000001.1	<i>Acinetobacter baumannii</i>	UH11608
2193	NZ_AY GK01000001.1	<i>Acinetobacter baumannii</i>	UH12208
2194	NZ_AY GJ01000001.1	<i>Acinetobacter baumannii</i>	UH12308
2195	NZ_AY GI01000001.1	<i>Acinetobacter baumannii</i>	UH12408
2196	NZ_JWXL03000001.1	<i>Acinetobacter baumannii</i>	UH126_102
2197	NZ_JW XJ03000001.1	<i>Acinetobacter baumannii</i>	UH126_106
2198	NZ_JW XF03000001.1	<i>Acinetobacter baumannii</i>	UH126_137
2199	NZ_AY GH01000001.1	<i>Acinetobacter baumannii</i>	UH12808
2200	NZ_JW VJ03000001.1	<i>Acinetobacter baumannii</i>	UH129_404
2201	NZ_JW VI03000001.1	<i>Acinetobacter baumannii</i>	UH129_408
2202	NZ_JW VH03000001.1	<i>Acinetobacter baumannii</i>	UH129_409
2203	NZ_JW VF03000001.1	<i>Acinetobacter baumannii</i>	UH129_415
2204	NZ_JW XA03000001.1	<i>Acinetobacter baumannii</i>	UH134_167
2205	NZ_JW WZ03000001.1	<i>Acinetobacter baumannii</i>	UH134_168
2206	NZ_JW WW03000001.1	<i>Acinetobacter baumannii</i>	UH134_192
2207	NZ_AY GG01000001.1	<i>Acinetobacter baumannii</i>	UH13908
2208	NZ_AY GF01000001.1	<i>Acinetobacter baumannii</i>	UH14508
2209	NZ_AY GE01000001.1	<i>Acinetobacter baumannii</i>	UH15208
2210	NZ_AY GD01000001.1	<i>Acinetobacter baumannii</i>	UH16008
2211	NZ_AY GC01000001.1	<i>Acinetobacter baumannii</i>	UH16108
2212	NZ_AY GB01000001.1	<i>Acinetobacter baumannii</i>	UH16208

	NCBI Reference Sequence ID#	Strain
2213	NZ_JWXB03000001.1	<i>Acinetobacter baumannii</i> UH17_151
2214	NZ_JWWY03000001.1	<i>Acinetobacter baumannii</i> UH17_182
2215	NZ_JWWT03000001.1	<i>Acinetobacter baumannii</i> UH17_202
2216	NZ_JWUR03000001.1	<i>Acinetobacter baumannii</i> UH17_465
2217	NZ_JWYK03000001.1	<i>Acinetobacter baumannii</i> UH17_52
2218	NZ_JZJB02000001.1	<i>Acinetobacter baumannii</i> UH175_674
2219	NZ_JWTP03000001.1	<i>Acinetobacter baumannii</i> UH175_677
2220	NZ_JWTO03000001.1	<i>Acinetobacter baumannii</i> UH175_679
2221	NZ_JWWE03000001.1	<i>Acinetobacter baumannii</i> UH184_295
2222	NZ_JWWA03000001.1	<i>Acinetobacter baumannii</i> UH184_309
2223	NZ_JWVZ03000001.1	<i>Acinetobacter baumannii</i> UH184_310
2224	NZ_AYGA01000001.1	<i>Acinetobacter baumannii</i> UH18608
2225	NZ_JWVU03000001.1	<i>Acinetobacter baumannii</i> UH189_348
2226	NZ_JWVT03000001.1	<i>Acinetobacter baumannii</i> UH189_349
2227	NZ_JWVS03000001.1	<i>Acinetobacter baumannii</i> UH189_355
2228	NZ_JWTX03000001.1	<i>Acinetobacter baumannii</i> UH195_560
2229	NZ_JWTV03000001.1	<i>Acinetobacter baumannii</i> UH195_568
2230	NZ_JWTT03000001.1	<i>Acinetobacter baumannii</i> UH195_573
2231	NZ_AYFZ01000080.1	<i>Acinetobacter baumannii</i> UH19608
2232	NZ_AYFY01000001.1	<i>Acinetobacter baumannii</i> UH19908
2233	NZ_AYFX01000001.1	<i>Acinetobacter baumannii</i> UH20108
2234	NZ_AYFW01000101.1	<i>Acinetobacter baumannii</i> UH2107
2235	NZ_JWVA03000001.1	<i>Acinetobacter baumannii</i> UH225_433
2236	NZ_JWUO03000001.1	<i>Acinetobacter baumannii</i> UH225_472
2237	NZ_JWUF03000001.1	<i>Acinetobacter baumannii</i> UH225_492
2238	NZ_JWUE03000001.1	<i>Acinetobacter baumannii</i> UH225_493
2239	NZ_AYFV01000001.1	<i>Acinetobacter baumannii</i> UH22908

