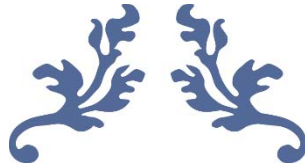


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Bioprospecting: The quest for novel extracellular polymers produced by soil-borne bacteria



A thesis presented in partial fulfilment of the
requirements for the degree of
Master of Science
In
Microbiology
at Massey University, Palmerston North,
New Zealand

Jason Smith

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Dedication

This thesis is dedicated to my dad.

Vaughan Peter Francis Smith

13 July 1955 – 27 April 2002

Though our time together was short
you are never far from my mind nor my heart.

Abstract

Bacteria are ubiquitous in nature, and the surrounding environment. Bacterially produced extracellular polymers, and proteins are of particular value in the fields of medicine, food, science, and industry. Soil is an extremely rich source of bacteria with over 100 million per gram of soil, many of which produce extracellular polymers. Approximately 90% of soil-borne bacteria are yet to be cultured and classified. Here we employed an exploratory approach and culture based method for the isolation of soil-borne bacteria, and assessed their capability for extracellular polymer production. Bacteria that produced mucoid (of a mucous nature) colonies were selected for identification, imaging, and polymer production. Here we characterised three bacterial isolates that produced extracellular polymers, with a focus on one isolate that formed potentially novel proteinaceous cell surface appendages. These appendages have an unknown function, however, I suggest they may be important for bacterial communication, signalling, and nutrient transfer. They may also serve to increase the bacteria's surface area for nutrient adsorption without compromising structural integrity of the cell. The results from this study contribute to the scientific body of knowledge and provide avenues for further research into bacterial appendage formation.

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List of abbreviations

A full list of abbreviations used

°C	Degrees Celsius
AIA	Actinomycete isolation agar
AIB	Actinomycete isolation broth
APS	Ammonium persulfate
BCA	Bicinchoninic acid
BLAST	Basic local alignment search tool
BSA	Bovine serum albumin
bp(s)	Base pair(s)
DMSO	Dimethylsulfoxide
DNA	Deoxyribonucleic acid
DNase	Deoxyribonuclease
dNTPs	Deoxyribonucleotide triphosphates
EDTA	Ethylenediaminetetraacetic acid
EtOH	Ethanol
g	Gravity/gram
<i>gyrA</i>	DNA gyrase subunit A
k	Kilo/thousand
kb	Kilo base(s)
kDa	Kilo Daltons
LB	Luria-Bertani broth
LBA	Luria-Bertani agar
MLST	Multilocus sequence typing

OMF	Outer membrane fraction
<i>parC</i>	DNA topoisomerase IV subunit A
PCR	Polymerase chain reaction
Psi	Pounds per square inch
RNA	Ribonucleic acid
RNase	Ribonuclease
rRNA	Ribosomal ribonucleic acid
<i>rpoB</i>	DNA-directed RNA polymerase β -subunit
rpm	Revolutions per minute
SDS	Sodium dodecyl sulphate
SDS-PAGE	Sodium dodecyl sulphate polyacrylamide gel electrophoresis
SEM	Scanning Electron Microscopy
TBE	Tris-Borate-EDTA buffer
TEM	Transmission Electron Microscopy
TEMED	Tetramethylethylenediamine
Tris	Trishydroxymethylaminomethane
v/v	Volume per volume
WEF	Whole envelope fraction
w/v	Weight per volume

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Chapter 1: Introduction

Bacteria are ubiquitous in nature and have evolved to survive and propagate in extreme environments once thought to be uninhabitable. Through this evolutionary process bacteria have developed the ability to utilise numerous substrates and produce innumerable others (Hibbing, Fuqua, Parsek, & Peterson, 2010). The diverse range of environments that bacteria can inhabit is exceeded by the number of different bacteria themselves, with diverse communities inhabiting the same environments in symbiotic, mutualistic or competitive/negative relationships with each other (Zook, 2015).

Bacteria's relationship with humans is very similar; we are inhabited by communities of bacteria that are either symbiotic, mutualistic, or harmful and every human has a unique bacterial make-up (Costello et al., 2009). This is important when considering the impacts of bacteria on human health. Some bacteria in the gastrointestinal tract protect against disease, aid in digestion, and influencing host immune and neuroendocrine systems (Palmer, Bik, DiGiulio, Relman, & Brown, 2007). However, if wiped out through antibiotic usage or other factors, disease causing bacteria such as *Clostridium difficile* may become established and be very difficult to treat (Cohen et al., 2010).

Pseudomonas aeruginosa, an important opportunistic bacterial pathogen of humans, produces large amounts of an extracellular polymer, alginate (Pugashetti, Metzger Jr, Vadas, & Feingold, 1982). Alginate itself is generally regarded as safe (GRAS) when harvested from brown seaweeds. Study by McHugh (1987) provided information regarding the structure, production, and the use of alginate in fields including medicine, food, pharmaceuticals, and industry. However when produced by *P. aeruginosa*, alginate becomes a major virulence factor particularly in cystic fibrosis patients (Pedersen, Høiby, Espersen, & Koch, 1992; Pedersen, Kharazmi, Espersen, & Høiby, 1990).

Alginate producing strains of *P. aeruginosa* are more likely to persist *in vivo* than non-alginate producing strains. There are many possible explanations for this including that alginate forms a layer around the bacteria preventing them from being engulfed by phagocytic cells or that thick layers of alginate prevent drugs from penetrating into the bacteria, and finally biofilm formation may prevent key immunomodulators from being visible to immune cells and complement (Matthew, 1984; Parsek & Singh, 2003).

While bacterially produced extracellular polymers can be associated with disease progression and persistence there are some that are potentially highly valuable in food, medicine, electronics, and industry (Vu, Chen, Crawford, & Ivanova, 2009). A brief review of these is provided below.

1.1 Bacterial extracellular polymers and food

As described above alginate is GRAS, and when extracted from brown seaweed is used in many food products particularly as a thickening and stabilising agent. Although it is produced by many bacteria, and most studied in the *Pseudomonas* and *Azotobacter* genera, bacterial alginate has no current commercial applications in food (Hay, Rehman, Moradali, Wang, & Rehm, 2013; Sabra, Zeng, & Deckwer, 2001).

Other bacterial extracellular polymers are widely used in foods for a range of purposes including as thickeners, stabilisers, and cryoprotectants. Two such polymers are the polysaccharide xanthan produced extensively by *Xanthomonas campestris* (Katzbauer, 1998) and the polyamide poly- γ -glutamate produced by *Bacillus* sp. (Kunioka, 1995).

Approximately 100,000 tons of xanthan (xanthan gum) is commercially produced per year using both traditional fermentation and solid state fermentation with around 65% used in food (Kreyenschulte, Krull, & Margaritis, 2014; Lopes et al., 2015; Stredansky & Conti, 1999) with 1 gram of xanthan gum costing around \$1 (NZD). Composed of pentasaccharide repeating units of alternate glucosyl residues on a poly- $[\beta-(1-4)\text{-D-Glcp}]$ backbone with α -(1-3) substitutions of charged trisaccharide sidechains $[\beta\text{-D-Manp-(1-4)-D-GlcAp-(1-2)-D-Manp}]$ (Tait, Sutherland, & Clarke-Sturman, 1986).

The structure and properties of xanthan make it soluble in hot and cold water and when in solution gives it qualities of a non-Newtonian fluid with high pseudoplasticity while also being stable over broad pH ranges (Katzbauer, 1998). These properties make xanthan excellent as a thickening agent, and it is used to thicken products ranging from acidic fruit juices and salad dressing through to dairy products like ice cream and butter (Lachke, 2004).

Poly- γ -glutamate (Poly- γ -glutamic acid) is a homo-polyamide composed of D- and L- glutamic acid units connected *via* amide linkages between α -amino and γ -carboxylic acid groups. Commercial production of poly- γ -glutamate is expensive due to substrate costs and low yields (Feng et al., 2015), as a result 1 gram of poly- γ -glutamic acid costs over

\$1300 (NZD). Although commercial production of poly- γ -glutamate is expensive, poly- γ -glutamate itself is naturally produced by *Bacillus* sp. including *B. subtilis*, *B. licheniformis*, and *B. megaterium* and is consumed in many fermented soya products across Asia (Chettri, Bhutia, & Tamang, 2016) such as natto in Japan (Kada, Ishikawa, Ohshima, & Yoshida, 2013).

Poly- γ -glutamate is water-soluble, anionic, non-toxic, edible, and has many applications in food, particularly as a cryoprotectant, thickener, and bitterness relieving agent (Chettri et al., 2016; Shih & Van, 2001).

1.2 Extracellular polymers and medicine

While microorganisms are a leading causative agent in disease and infection and some bacterially produced extracellular polymers cause disease. Such as extracellular polysaccharides synthesised by members of the *Streptococcus* genus, particularly *Streptococcus mutans* that causes dental carries (Birkhed, Rosell, & Granath, 1979) and alginate produced by *P. aeruginosa* in cystic fibrosis (Pedersen et al., 1992). Other bacterially produced extracellular polymers play an important role in treatment and recovery from disease, infection, and injury.

Dextran is an extracellular homo-polysaccharide composed of α -(1-2)/(1-3)/(1-4)-branched α -(1-6)-linked glucose monomers produced by *Leuconostoc* and *Streptococcus* species (Siddiqui, Aman, Silipo, Qader, & Molinaro, 2014). Dextran is utilised as a blood plasma extender and has properties of a Newtonian fluid when dissolved, with a viscosity that can be altered by varying concentration and temperature while also having low immunogenicity (Rehm, 2010).

While dextran is utilised internally as a fluid, bacterially produced cellulose has a range of applications with studies utilising bacterial cellulose in drug delivery (Stoica-Guzun, Stroescu, Tache, Zaharescu, & Grosu, 2007), for artificial blood vessels (Klemm, Schumann, Udhardt, & Marsch, 2001), and as a tissue/cartilage/bone scaffold (Kirdponpattara, Khamkeaw, Sanchavanakit, Pavasant, & Phisalaphong, 2015). Bacterial cellulose is a homo-polysaccharide composed of β -(1-4)-D-glucose monomers and produced by a variety of bacteria including plant pathogenic *Dickeya dadantii*, and *Erwinia chrysanthemi*, soil-borne bacteria *Burkholderia* sp. and *P. putida*, model bacteria *Escherichia coli* and *Salmonella enterica*, and commercially produced by *Acetobacter xylinum* (Rehm, 2010; Römling & Galperin, 2015). Bacterial cellulose has high

mechanical strength, wettability, and good biocompatibility and has been used successfully as an artificial skin in treatment of severe skin injuries, especially burns (Kucińska-Lipka, Gubanska, & Janik, 2015; Li et al., 2015).

Hyaluronic acid is an extremely important extracellular heteropolysaccharide produced by *Pasteurella multocida* and members of the *Streptococcus* genus, comprised of repeating β -(1-4)-linked glucuronate and N-acetyl glucosamine (Rehm, 2010). Hyaluronic acid is ubiquitous in the human body and is crucial for multiple cellular and tissue functions, and has been used clinically as a visco-protectant since the 1960s (Burdick & Prestwich, 2011; Kogan, Šoltés, Stern, & Gemeiner, 2007). Because hyaluronic acid is naturally present in the body, bacterially produced hyaluronic acid is immunoneutral and can be readily used or chemically modified to provide new physical forms through crosslinking (Burdick & Prestwich, 2011). These modified hyaluronic acid derivatives can be classified in one of two ways, depending on their modification and their ability to form new chemical bonds with living cells. Monolithic derivatives are modified at the terminal ends, cannot form new bonds in the presence of cells and tissue and must be further processed. In contrast living derivatives are able to interact and form new bonds in the presence of cells, tissue, and therapeutic agents, however it is important that the modifications are biologically compatible and stable (Burdick & Prestwich, 2011).

1.3 Extracellular polymers and industry

Extracellular polymer use is not just limited to medical and food products, heavy industry also utilises microbially produced polymers for a range of purposes.

Welan is a high molecular weight polysaccharide comprised of tetrasaccharide repeating units of D-glucose, D-glucuronic acid, D-glucose, and L-rhamnose with L-mannopyranosyl or L-rhamnopyranosyl side chains and is produced by *Alcaligenes sp.* (Ai et al., 2015). Because of this unique composition and structure, welan has a high viscosity and is stable in aqueous solutions across a broad pH range (2-12) and temperatures up to 150°C (Tako & Kiriaki, 1990). Industrial uses of welan are particularly focused in concrete production and enhancing oil recovery where it is used as a stabilising and viscosifying agent (Vu et al., 2009).

Alginate has multiple uses in industry including as a paper coating agent, and as thickening, surface penetration, and spread control agents in textiles. Due to alginate being a hydrocolloid with no free hydroxy groups that can compete with cotton, it is an

ideal thickener for dyeing fabrics (Lapasin, 2012). Bacterial alginates are easily modified to suit different industrial needs by engineering genes involved in synthesis resulting in alginates with unique properties, including increasing or decreasing mannuronic or guluronic acid, methylation, and acetylation ratios (Hay, Rehman, Ghafoor, & Rehm, 2010). These modifications are key to making custom bacterial alginates for industrial use (Hay et al., 2013).

1.4 Extracellular polymers and the environment

Since the industrial revolution the environment has become increasingly polluted with chemicals, heavy metals, and radioactive waste as a result of increased industry, mining, deforestation, and use of artificial fertilisers (Andrews, Brimblecombe, Jickells, Liss, & Reid, 2013; Eklöf et al., 2014; Grimaldi, Guédron, Grimaldi, Brearley, & Thomas, 2015; Sany et al., 2013; Su, 2014). As a result, remediation measures to reverse the damage have been increasingly moving toward bioremediation utilising bacteria, bacterially produced extracellular polymers, and biofilms to help remove heavy metals, toxins, and chemicals from the soil and waterways (Mukhtar & Griffin, 2015; Raj, Dalei, Chakraborty, & Das, 2016; Redmile-Gordon & Chen, 2016). Bacterial polymers have the advantage of being modifiable, and compatible with different compounds, they can also enhance the activity of materials such as nanoparticles (Raj et al., 2016; Rehm, 2010). The process of bioremediation can also support and increase the production of biopolymers and biofilms in soil bacteria which in turn increases the rate of remediation (Redmile-Gordon & Chen, 2016).

Waterway pollution is caused by multiple elements including heavy metals, and organic waste products. Bioremediation of nitrogen contaminated fresh waterways is the task of nitrifying and denitrifying bacteria such as *Klebsiella pneumonia* that utilises the organic substrate and produces extracellular polymers which in turn influences the floc structure, surface charge, and hydrophobicity increasing aggregation and biofilm formation (Padhi et al., 2013). Also, highly toxic heavy metals including cadmium, arsenic, zinc, lead, and mercury pollute waterways (Sany et al., 2013). Through bacteria resistant to these toxic compounds which are able to absorb, alter, and trap compounds in extracellular matrices and biofilms, bioremediation is possible (Naik & Dubey, 2017). Bacterial extracellular polymers have also been used to bio-augment nanoparticles to remove cadmium from solution (Raj et al., 2016).

1.5 Bio-prospecting, culturing, and the modern search for polymers

As the exploitation and depletion of non-renewable products intensifies there has been an increasing shift towards bio-prospecting (the search for and development of economically valuable products, produced in nature) for new sustainable alternatives (Arora, Behera, & Kumar, 2015). With the majority of microorganisms largely undiscovered or utilised especially when it comes to bio-prospecting, there is a need to develop and improve the ability to explore this diverse microbial potential (Overmann & Smith, 2017).

Before the early 1990's there was a period in which bio-prospecting and natural product research was extensively carried out by numerous countries and corporations, many of whom developed large libraries of organisms for screening (Borris, 2017). This screening process however was slow and the complex nature of the samples tested often made it difficult to establish exactly which compound was involved. To understand the action of the extracted product biochemical tests were developed and miniaturised, while automation was introduced to increase processing speeds effectively removing many barriers to discovery (Borris, 2017).

In the mid 1990's disputes over intellectual, financial, and ownership rights saw a significant reduction of bio-prospecting, although many of these issues have since been resolved through various statutes and agreements (Tvedt, 2017).

With the decrease in cost and increase in availability of genetic screening technology there has been a move away from traditional methods of culturing and biochemically defining bio-prospected materials. Metagenomic libraries are being compiled and screened for a particular gene or compound of interest, allowing researchers to quickly determine whether a sample is capable of production (Hicks & Prather, 2014).

Utilising a metagenomics based method has advantages of preserving microbial communities and quickly screening a complex sample without the need for culturing independent organisms, and carrying out biochemical testing to determine whether a desirable product is produced (Al-Amoudi et al., 2016). It has the disadvantage that if the scope of the search is too narrow or the bioinformatics approach is inappropriate other useful/novel compounds and properties could be missed (Lee & Lee, 2013).

1.6 Aims and objectives of this study

The primary aim of this study was to utilise an exploratory approach and culture based method of bio-prospecting soil-borne bacteria for the production of extracellular polymers.

Briefly, this research involved;

- Collection, and culturing of bacterial isolates from soil obtained beneath an organic waste pile,
- Screening for production of extracellular polymers,
- Characterisation, identification, and imaging of isolates and,
- The production, isolation, and identification of extracellular polymers.

However, during the course of identifying and imaging the bacteria, one isolate displaying novel structural appendages was discovered and the focus of this study shifted to the isolation and identification of these appendages.

Chapter 2: Materials and Methods

Unless otherwise mentioned, all reagents were purchased from Sigma-Aldrich (USA), Ajax Finechem (Australia), and Merck (Germany). Ultracentrifugation was performed using a Sorvall WX Ultra 80 (Thermo Scientific, USA).

2.1 Bacterial isolates and reference strains

The bacterial strains used in this study are listed in Tables 1, and 2 below.

2.1.1 Bacterial isolates

Table 1. *Bacterial isolates, isolated in this study*

Isolate	Genus based on 16S <i>rRNA</i> gene sequencing	Reference
X	<i>Pseudomonas</i>	This study
133	<i>Raoultella</i>	This study
134	<i>Luteimonas</i>	This study

2.1.2 Bacterial reference strains

Table 2. *Bacterial reference strains*

Bacterial strains	Strain ID	collection	Lot #	Reference
<i>Raoultella terrigena</i>	DSM 2687		0115	(Drancourt, Bollet, Carta, & Rousselier, 2001)
<i>Raoultella ornithinolytica</i>	DSM 7464		1010	(Drancourt et al., 2001)

2.2 Primers

The primers used in this study are listed in Tables 3, 4, and 5 below. All primers used were synthesised by Integrated DNA Technologies (NZ).

Table 3. *Primers used for 16S rRNA amplification and sequencing*

Primer name	Sequence for 5' to 3'	Reference
16SF	TTGGAGAGTTTGATCCTGGCTC	(Okhravi, Adamson, Matheson, Towler, & Lightman, 2000)
16SR	ACGTCATCCCCACCTTCCTC	(Okhravi et al., 2000)
1Spi16	AAAGCGTG GGGAGCAAACAGG	This study
2Spi16	GCTTGCACCCTCCGTATTACC	This study

Table 4. *Primers used for rpoB amplification and sequencing*

Primer name	Sequence for 5' to 3'	Reference
CM7	AACCAGTTCGCGTTGGCCTGG	(Drancourt et al., 2001)
CM31b	CCTGAACAACACGCTCGGA	(Drancourt et al., 2001)

Table 5. *Primers used for amplification and sequencing of Pseudomonas species*

Primer name	Sequence for 5' to 3'	Reference
PA-GS-F	GACGGGTGAGTAATGCCTA	(Spilker, Coenye, Vandamme, & LiPuma, 2004)
PA-GS-R	CACTGGTGTTTCCTTCCTATA	(Spilker et al., 2004)

2.3 Media

Unless otherwise stated all media was autoclaved at 121°C for at least 20 minutes before use and glycerol used was of purity >99% .

2.3.1 Liquid media

Luria-Bertani broth (LB) medium was prepared by adding 20 g per litre of Millipore water.

Nutrient broth medium was prepared by adding 13 g per litre of Millipore water.

Actinomycete isolation broth (AIB) medium was prepared by adding

Sodium propionate	4 g
Sodium caseinate	2 g
K ₂ HPO ₄	0.5 g
MgSO ₄ ·7H ₂ O	0.1 g
L-asparagine	0.1 g
FeSO ₄ ·7H ₂ O	0.001 g
Glycerol	5 mL

per litre of Millipore water.

2.3.2 Solid media

Unless stated otherwise, any addition of agar in preparation of solid media is bacteriological agar.

Actinomycete isolation agar (AIA) medium (Difco, USA) was prepared by adding 22 g per litre of Millipore water and supplementing with 5 mL glycerol.

Standard number 1 medium was prepared by adding

Peptone	15 g
Yeast extract	3 g
NaCl	6 g
D-glucose	1 g
Agar	12 g

per litre of Millipore water, and adjusting the pH to 7.5 prior to addition of agar.

LB agar medium was prepared by adding 15 g agar per litre of LB.

Nutrient agar medium was prepared by adding 15 g agar per litre of nutrient broth.

Blood agar (Fort Richard, NZ), MacConkey agar, and Mannitol salt agar (Oxoid, UK) mediums were purchased ready to use.

2.4 Bacterial cultivation conditions

Bacterial cultivation was carried out using either solid or broth media. Where broth media was used, bacteria were cultivated in capped flasks with an approximate ratio of 1:3 media to flask volume, and incubated at 30°C with continuous shaking ~150-250 rpm. Bacterial cultivation on solid media was carried out in aerobic conditions at 30°C.

2.5 Long term storage and revival of bacterial strains and isolates

2.5.1 Long term storage of bacterial strains and isolates

All bacterial strains and isolates were cultivated overnight in LB (section 2.3.1) media, one millilitre of culture was transferred to a sterile 1.8 mL cryotube (Thermo Scientific, USA) and 70 µL of filter sterilized dimethylsulfoxide (DMSO) was added. Strains and isolates were stored at -80°C until required.

2.5.2 Revival of bacterial strains and isolates

The bacterial strains and isolates were revived by using a sterile disposable loop to remove a fraction of frozen stock, which was used to inoculate AIA (section 2.3.2) media. This was incubated at 30°C for between one and three days depending on the bacteria being revived.

2.6 DNA and molecular cloning

2.6.1 Polymerase chain reaction

Polymerase chain reaction (PCR) was utilised to amplify targeted DNA regions (Sambrook, Fritsch, & Maniatis, 1989). PCR utilises repeated denaturation, annealing, and amplification steps, during which denaturation separates double stranded DNA (dsDNA) into single stranded DNA (ssDNA), allowing primers to bind to the ssDNA template during the annealing step, before DNA polymerase synthesises a new DNA strand complementary to the ssDNA template in the amplification step. The DNA polymerases used were *Taq* DNA polymerase and *Pfx* DNA polymerase (Invitrogen

Corporation, USA). For initial verification and troubleshooting *Taq* polymerase was used, and for sequencing purposes the high fidelity proofreading *Pfx* polymerase was used. Typical reaction mixtures for *Taq* and *Pfx* polymerase are presented in Tables 6 and 7 respectively.

Table 6. *Taq* polymerase reaction mixture

Reagents	Amounts
Glycerol (50%)	20 µL
DMSO	5 µL
10 X buffer	10 µL
MgCl ₂ (25 mM)	20 µL
Primer 1 (10 pmol/µL)	5 µL
Primer 2 (10 pmol/µL)	5 µL
dNTPs (10 mM of dATP, dGTP, dCTP, and dTTP)	10 µL
Template DNA	2 – 5 ng
<i>Taq</i> DNA polymerase (5 U/µL)	1 µL
Autoclaved Millipore water	To 100 µL

Table 7. *Pfx* polymerase reaction mixture

Reagents	Amounts
DMSO	2.5 µL
10 X PCR enhancer	22.5 µL
10 X <i>Pfx</i> buffer	20 µL
MgSO ₄ (50 mM)	2 µL
Primer 1 (10 pmol/µL)	3 µL
Primer 2 (10 pmol/µL)	3 µL
dNTPs (10 mM of dATP, dGTP, dCTP, and dTTP)	3 µL
Template DNA	2 – 5 ng
<i>Pfx</i> DNA polymerase (2.5 U/µL)	0.5 µL
Autoclaved Millipore water	To 100 µL

PCR was performed using a multigene optimax thermal cycler (Labnet International, USA). A typical program for PCR conditions utilising *Pfx* or *Taq* polymerase are shown in Tables 8 and 9 respectively.

Table 8. *PCR conditions for Pfx polymerase*

Step	Program conditions
1. Initial denature	94°C for five minutes
2. Denature	94°C for 40 seconds
3. Anneal	Optimal annealing temperature* for 30 seconds
4. Replication / Extension	68°C for one minute
5. Repeated cycle	Repeat steps 2 – 4 for 30 cycles
6. Final extension	68°C for two minutes
7. Hold	4°C

* An optimal temperature is dependent on the melting temperatures of the primer-DNA hybrid. Generally, the annealing temperature is set and performed at 5°C below the melting temperature of the primers, however optimisation by changing ($\pm$) the annealing temperature may be required.

Table 9. *PCR conditions for Taq polymerase*

Step	Program conditions
1. Initial denature	94°C for four minutes
2. Denature	95°C for 40 seconds
3. Anneal	Optimal annealing temperature* for 30 seconds
4. Replication / Extension	72°C for two minutes
5. Repeated cycle	Repeat steps 2 – 4 for 30 cycles
6. Final extension	72°C for four minutes
7. Hold	10°C

* An optimal temperature is dependent on the melting temperatures of the primer-DNA hybrid. Generally, the annealing temperature is set and performed at 5°C below the melting temperature of the primers, however optimisation by changing ($\pm$) the annealing temperature may be required.

2.6.2 Agarose gel electrophoresis

Agarose gel electrophoresis (AGE) was performed as outlined elsewhere (Sambrook et al., 1989). PCR products were separated by AGE using a horizontal slab gel apparatus in 1x Tris-Borate-EDTA (TBE) buffer. In this study, 1% agarose gels were made with 1x TBE buffer and used to resolve the DNA products resulting from PCR. DNA samples were mixed with 6x DNA loading dye before being loaded onto the agarose gel. Electrophoresis was carried out at 120 V for 50 minutes. Resulting agarose gels were stained in a bath containing 0.01% (v/v) ethidium bromide in distilled water for at least 20 minutes and destained in distilled water for one minute. The gels were visualised using a UV transilluminator at a wave length of 254 nm (Gel Doc 2000, Bio-Rad Laboratories, USA) and image lab software (version 5.1, Bio-Rad Laboratories, USA). When DNA fragments were required to be excised from the gel, SYBR safe DNA gel stain (Invitrogen, USA) was included according to the manufacturer's instructions, and the resulting gel visualised using a Safe Imager™ 2.0 Blue-Light Transilluminator (Invitrogen, USA). The composition of the 6x DNA loading dye and 10x TBE buffer are outlined below:

DNA loading dye (6x):

Urea	4 M
Sucrose	50% (v/v)
EDTA	50 mM
Bromophenol Blue	0.1%

TBE buffer (10x):

Tris-HCl	500 mM
Boric acid	500 mM
EDTA	25 mM
Adjust to roughly pH 8.5 using HCl	

2.6.2.1 DNA ladder standards

A suitable DNA ladder was used to estimate the size of DNA fragments on AGE. 1 Kb plus DNA ladder (Invitrogen, USA) was used in this study to determine the size of DNA fragments and was mixed with 10x DNA dye and stored at -20°C for future use. It was used according to the manufacturer's instructions, and the size of DNA fragments are shown in Table 10.