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2240	NZ_AYFU01000001.1	<i>Acinetobacter baumannii</i>	UH2307
2241	NZ_JWXV03000001.1	<i>Acinetobacter baumannii</i>	UH236_84
2242	NZ_JWXU03000001.1	<i>Acinetobacter baumannii</i>	UH236_85
2243	NZ_JWXT03000001.1	<i>Acinetobacter baumannii</i>	UH236_87
2244	NZ_JWYS03000001.1	<i>Acinetobacter baumannii</i>	UH243_14
2245	NZ_JWYP03000001.1	<i>Acinetobacter baumannii</i>	UH243_33
2246	NZ_JWYL03000001.1	<i>Acinetobacter baumannii</i>	UH243_43
2247	NZ_JWYJ03000001.1	<i>Acinetobacter baumannii</i>	UH243_54
2248	NZ_JWYI03000001.1	<i>Acinetobacter baumannii</i>	UH243_55
2249	NZ_JWYH03000001.1	<i>Acinetobacter baumannii</i>	UH243_56
2250	NZ_JWYG03000001.1	<i>Acinetobacter baumannii</i>	UH243_57
2251	NZ_JWYA03000001.1	<i>Acinetobacter baumannii</i>	UH243_66
2252	NZ_JWXZ03000001.1	<i>Acinetobacter baumannii</i>	UH243_68
2253	NZ_JWXY03000001.1	<i>Acinetobacter baumannii</i>	UH243_73
2254	NZ_AYFT01000001.1	<i>Acinetobacter baumannii</i>	UH2707
2255	NZ_JWXW03000001.1	<i>Acinetobacter baumannii</i>	UH280_81
2256	NZ_JWXS03000001.1	<i>Acinetobacter baumannii</i>	UH280_92
2257	NZ_JWXR03000001.1	<i>Acinetobacter baumannii</i>	UH280_93
2258	NZ_JWXS03000001.1	<i>Acinetobacter baumannii</i>	UH280_99
2259	NZ_AYFS01000001.1	<i>Acinetobacter baumannii</i>	UH2907
2260	NZ_JWVP03000001.1	<i>Acinetobacter baumannii</i>	UH293_373
2261	NZ_JWVO03000001.1	<i>Acinetobacter baumannii</i>	UH293_377
2262	NZ_JWVG03000001.1	<i>Acinetobacter baumannii</i>	UH293_412
2263	NZ_JWVX03000001.1	<i>Acinetobacter baumannii</i>	UH299_338
2264	NZ_JWVW03000001.1	<i>Acinetobacter baumannii</i>	UH299_341
2265	NZ_JWVV03000001.1	<i>Acinetobacter baumannii</i>	UH299_342
2266	NZ_JWXN03000001.1	<i>Acinetobacter baumannii</i>	UH315_100

	NCBI Reference Sequence ID#	Strain
2267	NZ_JWXM03000001.1	<i>Acinetobacter baumannii</i> UH315_101
2268	NZ_JWYN03000001.1	<i>Acinetobacter baumannii</i> UH315_39
2269	NZ_JWYF03000001.1	<i>Acinetobacter baumannii</i> UH315_58
2270	NZ_JWUX03000001.1	<i>Acinetobacter baumannii</i> UH326_445
2271	NZ_JWUS03000001.1	<i>Acinetobacter baumannii</i> UH326_461
2272	NZ_JWUD03000001.1	<i>Acinetobacter baumannii</i> UH326_495
2273	NZ_JWYT03000001.1	<i>Acinetobacter baumannii</i> UH348_13
2274	NZ_JWYR03000001.1	<i>Acinetobacter baumannii</i> UH348_25
2275	NZ_JWYQ03000001.1	<i>Acinetobacter baumannii</i> UH348_27
2276	NZ_JWUB03000001.1	<i>Acinetobacter baumannii</i> UH355_545
2277	NZ_JWTU03000001.1	<i>Acinetobacter baumannii</i> UH355_569
2278	NZ_JWTZ03000001.1	<i>Acinetobacter baumannii</i> UH367_548
2279	NZ_JWTY03000001.1	<i>Acinetobacter baumannii</i> UH367_558
2280	NZ_JWTW03000001.1	<i>Acinetobacter baumannii</i> UH367_565
2281	NZ_JWWM03000001.1	<i>Acinetobacter baumannii</i> UH370_269
2282	NZ_JWWB03000001.1	<i>Acinetobacter baumannii</i> UH370_301
2283	NZ_AYFR01000001.1	<i>Acinetobacter baumannii</i> UH3807
2284	NZ_JWUP03000001.1	<i>Acinetobacter baumannii</i> UH381_467
2285	NZ_JWUM03000001.1	<i>Acinetobacter baumannii</i> UH381_482
2286	NZ_JZJA02000001.1	<i>Acinetobacter baumannii</i> UH381_484
2287	NZ_JWUY03000001.1	<i>Acinetobacter baumannii</i> UH384_444
2288	NZ_JWUV03000001.1	<i>Acinetobacter baumannii</i> UH384_450
2289	NZ_JWUC03000001.1	<i>Acinetobacter baumannii</i> UH392_536
2290	NZ_JWTR03000001.1	<i>Acinetobacter baumannii</i> UH392_659
2291	NZ_JWTN03000001.1	<i>Acinetobacter baumannii</i> UH392_684
2292	NZ_JWUL03000001.1	<i>Acinetobacter baumannii</i> UH41_486
2293	NZ_JWUK03000001.1	<i>Acinetobacter baumannii</i> UH41_487

	NCBI Reference Sequence ID#	Strain	
2294	NZ_JWUJ03000001.1	<i>Acinetobacter baumannii</i>	UH41_488
2295	NZ_JWUI03000001.1	<i>Acinetobacter baumannii</i>	UH41_489
2296	NZ_JWUH03000001.1	<i>Acinetobacter baumannii</i>	UH41_490
2297	NZ_JWUG03000001.1	<i>Acinetobacter baumannii</i>	UH41_491
2298	NZ_JWXX03000001.1	<i>Acinetobacter baumannii</i>	UH410_103
2299	NZ_JWXI03000001.1	<i>Acinetobacter baumannii</i>	UH410_108
2300	NZ_JWXH03000001.1	<i>Acinetobacter baumannii</i>	UH410_128
2301	NZ_JWXP03000001.1	<i>Acinetobacter baumannii</i>	UH410_96
2302	NZ_JWUT03000001.1	<i>Acinetobacter baumannii</i>	UH430_459
2303	NZ_JWUQ03000001.1	<i>Acinetobacter baumannii</i>	UH430_466
2304	NZ_JWUN03000001.1	<i>Acinetobacter baumannii</i>	UH430_478
2305	NZ_JWYO03000001.1	<i>Acinetobacter baumannii</i>	UH455_38
2306	NZ_JWYU03000001.1	<i>Acinetobacter baumannii</i>	UH455_6
2307	NZ_JWYE03000001.1	<i>Acinetobacter baumannii</i>	UH455_61
2308	NZ_JWYD03000001.1	<i>Acinetobacter baumannii</i>	UH455_62
2309	NZ_JWWV03000001.1	<i>Acinetobacter baumannii</i>	UH475_197
2310	NZ_JWWR03000001.1	<i>Acinetobacter baumannii</i>	UH475_239
2311	NZ_JZJF02000001.1	<i>Acinetobacter baumannii</i>	UH475_361
2312	NZ_JWYM03000001.1	<i>Acinetobacter baumannii</i>	UH487_41
2313	NZ_JWYC03000001.1	<i>Acinetobacter baumannii</i>	UH487_63
2314	NZ_JWYB03000001.1	<i>Acinetobacter baumannii</i>	UH487_64
2315	NZ_JWXX03000001.1	<i>Acinetobacter baumannii</i>	UH487_78
2316	NZ_JWWP03000001.1	<i>Acinetobacter baumannii</i>	UH507_247
2317	NZ_JWWO03000001.1	<i>Acinetobacter baumannii</i>	UH507_263
2318	NZ_JWWC03000001.1	<i>Acinetobacter baumannii</i>	UH507_300
2319	NZ_AYFQ01000001.1	<i>Acinetobacter baumannii</i>	UH5107
2320	NZ_JWWG03000001.1	<i>Acinetobacter baumannii</i>	UH514_287

	NCBI Reference Sequence ID#	Strain
2321	NZ_JWWF03000001.1	<i>Acinetobacter baumannii</i> UH514_288
2322	NZ_JZJG02000001.1	<i>Acinetobacter baumannii</i> UH514_289
2323	NZ_AYFP01000001.1	<i>Acinetobacter baumannii</i> UH5207
2324	NZ_AYFO01000001.1	<i>Acinetobacter baumannii</i> UH5307
2325	NZ_JWVN03000001.1	<i>Acinetobacter baumannii</i> UH532_386
2326	NZ_JWVM03000001.1	<i>Acinetobacter baumannii</i> UH532_387
2327	NZ_JWVK03000001.1	<i>Acinetobacter baumannii</i> UH532_392
2328	NZ_JWVE03000001.1	<i>Acinetobacter baumannii</i> UH535_418
2329	NZ_JWVD03000001.1	<i>Acinetobacter baumannii</i> UH535_419
2330	NZ_JWVC03000001.1	<i>Acinetobacter baumannii</i> UH535_423
2331	NZ_AYFN01000001.1	<i>Acinetobacter baumannii</i> UH5707
2332	NZ_JWTS03000001.1	<i>Acinetobacter baumannii</i> UH588_656
2333	NZ_JWTQ03000001.1	<i>Acinetobacter baumannii</i> UH588_663
2334	NZ_JZIY02000001.1	<i>Acinetobacter baumannii</i> UH592_583
2335	NZ_JZJE02000001.1	<i>Acinetobacter baumannii</i> UH592_595
2336	NZ_JZJD02000001.1	<i>Acinetobacter baumannii</i> UH592_599
2337	NZ_AYFM01000001.1	<i>Acinetobacter baumannii</i> UH6107
2338	NZ_AYFL01000001.1	<i>Acinetobacter baumannii</i> UH6207
2339	NZ_AYFK01000001.1	<i>Acinetobacter baumannii</i> UH6507
2340	NZ_JWWQ03000001.1	<i>Acinetobacter baumannii</i> UH66_241
2341	NZ_JZIZ02000001.1	<i>Acinetobacter baumannii</i> UH66_253
2342	NZ_JWWN03000001.1	<i>Acinetobacter baumannii</i> UH66_268
2343	NZ_JZIX02000001.1	<i>Acinetobacter baumannii</i> UH66_271
2344	NZ_JWWK03000001.1	<i>Acinetobacter baumannii</i> UH66_276
2345	NZ_AYFJ01000001.1	<i>Acinetobacter baumannii</i> UH6907
2346	NZ_AYFI01000019.1	<i>Acinetobacter baumannii</i> UH7007
2347	NZ_JWWJ03000001.1	<i>Acinetobacter baumannii</i> UH71_277