Table 10. *DNA Ladder: 1 Kb plus*

DNA Ladder	Fragment sizes (bp)
1 Kb plus	12000, 11000, 10000, 9000, 8000, 7000, 6000, 5000, 4000, 3000, 2000, 1650, 1000, 850, 650, 500, 400, 300, 200, 100

2.6.3 Clean-up of PCR products

Amplified PCR products were cleaned up to remove salts and other by-products from the amplified DNA prior to sequencing using the DNA Clean and Concentrator™ (Zymo Research, USA) kit, according to manufacturer's instructions.

2.6.3.1 Recovery of DNA fragments from agarose gels

DNA fragments separated by AGE with SYBR safe DNA gel stain (section 2.6.2) were recovered using the Zymoclean™ Gel DNA Recovery Kit (Zymo Research, USA), according to manufacturer's instructions.

2.6.4 DNA sequencing

DNA sequencing of PCR products was performed by the Massey Genome Service (Massey University, Palmerston North, NZ) using a 3730 DNA analyser (Applied Biosystems Inc., USA). DNA sequencing reactions were prepared in sterile 0.2 mL thin-walled PCR tubes (Axygen, USA) containing a DNA concentration of 4 ng / 100 bps, and 5.5 pmol of primer in a total volume of 20 µL. The results were presented in ABI format and analysed using Vector NTI version 10 (Thermo Fisher, USA).

2.6.5 Genomic DNA isolation

Bacterial genomic DNA was isolated using the PureLink™ Genomic DNA kit (Invitrogen), according to manufacturer's instructions.

2.6.6 Bacterial identification

Analysed DNA sequences were compared to the National Center for Biotechnology Information (NCBI) database using the nucleotide basic local alignment search tool (BLAST). BLAST analysis of the DNA sequences allowed the sample to be aligned to a known genus. Multilocus sequence typing (MLST) was used to compare housekeeping genes to related bacteria, the comparison was carried out using genes and strains similar

to the study by Kimura, Chung, Itoh, Hiraishi, and Okabe (2014). Briefly *rpoB*, *gyrA*, and *parC* genes were selected, and *Raoultella ornithinolytica*, *R. terrigena*, and *R. planticola* were selected for comparison.

2.7 Isolation of outer membrane proteins

Isolation of outer membrane proteins was performed through cell harvesting, cell disruption, and enzymatic digest.

2.7.1 Cellular harvesting

Where bacteria were grown on solid media, cells were harvested by scraping them from the solid media using a sterile spatula into 20-50 mL of either 0.9% sterile saline, 30 mM Tris-HCl buffer, or 20 mM Tris-HCl + 150 mM NaCl buffer, vortexed, and collected by centrifuging at 9000 x *g* for 20-30 minutes at 4°C, before repeating the suspension, vortexing, and centrifugation steps twice more to wash. Where bacteria were grown in broth media, cells were harvested by initial centrifugation at 9000 x *g* for 20-30 minutes at 4°C, before suspending the pellet in 20 mL of either 0.9% sterile saline, 30 mM Tris-HCl buffer, or 20 mM Tris-HCl + 150 mM NaCl, vortexing, and collecting by centrifugation as above twice to wash. The compositions of 0.9% saline, 30 mM Tris-HCl buffer, and 20 mM Tris-HCl + 150 mM NaCl buffer are outlined below:

0.9% Saline:

NaCl 9 g
per litre of Millipore water

30 mM Tris-HCl buffer:

Tris buffer 3.6 g
per litre of Millipore water
adjusted to pH 8.3 with HCl

20 mM Tris-HCl + 150 mM NaCl buffer:

Tris-HCl buffer 31.52 g
NaCl 8.766 g
per litre of Millipore water
adjusted to pH 7.8 with NaOH

2.7.2 Cellular disruption

Cells were disrupted using several methods as described in sections 2.7.2.1 and 2.7.2.2.

2.7.2.1 Mechanical cell disruption

Harvested cells (section 2.7.1) were suspended in 5 mL 30 mM Tris-HCl and passed twice through a mechanical cell disrupter set to 20 kPsi (Constant Cell Disruption Systems, UK). Disrupted cell lysates were centrifuged at 11000 x *g* for 30 minutes at 4°C. The supernatant was separated into a sterile 15 mL falcon tube using a sterile pipette, the pelleted cells were then re-suspended in 1 mL of supernatant. The suspended disrupted cells were then stored at -20°C before purification by ultracentrifugation in combination with glycerol gradients (section 2.7.4.1).

2.7.2.2 Enzymatic cell disruption

Harvested cells (section 2.7.1) were subjected to enzymatic disruption using a modified method (Moradali, Donati, Sims, Ghods, & Rehm, 2015). Harvested cells were suspended in 20 mL 30 mM Tris-HCl containing 0.5 mg/mL DNase I, 0.5 mg/mL RNase A, 0.5 mg/mL lysozyme, and 4 mL of Roche EDTA free complete protease inhibitor (Sigma-Aldrich) (one tablet dissolved in 10 mL 30 mM Tris-HCl), on ice for 20 minutes. Followed by 5 minutes sonication using 10 cycles of 30 seconds each. Cellular debris and unbroken cells were removed by centrifugation at 8000 x *g* for 5 minutes at 4°C. The whole envelope fraction was then isolated by centrifugation at 43000 x *g* for 1 hour at 4°C before further purification (section 2.7.4.2).

2.7.3 Enzymatic digestion of outer membrane proteins

Cells were harvested in 20 mM Tris-HCl + 150 mM NaCl (section 2.7.1) and prepared for enzymatic digestion using a modified method (Severin et al., 2007). Cells were suspended in 2 mL 20 mM Tris-HCl + 150 mM NaCl to which 20 µL 1 M L-arabinose, 20 µL 10 mM CaCl₂, and 10 µL 400 mg/mL trypsin were added. Following the addition of trypsin the suspended cell mixture was vortexed and incubated at 37°C for 4 hours with continuous shaking. The suspension was then plunged into an ice bath to prevent further enzymatic activity, before being transferred to sterile 15 mL falcon tubes. Centrifugation to separate cells from suspension was carried out at 14000 x *g* for 25 minutes at 4°C. The supernatant was removed carefully and sterilised through a 0.2 µm

filter prior to storage at -20°C alongside the cell pellet. The compositions of 1 M L-arabinose, 10 mM CaCl_2 , and 400 mg/mL trypsin are outlined below:

1 M L-arabinose

L-arabinose 150.13g
per litre of Millipore water

10 mM CaCl_2

$\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$ 1.47g
per litre of Millipore water

400 mg/mL trypsin

Trypsin 400mg
per mL of 50 mM acetic acid

2.7.4 Purification of outer membrane proteins

Purification of outer membrane proteins was carried out using various methods including ultracentrifugation with glycerol gradients, and solubilisation.

2.7.4.1 Ultracentrifugation with glycerol gradients

Outer membrane proteins were purified from cell lysates (section 2.7.2.1) using ultracentrifugation and glycerol gradients (Korhonen, Nurmiaho, Ranta, & Eden, 1980), five types of glycerol gradients made with Millipore water were used. Cell lysates were loaded on glycerol gradients consisting of layers containing 10%, 25%, 40%, 60%, and 80% glycerol. After ultracentrifugation at $100000 \times g$ for 20 hours at 4°C , interfaces formed which could be separated. The process for ultracentrifugation with glycerol gradients is shown in Figure 1.

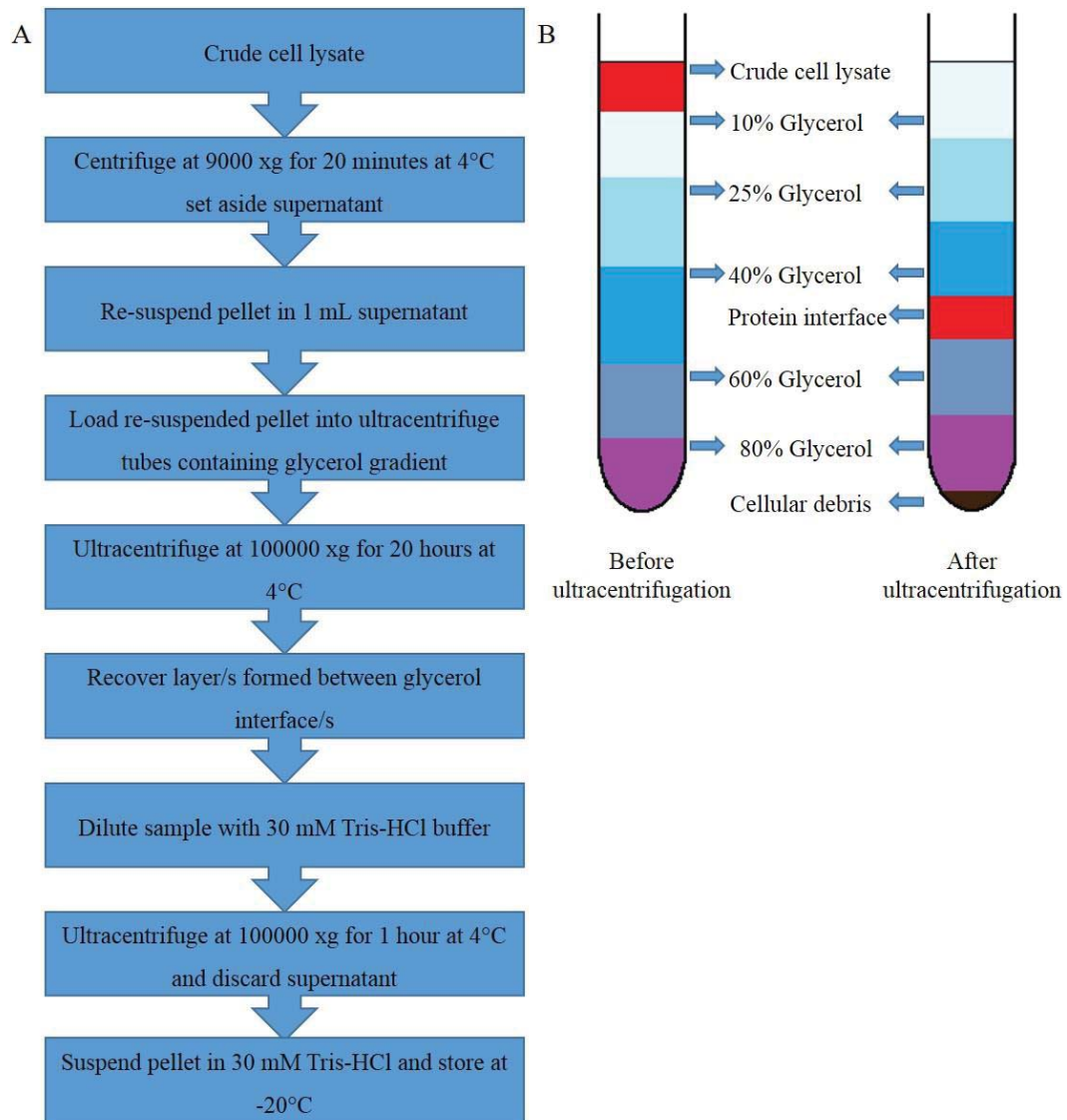


Figure 1. Schematic overview of protein isolation after mechanical disruption. (A) The process of isolating protein from disrupted crude cell lysate using ultracentrifugation and glycerol gradients. (B) Protein layer in glycerol gradient before and after ultracentrifugation.

2.7.4.2 Purification of outer membrane proteins via solubilisation

The outer membrane fraction was obtained by solubilisation of the whole envelope fraction (Rehman & Rehm, 2013). The whole envelope fraction (section 2.7.2.2) was suspended in 10 mL 30 mM Tris-HCl containing 0.7% (w/v) N-lauroyl-sarcosine and subjected to continuous shaking on ice for 20 minutes to solubilise the inner membrane fraction. This was centrifuged at 43000 x *g* for 1 hour at 4°C, the supernatant was discarded and the resulting pellet containing the outer membrane fraction, was re-suspended in 30 mM Tris-HCl and centrifuged as above to remove residual detergent. The outer membrane fraction was suspended in 100 µL 30 mM Tris-HCl and the total

protein concentration was determined *via* bicinchoninic acid (BCA) assay (section 2.8.1) before analysis using sodium dodecylsulfate polyacrylamide gel electrophoresis (SDS-PAGE) (section 2.8.2).

2.8 General methods for protein analysis

2.8.1 Determination of protein concentration

The BCA assay method was used to determine the concentration of proteins from membrane fractions, as previously described (Walker, 2002). The Pierce™ BCA protein assay kit (Thermo Scientific, USA) was used according to manufacturer's instructions. In that reagent B was added to reagent A in a ratio of 1:50. Serial dilutions of membrane fraction sample and a known concentration of bovine serum albumin (BSA, Sigma-Aldrich, USA) were prepared in sterile 1.7 mL microfuge tubes to which reagents A+B was added. The samples were incubated at 37°C for 30 minutes on an orbital rotator to stabilise the reaction. Once stabilised the samples were loaded in duplicate to a microtitre plate and read at 562 nm using an ELx808 ultra microplate reader (Bio-Tek instruments, Inc., USA). A standard curve was constructed using the BSA sample results and protein in the membrane samples was estimated.

2.8.2 Sodium dodecylsulfate polyacrylamide gel electrophoresis

SDS-PAGE has been outlined previously (Sambrook et al., 1989). This method was performed using 1x electrode running buffer in a vertical slab gel electrophoresis apparatus to separate protein samples. Each Bis-Tris gel consists of two layers: a lower resolving gel layer (10%, w/v) and an upper stacking gel layer (4%, w/v). The gels were made in a glass cassette (10 cm x 7 cm) yielding a gel of 1 mm thick. The composition of electrode running buffer for SDS-PAGE is outlined below:

Electrode running buffer

100 mL 5x high or low molecular weight running buffer

2.5 mL 200x reducing agent

make up to 500 mL with Millipore water

5x high molecular weight running buffer

(used for separating proteins >20 kDa)

250 mM MOPS	52 g/L
250 mM Tris buffer	30 g/L
0.5% SDS	5 g/L
5 mM EDTA	2 g/L

5x low molecular weight running buffer

(used for separating proteins 2 – 50 kDa)

250 mM MES	53 g/L
250 mM Tris buffer	30 g/L
0.5% SDS	5 g/L
5 mM EDTA	1.9 g/L

200x reducing agent

1 M sodium bisulfite 10.4 g

make up to 100 mL with Millipore water

The resolving gel was prepared and degassed by adding 1 – 3 mg of Na_2SO_3 to avoid air bubble formation. Polymerisation of the gel solution was initiated by adding N, N, N', N'-tetramethylethyl-endiamin (TEMED) and 10% (w/v) ammonium persulfate (APS). The mixture was then poured into the glass cassette and overlaid with isopropanol. After allowing 30 minutes for polymerisation, the isopropanol was poured off and rinsed with water to remove residual isopropanol in preparation for the stacking gel. The composition of the resolving gel is outlined below:

Resolving gel

Bis-Tris gel buffer	2.86 mL
30% Bis-Acrylamide	3.33 mL
Water	3.81 mL
10% APS	25 μL
TEMED	7 μL

Bis-Tris gel buffer

1.25 M Bis-Tris 65.4g

make up to 450 mL with Millipore water

adjust to pH 6.5 – 6.8 with HCl

The stacking gel was prepared and as with the resolving gel 10% APS and TEMED were added to initialise the polymerisation. This solution was poured on top of the resolving gel and a plastic comb was immediately inserted to allow the formation of wells. After 30 minutes for polymerisation the plastic comb was removed carefully and the gel was either used straight away or stored in damp tissue at 4°C until required. The composition of the stacking gel is outlined below:

Stacking gel

Bis-Tris gel buffer	1.43 mL
30% Bis-Acrylamide	0.65 mL
Water	2.92 mL
10% APS	4 µL
TEMED	3.5 µL

2.8.2.1 Sample preparation for SDS-PAGE and electrophoresis conditions

Generally 10 – 20 µL of sample was loaded onto the gel for electrophoresis. Five volumes of sample was mixed with one volume of SDS loading buffer (6x) in a 1.7 mL microfuge tube and incubated for 15 minutes at 95°C. The denatured samples were cooled to room temperature prior to loading onto the gel. A protein standard, GangNam-stain™ (iNtRON biotechnology, Korea; see table 11), was also loaded onto the gel and used to estimate the size of proteins on SDS-PAGE. The electrophoresis running conditions were 150 V for approximately 1 hour. The composition for the SDS loading buffer is outlined below:

6x SDS loading buffer

4x Stacking gel buffer	7 mL
Glycerol	3 mL
SDS	1 g
DTT	0.93 g
Bromothymol blue	1.2 mg

4x Stacking gel buffer

1.5 M Tris-HCl	181.7 g/L
SDS	4 g/L
adjust to pH 8.9	

Table 11. *Protein marker*

Protein marker	Molecular weight (kDa)
GangNam stain	235, 170, 130, 100, 70, 53, 41, 30, 22, 18, 14, 9

2.8.2.2 Protein staining and destaining

The SDS-PAGE gel was carefully removed from the glass cassette and stained with Coomassie Brilliant Blue Staining solution for 20 minutes on a tilt shaker (Labnet International, USA) at slow speed. After staining the gel was washed with distilled water and destained with destaining solution for an hour as above until the protein bands were visible and the background colour from the staining solution was removed. Gels were visualised using a white light transilluminator (Gel Doc 2000, Bio-Rad Laboratories, USA), and image lab software (version 5.1, Bio-Rad Laboratories, USA). The composition of staining and destaining solutions are outlined below:

Coomassie Brilliant Blue Staining solution:

Coomassie blue R-250	4 g
Methanol	450 mL
Acetic acid	90 mL
Millipore water	460 mL

Destaining solution:

Methanol	660 mL
Acetic acid	200 mL
Millipore water	1140 mL

2.9 Characterisation of extracellular polymers

Extracellular polymers were prepared (section 2.9.1) and harvested from bacterial isolates (section 2.1.1) grown on solid AIA media (section 2.3.2).

2.9.1 Preparation and harvest of extracellular polymers

Extracellular polymers from solid media were prepared and harvested utilising a similar method to that described previously (Remminghorst & Rehm, 2006). Briefly, frozen stock (section 2.5.2) was used to inoculate AIA media (section 2.3.2). After 24 hours incubation at 30°C, a single colony was used to inoculate 50 mL of LB media (section 2.3.1). After

17 hours incubation (shaking at 30°C), the culture was transferred to 50 mL falcon tubes and centrifuged at 9000 x *g* for 30 minutes to pellet the cells. Supernatant was discarded and the cell pellet washed twice with 0.9% saline (section 2.7.1), and centrifuged as above with the supernatant discarded between washes. The washed cell pellet was then suspended in 2.5 mL of 0.9% saline and 100 µL of this was spread on individual AIA media using a sterile plastic spreader. After 74 hours incubation at 30°C the biomass was harvested (section 2.7.1) by scraping into 20 mL 0.9% saline, vortexed, and centrifuged as above. The supernatant was then precipitated by pouring into 1x volume of ice cold isopropanol with constant stirring using a magnetic flea. Cell pellets, and crude extracellular polymers were freeze dried. For freeze drying, samples were either plunged into liquid nitrogen for 30 minutes or stored at -80°C for 24 hours before drying at room temperature for at least 24 hours using a floor model freeze drier (Dura-Dry MP Model # FD2085C0000, FTS Systems, USA). Freeze drying sublimates the frozen water under a reduced atmosphere of pressure, and dehydrates the sample. The freeze dried cell pellet and crude extracellular polymer were then weighed before solubilising the crude polymer in buffer containing 50 mM Tris-HCl and 10 mM MgCl₂ to a final concentration of 0.5% (w/v). DNase I and RNase A (15 µg/mL) were added to the solubilised crude polymer and incubated at 37°C with continuous shaking for 6 hours to remove nucleic acids. Proteinase E (20 µg/mL) was added to remove protein contaminants and inactivate the DNase and RNase, and incubated as above for 18 hours. This was dialysed in 12400 Da tubing against 5 L of water at 4°C for 24 hours. Post dialysis the sample was precipitated with ice cold isopropanol, freeze dried and weighed as above. These purified samples were dissolved in Millipore water to a 0.5 mg/mL concentration and further diluted to 0.25 – 0.125 mg/mL before uronic acid content was determined (section 2.9.2).

2.9.2 Anthrone assay – uronic acid determination

Concentration of uronic acid in samples was determined *via* anthrone assay as described previously (Loewus, 1952). Prepared samples (section 2.9.1) and samples of glucose with known concentration were mixed with 75% H₂SO₄ and anthrone reagent before boiling at 100°C for 15 minutes. Boiled samples were cooled to room temperature before transferring to glass cuvettes and reading absorbance at 620 nm. Absorbance readings were normalised against the H₂SO₄ and anthrone mixture background, and a standard curve produced from the glucose sample, the prepared samples absorbance were compared to the standard and a glucose equivalence recorded.

2.10 Bacterial capsule

The bacterial capsule was visualised using 10% aqueous nigrosin as described previously (Kapale, Chaudhary, Chande, Shrikhande, & Fule, 2003). Bacteria were spread in saline to form a film on a glass slide, heat fixed and stained with carbol fuchsin. This was rinsed with water and blotted dry before spreading 10% aqueous nigrosin across the slide until a thin film covers the sample and allowed to air dry before visualising the preparation using a light microscope at 400x (10x eye piece and 40x objective lens) magnification. Bacteria returning a positive capsular stain were subjected to capsule extraction (section 2.10.1).

2.10.1 Capsular extraction

Extraction of the bacterial capsule was performed as previously described (Domenico, Diedrich, & Cunha, 1989). Bacteria were harvested from solid media (section 2.7.1) and suspended in 0.9% saline before centrifuging at 17700 x *g* for 30 minutes at 4°C. The cell pellet was washed twice in 0.9% saline with centrifugation as above between washes. The washed cell pellet was then suspended in 50 mM citrate buffer with the addition of 0.1 or 0.2% zwittergent (w/v) and incubated with continuous shaking at 42°C for 30 minutes. Treated cells were centrifuged as above for 5 minutes, the supernatant was removed and run on SDS-PAGE (section 2.8.2.1), and the treated cell pellet was sent for imaging at the Manawatu Microscopy and Imaging Centre (MMIC, Palmerston North, NZ). The composition of citrate buffer is outlined below:

1 M Citrate buffer:

Trisodium citrate dihydrate 294.1 g/L

Citric acid monohydrate 210.1 g/L

2.11 Standard microbiological techniques

2.11.1 Gram staining

Gram staining described in detail by Bartholomew and Mittwer (1952) was performed on bacterial isolates to determine gram reaction. Briefly, bacteria were smeared with water on a clean glass slide, and allowed to dry before heat fixing by running the slide quickly through a flame twice. Crystal violet stain was flooded over the smear and allowed to sit for 1 minute before washing with water. Gram's iodine was then flooded over slide and

allowed to sit for 1 minute before washing with water. An acetone and ethyl alcohol mix was added and left for 5 – 10 seconds until the colour ran from the slide and then washed with water. Finally safranin was flooded over the slide and allowed to sit for 1 minute before washing with water. The stained slide was then allowed to air dry before viewing with a light microscope under the oil immersion lens at 1000x (10x eye piece and 100x objective lens) magnification. Gram negative bacteria appear pink, while gram positive bacteria appear purple.

2.11.2 Electron microscopy

Samples for transmission electron microscopy (TEM) (section 2.11.2.1) and scanning electron microscopy (SEM) (section 2.11.2.2), were prepared and imaged by MMIC.

2.11.2.1 Transmission electron microscopy sample preparation

Cells were removed from solid media or pellet if from broth, and fixed for at least 2 hours at room temperature in primary fixative (3% glutaraldehyde, 0.25% ruthenium red (ProSciTech, Australia) in phosphate buffer, pH 7.2). Make 20 mL 3% low temperature melting point agarose (sets at 37°C) (0.6g agarose in 20ml reverse osmosis H₂O). Centrifuge samples at 4000 rpm in a Minispinner centrifuge for 4 minutes. Pipette off Fixative and discard. Add cooled but still molten agarose and quickly mix, before centrifuging again as above. Allow to set, remove pellet from tube, cut off excess agarose and discard. Slice pellet into thin pieces using half of a double-sided razor blade. Buffer wash in 0.1 M phosphate buffer (pH 7.2) three times for 10 minutes each. Post fix in 1% osmium tetroxide (OsO₄) in 0.1M phosphate buffer for 30 minutes to 1 hour max at room temperature. Buffer wash as above. Dehydrate through a graded acetone series (25%, 50%, 75%, 95%, 100%) for 10-15 minutes each, followed by two changes of 100% acetone for one hour each. Samples were transferred into 50:50 resin:acetone and stirred overnight. Replace with fresh 100% resin (Procure 812, ProSciTech, Australia) and stir for 8 hours. Repeat this step twice more (overnight in 100% resin, 8 hours in 100% resin). Embed samples in moulds with fresh resin and cure in a 60°C oven for 48 hours. Light microscope sections were cut at 1 micron using a glass knife on the ultramicrotome (Leica EM UC7, Germany) and heat fixed onto glass slides. These were stained with 0.05% toluidine blue for approximately 12 seconds and viewed under the light microscope. The block was trimmed down to the selected area and cut using a diamond knife (Diatome, Austria) at 100 nm. These were stretched with chloroform and mounted on a grid using a

Quick Coat G pen (Saiko, Japan). Grids were stained in saturated uranyl acetate in 50% ethanol for 4 minutes, washed with 50% ethanol and MilliQ water and then stained in lead citrate (Venable and Coggeshall, 1965) for a further four minutes. This was followed by a wash in MilliQ water. Samples were viewed using an FEI Tecnai G2 Spirit BioTWIN Transmission Electron Microscope (Czech Republic).

2.11.2.2 Scanning electron microscopy sample preparation

Cells were removed from solid media or pellet if from broth, and fixed in modified Karnovsky's fixative (3% glutaraldehyde, 2% formaldehyde in 0.1 M phosphate buffer, pH 7.2) for at least 8 hours. Samples were centrifuged at 4000 rpm (Savant Speed Fuge HSC10K) for 4 minutes. A drop of each pelleted solution was clamped between two membrane filters (0.4 µm, Isopore, Merck Millipore Ltd., USA), in an aluminium clamp and processed as follows: three times 0.1 M phosphate buffer washes (15 minutes each), dehydrated in a graded series of ethanol steps (25%, 50%, 75%, 95%, and 100%) for 15 minutes each, and a final 100% for 1 hour. Samples were critical point dried using liquid CO₂ as the CP fluid and 100% ethanol as the intermediary (Polaron E3000 series II critical point drying apparatus). The samples were mounted onto aluminium stubs and sputter coated with gold (BAL-TEC SCD 005 sputter coater) and viewed in a FEI Quanta 200 scanning electron microscope at an accelerating voltage of 25kV.

Preparation for isolate 133 varied slightly from above. Briefly; three times 0.1 M phosphate buffer washes (15 minutes each), post-fixed for 1 hour in 1% osmium tetroxide (OsO₄) at room temperature then buffer washed an additional three times in 0.1 M phosphate buffer (15 minutes each), before being dehydrated as above.

2.11.3 Biochemical testing

Biochemical testing was carried out using two commercially available kits [Microgen™ GnA+B-ID, (Microgen Bioproducts Ltd., U.K.) and BBL Crystal™ Enteric/Nonfermenter ID Kit, (Becton, Dickinson and Company, USA)] according to manufacturer's instructions.