	NCBI Reference Sequence ID#	Strain	
2348	NZ_JWWI03000001.1	<i>Acinetobacter baumannii</i>	UH71_278
2349	NZ_JWWH03000001.1	<i>Acinetobacter baumannii</i>	UH71_279
2350	NZ_JWWD03000001.1	<i>Acinetobacter baumannii</i>	UH71_296
2351	NZ_AYFH01000057.1	<i>Acinetobacter baumannii</i>	UH7607
2352	NZ_AYFG01000001.1	<i>Acinetobacter baumannii</i>	UH7707
2353	NZ_AYFF01000001.1	<i>Acinetobacter baumannii</i>	UH7807
2354	NZ_AYFE01000001.1	<i>Acinetobacter baumannii</i>	UH7907
2355	NZ_JWVR03000001.1	<i>Acinetobacter baumannii</i>	UH81_364
2356	NZ_JWVQ03000001.1	<i>Acinetobacter baumannii</i>	UH81_366
2357	NZ_JWVL03000001.1	<i>Acinetobacter baumannii</i>	UH81_389
2358	NZ_JWUU03000001.1	<i>Acinetobacter baumannii</i>	UH81_452
2359	NZ_AYFD01000001.1	<i>Acinetobacter baumannii</i>	UH8107
2360	NZ_AYFC01000001.1	<i>Acinetobacter baumannii</i>	UH8407
2361	NZ_AYFB01000001.1	<i>Acinetobacter baumannii</i>	UH8707
2362	NZ_AYFA01000001.1	<i>Acinetobacter baumannii</i>	UH8807
2363	NZ_AYEZ01000001.1	<i>Acinetobacter baumannii</i>	UH8907
2364	NZ_AYFY01000001.1	<i>Acinetobacter baumannii</i>	UH9007
2365	NZ_AYEX01000118.1	<i>Acinetobacter baumannii</i>	UH9707
2366	NZ_AYOH01000010.1	<i>Acinetobacter baumannii</i>	UH9907
2367	NZ_AYEW01000001.1	<i>Acinetobacter baumannii</i>	UH9907
2368	NZ_AEPK01000118.1	<i>Acinetobacter baumannii</i>	UMB001
2369	NZ_AEPL01000074.1	<i>Acinetobacter baumannii</i>	UMB002
2370	NZ_CP020595.1	<i>Acinetobacter baumannii</i>	USA15
2371	NZ_CP020592.1	<i>Acinetobacter baumannii</i>	USA2
2372	NZ_PESS01000100.1	<i>Acinetobacter baumannii</i>	VB17782
2373	NZ_LTAJ01000001.1	<i>Acinetobacter baumannii</i>	VB22595
2374	NZ_PESU01000100.1	<i>Acinetobacter baumannii</i>	VB2265

	NCBI Reference Sequence ID#	Strain	
2375	NZ_PESR01000100.1	<i>Acinetobacter baumannii</i>	VB23193
2376	NZ_PEST01000100.1	<i>Acinetobacter baumannii</i>	VB3373
2377	NZ_MJBM01000001.1	<i>Acinetobacter baumannii</i>	VB3552
2378	NZ_MJBK01000001.1	<i>Acinetobacter baumannii</i>	VB36560
2379	NZ_MJBL01000001.1	<i>Acinetobacter baumannii</i>	VB39358
2380	NZ_AIEH01000133.1	<i>Acinetobacter baumannii</i>	W7282
2381	NZ_JXOC01000001.1	<i>Acinetobacter baumannii</i>	WA2859
2382	NZ_MLYW01000001.1	<i>Acinetobacter baumannii</i>	WA2859
2383	NZ_AMZT01000001.1	<i>Acinetobacter baumannii</i>	WC-348
2384	NZ_AMGG01000001.1	<i>Acinetobacter baumannii</i>	WC-692
2385	NZ_AMTA01000001.1	<i>Acinetobacter baumannii</i>	WC-A-694
2386	NZ_AMFU01000001.1	<i>Acinetobacter baumannii</i>	WC-A-92
2387	NZ_CP027246.1	<i>Acinetobacter baumannii</i>	WCHAB005078
2388	NZ_CP026750.1	<i>Acinetobacter baumannii</i>	WCHAB005133
2389	NZ_QCXT01000001.1	<i>Acinetobacter baumannii</i>	WE1572
2390	NZ_CP020598.1	<i>Acinetobacter baumannii</i>	WKA02
2391	NZ_FBXB01000001.1	<i>Acinetobacter baumannii</i>	WM98
2392	NZ_AERY01000162.1	<i>Acinetobacter baumannii</i>	WM99c
2393	NZ_CP018421.1	<i>Acinetobacter baumannii</i>	XDR-BJ83
2394	NZ_MDWH01000001.1	<i>Acinetobacter baumannii</i>	XH181
2395	NZ_MDWJ01000001.1	<i>Acinetobacter baumannii</i>	XH182
2396	NZ_MDWK01000001.1	<i>Acinetobacter baumannii</i>	XH183
2397	NZ_MDWL01000001.1	<i>Acinetobacter baumannii</i>	XH184
2398	NZ_MDWG01000001.1	<i>Acinetobacter baumannii</i>	XH191
2399	NZ_MDWI01000001.1	<i>Acinetobacter baumannii</i>	XH192
2400	NZ_MDWF01000001.1	<i>Acinetobacter baumannii</i>	XH193
2401	NZ_MDWM01000001.1	<i>Acinetobacter baumannii</i>	XH198

	NCBI Reference Sequence ID#	Strain	
2402	NZ_CP010779.1	<i>Acinetobacter baumannii</i>	XH386
2403	NZ_LYLM01000001.1	<i>Acinetobacter baumannii</i>	XH506
2404	NZ_LYLL01000001.1	<i>Acinetobacter baumannii</i>	XH507
2405	NZ_LYLK01000001.1	<i>Acinetobacter baumannii</i>	XH508
2406	NZ_LY LJ01000001.1	<i>Acinetobacter baumannii</i>	XH509
2407	NZ_LY LJ01000001.1	<i>Acinetobacter baumannii</i>	XH510
2408	NZ_LY LH01000001.1	<i>Acinetobacter baumannii</i>	XH511
2409	NZ_LY LG01000001.1	<i>Acinetobacter baumannii</i>	XH512
2410	NZ_LY LF01000001.1	<i>Acinetobacter baumannii</i>	XH513
2411	NZ_LY LE01000001.1	<i>Acinetobacter baumannii</i>	XH514
2412	NZ_LY LD01000001.1	<i>Acinetobacter baumannii</i>	XH515
2413	NZ_LY LC01000001.1	<i>Acinetobacter baumannii</i>	XH545
2414	NZ_LY LB01000001.1	<i>Acinetobacter baumannii</i>	XH546
2415	NZ_LY LA01000001.1	<i>Acinetobacter baumannii</i>	XH547
2416	NZ_LY KZ01000001.1	<i>Acinetobacter baumannii</i>	XH548
2417	NZ_LY KY01000001.1	<i>Acinetobacter baumannii</i>	XH549
2418	NZ_LY KX01000001.1	<i>Acinetobacter baumannii</i>	XH550
2419	NZ_LY KV01000001.1	<i>Acinetobacter baumannii</i>	XH552
2420	NZ_LY KU01000001.1	<i>Acinetobacter baumannii</i>	XH553
2421	NZ_LY KT01000001.1	<i>Acinetobacter baumannii</i>	XH554
2422	NZ_LY KS01000001.1	<i>Acinetobacter baumannii</i>	XH595
2423	NZ_LY KR01000001.1	<i>Acinetobacter baumannii</i>	XH606
2424	NZ_LY JO01000001.1	<i>Acinetobacter baumannii</i>	XH608
2425	NZ_LY KQ01000001.1	<i>Acinetobacter baumannii</i>	XH639
2426	NZ_LY KP01000001.1	<i>Acinetobacter baumannii</i>	XH640
2427	NZ_LY KO01000001.1	<i>Acinetobacter baumannii</i>	XH641
2428	NZ_LY KN01000001.1	<i>Acinetobacter baumannii</i>	XH642