2.11.4 Sample collection and preparation

Soil samples were collected from beneath an organic waste pile on two occasions from Carroll Street, Palmerston North. A slurry was made by mixing soil with 0.9% saline

before 10-fold dilutions were prepared in 0.9% saline and plated out by spreading 20 μ L of prepared dilutions using a sterile spreader across a range of solid media (section 2.3.2).

Chapter 3: Results

3.1 Introduction

To achieve the aim of this study of bioprospecting soil-borne bacteria for novel extracellular polymers, soil was collected and dilution plated. The resulting bacterial colonies visually screened for a mucoid phenotype, where mucoidity was judged as a wet, glossy colony appearance with a consistency similar to mucous.

Over 130 colonies displaying a mucoid phenotype were generated before the final selection of 3 colonies for further study was made based on production of large amounts of extracellular polymer (Isolates X, 133, and 134). Isolate 133 became the major target for investigation after SEM imaging revealed the presence of unknown structures extending outwards from the bacteria.

3.2 Generation and characterisation of bacterial isolates

Dilutions of collected soil (section 2.11.4) were spread on solid media (LB, AIA, and nutrient agar) (section 2.3.2) and cultured (section 2.4). Bacterial isolates with mucoid phenotypes were further identified and characterised by gram staining, electron microscopy, PCR and 16S *rRNA* gene sequencing, cellular harvesting, protein analysis, characterisation of extracellular polymer produced, and biochemical testing (sections 2.6.1, 2.7.1, 2.8, 2.9, 2.11.1, 2.11.2, 2.11.3). The results for each isolate are presented below.

3.2.1 Isolate X

Isolate X produced white/cream heavily mucoid colonies (Figure 2), and is a long gram negative rod.

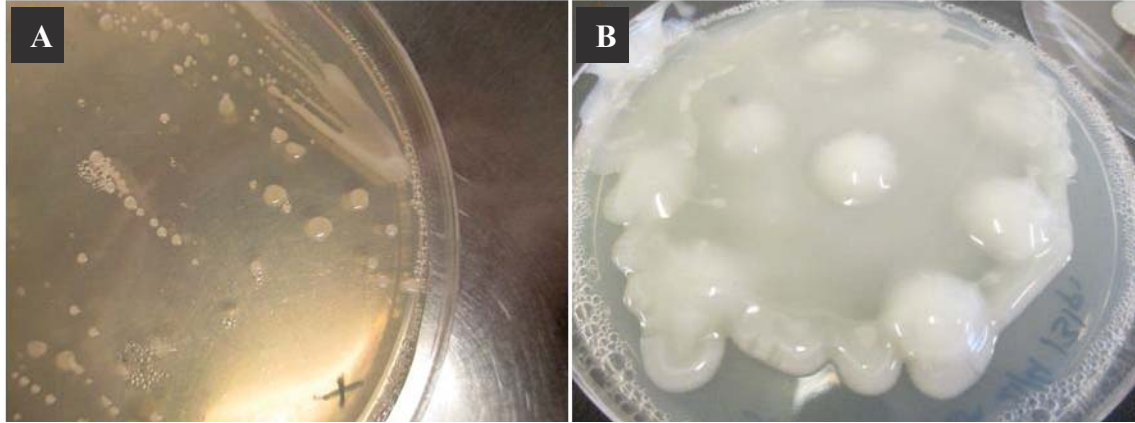


Figure 2. Isolate X – mucoid colonies and lawn. (A) Mucoid white colonies formed by isolate X when grown on Actinomycete isolation agar. (B) Mucoid lawn produced by isolate X on Actinomycete isolation agar after storage at 4°C for a week post incubation.

3.2.1.1 Electron microscopy imaging

SEM imaging (section 2.11.2) revealed a polymer network and conserved shape across various conditions, including storage temperature and length of incubation (Figures 3, 4, and 5).

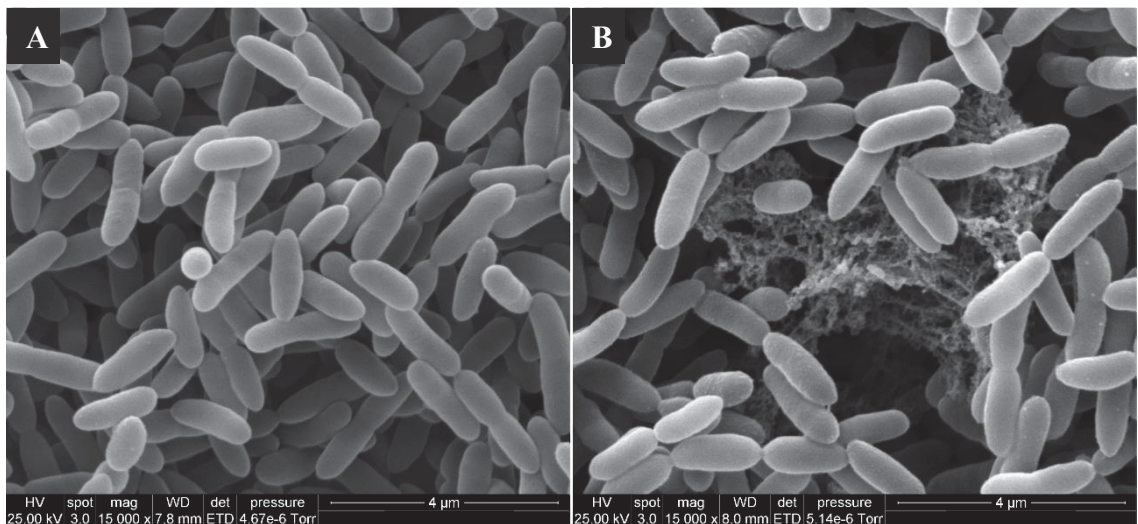


Figure 3. SEM images of isolate X grown on Actinomycete isolation agar. (A) Bacteria display a regular size and shape with a smooth appearance. (B) Bacterial interactions with the polymer matrix appear limited. The polymer matrix appears to have multiple dimensions.

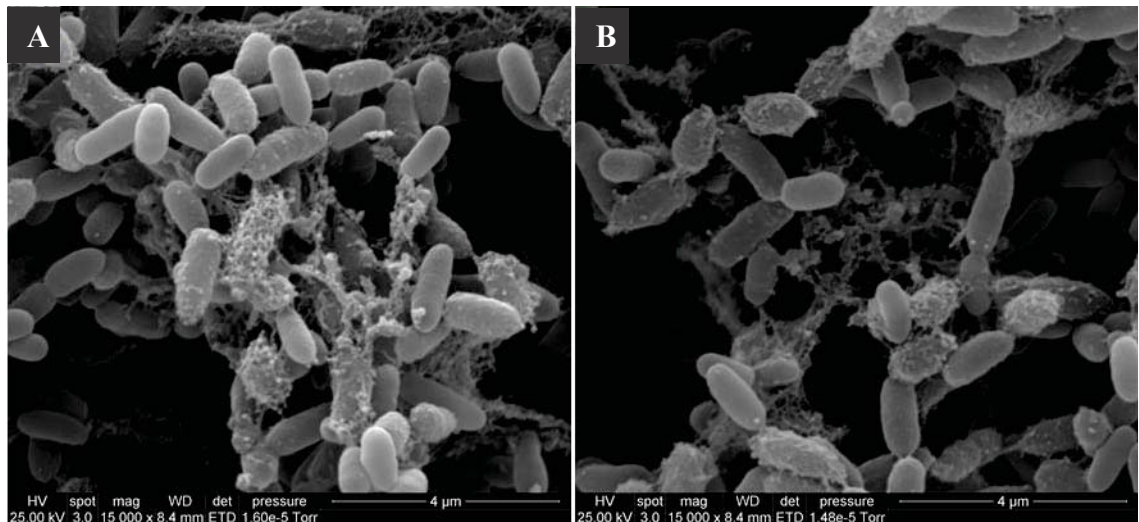


Figure 4. SEM images of isolate X after storage at 4°C for 7 days. (A) Bacteria maintain a regular size and shape, an increase in polymer surrounding the bacteria resulting in a rough appearance. (B) Bacterial interactions with the polymer matrix increases as more bacteria produce polymer. The polymer matrix appears to become less dimensional but more heavily linked to the bacteria.

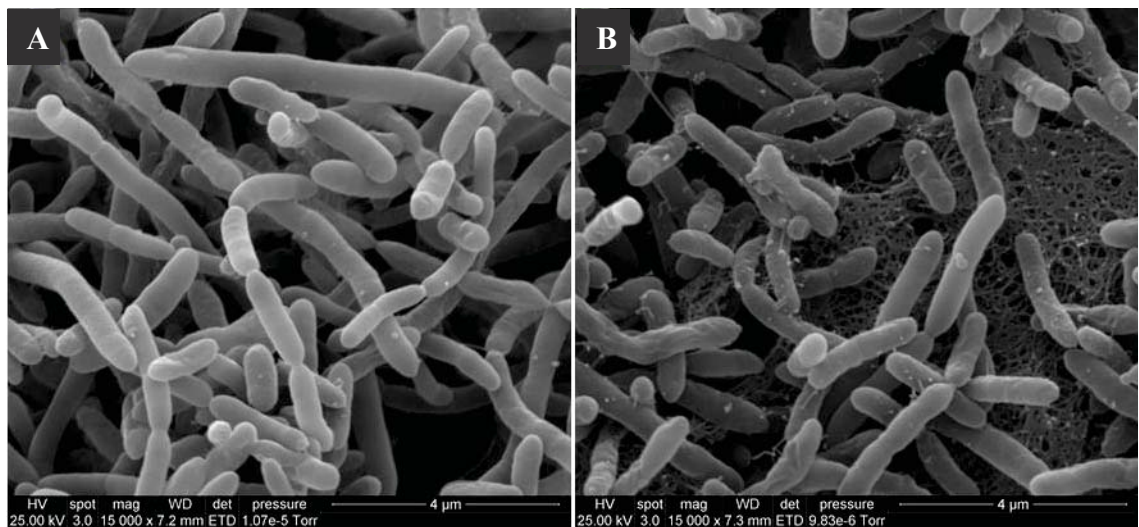


Figure 5. SEM images of isolate X after storage at 30°C for 7 days. (A) Bacteria lose their regular size and shape, becoming elongated and thicker, their smooth appearance becomes pitted and rough. (B) Bacterial interactions with the polymer matrix appears heavily reduced. The polymer matrix loses its multidimensional structure and appears as a dense flat web.

3.2.1.2 Genetic analysis – 16S *rRNA* encoding gene sequencing

Initial PCR (section 2.6.1) and sequencing (section 2.6.4) with 16S *rRNA* encoding gene primers (table 3, section 2.2) revealed a sequence similarity to *Pseudomonas* genus (Figure 6) and further PCR and sequencing with *Pseudomonas* specific primers (table 5, section 2.2) confirmed isolate X is likely a *Pseudomonas* sp..



Figure 6. Isolate X – *Pseudomonas* sp. – 16S *rRNA* gene sequence results and BLAST top hit. Sequence generated by sequencing isolate X using 16S *rRNA* encoding gene specific primers, and the resulting top match against NCBI's BLAST database.

3.2.1.3 Extracellular polymer production

Extracellular polymer harvest and purification (section 2.9) (table 12) resulted in 15.9 mg of purified sample and an averaged glucose equivalence of 19.2% by anthrone assay (section 2.9.2) (Figure 7) (table 13).

Table 12. *Harvest of biomass and extracellular polymer from isolate X*

Sample	Freeze dried cell mass (mg)	Freeze dried precipitate mass (mg)
Raw sample	84.6	142.8
Purified sample		15.9

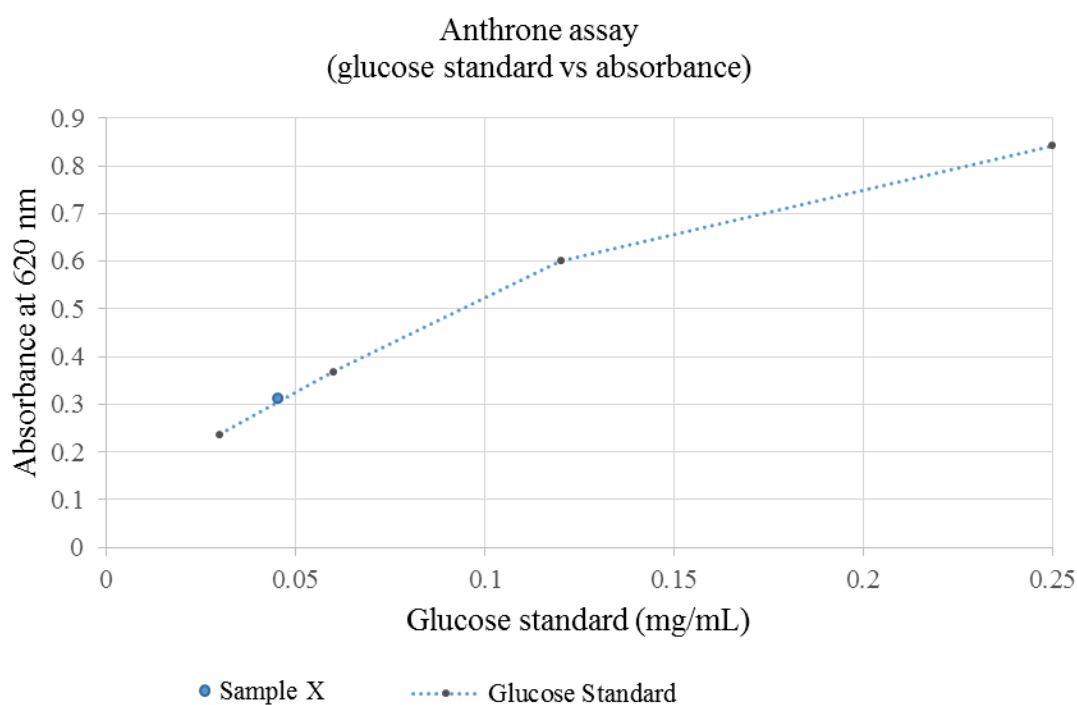


Figure 7. Graphical representation of anthrone assay results. Dilutions of purified extracellular polymer from isolate X were prepared and plotted against the glucose standard based on the absorbance reading of each sample.

Table 13. *Glucose equivalence of purified extracellular polymer from isolate X*

Concentration of X (mg/mL)	Concentration of glucose (mg/mL)	Glucose equivalence (glucose concentration / X concentration)	Glucose equivalence (%)
0.125	0.026	0.208	20.8
0.25	0.044	0.176	17.6
	Averaged	0.192	19.2

3.2.2 Isolate 134

Isolate 134 produced mustard yellow mucoid colonies (Figure 8), and is a gram negative rod.

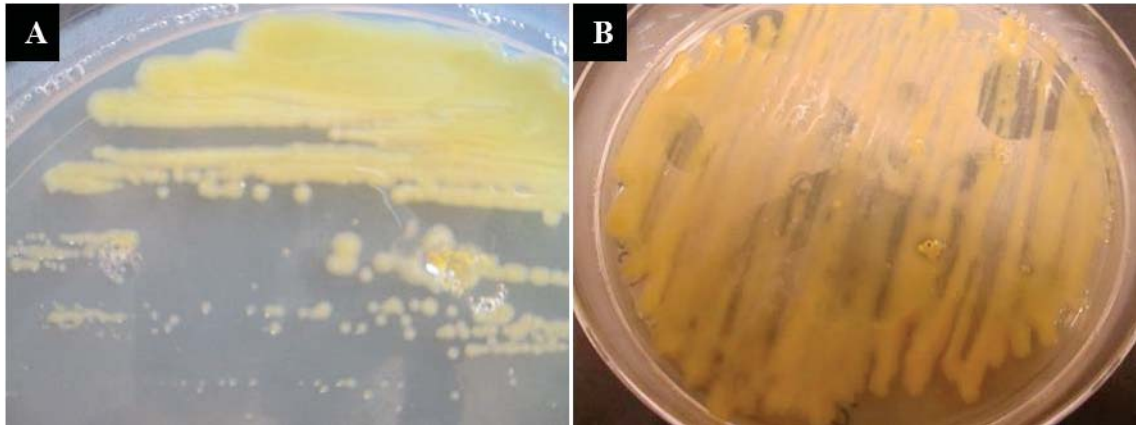


Figure 8. Isolate 134 – mucoid colonies and lawn. (A) Mucoid yellow colonies formed by isolate 134 when grown on Actinomycete isolation agar. (B) Mucoid lawn produced by isolate 134 on Actinomycete isolation agar after incubation at 30°C for 3 days.

3.2.2.1 Electron microscopy imaging

SEM imaging (section 2.11.2) revealed a polymer network and bacteria with conserved shape of various lengths (Figures 9, 10, and 11) although storage temperature appears to have an impact on both polymer formation and bacteria (Figure 10).

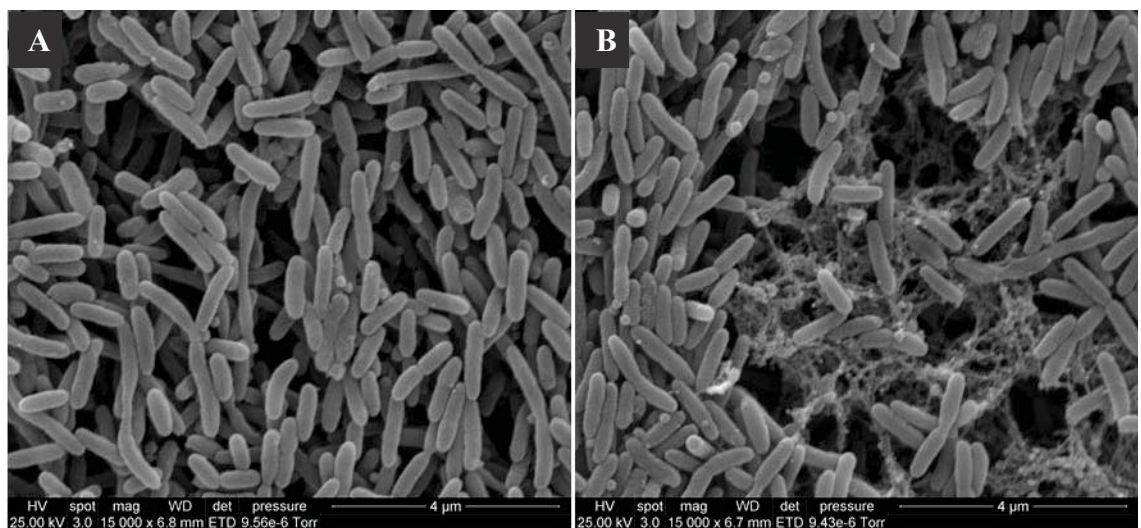


Figure 9. SEM images of isolate 134 grown on Actinomycete isolation agar. (A) Bacteria have a regular shape and appear smooth, but elongate and appear to pinch in the middle when dividing. (B) Bacteria interact with a polymer network.

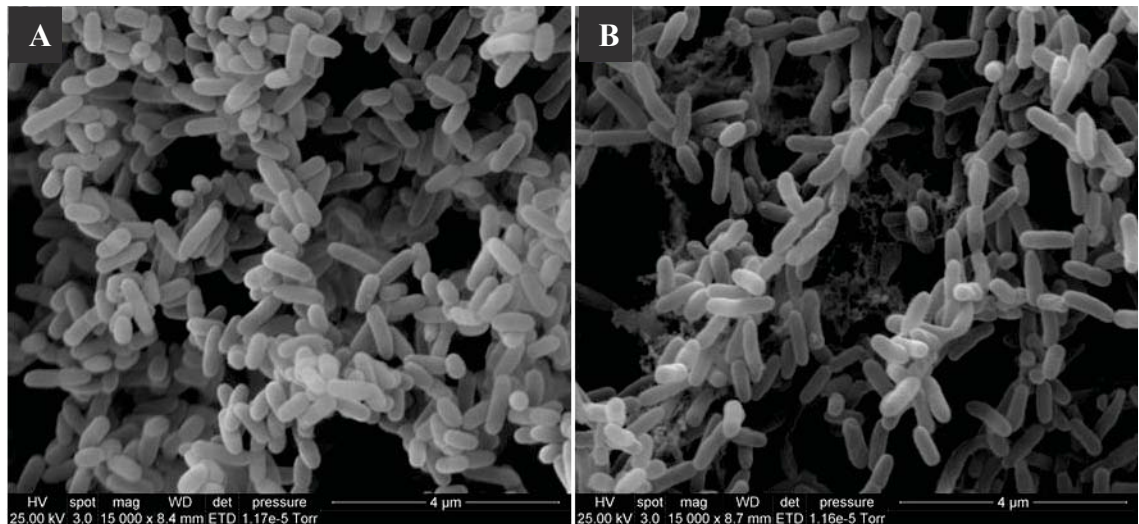


Figure 10. SEM images of isolate 134 after storage at 4°C for 7 days. (A) Bacteria appear to have a highly ordered structure with a regular shape, size, and length. (B) Bacteria appear with a highly ordered structure, and polymer network.

Storage at 30°C for 7 days has a marked effect on isolate 134, with some bacteria appearing misshapen, and desiccated. A polymer sheet has formed over the top of some bacteria, and bacteria beneath it appear to be more protected from desiccation caused by the storage temperature (Figure 11).

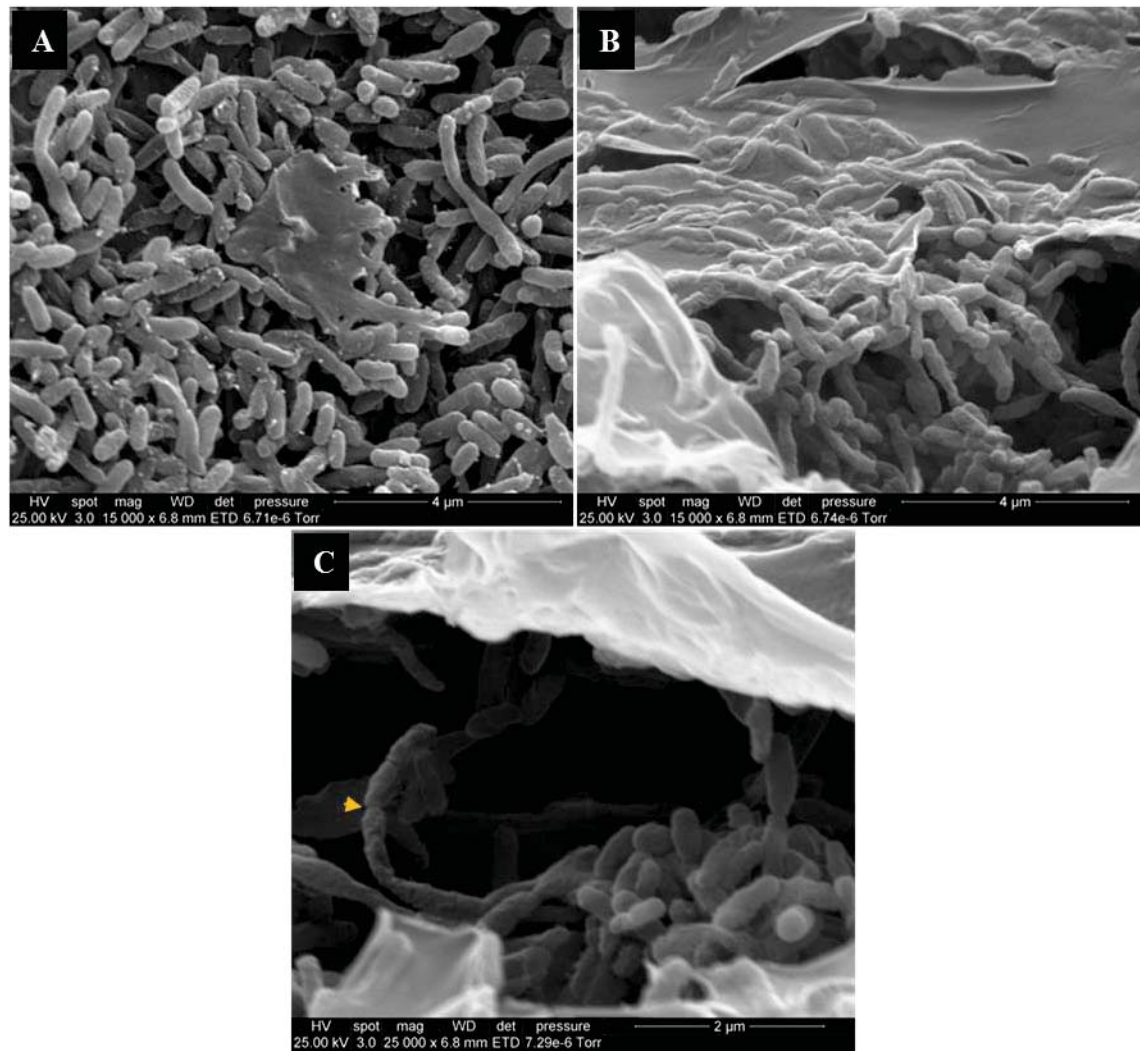


Figure 11. SEM images of isolate 134 after storage at 30°C for 7 days. (A) A polymer sheet covers some bacteria. (B) A polymer sheet with embedded bacteria. (C) Increased magnification shows the polymer sheet at top with bacteria beneath. Some bacteria outside the polymer sheet (arrow head) appear desiccated and misshapen.

3.2.2.2 Genetic analysis – 16S *rRNA* encoding gene sequencing

Initial PCR (section 2.6.1) and sequencing (section 2.6.4) with 16S *rRNA* gene primers (table 3, section 2.2) revealed a sequence similarity to *Luteimonas* genus (Figure 12).

TGCAAGTCGAACGGCAGCACAGAGGAGCTTGCTCCTTGGGTGGCGAGT GGCGGACGGGTGAGGAATACATCGGAATCTGCCTATTTGTGGGGGATAA CGTAGGGAAACTTACGCTAATACCGCATACGACCTACGGGTGAAAGCG GAGGACCTTCGGGCTTCGCGCAGATAGATGAGCCGATGTCGGATTAGCT AGTTGGCGGGGTAAAGGCCACCAAGGCGACGATCCGTAGCTGGTCTG AGAGGATGATCAGCCACACTGGAAGTGAAGACACGGTCCAGACTCCTAC GGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCA GCCATGCCGCGTGGGTGAAGAAGGCCTTCGGGTGTAAAGCCCTTTTG TTGGGAAAGAAAAGCAGTCGGTTAATACCCGATTGTTCTGACGGTACCC AAAGAATAAGCACCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGA AGGGTGCAAGCGTTACTCGGAATTACTGGGCGTAAAGCGTGCGTAGGT GGTTTGTTAAGTCTGATGTGAAAGCCCTGGGCTCAACCTGGGAATTGC ATTGGATACTGGCAGGCTAGAGTGCGGTAGAGGGTAGTGGAATTCCTCG GTGTAGCAGTGAAATGCGTAGAGATCGGGAGGAACATCCGTGGCGAAG GCGACTACCTGGACCAGCACTGACACTGAGGCACGAAAGCGTGGGGA GCAAACAGGATTAGATAACCCTGGTAGTCCACGCCCTAAACGATGCGAA CTGGATGTTGGGTTCAACTAGGAACTCAGTATCGAAGCTAACGCGTTAA GTTTCGCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATT GACGGGGGCCCCGCACAAGCGGTGGAGTATGTGGTTTAATTTCGATGCAA CGCGAAGAACCTTACCTGGCCTTGACATGCACGGAACCTTCCAGAGAT GGATTGGTGCCTTCGGGAACCGTGACACAGGTGCTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGATTAAAGTCCCGCAACGAGCGCAACC						
Description	Max score	Total score	Query cover	E value	Ident	Accession
☐ Luteimonas aestuarii strain JM-R9 16S ribosomal RNA gene, partial sequence	1951	1951	100%	0.0	99%	KF876901.1

Figure 12. Isolate 134 – *Luteimonas* sp. – 16S *rRNA* gene sequence results and BLAST top hit. Sequence generated by sequencing isolate 134 using 16S *rRNA* encoding gene specific primers, and the resulting top match against NCBI's BLAST database.

3.2.2.3 Extracellular polymer production

Raw extracellular polymer production was assessed across four replicates of four AIA plates (table 14).

Table 14. *Raw extracellular polymer production by isolate 134*

Freeze dried mass (mg)			
Replica	Cells	Polymer	Raw polymer as a percentage of total mass
A	146.4	117.7	44.57%
B	154.5	138.4	47.25%
C	207.5	142.7	40.75%
D	216.1	156.0	41.92%
Average	181.1	138.7	43.37%

3.2.3 Isolate 133

Isolate 133 produced clear/cream mucoid colonies (Figure 13), and is a gram negative rod.

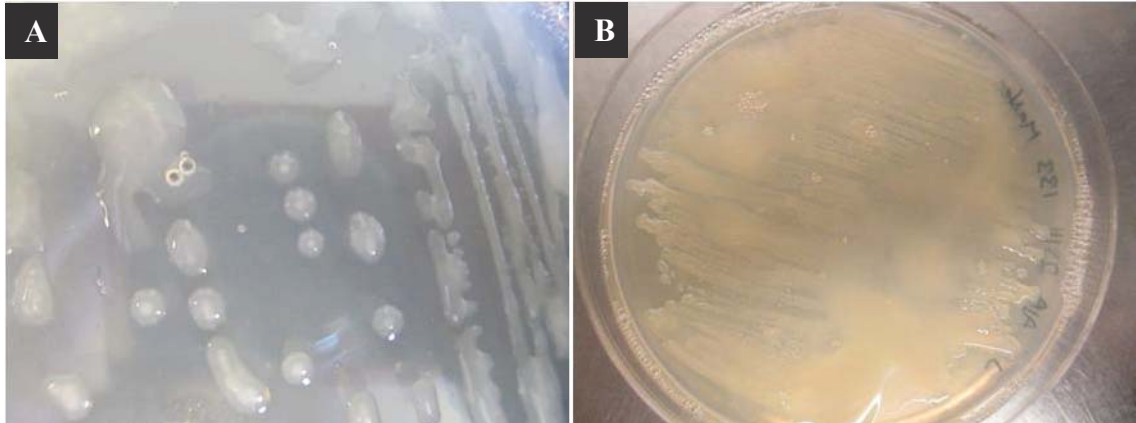


Figure 13. Isolate 133 – mucoid colonies and lawn. (A) Mucoid clear/cream colonies formed by isolate 133 when grown on Actinomycete isolation agar. (B) Mucoid lawn produced by isolate 133 on Actinomycete isolation agar after incubation at 30°C for 3 days.

3.2.3.1 Electron microscopy imaging

SEM imaging (section 2.11.2) revealed striking appendages extending from the bacteria's surface when grown on AIA (section 2.3.2) (Figures 14, and 15) but not when grown on other solid media or in liquid media (section 2.3.1) (Figures 16, and 17). TEM imaging (section 2.11.2) confirmed these structures are attached to the bacteria, extend outwards from beyond the outer membrane (Figure 18) and link bacteria to each other (Figure 19). TEM imaging reveals these structures extend large distances from the bacteria (Figure 20), and can split (Figure 21). Electron density and the stain used in TEM suggest these structures are proteinaceous (section 2.10.1).

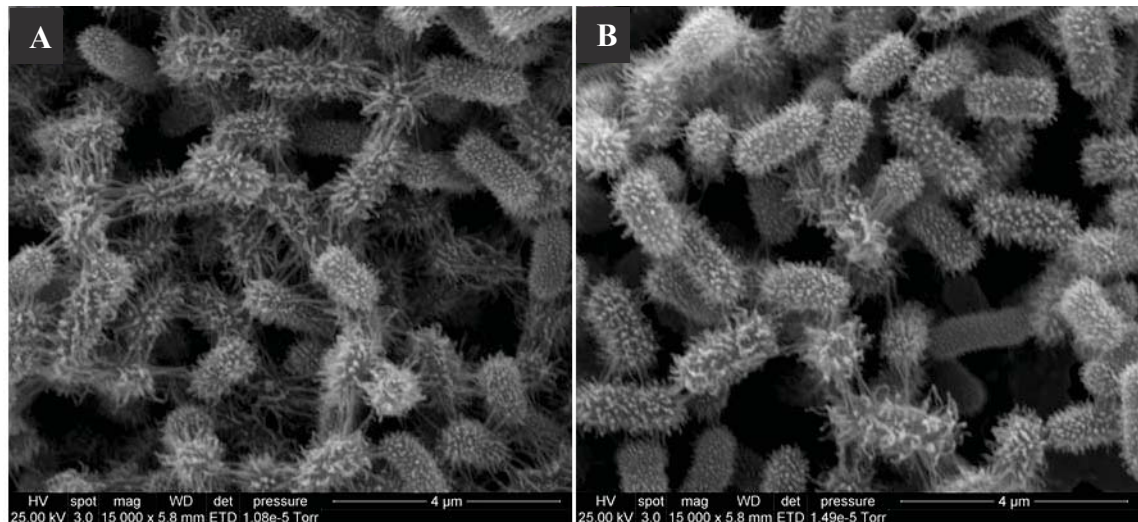


Figure 14. SEM of isolate 133 reveals striking appendages. Appendages extend outwards in all directions from isolate 133 grown on Actinomycete isolation agar. (A) Masses of appendaged bacteria form an interconnecting network, with multiple connections per bacteria. (B) Bacteria produce appendages of increasing length until contact occurs with another bacteria.

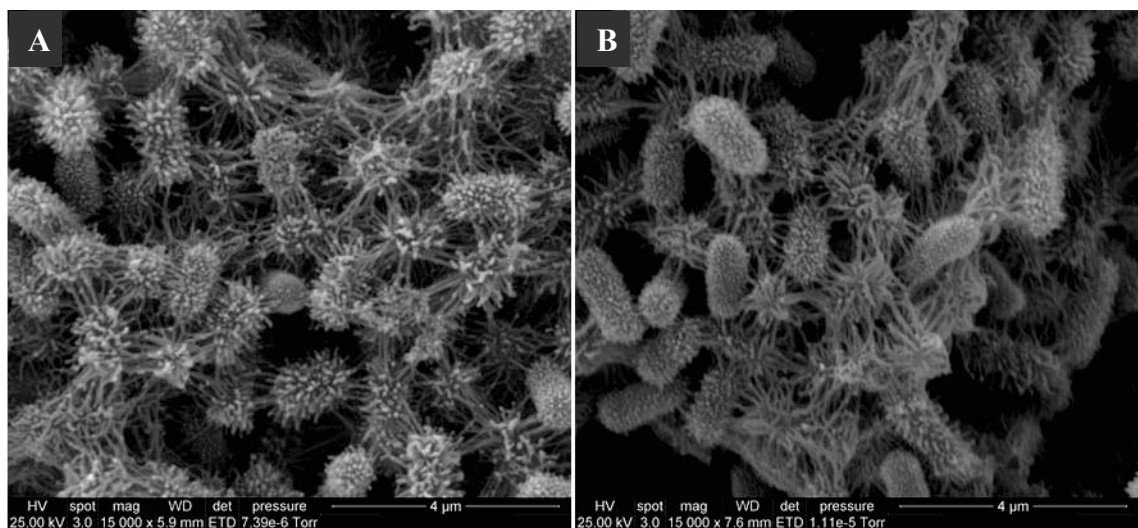


Figure 15. Temperature and storage have no effect on appendage formation. Isolate 133 grown on Actinomycete isolation agar and stored (post incubation) for one week at two different temperatures and although not controlled, moisture levels (fridge vs controlled room) produced appendages and form interconnecting networks. (A) Bacteria stored at 4°C for one week. (B) Bacteria stored at 30°C for one week.

Isolate 133 produced striking appendages when grown on Actinomycete isolation agar (AIA), and was able to grow on a range of media. SEM imaging was performed to assess if 133 would produce appendages when grown on other solid media. Isolate 133 produced striking appendages only when grown on solid AIA (Figure 16).

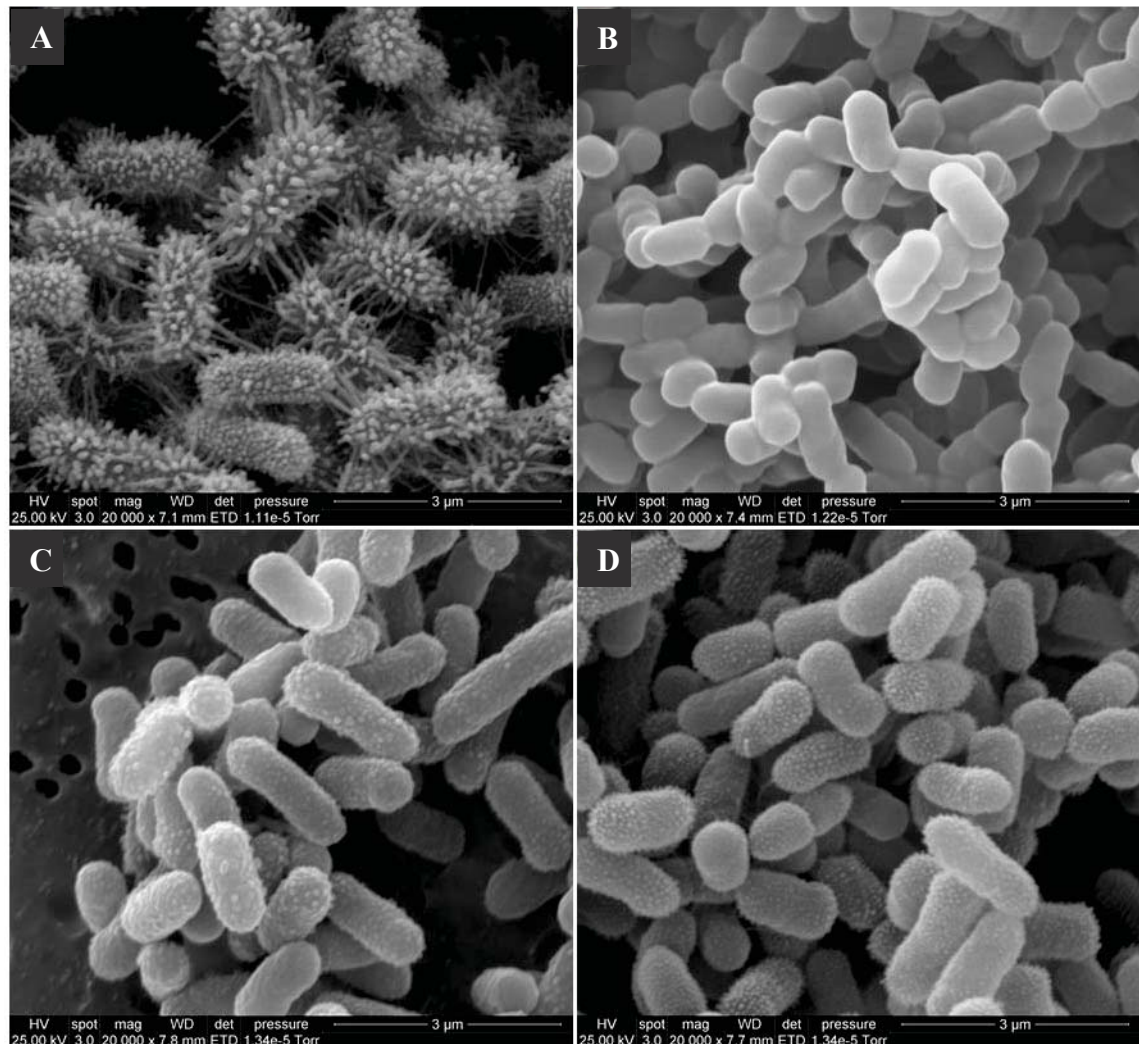


Figure 16. SEM comparison of isolate 133 across solid media. (A) Isolate 133 grown on AIA, the surface is covered in appendages, and there is a visible thick network structure. (B) Isolate 133 grown on Luria-Bertani broth agar, bacteria are free of appendages, appear smooth, and no visible network structure is present. (C) Isolate 133 grown on MacConkey agar, bacteria are free from appendages, have a rough uneven surface with sporadic bumps, and no visible network structure. (D) Isolate 133 grown on blood agar, bacteria are free of appendages, the surface of some bacteria is covered in small bumps while other bacteria are bald in some spots, and there is a limited amount of thin network.

SEM imaging was performed to assess if 133 produced appendages when grown in broth media (Figure 17) including Actinomycete isolation broth (AIB) which contains the same nutrients as AIA.

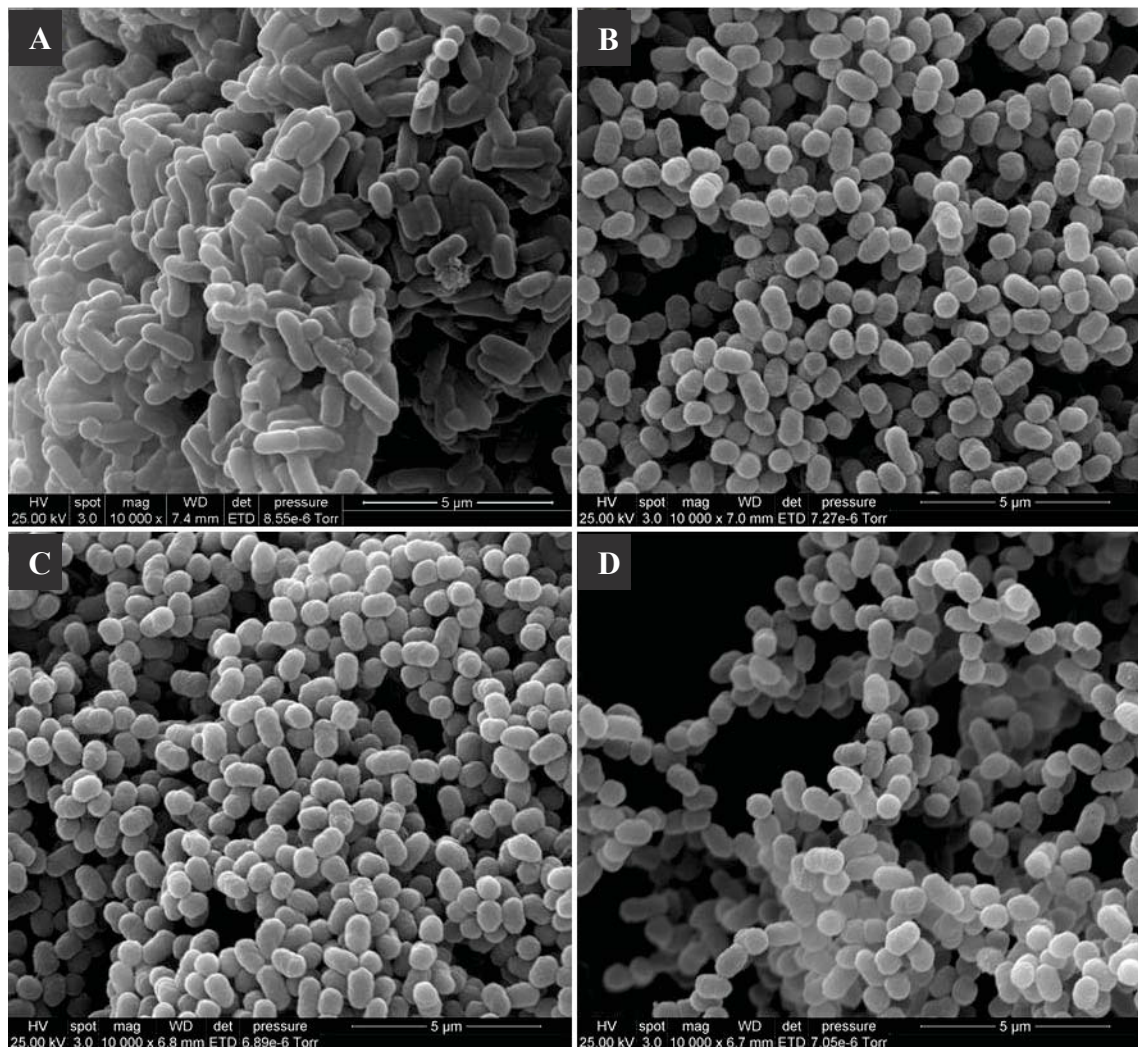


Figure 17. SEM imaging of isolate 133 in broth media. (A) Isolate 133 grown in Actinomycete isolation broth, no appendages are present and bacteria appear smooth and tightly associated. (B) Isolate 133 grown in Luria-Bertani broth, no appendages are present and bacteria appear smooth and loosely associated. (C) Subculture of isolate 133 (from B) grown in Luria-Bertani broth. (D) Isolate 133 subcultured twice (from B) and grown in Luria-Bertani broth.

Bacteria appear to connect to each other *via* appendages in SEM images and TEM imaging investigated this further. Bacteria connect *via* appendages which are only nano-meters thick but hundreds of nano-meters long (Figures 19, and 20). Increasing magnification of appendage threads revealed an unwinding and splitting of a main appendage thread into thinner branches (Figure 21).

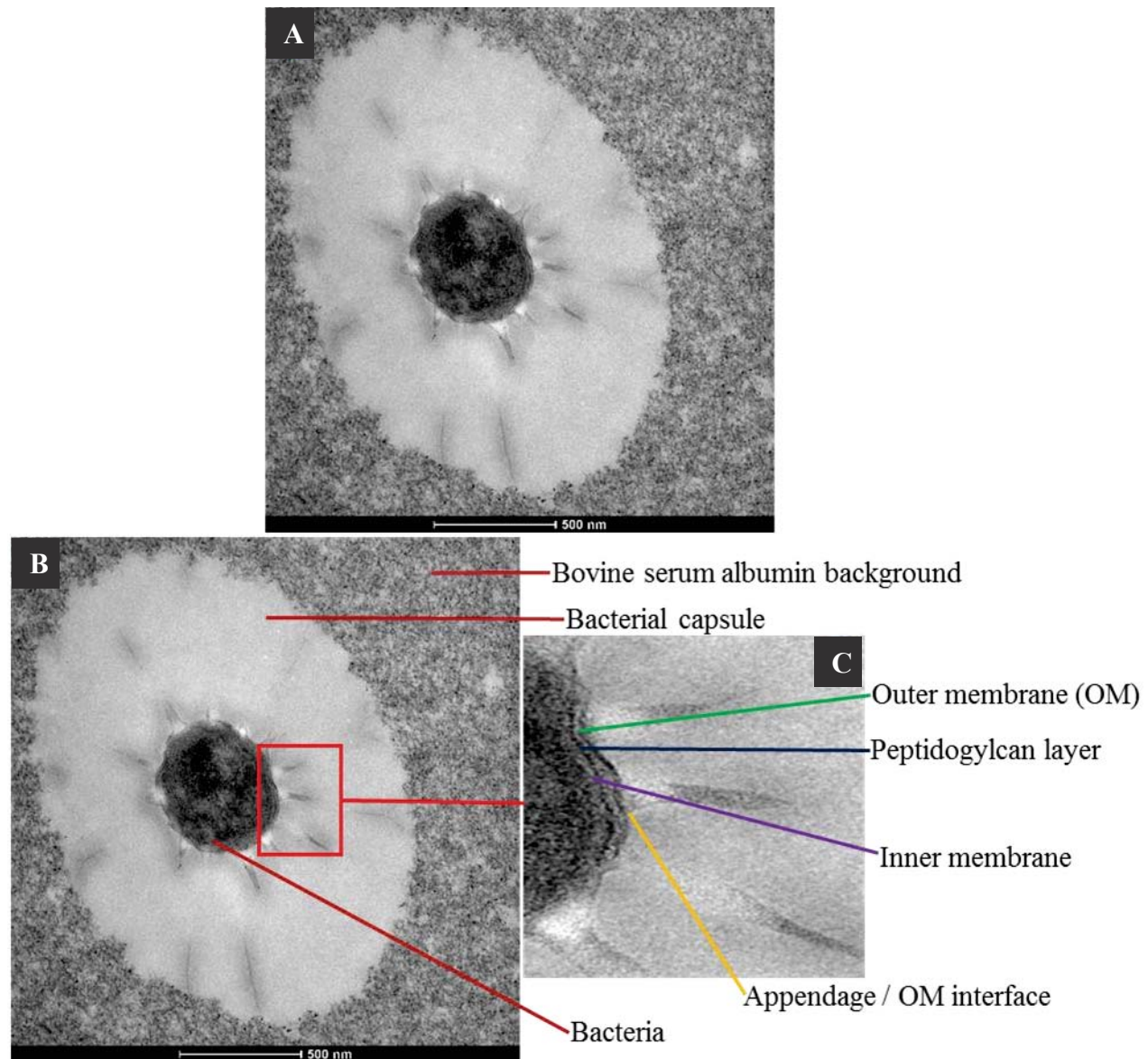


Figure 18. TEM images of isolate 133 – outlining features of importance. The labelling seen in this figure is consistent with all other TEM images of isolate 133, with the bovine serum albumin (BSA) background always appearing as an electron dense fuzzy cloud, the bacterial capsule (if present) appearing as a white electron empty zone surrounding the bacteria with electron dense appendages present. (A) Original TEM image of isolate 133 without labels. (B) Isolate 133 with labelling for bacterial capsule, BSA background, bacteria, and area of enlargement. (C) Enlarged image displaying the outer membrane, peptidoglycan layer, inner membrane, and the appendage / outer membrane interface.

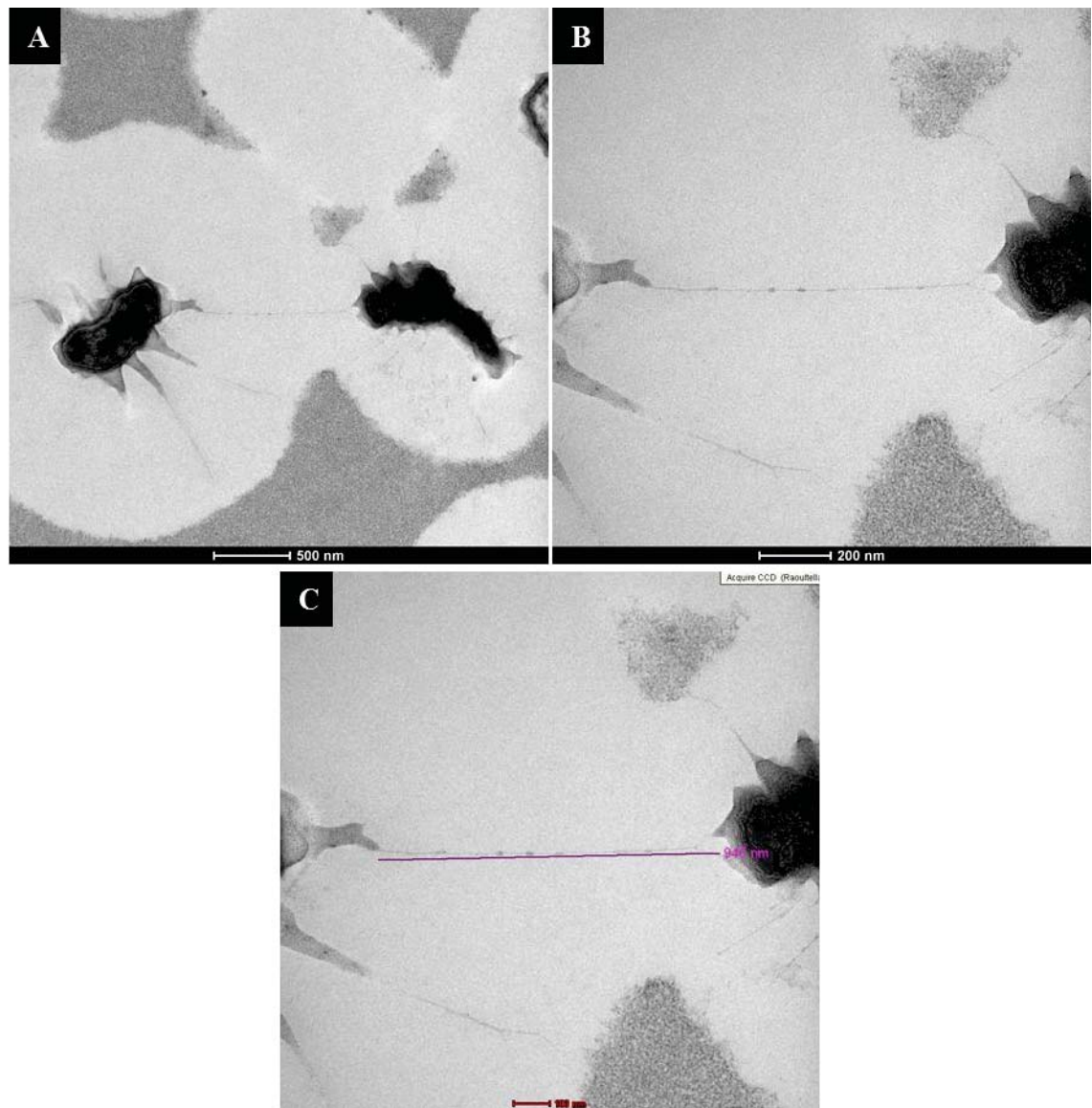


Figure 19. TEM images of bacterial connectivity via an appendage. (A) Bacteria producing appendages are connected by a single thread. (B) An increase in magnification reveals droplets or thickening at points along the thread. (C) Increased magnification with a rough measurement of the thread from thick appendage to thick appendage, revealing a connection over a distance of around 940 nm and an estimated distance of over 1 micron from outer membrane to outer membrane.