	NCBI Reference Sequence ID#	Strain	
2429	NZ_LYKMM01000001.1	<i>Acinetobacter baumannii</i>	XH643
2430	NZ_LYKLL01000001.1	<i>Acinetobacter baumannii</i>	XH644
2431	NZ_LYKKK01000001.1	<i>Acinetobacter baumannii</i>	XH645
2432	NZ_LYKJ01000001.1	<i>Acinetobacter baumannii</i>	XH646
2433	NZ_LYKIO1000001.1	<i>Acinetobacter baumannii</i>	XH647
2434	NZ_LYKHO1000001.1	<i>Acinetobacter baumannii</i>	XH648
2435	NZ_LYKGO1000001.1	<i>Acinetobacter baumannii</i>	XH649
2436	NZ_LYKFO1000001.1	<i>Acinetobacter baumannii</i>	XH650
2437	NZ_LYKCO1000001.1	<i>Acinetobacter baumannii</i>	XH661
2438	NZ_LYKA01000001.1	<i>Acinetobacter baumannii</i>	XH663
2439	NZ_LYJZ01000001.1	<i>Acinetobacter baumannii</i>	XH664
2440	NZ_LYJY01000001.1	<i>Acinetobacter baumannii</i>	XH665
2441	NZ_LYJX01000001.1	<i>Acinetobacter baumannii</i>	XH666
2442	NZ_LYJW01000001.1	<i>Acinetobacter baumannii</i>	XH667
2443	NZ_LYJV01000001.1	<i>Acinetobacter baumannii</i>	XH668
2444	NZ_LYJU01000001.1	<i>Acinetobacter baumannii</i>	XH669
2445	NZ_LYJT01000001.1	<i>Acinetobacter baumannii</i>	XH670
2446	NZ_LYJS01000001.1	<i>Acinetobacter baumannii</i>	XH671
2447	NZ_LYJR01000001.1	<i>Acinetobacter baumannii</i>	XH672
2448	NZ_LYJQ01000001.1	<i>Acinetobacter baumannii</i>	XH673
2449	NZ_LYJP01000001.1	<i>Acinetobacter baumannii</i>	XH674
2450	NZ_LYJK01000001.1	<i>Acinetobacter baumannii</i>	XH679
2451	NZ_LYJI01000001.1	<i>Acinetobacter baumannii</i>	XH680
2452	NZ_LYJH01000001.1	<i>Acinetobacter baumannii</i>	XH681
2453	NZ_LYJG01000001.1	<i>Acinetobacter baumannii</i>	XH682
2454	NZ_LYJF01000001.1	<i>Acinetobacter baumannii</i>	XH683
2455	NZ_LYJE01000001.1	<i>Acinetobacter baumannii</i>	XH684

	NCBI Reference Sequence ID#	Strain	
2456	NZ_LYJE01000001.1	<i>Acinetobacter baumannii</i>	XH685
2457	NZ_LYJD01000001.1	<i>Acinetobacter baumannii</i>	XH686
2458	NZ_LYJC01000001.1	<i>Acinetobacter baumannii</i>	XH687
2459	NZ_LYJB01000001.1	<i>Acinetobacter baumannii</i>	XH688
2460	NZ_LYJA01000001.1	<i>Acinetobacter baumannii</i>	XH689
2461	NZ_LYIZ01000001.1	<i>Acinetobacter baumannii</i>	XH690
2462	NZ_LYIY01000001.1	<i>Acinetobacter baumannii</i>	XH693
2463	NZ_LYIW01000001.1	<i>Acinetobacter baumannii</i>	XH697
2464	NZ_LYIV01000001.1	<i>Acinetobacter baumannii</i>	XH698
2465	NZ_LYIU01000001.1	<i>Acinetobacter baumannii</i>	XH701
2466	NZ_LYIT01000001.1	<i>Acinetobacter baumannii</i>	XH702
2467	NZ_LYIS01000001.1	<i>Acinetobacter baumannii</i>	XH703
2468	NZ_LYIR01000001.1	<i>Acinetobacter baumannii</i>	XH704
2469	NZ_LYIQ01000001.1	<i>Acinetobacter baumannii</i>	XH705
2470	NZ_LYIP01000001.1	<i>Acinetobacter baumannii</i>	XH706
2471	NZ_LYIO01000001.1	<i>Acinetobacter baumannii</i>	XH707
2472	NZ_LYIN01000001.1	<i>Acinetobacter baumannii</i>	XH708
2473	NZ_LYIM01000001.1	<i>Acinetobacter baumannii</i>	XH709
2474	NZ_LYIL01000001.1	<i>Acinetobacter baumannii</i>	XH710
2475	NZ_LYIK01000001.1	<i>Acinetobacter baumannii</i>	XH713
2476	NZ_LYIJ01000001.1	<i>Acinetobacter baumannii</i>	XH714
2477	NZ_LYII01000001.1	<i>Acinetobacter baumannii</i>	XH715
2478	NZ_LYIH01000001.1	<i>Acinetobacter baumannii</i>	XH717
2479	NZ_LYIG01000001.1	<i>Acinetobacter baumannii</i>	XH718
2480	NZ_LYIF01000001.1	<i>Acinetobacter baumannii</i>	XH719
2481	NZ_LYIE01000001.1	<i>Acinetobacter baumannii</i>	XH720
2482	NZ_LYID01000001.1	<i>Acinetobacter baumannii</i>	XH721