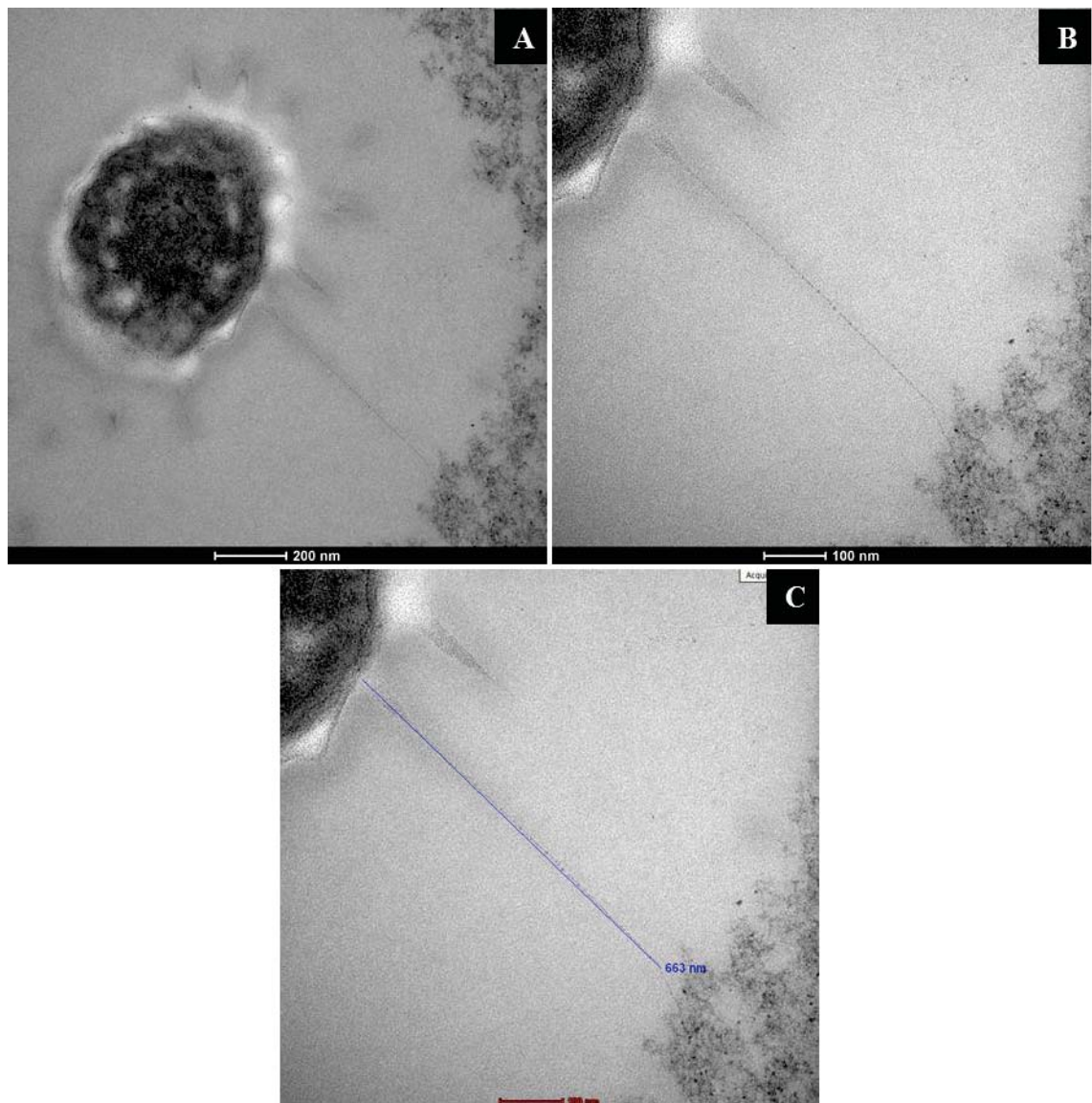


Figure 20. TEM images of bacterial appendage extension. (A) Bacteria producing appendages. (B – C) Increased magnification and rough measurement of an appendage extending over 600 nm.

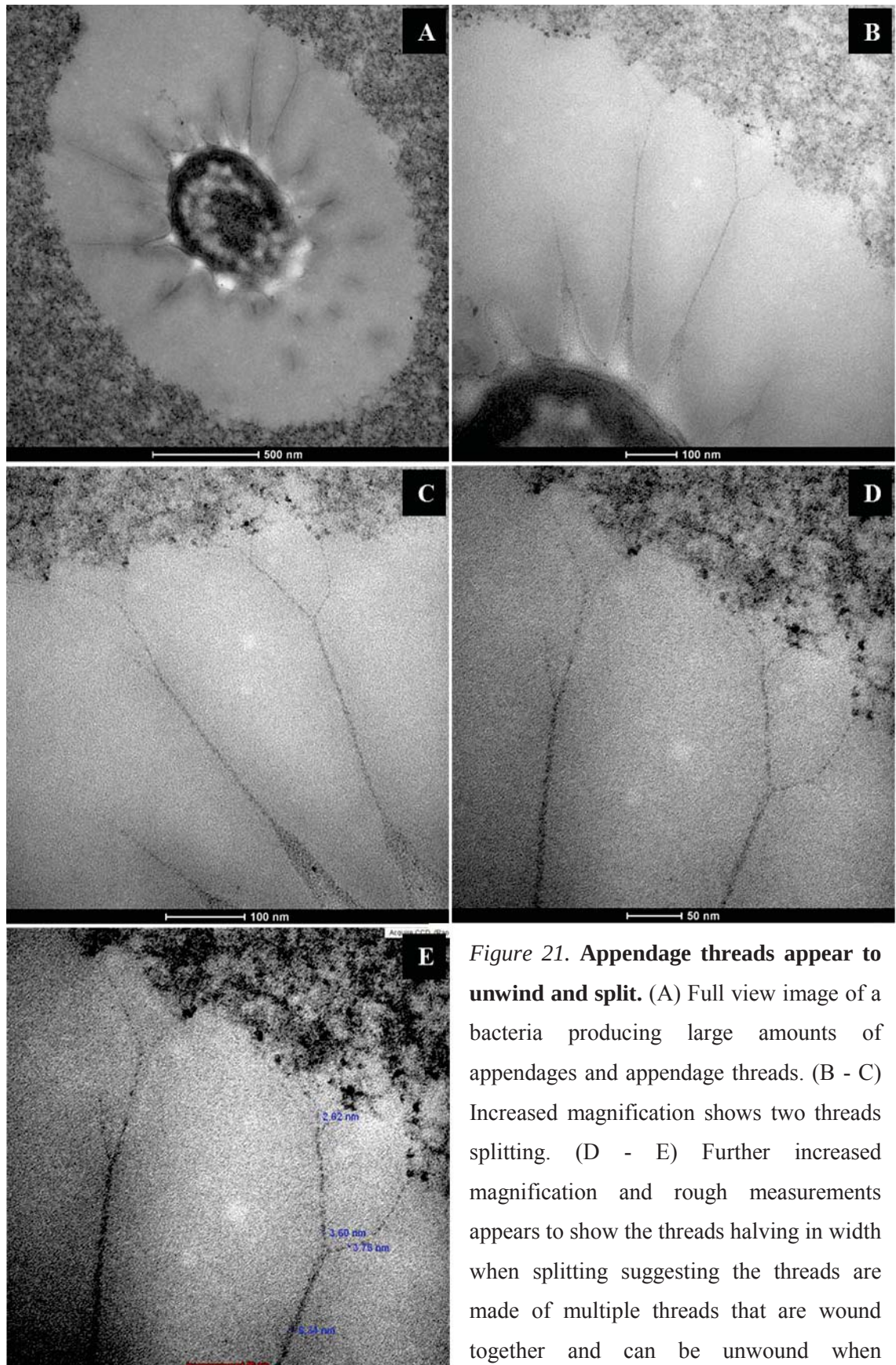


Figure 21. Appendage threads appear to unwind and split. (A) Full view image of a bacteria producing large amounts of appendages and appendage threads. (B - C) Increased magnification shows two threads splitting. (D - E) Further increased magnification and rough measurements appears to show the threads halving in width when splitting suggesting the threads are made of multiple threads that are wound together and can be unwound when extending far enough from the main appendage and cell.

3.2.3.2 Genetic analysis – 16S *rRNA* encoding gene and whole genome sequencing

Initial PCR (section 2.6.1) and sequencing (section 2.6.4) with 16S *rRNA* encoding gene primers (table 3, section 2.2) revealed a sequence similarity to *Raoultella* genus (Figure 22). The entire genome of 133 was sequenced by New Zealand Genomics Limited using Illumina MiSeq 2 x 250 base paired end library preparation and generated 140x coverage.



Figure 22. Isolate 133 – *Raoultella* sp. – 16S *rRNA* encoding gene sequence results and BLAST top hit. Sequence generated by sequencing isolate 133 using 16S *rRNA* encoding gene specific primers, and the resulting top match against NCBI's BLAST database reveals a 99% identity to *Raoultella terrigena*.

3.2.3.2.1 Whole genome sequence analysis

The entire genome of isolate 133 – *Raoultella* sp. was sequenced using an Illumina MiSeq 2 x 250 base paired end library preparation. Initial assembly of the genomic data was

carried out using SPAdes (version 3.9.1, Center for Algorithmic Biotechnology, St. Petersburg State University, Russia). Analysis of the assembled contigs (nodes) was carried out using QUAST (quality assessment tool for genome assemblies, Center for Algorithmic Biotechnology, St. Petersburg State University). The entire assembly (above 500 bp) after removing contaminating DNA sequences was submitted to NCBI, processed and annotated by the NCBI prokaryotic genome annotation pipeline (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/). The master accession number for this project is MUBF00000000.

QUAST analysis (Appendix II) revealed, an assembly of 56 contigs, containing 5,832,040 nucleotides, with a GC ratio of 57%, and 5460 predicted unique genes.

Using multilocus sequence typing (section 2.6.6), isolate 133 was revealed to be identical to *R. terrigena* across all three housekeeping gene comparisons (tables 15, 16, and 17) and was assigned the strain name NZ133. The complete name as recorded in NCBI records is *Raoultella terrigena* strain NZ133.

Table 15. *parC* housekeeping gene comparison

	Isolate 133	<i>R. ornithinolytica</i>	<i>R. terrigena</i>	<i>R. planticola</i>
DNA topoisomerase IV subunit A (<i>parC</i>)				
Isolate 133	x	x	x	x
<i>Raoultella ornithinolytica</i>	0.905	x	x	x
<i>Raoultella terrigena</i>	1	0.905	x	x
<i>Raoultella planticola</i>	0.909	0.993	0.909	x

Table 16. *gyrA* housekeeping gene comparison

	Isolate 133	<i>R. ornithinolytica</i>	<i>R. terrigena</i>	<i>R. planticola</i>
DNA gyrase, subunit A (<i>gyrA</i>)				
Isolate 133	x	x	x	x
<i>Raoultella ornithinolytica</i>	0.960	x	x	x
<i>Raoultella terrigena</i>	1	0.960	x	x
<i>Raoultella planticola</i>	0.963	0.997	0.963	x

Table 17. *rpoB* housekeeping gene comparison

	Isolate 133	<i>R. ornithinolytica</i>	<i>R. terrigena</i>	<i>R. planticola</i>
DNA-directed RNA polymerase subunit Beta (<i>rpoB</i>)				
Isolate 133	x	x	x	x
<i>Raoultella ornithinolytica</i>	0.953	x	x	x
<i>Raoultella terrigena</i>	1	0.953	x	x
<i>Raoultella planticola</i>	0.953	0.985	0.953	x

Circos plots were created and display a range of genetic information (Figures 24, and 25), including the nodes length, where the nucleotide sequence matches to the NCBI database, forward encoding genes, reverse encoding genes, and where the translated protein sequence matches to the NCBI database (Appendix V), tags of important gene products (Appendix IV), and the GC content across the nodes (Figure 23).

Important genes tagged include genes encoding for pilus, fimbrial, type IV secretion system, and type II secretion system assembly, polysaccharide synthase, enzymes, lipopolysaccharide, and biofilm associated genes, antibiotic synthesis, and bacteriophage related proteins. Genes important for bacterial survival and pathogenicity including efflux pumps, resistance genes to drugs, antibiotics, and heavy metals, genes encoding toxins and virulence factors as well as haemolytic factors.

The node each gene is positioned in can be found in Appendix VI. Individual circos plots for nodes 1 – 25 can be found in Appendix III.

Genes and nucleotide identities can be either of *Raoultella* sp. (green), bacterial (non-*Raoultella*) (pink), uncharacterised (black), or eukaryotic (orange) in origin.

Circos plots are arranged from largest node to smallest node for illustrative purposes only.

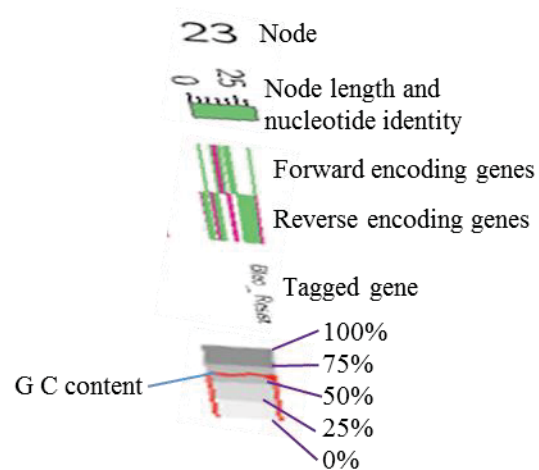


Figure 23. How to read circos plot information. Node represents the assembly of nucleotides. Node length large scale indication 25,000 nucleotides, small scale indication 5,000 nucleotides (unless otherwise labelled). Nucleotide identity is the match to NCBI database based on overall nucleotide sequence. Forward and reverse encoding genes colour indication is based on translated protein sequence match to NCBI database. Tagged gene is a gene of interest and information can be found in Appendix IV. GC content is the percentage of G's and C's every 100 bps (red line), while the grey bars represent 0 – 100% GC content in 25% steps.

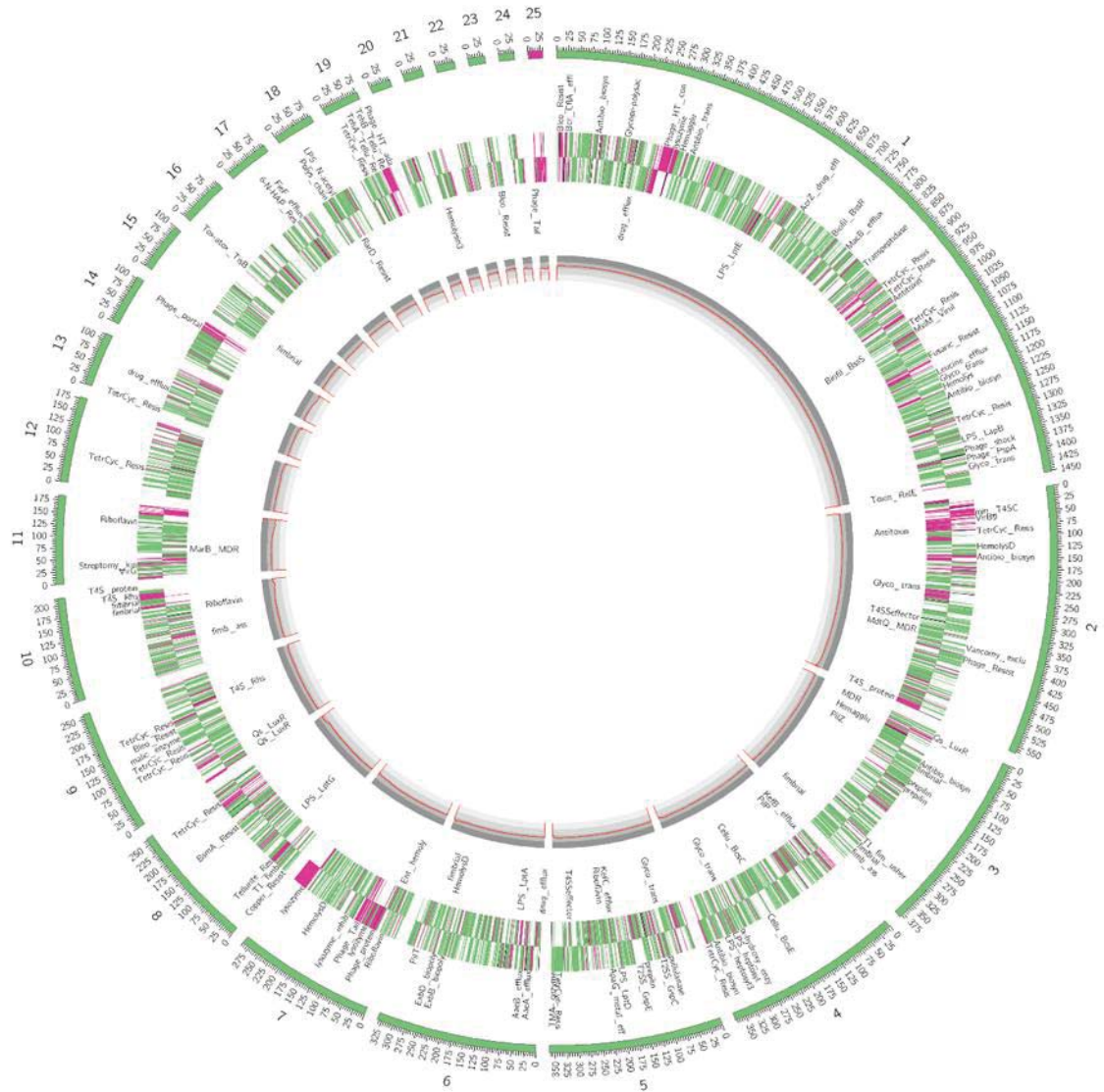


Figure 24. Circos plot of nodes 1 - 25, displaying GC content, forward, and reverse encoding genes, and genetic match. Node length is 1:1000 (1 = 1000 bps).



Figure 25. Circos plot of nodes 26 - 50, displaying GC content, forward, and reverse encoding genes, and genetic match. Node length is 1:1 (1 = 1 bp). Nodes 30, 38, 42, 45, 46, and 49 are all non-encoding regions.

3.2.3.3 Extracellular polymer production

Extracellular polymer was harvested and purified (section 2.9) from 10 AIA plates (table 18).

Table 18. Polymer production by isolate 133

Freeze dried	Raw polymer	Purified polymer
Sample 133	127 mg	22.5 mg

The purified polymer was sent to collaborators at the Technical University of Munich for analysis. However at the time of submission these results were not available. There is a cluster of cellulose biosynthesis genes present in the genomic data and this suggests the polymeric analysis would reveal the polymer to be bacterial cellulose.

3.2.3.3.1 Capsular polysaccharide

Capsular polysaccharide (CPS) presence was observed *via* nigrosin staining (section 2.10) (Figure 26) and TEM imaging (section 2.11.2) (Figure 27). Extraction of the CPS (section 2.10.1) was carried out to assess the impact on appendage formation.

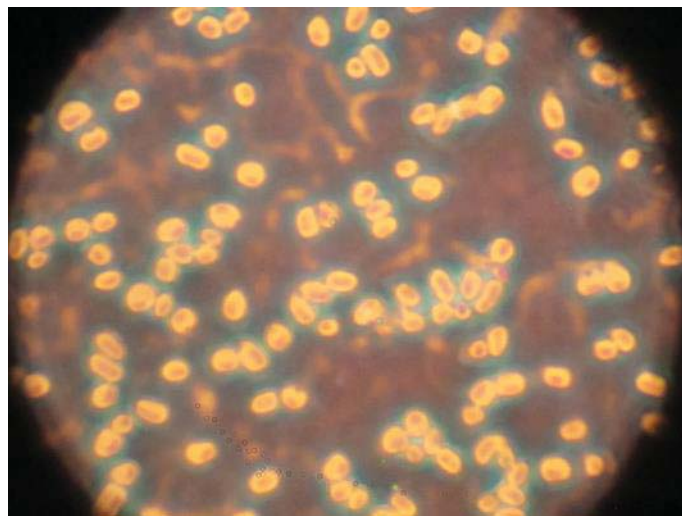


Figure 26. Nigrosin stain reveals capsule of isolate 133. Bacteria (stained pink/red) appear to have a halo (capsule) around them against a purple/brown background.

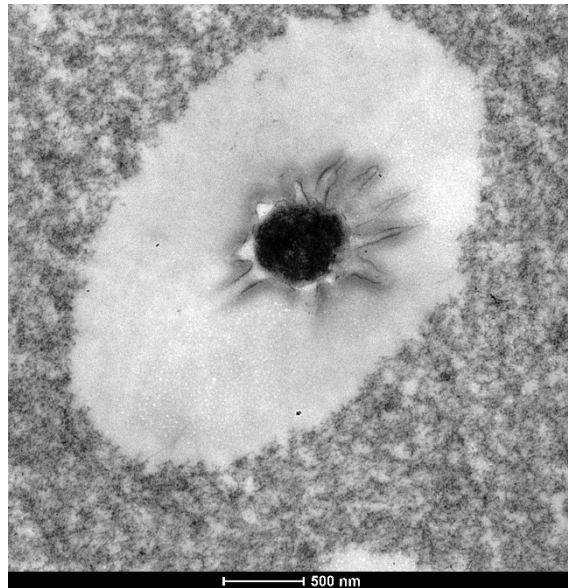


Figure 27. TEM image of isolate 133 before capsular extraction. A thick white space (capsule) is visible between the bacteria and the bovine serum albumin background. Bacterial appendages are visible within the capsular space.

The capsule appears reduced after treatment with 0.1% zwittergent and citrate buffer and appendages are still present within the capsular space (Figure 28).

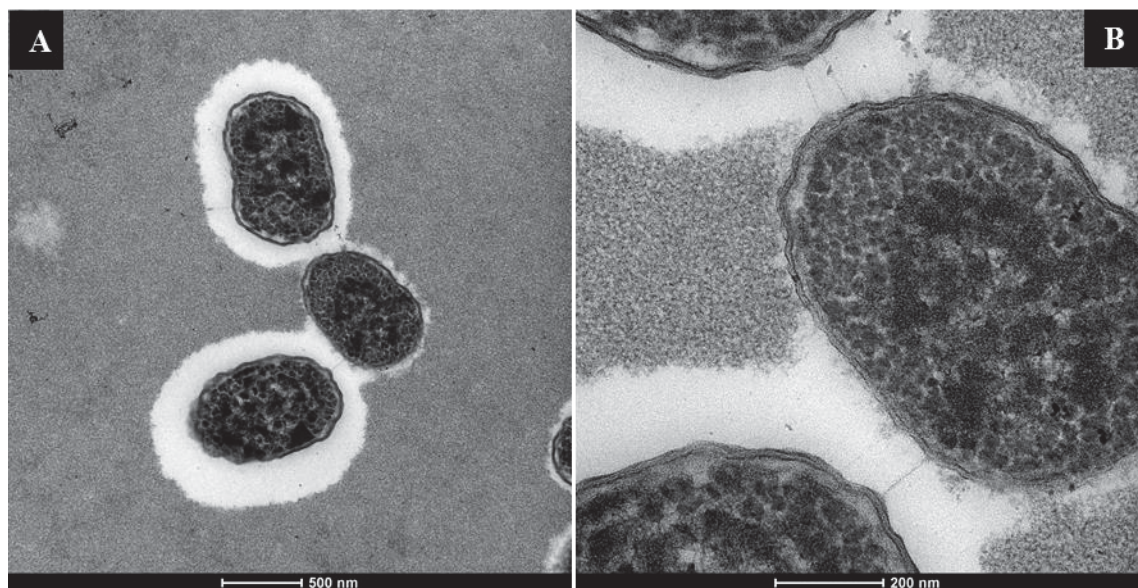


Figure 28. TEM images of isolate 133 after capsular extraction with 0.1% zwittergent. (A) Three bacteria with reduced capsule and thin appendages. (B) Increased magnification shows two thin appendages connecting the middle bacteria to each of the other bacteria.

The capsule appears heavily reduced or completely absent after treatment with 0.2% zwittergent and citrate buffer. Appendages are still present but more difficult to visualise against the bovine serum albumin background (Figure 29).

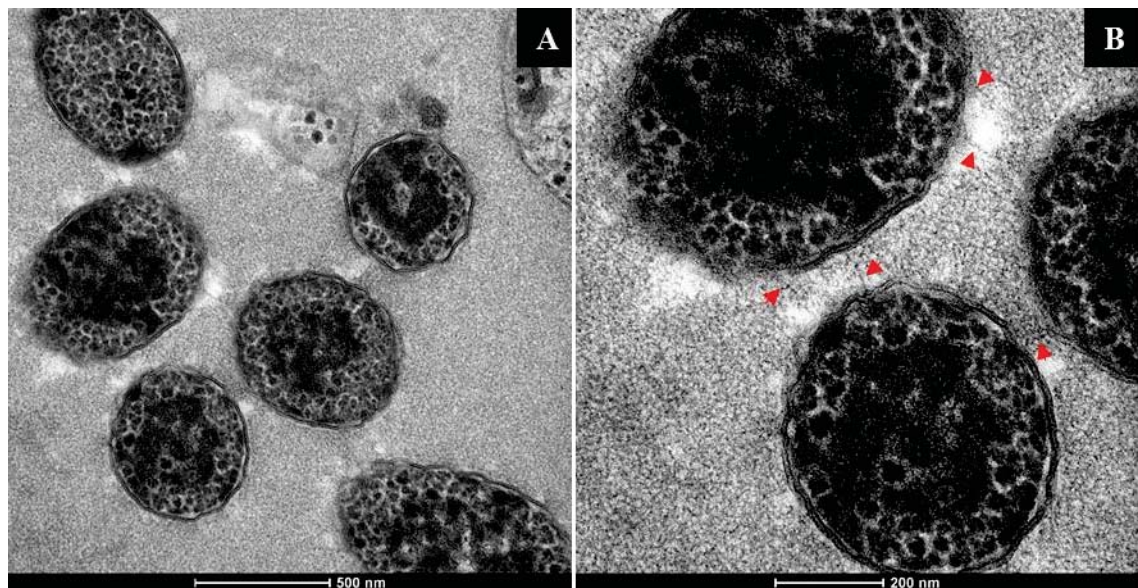


Figure 29. TEM images of isolate 133 after capsular extraction with 0.2% zwittergent. (A) Bacteria with either a heavily reduced and patchy capsule or complete lack of capsule. (B) Increased magnification makes appendages (indicated by red arrow heads) more visible.

3.2.3.4 Proteomics

To determine differences in protein expression between appendage producing isolate 133 grown on AIA media and appendage-lacking isolate 133 grown in AIB media, SDS-PAGE was used. Initially whole cell lysate was enzymatically prepared (section 2.7.2.2) before loading and running on an SDS gel (Figure 30).

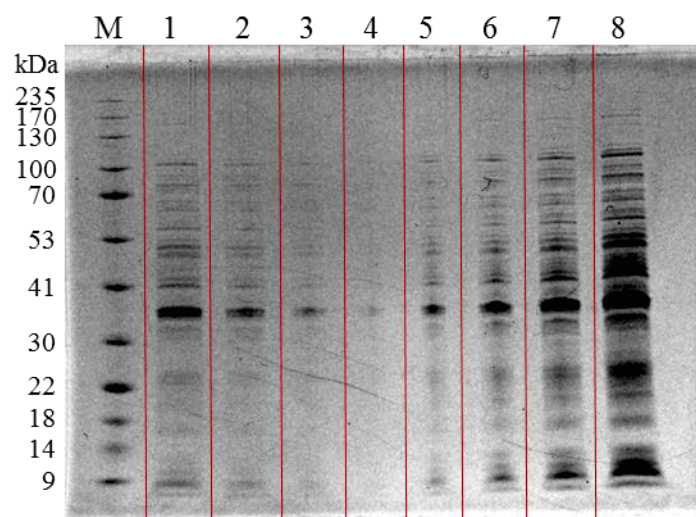


Figure 30. SDS gel of prepared whole cell lysate from isolate 133. Lanes (M) Molecular standard Gangnam stain. (1 – 4) 20, 10, 5, 2.5 μ L of loaded lysate from bacteria grown on solid media. (5 – 8) 2.5, 5, 10, 20 μ L of loaded lysate from bacteria grown in liquid media.

The whole envelope fragment and outer membrane fragment were prepared (section 2.7.4.2) and examined by SDS gel electrophoresis (Figure 31). This appeared to show a difference in protein pattern between solid and liquid media prepared bacteria at around the 22 kDa range.

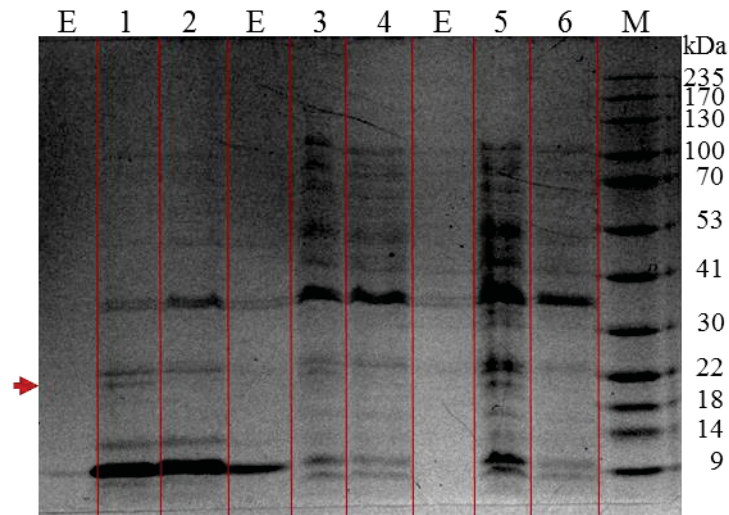


Figure 31. SDS gel of membrane fragments from isolate 133 reveals difference at ~22 kDa. Lanes (E) Empty. (M) Molecular standard Gangnam stain. (1) 0.9 mg/mL outer membrane fragment from solid media. (2) 0.9 mg/mL outer membrane fragment from liquid media. (3) 0.9 mg/mL whole envelope fragment from solid media. (4) 0.9 mg/mL whole envelope fragment from liquid media. (5) Neat whole envelope fragment from solid media. (6) Neat whole envelope fragment from liquid media.

Ultracentrifugation utilising mechanically disrupted cells (section 2.7.2.1) and glycerol gradients (section 2.7.4.1) was used to visualise and collect differences in density between liquid and solid cultivated bacteria (Figure 32).

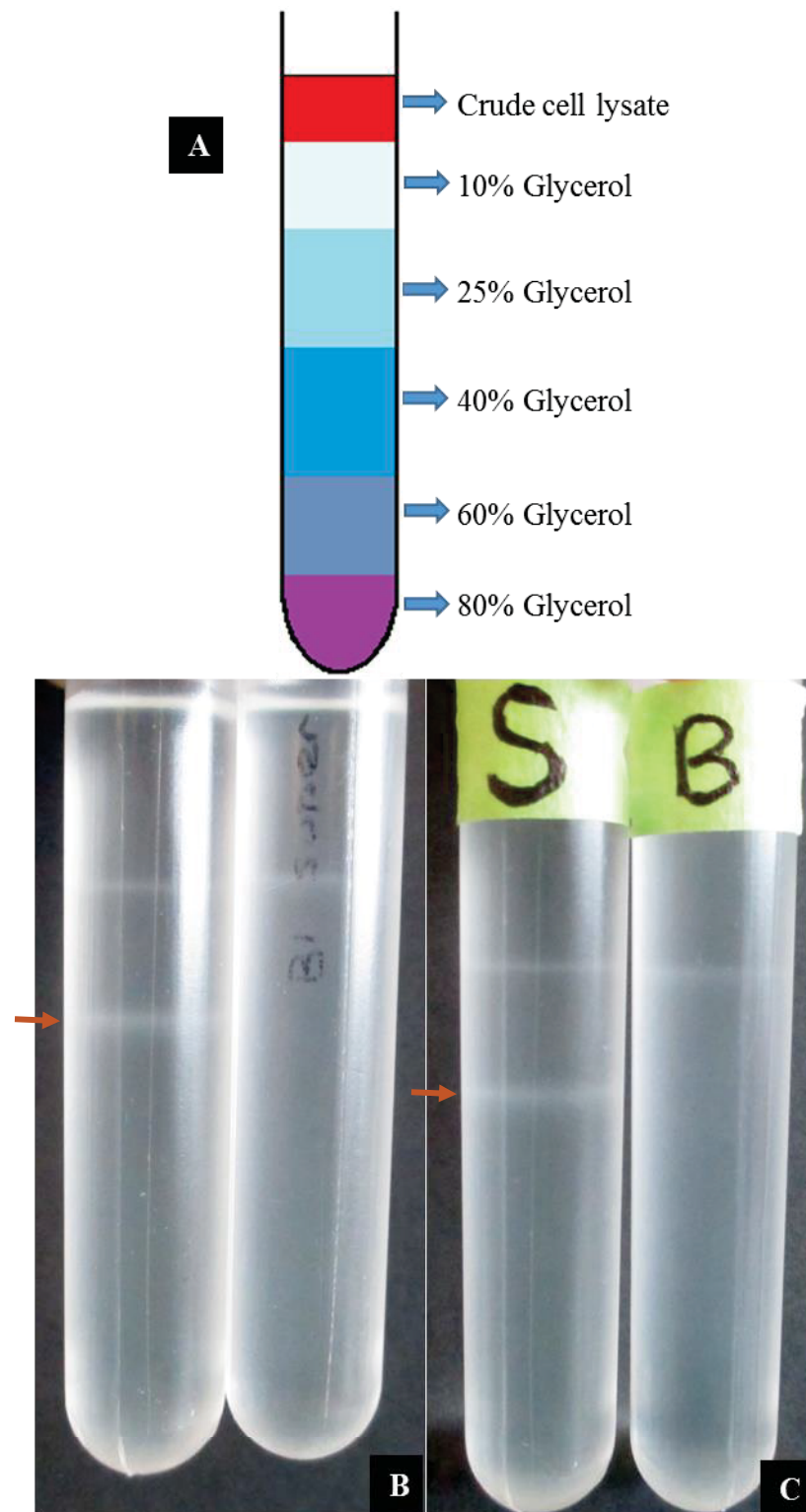


Figure 32. Density difference observed after ultracentrifugation for 20 hours. (A) Schematic representation of ultracentrifuge tube loading before run. (B) Extra high density band observed (arrow) in unmarked tube which was loaded with disrupted cells from solid media. (C) Duplicate of (B) with labelling where “S” is a solid media cell harvest and “B” is a liquid media cell harvest.

Enzymatic digestion of isolate 133 cells grown either on AIA or in AIB with trypsin (section 2.7.3) was carried out to assess if the appendage structures present could be removed and isolated. SEM imaging was utilised to assess digestion efficiency (Figures 33 and 34).

No difference is seen when viewing bacteria grown in AIB whether treated with trypsin or not. However there is a difference between the treated and untreated bacteria grown on AIA, and while not totally absent of appendages the trypsin treated bacteria are patchy while non-treated bacteria are heavily covered in appendages (Figures 33 and 34).

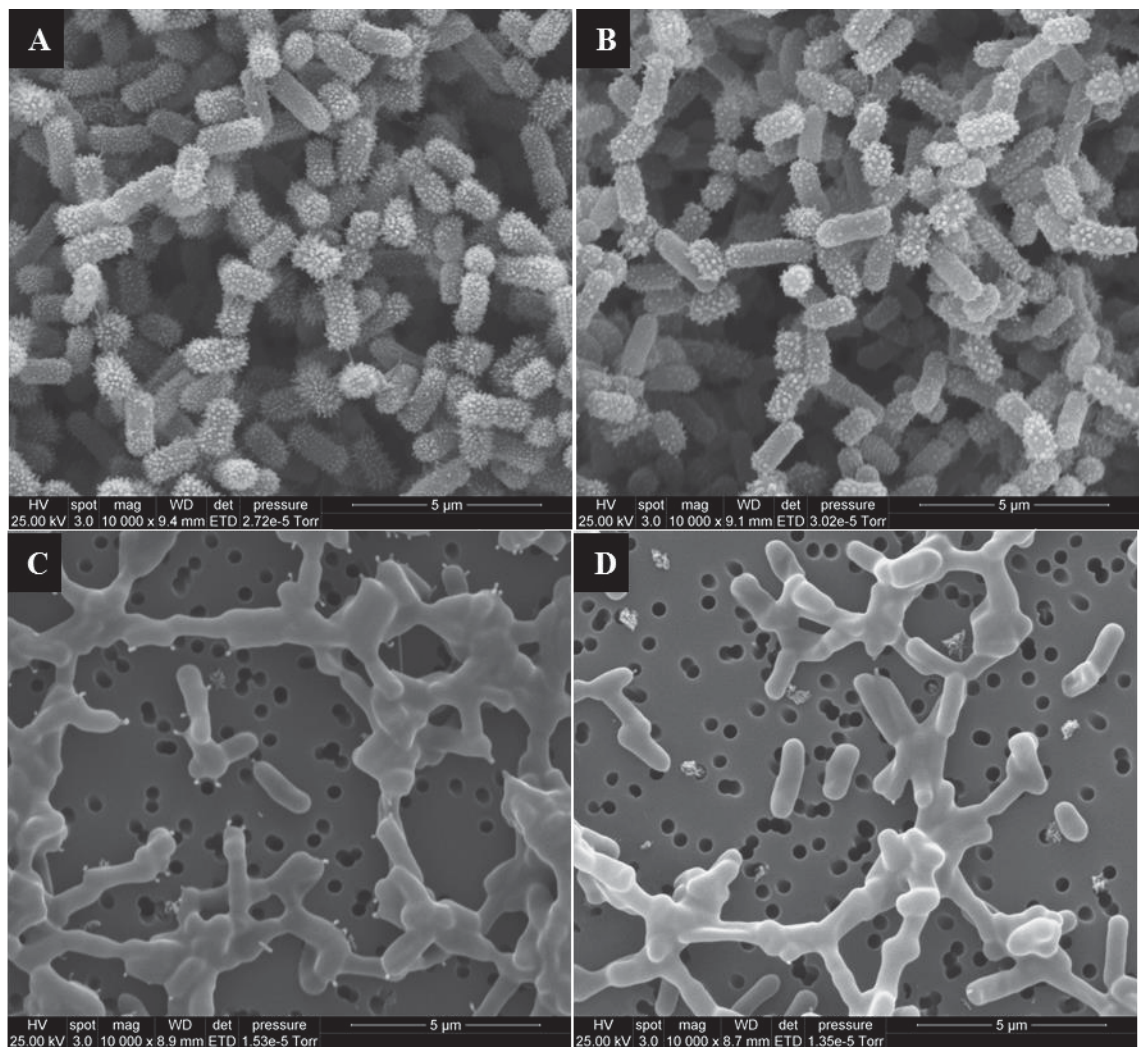


Figure 33. SEM images of isolate 133 before and after enzymatic digestion. (A) Untreated bacteria grown on AIA. (B) Trypsin treated bacteria grown on AIA. (C) Untreated bacteria grown in AIB. (D) Trypsin treated bacteria grown in AIB.

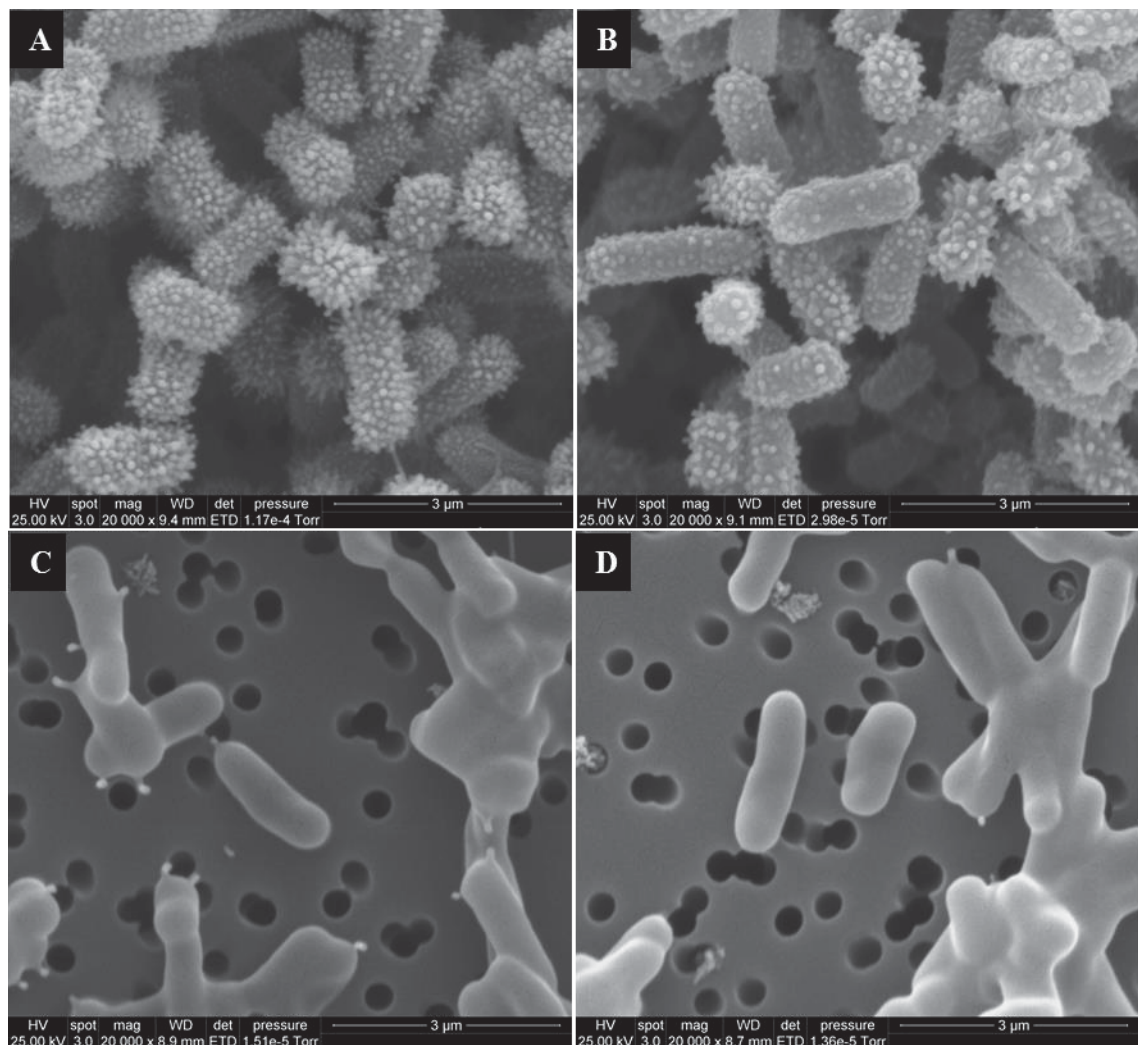


Figure 34. SEM images of isolate 133 before and after enzymatic digestion at increased magnification. (A) Untreated bacteria grown on AIA. (B) Trypsin treated bacteria grown on AIA. (C) Untreated bacteria grown in AIB. (D) Trypsin treated bacteria grown in AIB.

3.2.3.5 Biochemical testing

Utilising commercial biochemical test kits (section 2.11.3) isolate 133 was compared to the reference strains obtained from DSMZ (the German collection of microorganisms and cell cultures). The results revealed differences in substrate utilisation between isolate 133 and the reference strains *R. ornithinolytica* and *R. terrigena* (tables 19, and 20).

Table 19. *GnA+B-ID* reaction result comparison for isolate 133, *R. terrigena*, and *R. ornithinolytica*

Reaction	133	<i>R. terrigena</i>	<i>R. ornithinolytica</i>
Oxidase	-	-	-
Motility	-	-	-
Nitrate	+	-	+
Lysine	+	+	+
Ornithine	-	-	+
H ₂ S	-	-	-
Glucose	+	+	+
Mannitol	+	+	+
Xylose	+	+	+
ONPG	+	+	+
Indole	-	-	+
Urease	+	+	+
V.P.	-	-	+
Citrate	+	+	+
TDA	-	-	-
Gelatine	-	-	-
Malonate	+	+	+
Inositol	+	+	+
Sorbitol	+	+	+
Rhamnose	+	+	+
Sucrose	+	+	+
Lactose	-	-	-
Arabinose	+	+	+
Adonitol	+	+	+
Raffinose	+	+	+
Salicin	+	+	+
Arginine	+	-	-

Table 20. Isolate 133, *R. terrigena*, and *R. ornithinolytica* – BBL enteric/nonfermenter ID well reaction results comparison.

Well	A	B	C	D	E	F	G	H	I	J
133										
4	+	+	+	+	+	+	+	+	+	+
2	-	+	+	-	+	+	+	-	-	+
1	+	+	-	+	-	+	+	+	+	+
<i>R. ter</i>										
4	+	+	+	+	+	+	+	+	+	+
2	-	+	+	-	+	+	+	-	-	+
1	+	+	-	+	-	+	+	+	-	+
<i>R. orn</i>										
4	+	+	+	+	+	+	+	+	+	+
2	-	+	+	-	+	+	+	-	-	+
1	-	+	-	+	-	+	+	+	+	+

NB: Well reactions for the BBL crystal enteric/nonfermenter ID kits can be found in Appendix I.

Chapter 4: Discussion

4.1 Experimental approach

The sampling and culturing of microbes from the environment is important in both environmental monitoring and within industrial processes, where bioburden testing, sterilisation, contamination risk and monitoring are being constantly carried out to ensure the end products are sterile. Microbiological monitoring of waterways for drinking, bathing, and swimming, is highly important to monitor bacterial levels and ensuring that exposure to the water or food obtained from the water is safe. Each of these employ collection and culture methods to assess risk, and while this project is not about assessing risk it does employ the same principle.

The bioprospecting strategy of culturing and screening bacteria isolated from a soil sample, for the production of extracellular polymers, was effective with over 130 isolates showing the potential to be polymer producers. While only three isolates were selected for further analysis due to time constraints, the use of different solid media, and dilution plating of the sample prevented populous bacterial species from overgrowing other bacteria.

The use of a culture based method for bioprospecting bacterial species for polymers, or other potentially useful products is seen by some (Bull, Ward, & Goodfellow, 2000; Firn, Jones, Xue, & Zhang, 1998) as unreliable and approaches using meta-genomics, and genome mining are preferred. While others (Hoefel et al., 2006; Pham & Kim, 2012) utilise a culture based method and encourage the continual exploration and advancement of culture media, and technique to increase our knowledge and understanding of bacteria that meta-genomics and other culture-independent methods fail to answer.

The use of meta-genomics, and high throughput sequencing could have been utilised for uncovering a broader range of bacterial species from the diverse and heavily populated sample. Allowing quick screening for the production of extracellular polymers that traditional culture based techniques may fail to isolate. However by culturing bacteria and physically screening for polymer production it becomes possible to immediately select isolates which have potential and only select those for further analysis. Issues surrounding a meta-genomics approach include: That while known gene clusters may be present within the data, there may be other modifiers that influence the gene products that are

missed when looking for specifics. While bacteria may produce a polymer, other bacteria may have different genes for that same polymer. The paper by Valla, Ertesvåg, Tonouchi, and Fjærvik (2009) outlines the different genes involved in the synthesis of bacterial cellulose, with some bacteria sharing similar genes and others with completely different genes. Another issue is that databases are not complete and if indeed a novel polymer or compound is produced it may not be annotated within the database, leading to it being overlooked. The meta-genomics approach also means having to engineer bacteria or construct plasmids to encode your genes of interest.

In contrast, culturing bacteria and screening allows you to establish if bacteria produce a polymer, allows for the isolation, and identification of that polymer even if it is novel, and represents the naturally produced form of that polymer. Once the polymer is isolated, you also have access to the bacteria and can manipulate the bacteria to affect the polymers composition and/or production.

4.2 Bacterial identification and characterisation

Genetic sequencing of the 16S *rRNA* encoding gene is a widely-accepted method for determining bacterial identity, however the 16S *rRNA* encoding gene alone is not enough to give a definitive identity at species level but is useful for identifying bacteria to at least genus level, and can provide a lead to other genes to sequence for an accurate identification. The bacteria isolated in this study had their 16S *rRNA* encoding gene sequenced after amplification with PCR using universal primers.

Universal primers amplify the specific sequence they are designed to amplify no matter the sample, and so one must be extremely careful that contamination doesn't occur during preparation of the PCR reaction, or there is a risk of amplifying the wrong product. To reduce the possibility of contamination, isolated colonies of the bacteria to be identified were selected and a negative control which contained no DNA was included in the PCR step. If a band was observed on the resolving gel after PCR amplification, all of the amplified products were disposed of and an investigation as to the contamination source was carried out.

Sequencing PCR amplicons carries problems as the polymerase may lack proof reading capability and can incorporate the incorrect nucleotide into the extending sequence, miss a nucleotide or add additional nucleotides particularly in heavily repeated regions, resulting in an erroneous sequence. Errors may also be introduced by the sequencing

method, and some reads may be unclear, relying on reading the chromatic graphic results carefully and may still result in an incorrect base calling.

A more accurate and informative but costly method for bacterial identification is whole genome sequencing using next generation technologies such as MiSeq. The Illumina MiSeq platform was used to identify isolate 133. This technology is more accurate, because more reads span a region of the genome, which when assembled overlap each other, providing an extended sequence. The fact that every piece of DNA present gets amplified can cause issues with the end result being impure, and the method of library preparation can lead to information being lost if multiple samples are run.

Once the sequencing data is available it must be assembled. Assembly may lead to errors, especially when there are multiple regions of repeat DNA. However, software designers are continually improving the algorithms to increase the accuracy of assembly. The assembled DNA sequences are split into contigs depending on how well the DNA could be assembled. Ideally this results in a single contig representing the entire genome. A low L50 score that represents where 50% of contigs assemble to 50% of the sequence length and a high N50 score which represents the average length of all contigs that make up the L50 are desirable.

The contigs resulting from the sequencing of isolate 133, were compared to the NCBI database using BLAST, and this revealed that among the contigs of isolate 133 sequence there was contamination from eukaryotic and viral sources. The eukaryotic sequences were related to a range of families including *Hominidae*, *Hylobatidae*, *Physeteridae*, and *Plasmodiidae*, while the viral sequence was that of *PhiX* a virus commonly used as a control for next generation sequencing. This contamination raises questions about what the accepted level of contamination is when carrying out next generation sequencing, and although the sample sequenced in this case was bacterial and could be easily distinguished from the contaminating sequences, samples of eukaryotic origin may encounter issues with foreign sequences being included with their sequence.

The sequencing of isolate 133 using a paired end library preparation resulted in an incomplete genome assembly comprised of 41 contigs of bacterial DNA. Resequencing using a mate paired library preparation could be used for completion. From the sequencing data housekeeping genes from isolate 133 which had been identified to genus level as *Raoultella* could be aligned and compared to other known *Raoultella* sp. and

allowed for isolate 133 to be identified as *R. terrigena*. Although these housekeeping genes were identical to the reference genome *R. terrigena* there were differences in non-housekeeping genes. This and geographical separation of the isolate from the reference led to a new strain name being assigned to isolate 133 of NZ133 where NZ stands for the country of origin, New Zealand, and 133 being the isolates reference during the course of the investigation. The full identification of isolate 133 is therefore *Raoultella terrigena* strain NZ133.

Bacterial characterisation of *R. terrigena* NZ133 was carried out using commercial biochemical test kits and the reference organisms, *R. ornithinolytica* and *R. terrigena* for comparison. The biochemical test results revealed differences in substrate utilisation between the tested bacteria, however there were inconsistencies between kits and tests, with one kit testing positive for utilisation and the other testing negative, and repetition of tests with the same kit having varying results. The differences seen between kits could be due to differences in the principle used to test substrate utilisation. For example one kit may test anaerobic fermentation of a substrate where another kit tests aerobic utilisation. While both of these tests look at the utilisation of the same substrate, bacteria capable of only one form of utilisation will test negative to one kit.

An issue surrounding interpretation of results from colourimetric biochemical test kits is that unless an appropriate reader is available the results are open for interpretation and will vary depending on the person reading the colour change. This is particularly true if the difference in colour change between a positive and negative result is minor or ambiguous, for example between aqua and turquoise.

Other issues surrounding the use of biochemical test kits are the deterioration of reagents, and manual addition of reagents to kits. While some kits may avoid having to manually add additional reagents by having the correct concentration and composition already provided, these reagents deteriorate over time. The manual addition of additional reagents may not be consistent and if not provide with the kit are subject to batch variation. This can be overcome by using a carefully programmed fully automated system and frequent preparation of reagents to prevent deterioration. However this would be expensive and impractical when researching in the field environment.

Overall, miniaturised biochemical tests are useful for simple and quick biochemical analysis, and can provide a guide as to other biochemical tests to be carried out. They can

also be used to distinguish species of a genus based on substrate utilisation. This must be approached with some caution as bacteria within a species may test differently, as seen in *R. terrigena* NZ133 and the reference *R. terrigena*.

4.3 Polymer analysis

Although the method of extraction and analysis of extracellular polymer, has been used previously. The isopropanol precipitation step during the extraction process can be challenging when the extracellular polymer is of low molecular weight. When the polymer is high molecular weight it precipitates out of solution often forming a thick gel that can be easily separated. However, when the polymer is low molecular weight it precipitates out of solution as small flecks similar to desiccated coconut, and does not form a gel, requiring extra steps to collect the precipitate which can lead to some loss of sample. There is also a risk when dialysing low molecular weight polymer, as the dialysis tubing cut off can be too large and the sample will be lost to the dialysate, and may be unrecoverable. Extracellular polymer production can be enhanced by storing a culture at 4°C allowing for greater amounts to be harvested at the expense of increased time delay. Theory suggests that storing the culture at low temperatures causes a shift away from substrate utilisation for growth and replication, towards utilising the substrate for polymer production.

The information gained from polymer analysis can vary depending on the method used. In this experiment isolate X was stored at 4°C before harvesting the polymer and assayed using the anthrone assay which results in a percentage glucose equivalence. The anthrone assay is a colourimetric assay that tests the reducing potential of known glucose concentrations, and represents the amount of free polysaccharides the unknown contains. Because complex polysaccharide chains are less susceptible to reduction only polysaccharide moieties that are loosely associated or open to reaction will cause a colour change resulting in an estimate of glucose equivalence. As there is no structural or chemical analysis of the polymer the only information that can be gained from this method is that the polymer is comprised of polysaccharide units, however the exact composition of polysaccharides is unknown.

The polymer extracted from isolate 133, was purified and sent to collaborators in Germany for analysis. The results for the analysis were not available at the time of submission. While having an analytical report would have been advantageous in knowing

the polymers composition and identity, there is a cluster of cellulose biosynthesis genes present in the genomic data, and this suggests the polymer is likely bacterial cellulose. Even with a cluster of biosynthetic genes present there may be side chain modifications present on the polymer which would only be detected through the analysis of the polymer.

4.4 Appendages and proteomic approach

During the course of SEM imaging the bacterial isolates, isolate 133 appeared to have appendage-like structures extending outwards from the surface of the bacteria. These structures were novel and extensive searches of literature and images of other bacteria failed to yield a result as to what they were. TEM imaging confirmed that these appendage structures were associated with but not anchored to the outer membrane of the bacteria, and there was no evidence of extension or anchoring of the structures beyond the outer membrane. Comparison of known structures produced by bacteria, including pili, fimbriae, flagella, and type IV secretion systems to the appendages of isolate 133 revealed little similarity.

The appendages of isolate 133 vary in length and can be over 1 micron long and around 5 – 6 nm thick, and are extremely straight; the samples viewed by TEM are generally between 90 – 100 nm thick, so even small amounts of curvature result in an uneven appearance. The appendages also branch and split at the ends multiple times into Y-shaped structures with each split approximately halving the thread thickness. These appendages appear thicker near the outer membrane of the bacteria with a triangular form as the base from which thinner strands extend, and are present around the entire surface of the bacteria, but only when cultured on solid AIA media.