	NCBI Reference Sequence ID#	Strain	
2483	NZ_LYIC01000001.1	<i>Acinetobacter baumannii</i>	XH722
2484	NZ_LYIB01000001.1	<i>Acinetobacter baumannii</i>	XH723
2485	NZ_LYIA01000001.1	<i>Acinetobacter baumannii</i>	XH724
2486	NZ_LYHZ01000001.1	<i>Acinetobacter baumannii</i>	XH726
2487	NZ_LYHY01000001.1	<i>Acinetobacter baumannii</i>	XH727
2488	NZ_LYHX01000001.1	<i>Acinetobacter baumannii</i>	XH728
2489	NZ_LYHW01000001.1	<i>Acinetobacter baumannii</i>	XH729
2490	NZ_LYHV01000001.1	<i>Acinetobacter baumannii</i>	XH730
2491	NZ_LYHU01000001.1	<i>Acinetobacter baumannii</i>	XH731
2492	NZ_LYHT01000001.1	<i>Acinetobacter baumannii</i>	XH732
2493	NZ_LYHS01000001.1	<i>Acinetobacter baumannii</i>	XH733
2494	NZ_LYHR01000001.1	<i>Acinetobacter baumannii</i>	XH735
2495	NZ_LYHQ01000001.1	<i>Acinetobacter baumannii</i>	XH736
2496	NZ_LYHP01000001.1	<i>Acinetobacter baumannii</i>	XH737
2497	NZ_LYHO01000001.1	<i>Acinetobacter baumannii</i>	XH738
2498	NZ_LYHN01000001.1	<i>Acinetobacter baumannii</i>	XH739
2499	NZ_LYHM01000001.1	<i>Acinetobacter baumannii</i>	XH740
2500	NZ_LYHL01000001.1	<i>Acinetobacter baumannii</i>	XH741
2501	NZ_LYHK01000001.1	<i>Acinetobacter baumannii</i>	XH742
2502	NZ_LYHJ01000001.1	<i>Acinetobacter baumannii</i>	XH743
2503	NZ_LYHI01000001.1	<i>Acinetobacter baumannii</i>	XH744
2504	NZ_LYHH01000001.1	<i>Acinetobacter baumannii</i>	XH745
2505	NZ_LYHG01000001.1	<i>Acinetobacter baumannii</i>	XH746
2506	NZ_LYHF01000001.1	<i>Acinetobacter baumannii</i>	XH747
2507	NZ_LYHE01000001.1	<i>Acinetobacter baumannii</i>	XH748
2508	NZ_LYHD01000001.1	<i>Acinetobacter baumannii</i>	XH749
2509	NZ_LYHC01000001.1	<i>Acinetobacter baumannii</i>	XH750

	NCBI Reference Sequence ID#	Strain	
2510	NZ_LYHB01000001.1	<i>Acinetobacter baumannii</i>	XH751
2511	NZ_LYHA01000001.1	<i>Acinetobacter baumannii</i>	XH752
2512	NZ_LYGA01000001.1	<i>Acinetobacter baumannii</i>	XH753
2513	NZ_LYGY01000001.1	<i>Acinetobacter baumannii</i>	XH754
2514	NZ_LYGX01000001.1	<i>Acinetobacter baumannii</i>	XH755
2515	NZ_LYGW01000001.1	<i>Acinetobacter baumannii</i>	XH756
2516	NZ_LYGV01000001.1	<i>Acinetobacter baumannii</i>	XH757
2517	NZ_LYGT01000001.1	<i>Acinetobacter baumannii</i>	XH763
2518	NZ_LYGS01000001.1	<i>Acinetobacter baumannii</i>	XH764
2519	NZ_LYQQ01000001.1	<i>Acinetobacter baumannii</i>	XH766
2520	NZ_LYGP01000001.1	<i>Acinetobacter baumannii</i>	XH767
2521	NZ_LYGO01000001.1	<i>Acinetobacter baumannii</i>	XH768
2522	NZ_LYGN01000001.1	<i>Acinetobacter baumannii</i>	XH769
2523	NZ_LYGM01000001.1	<i>Acinetobacter baumannii</i>	XH770
2524	NZ_LYGL01000001.1	<i>Acinetobacter baumannii</i>	XH771
2525	NZ_LY GK01000001.1	<i>Acinetobacter baumannii</i>	XH778
2526	NZ_LY GJ01000001.1	<i>Acinetobacter baumannii</i>	XH779
2527	NZ_LY FE01000001.1	<i>Acinetobacter baumannii</i>	XH780
2528	NZ_LY FD01000001.1	<i>Acinetobacter baumannii</i>	XH781
2529	NZ_LY GI01000001.1	<i>Acinetobacter baumannii</i>	XH786
2530	NZ_LY GH01000001.1	<i>Acinetobacter baumannii</i>	XH787
2531	NZ_LY GG01000001.1	<i>Acinetobacter baumannii</i>	XH792
2532	NZ_LY GF01000001.1	<i>Acinetobacter baumannii</i>	XH793
2533	NZ_LY GD01000001.1	<i>Acinetobacter baumannii</i>	XH795
2534	NZ_LY GB01000001.1	<i>Acinetobacter baumannii</i>	XH797
2535	NZ_LY GA01000001.1	<i>Acinetobacter baumannii</i>	XH798
2536	NZ_LY FZ01000001.1	<i>Acinetobacter baumannii</i>	XH799