Flagella tend to be curved and often appear unevenly when viewed by TEM. They are also either in a polar, peritrichous, or amphitrichous orientation, and associated with motility especially in liquid media and are attached to the cell *via* an intramembranous motor. Because *Raoultella* sp. are non-motile bacteria, and do not produce flagella, as well as the fact the appendages only appear on a single type of solid media suggests it is improbable the appendages are flagella.

Pili can be extremely long, and straight, and include sex pilus capable of connecting two bacteria together; however, sex pili are generally thick and only produced at less than 10 per bacterium. Type IV pili are associated with twitching motility, but are incorporated in the outer membrane. Although there are genes encoding type IV pili, present in the

genome of isolate 133, the numerous appendages extending from isolate 133 and their ability to branch suggest the appendages are not pili or type IV pili.

Fimbriae are extensively produced around the surface of bacteria and present in extremely large numbers (>200), and are associated with bacterial adhesion. However, they are much shorter and thinner than pili and often difficult to visualise clearly in TEM and SEM imaging. Because the appendages present on isolate 133 are clearly visible in both SEM and TEM, and their length this suggests that they are not fimbriae.

Although appendages were visualised only when grown on AIA media, attempts to visualise a difference in banding pattern on SDS-PAGE gel between whole cell lysate, outer membrane fractions (OMF) and whole envelope fractions (WEF) between isolate 133 samples cultured in liquid media and on AIA were unsuccessful. A difference in banding pattern between liquid culture and solid culture appeared once, however it was not repeatable. Ultracentrifugation of WEF from AIA and liquid cultures, using glycerol gradients to separate differences in density showed that WEF prepared from AIA contained an extra density that was not present in broth preparations. However, extraction of this extra density proved difficult, and further repetitions with increased sample input yielded the same result. Although the extra density appeared to change position between samples. To investigate further, freshly prepared and frozen samples of WEF extracted from both AIA and liquid media were ultracentrifuged simultaneously. The results showed an extra density present in only the solid WEF from frozen and not in either broth extracts nor the freshly prepared WEF from AIA. As a result, I concluded that the extra density band was an artefact of the freezing process.

Although the attempts to isolate the appendages failed, the mode of investigating the appendages as proteinaceous is supported by several experiments and electron microscopy imaging. (i) TEM imaging utilising protein specific staining, resulted in the appendages and threads appearing electron dense; (ii) the presence of the appendage threads after treatment and removal of the capsule surrounding the bacteria; and (iii) reduction and removal of appendages from the surface of cells from AIA treated with trypsin compared to the same cells without the addition of trypsin.

The appendages produced by isolate 133 appear to have many unique characteristics that have not been observed in extracellular structures previously. These include the production of appendages solely on a single media type, the ability of the appendage

threads to extend large distances, while remaining incredibly straight, and having the ability to fray much like rope, splitting into thinner threads. Being able to connect between bacteria, and always connecting *via* the appendage base, and being membrane associated but having no clear membrane anchoring point.

The ability for the appendages to fray and almost perfectly halving in thickness suggests they are comprised of many filaments wound together to form a strong thread. These filaments also appear to be capable of connecting multiple appendage bases even after splitting. The purpose of connecting to each other remains unclear. However, I suggest that this could be for several reasons. Including that these threads are hollow and capable of transporting small molecules between the bacteria, much like a sex pilus, as well as for transporting externally produced materials, like extracellular polymer along the outside of the threads much like a pulley type clothes line and or used for structural support of the bacterial colony.

Alternately these threads could be a super highway for information exchange, and would certainly be useful in the environment where other organisms are producing extracellular signals which may affect the isolates' ability to quorum sense. By having a secure line as such, members of the community linked by these appendages, could exchange information rapidly *via* numerous linkages, at an exponential rate. Thus allowing all members of the community to respond simultaneously without the need to produce large amounts of signal peptides. This may be advantageous as it allows the connected bacteria to respond to the environmental situation, preventing competing bacteria from detecting the response, and allowing the quorum sensing regions of the connected bacteria to detect signals being sent by the surrounding bacterial community.

These appendages may also be an effective transport system for ferrying nutrients from nutrient dense regions of the colony into nutrient poor regions of the community such as the core. They may increase the surface area of the bacteria without compromising cellular integrity allowing for greater adsorption of nutrients, or for ferrying toxic compounds out of vital regions of the community.

Another possible explanation for the appendages is in microbial warfare, with these appendages being thrust into the surrounding environment where bacteria not producing the appendages have their membrane pierced causing them to lyse, and then having the spilled nutrients, DNA, etc. absorbed for use by the appendaged community.

Each of the possible explanations would provide an advantage to the bacteria producing the appendages, and could suggest why these appendages are only produced under certain circumstances where it is advantageous for the bacteria.

4.5 Future work

Future work to complete this project would include

- Sequencing of isolates X and 134 to determine species.
- A mate-paired library preparation of *Raoultella terrigena* NZ133 to obtain a complete genome sequence.
- Production, purification, and analysis of extracellular polymer from isolates X and 134, similar to that done for isolate 133.
- Extraction and identification of the capsule produced by isolate 133.
- Isolation, purification, and identification of the appendages produced by isolate 133 (particularly reattempting the trypsin digestion).

4.6 Final thoughts

The objective of this project was originally to bio-prospect soil-borne bacteria for novel extracellular polymers. While this wasn't achieved as such, a potentially novel outer membrane-associated structure was discovered which can lead to further exploration in the field of microbiology. This work also contributes to the body of scientific knowledge by providing another set of whole genome sequencing data relating to *R. terrigena*. As well as raising many questions regarding the purpose of the appendages produced by *R. terrigena* NZ133, what they are comprised of, and what potential information that could provide regarding bacterial interactions.

Appendix I: BBL Reagents

This Appendix contains the biochemical reagent reactions for the BBL crystal enteric/nonfermenter kits (section 3.2.3.5).

Well	Well code	Reaction ingredient
4A	ARA	Arabinose
4B	MNS	Mannose
4C	SUC	Sucrose
4D	MEL	Melibiose
4E	RHA	Rhamnose
4F	SOR	Sorbitol
4G	MNT	Mannitol
4H	ADO	Adonitol
4I	GAL	Galactose
4J	INO	Inositol
2A	PHO	p-n-p-phosphate
2B	BGL	p-n-p α - β -glucoside
2C	NPG	p-n-p- β -galactoside
2D	PRO	Proline nitroanilide
2E	BPH	p-n-p bis-phosphate
2F	BXY	p-n-p-xyloside
2G	AAR	p-n-p- α -arabinoside
2H	PHC	p-n-p-phosphorylcholine
2I	GLR	p-n-p- β -glucuronide
2J	NAG	p-n-p-N-acetyl glucosaminide
1A	GGL	γ -L-glutamyl p-nitroanilide
1B	ESC	Esculin
1C	PHE	p-nitro-DL-phenylalanine
1D	URE	Urea
1E	GLY	Glycine
1F	CIT	Citrate
1G	MLO	Maloric acid
1H	TTC	Triphenyl tetrazolium chloride
1I	ARG	Arginine
1J	LYS	Lysine

Appendix II: QUASt Report

This appendix contains the QUASt report generated for the whole genome sequencing of isolate 133 – *Raoultella* sp. (Note: contig and node are used interchangeably)

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs.)

Statistics without reference	scaffolds
# contigs	56
# contigs (≥ 0 bp)	193
# contigs (≥ 1000 bp)	40
# contigs (≥ 5000 bp)	28
# contigs (≥ 10000 bp)	26
# contigs (≥ 25000 bp)	26
# contigs (≥ 50000 bp)	19
Largest contig	1,452,774
Total length	5,832,040
Total length (≥ 0 bp)	5,885,978
Total length (≥ 1000 bp)	5,821,607
Total length (≥ 5000 bp)	5,795,765
Total length (≥ 10000 bp)	5,783,025
Total length (≥ 25000 bp)	5,783,025
Total length (≥ 50000 bp)	5,535,337
N50	362,189
N75	216,584
L50	5
L75	10
GC (%)	57.44
Mismatches	
# N's	159
# N's per 100 kbp	2.73

Statistics without reference scaffolds

Predicted genes

# predicted genes (unique)	5460
# predicted genes (≥ 0 bp)	5462
# predicted genes (≥ 300 bp)	4887
# predicted genes (≥ 1500 bp)	693
# predicted genes (≥ 3000 bp)	62

N50/75 is the length for which the collection of all contigs of that length or longer covers at least 50/75% of an assembly.

L50/75 is the number of contigs equal to or longer than N50/75. L50, for example, is the minimal number of contigs that cover 50% of the assembly.

N's are the number of uncalled bases in the assembly

Appendix III: Circos Plots

This Appendix contains individual circos plots for the first 25 nodes. Genes and nucleotide identities can be either of *Raoultella* sp. (green), bacterial (non-*Raoultella*) (pink), uncharacterised (black), or eukaryotic (orange) in origin. (Refer to page 48 Figure 23 for how to read circos plot information)

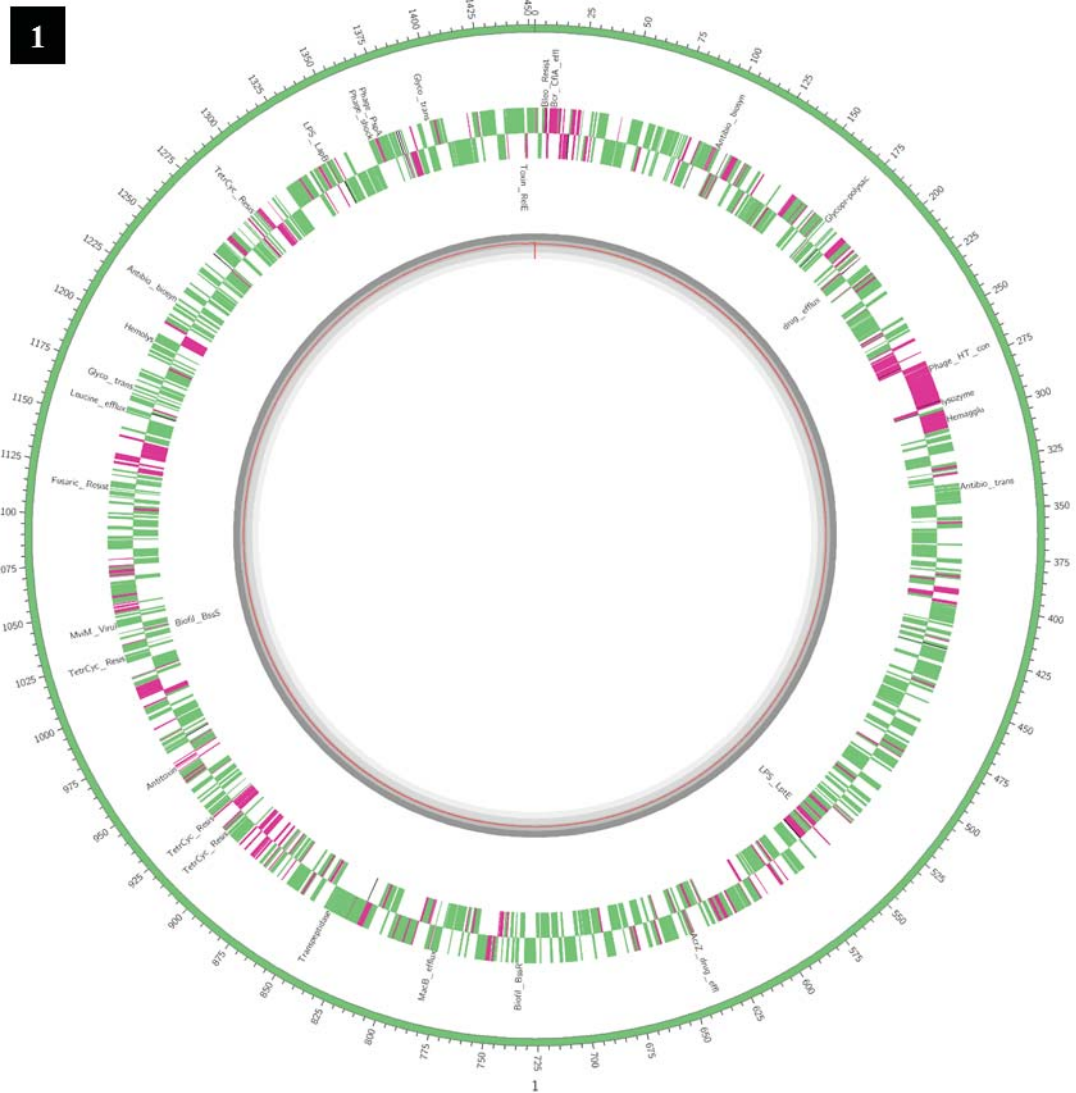


Figure 35. Individual circos plot of node 1. The nucleotide identity is that of *Raoultella* (green). There are very few non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin with a few uncharacterised genes (black). The tagged genes are mostly associated with resistance and virulence factors. Node ratio 1:1000 (1 = 1000 bps).



Figure 36. Individual circos plot of node 2. The nucleotide identity is that of *Raoultella* (green). There are many scattered small non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin with a few uncharacterised genes (black). The tagged genes are mostly associated with resistance, virulence factors and type IV secretion. There are several clusters that identify with other bacteria. Node ratio 1:1000 (1 = 1000 bps).

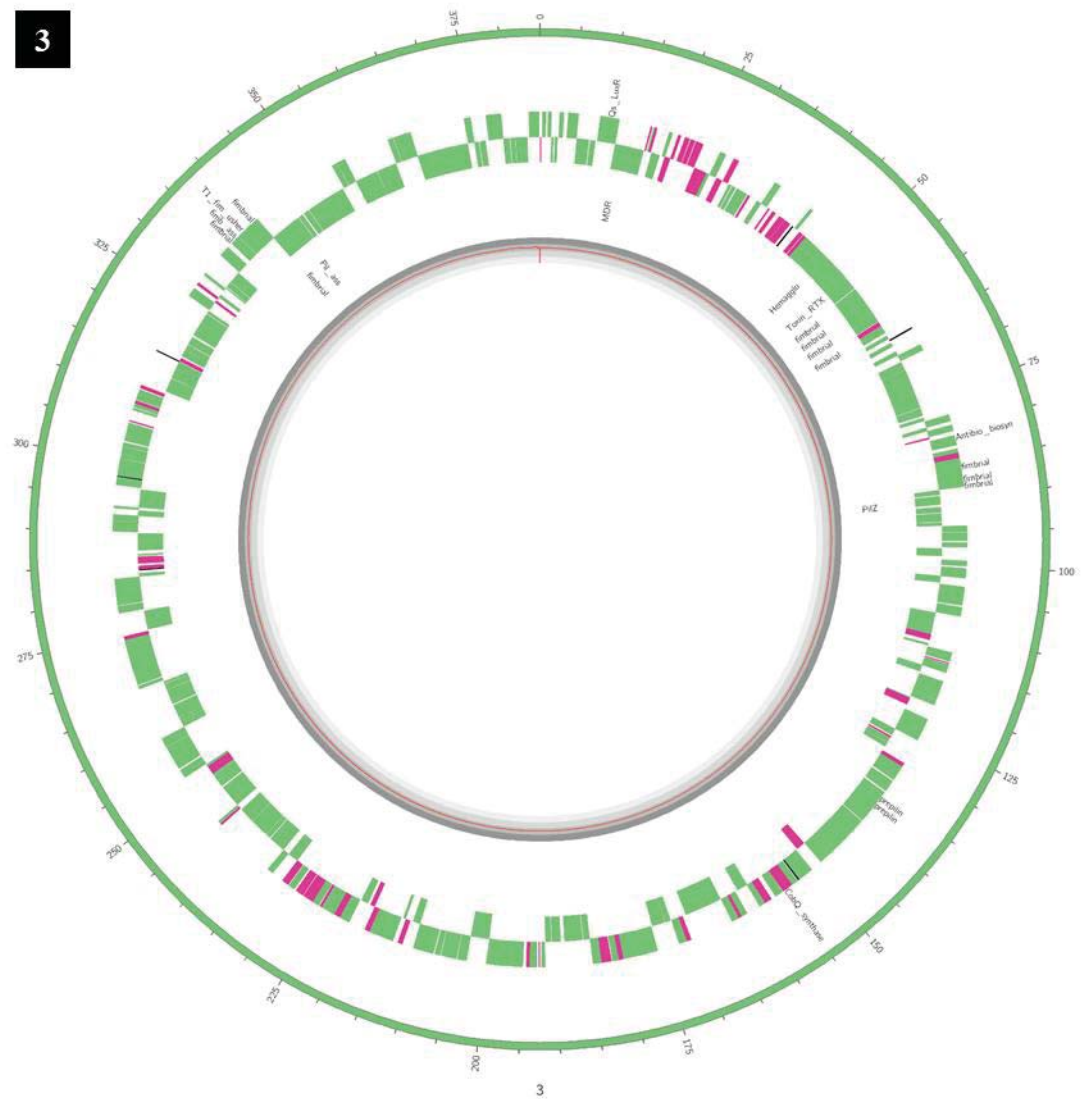
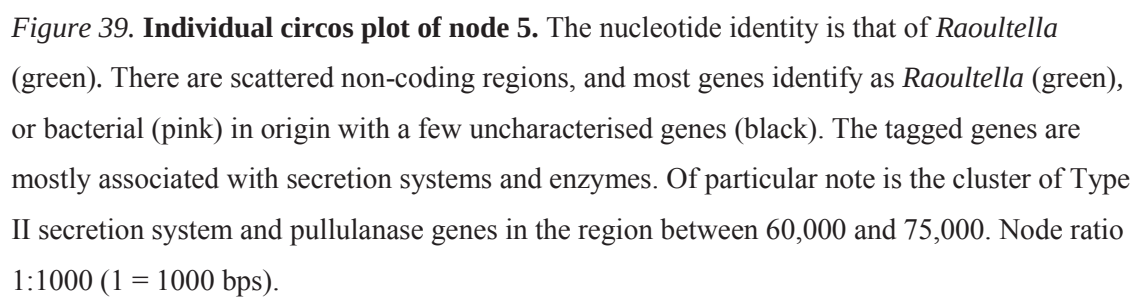


Figure 37. Individual circos plot of node 3. The nucleotide identity is that of *Raoultella* (green). There are scattered small non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin with a few uncharacterised genes (black). The tagged genes are mostly associated with pili and fimbrial assembly. Node ratio 1:1000 (1 = 1000 bps).



ratio 1:1000 (1 = 1000 bps).



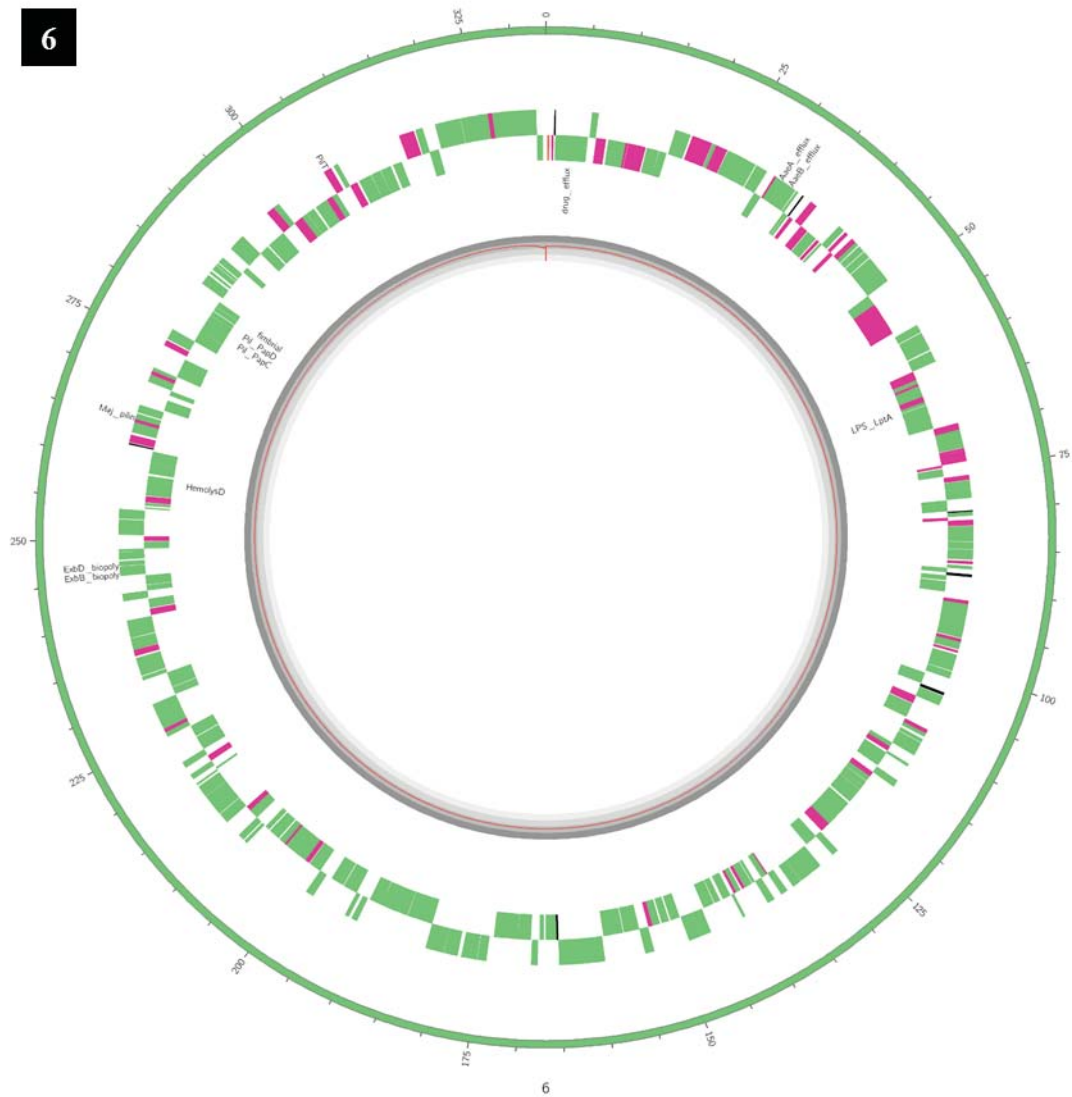


Figure 40. Individual circos plot of node 6. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin with a few uncharacterised genes (black), and a single gene of eukaryotic (orange) origin. The tagged genes are mostly associated with efflux and pili. Node ratio 1:1000 (1 = 1000 bps).

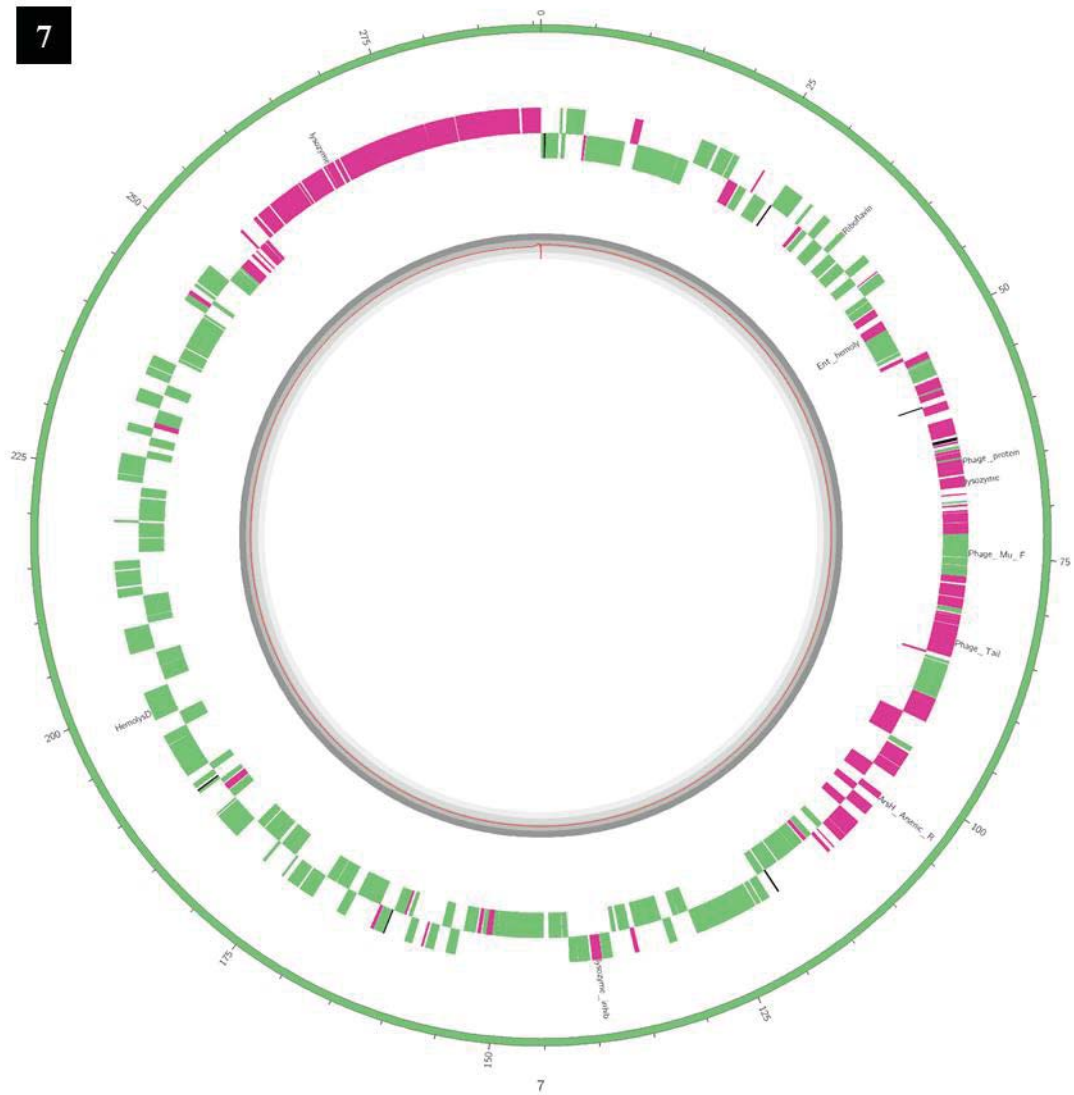


Figure 41. Individual circos plot of node 7. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin with a few uncharacterised genes (black). The tagged genes are mostly associated with phage, and enzymes. There are multiple clusters of bacterial (pink) origin. Node ratio 1:1000 (1 = 1000 bps).