	NCBI Reference Sequence ID#	Strain	
2537	NZ_LYFY01000001.1	<i>Acinetobacter baumannii</i>	XH800
2538	NZ_LYFX01000001.1	<i>Acinetobacter baumannii</i>	XH801
2539	NZ_LYFW01000001.1	<i>Acinetobacter baumannii</i>	XH802
2540	NZ_LYFV01000001.1	<i>Acinetobacter baumannii</i>	XH803
2541	NZ_LYFU01000001.1	<i>Acinetobacter baumannii</i>	XH804
2542	NZ_LYFT01000001.1	<i>Acinetobacter baumannii</i>	XH805
2543	NZ_LYFS01000001.1	<i>Acinetobacter baumannii</i>	XH810
2544	NZ_LYFR01000001.1	<i>Acinetobacter baumannii</i>	XH811
2545	NZ_LYFQ01000001.1	<i>Acinetobacter baumannii</i>	XH819
2546	NZ_LYFP01000001.1	<i>Acinetobacter baumannii</i>	XH820
2547	NZ_LYFC01000001.1	<i>Acinetobacter baumannii</i>	XH821
2548	NZ_LYFB01000001.1	<i>Acinetobacter baumannii</i>	XH822
2549	NZ_LYFO01000001.1	<i>Acinetobacter baumannii</i>	XH823
2550	NZ_LYFA01000001.1	<i>Acinetobacter baumannii</i>	XH827
2551	NZ_LYEZ01000001.1	<i>Acinetobacter baumannii</i>	XH828
2552	NZ_LYFM01000001.1	<i>Acinetobacter baumannii</i>	XH829
2553	NZ_LYFL01000001.1	<i>Acinetobacter baumannii</i>	XH830
2554	NZ_LYFK01000001.1	<i>Acinetobacter baumannii</i>	XH833
2555	NZ_LYFJ01000001.1	<i>Acinetobacter baumannii</i>	XH834
2556	NZ_LYFI01000001.1	<i>Acinetobacter baumannii</i>	XH835
2557	NZ_LYFH01000001.1	<i>Acinetobacter baumannii</i>	XH836
2558	NZ_LYFG01000001.1	<i>Acinetobacter baumannii</i>	XH837
2559	NZ_LYFF01000001.1	<i>Acinetobacter baumannii</i>	XH838
2560	NZ_LYFY01000001.1	<i>Acinetobacter baumannii</i>	XH839
2561	NZ_LYEX01000001.1	<i>Acinetobacter baumannii</i>	XH840
2562	NZ_LYJN01000001.1	<i>Acinetobacter baumannii</i>	XH850
2563	NZ_LYJM01000001.1	<i>Acinetobacter baumannii</i>	XH851

	NCBI Reference Sequence ID#	Strain	
2564	NZ_LYJL01000001.1	<i>Acinetobacter baumannii</i>	XH854
2565	NZ_CP014541.1	<i>Acinetobacter baumannii</i>	XH856
2566	NZ_CP014540.1	<i>Acinetobacter baumannii</i>	XH857
2567	NZ_CP014528.1	<i>Acinetobacter baumannii</i>	XH858
2568	NZ_CP014539.1	<i>Acinetobacter baumannii</i>	XH859
2569	NZ_CP014538.1	<i>Acinetobacter baumannii</i>	XH860
2570	NZ_CP014215.1	<i>Acinetobacter baumannii</i>	YU-R612
2571	NZ_MIFW01000001.1	<i>Acinetobacter baumannii</i>	ZJ06-200P5-1
2572	NZ_CM008887.2	<i>Acinetobacter baumannii</i>	ZQ1
2573	NZ_CM009030.2	<i>Acinetobacter baumannii</i>	ZQ10
2574	NZ_CM009049.2	<i>Acinetobacter baumannii</i>	ZQ2
2575	NZ_CM009028.2	<i>Acinetobacter baumannii</i>	ZQ3
2576	NZ_CM009038.2	<i>Acinetobacter baumannii</i>	ZQ6
2577	NZ_CM009036.2	<i>Acinetobacter baumannii</i>	ZQ7
2578	NZ_CM009033.2	<i>Acinetobacter baumannii</i>	ZQ8
2579	NZ_CM009083.2	<i>Acinetobacter baumannii</i>	ZQ9
2580	NC_023028.1	<i>Acinetobacter baumannii</i>	ZW85-1
2581	NZ_AMGR01000001.1	<i>Acinetobacter baumannii</i>	ZWS1122
2582	NZ_AMGS01000001.1	<i>Acinetobacter baumannii</i>	ZWS1219

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