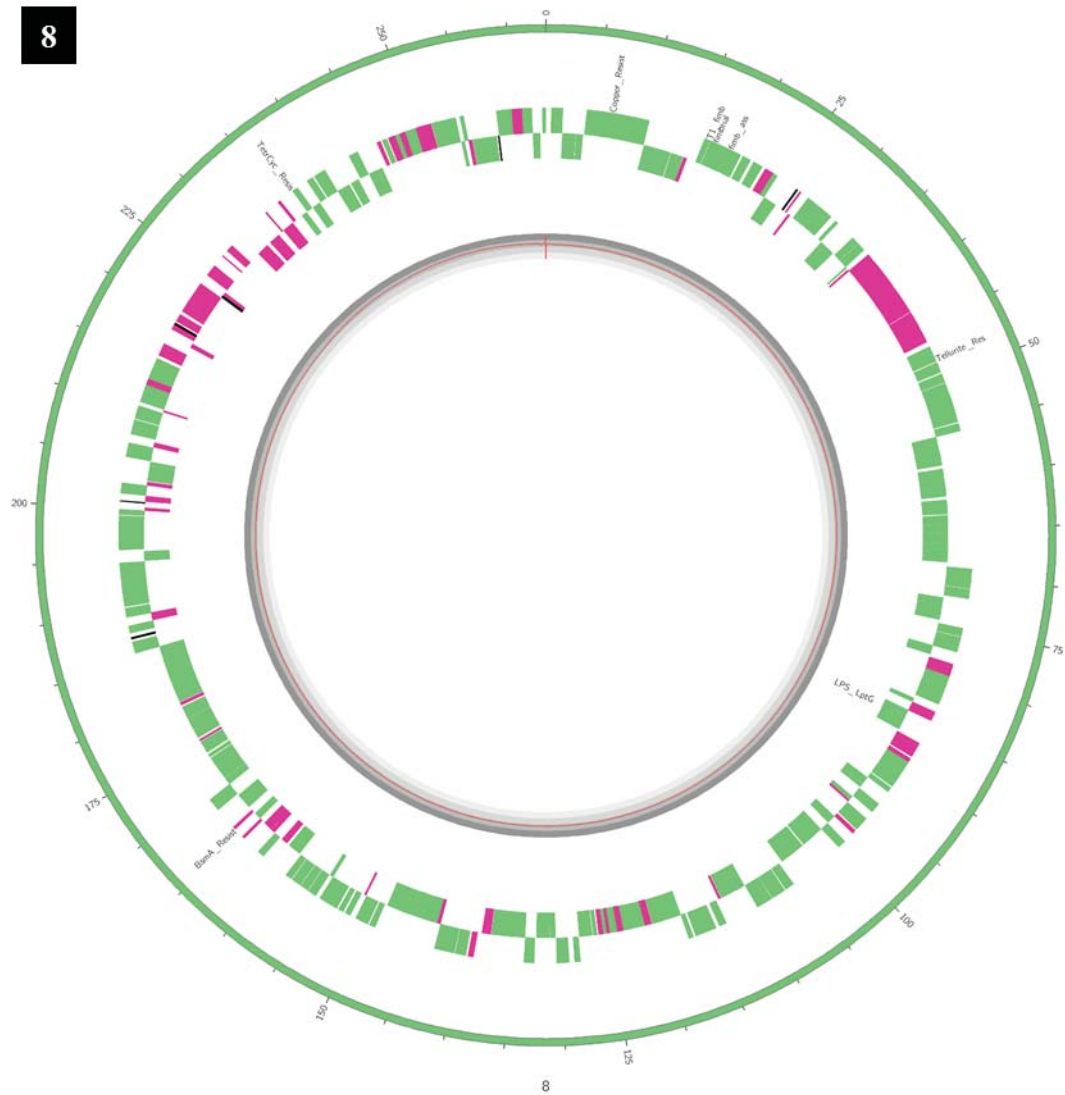


Figure 42. Individual circos plot of node 8. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin with a few uncharacterised genes (black). The tagged genes are mostly associated with fimbriae, and resistance. Node ratio 1:1000 (1 = 1000 bps).

9

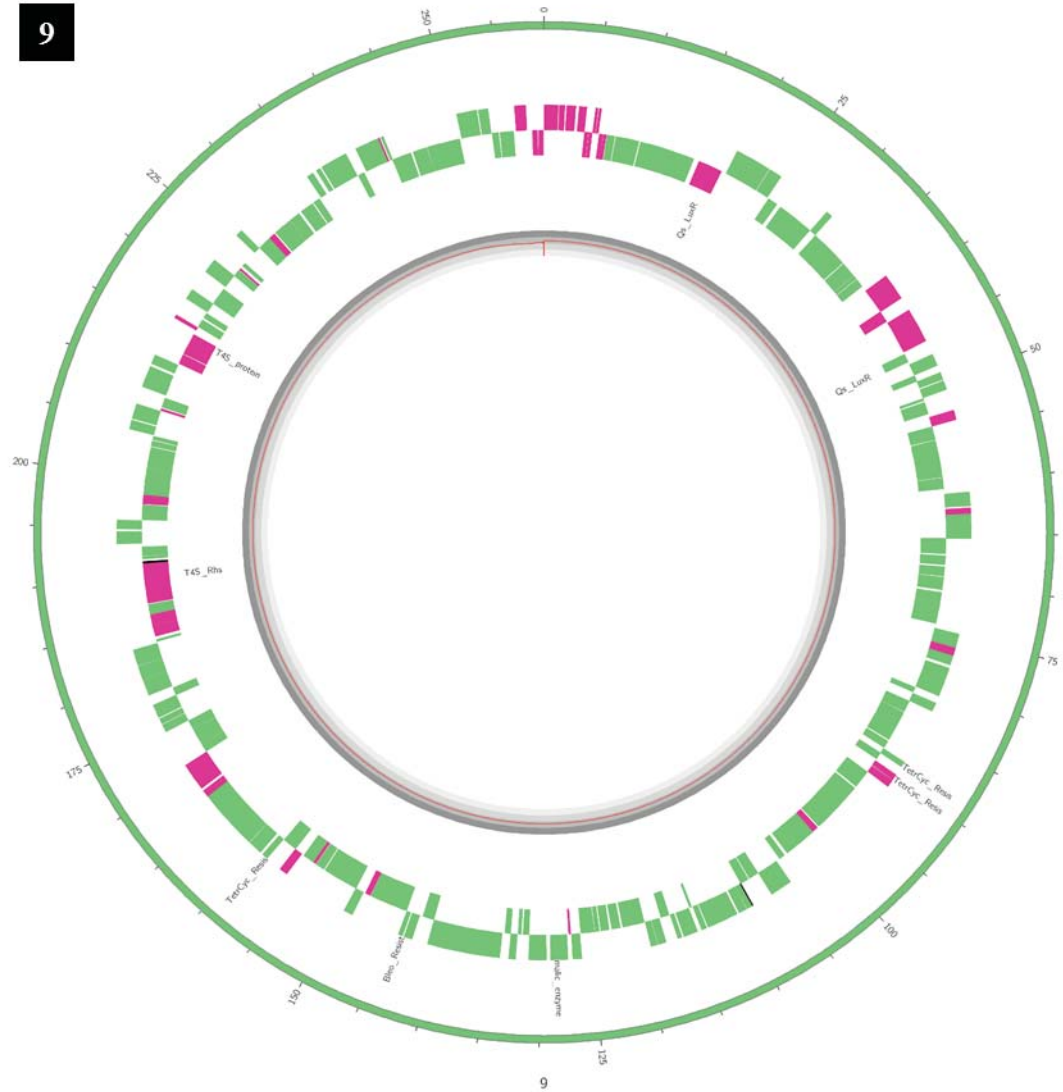


Figure 43. Individual circos plot of node 9. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin with a few uncharacterised genes (black). The tagged genes are mostly associated with quorum sensing, and resistance. Node ratio 1:1000 (1 = 1000 bps).

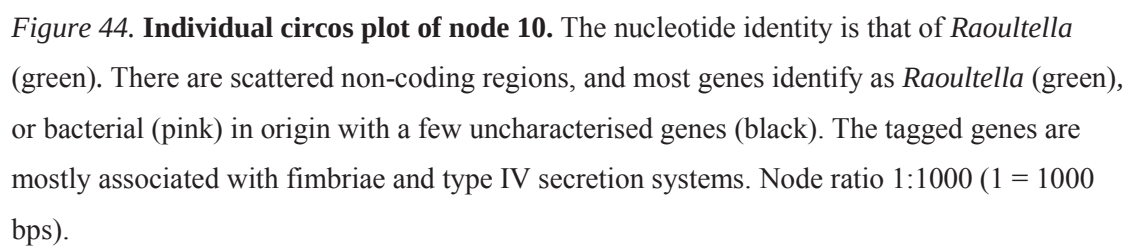




Figure 45. Individual circos plot of node 11. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin with a few uncharacterised genes (black). The tagged genes are mostly associated with resistance and virulence. Node ratio 1:1000 (1 = 1000 bps).

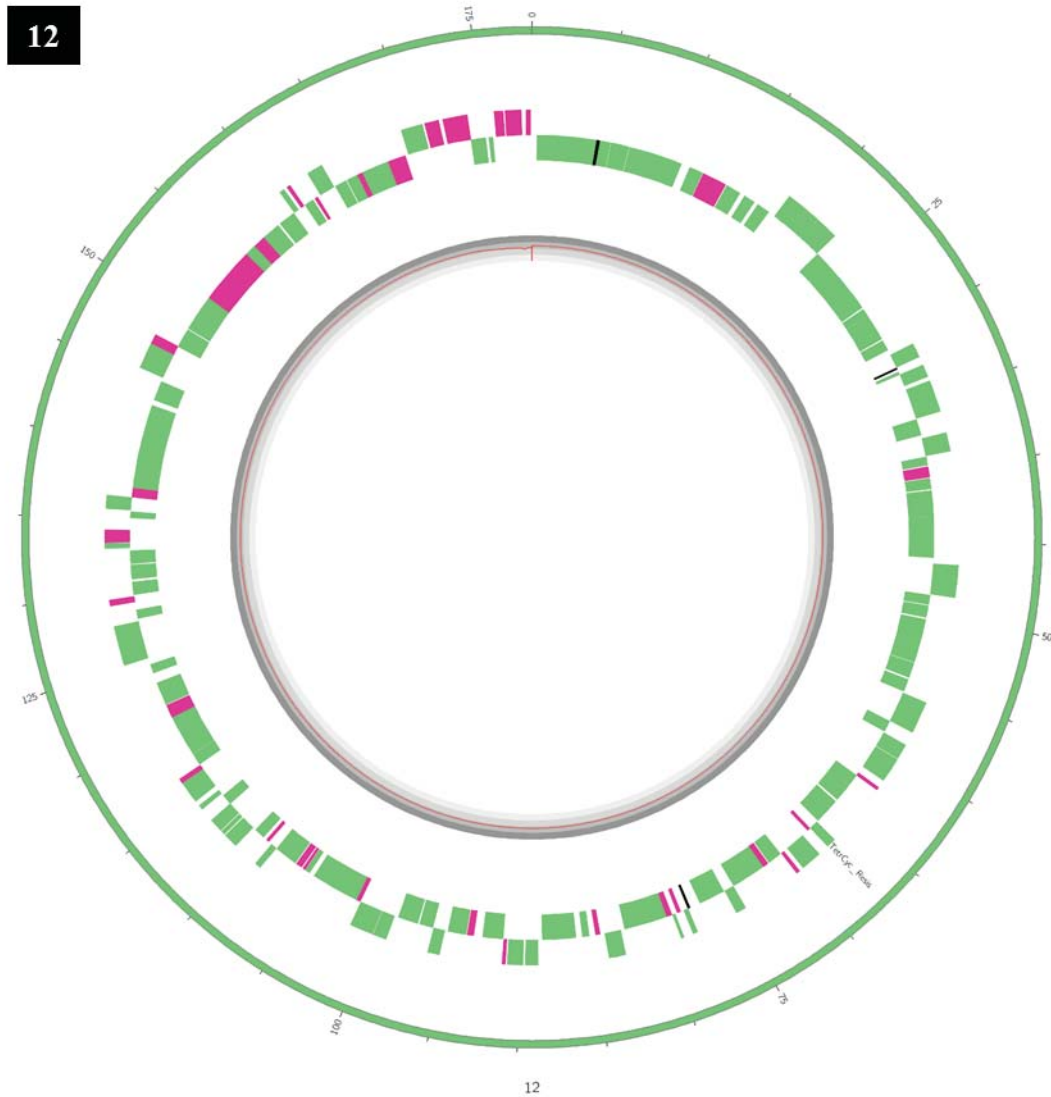


Figure 46. Individual circos plot of node 12. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin with a few uncharacterised genes (black). The tagged gene is associated with resistance. Node ratio 1:1000 (1 = 1000 bps).

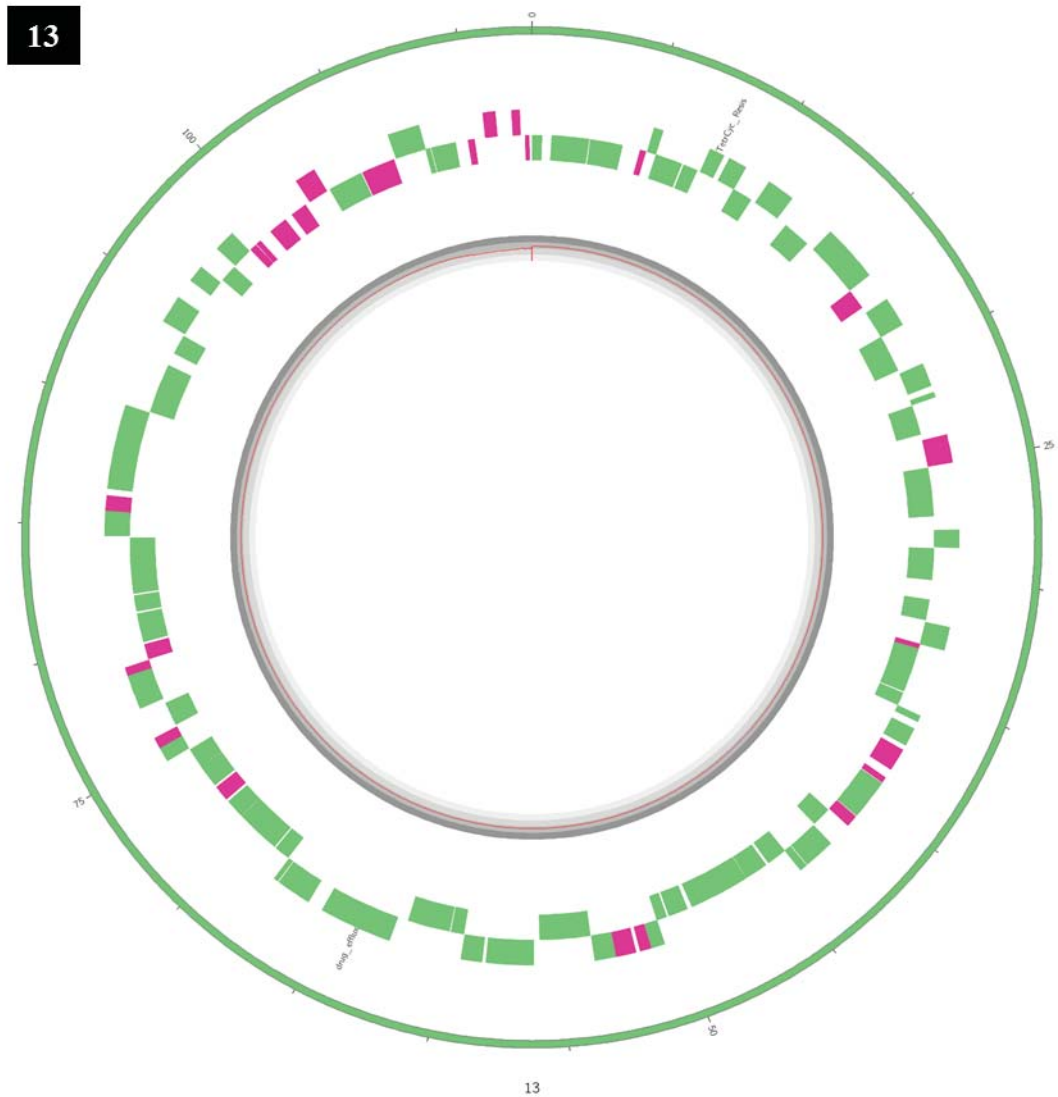


Figure 47. Individual circos plot of node 13. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin. The tagged genes are associated with resistance. Node ratio 1:1000 (1 = 1000 bps).

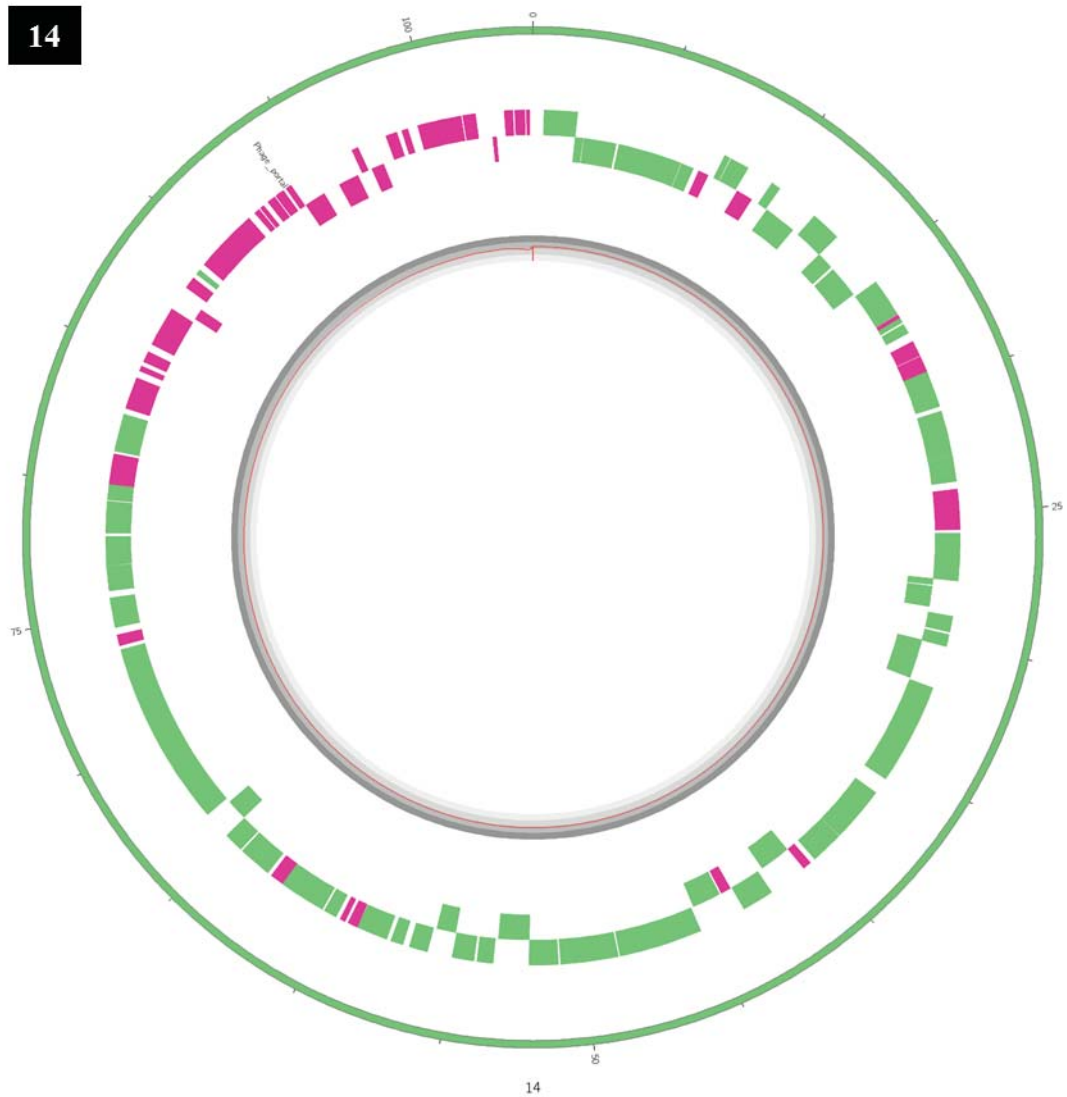


Figure 48. Individual circos plot of node 14. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin. The tagged gene is associated with phage. Node ratio 1:1000 (1 = 1000 bps).

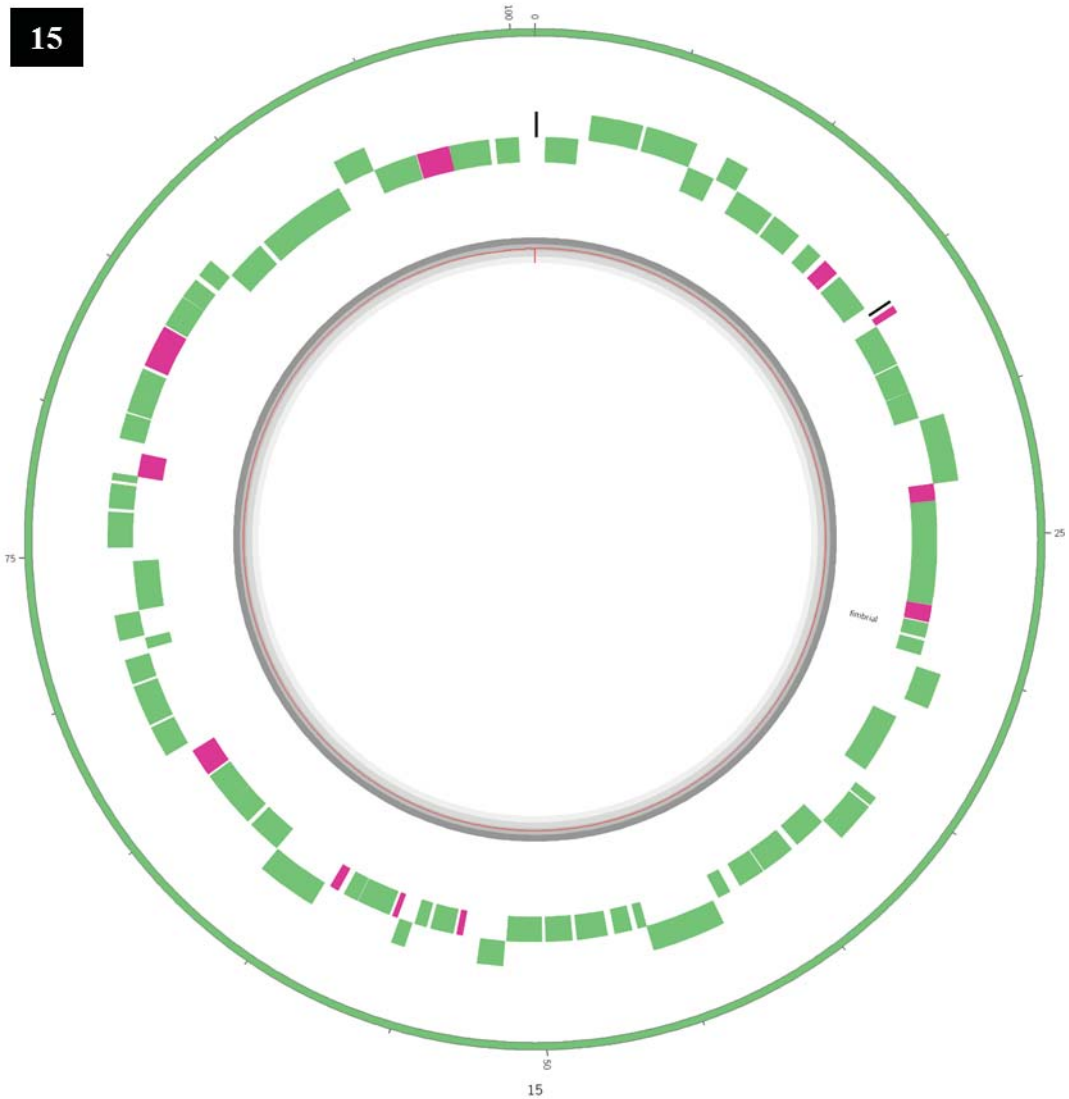


Figure 49. Individual circos plot of node 15. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin with a few uncharacterised genes (black). The tagged gene is associated with fimbriae. Node ratio 1:1000 (1 = 1000 bps).

16

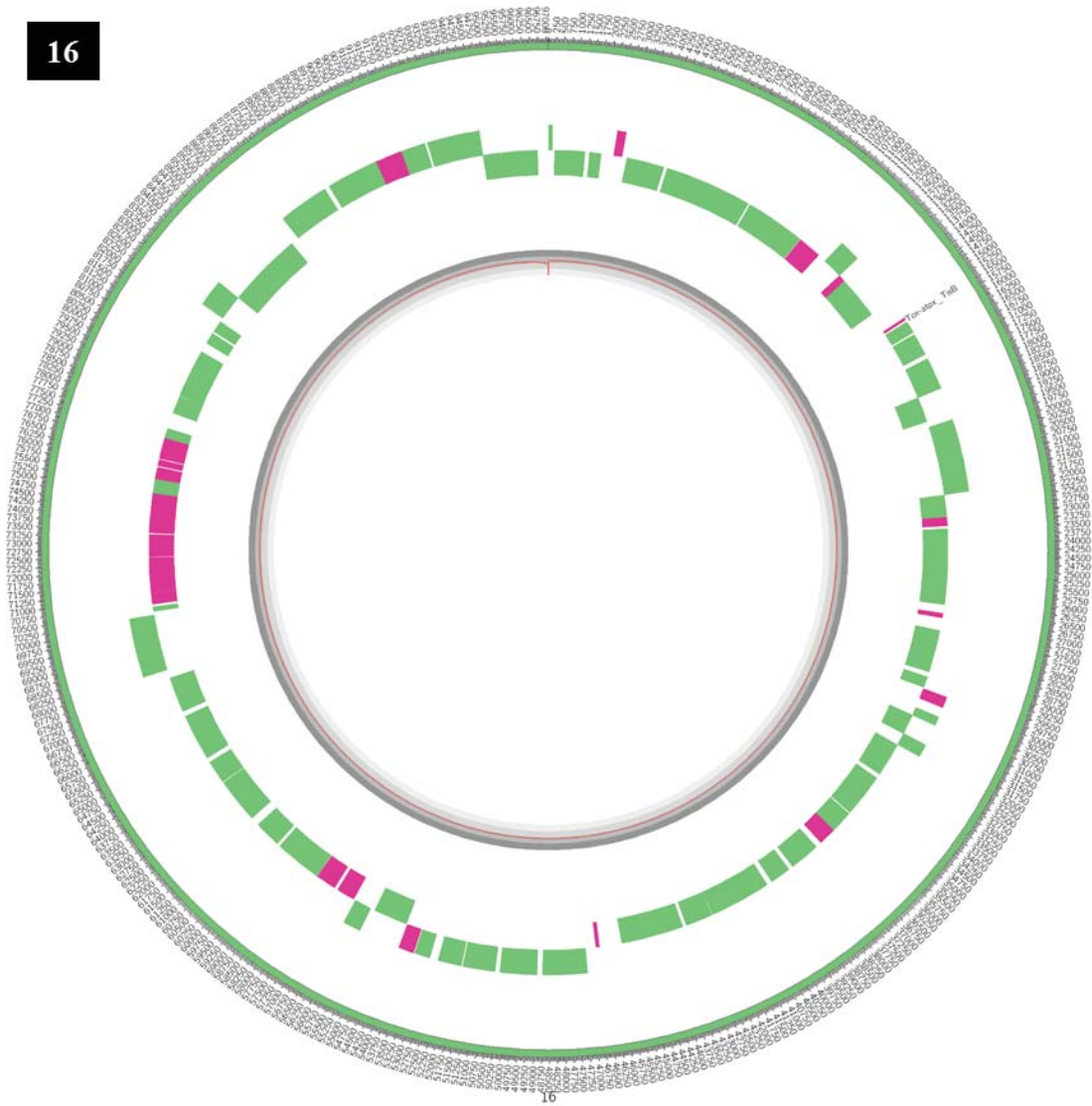


Figure 50. Individual circos plot of node 16. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin. The tagged gene is associated with toxins. Node ratio 1:1 (1 = 1 bp).

17



Figure 51. Individual circos plot of node 17. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin with an uncharacterised gene (black), and a gene of eukaryotic origin (orange). The tagged genes are associated with resistance. Node ratio 1:1 (1 = 1 bp).

18

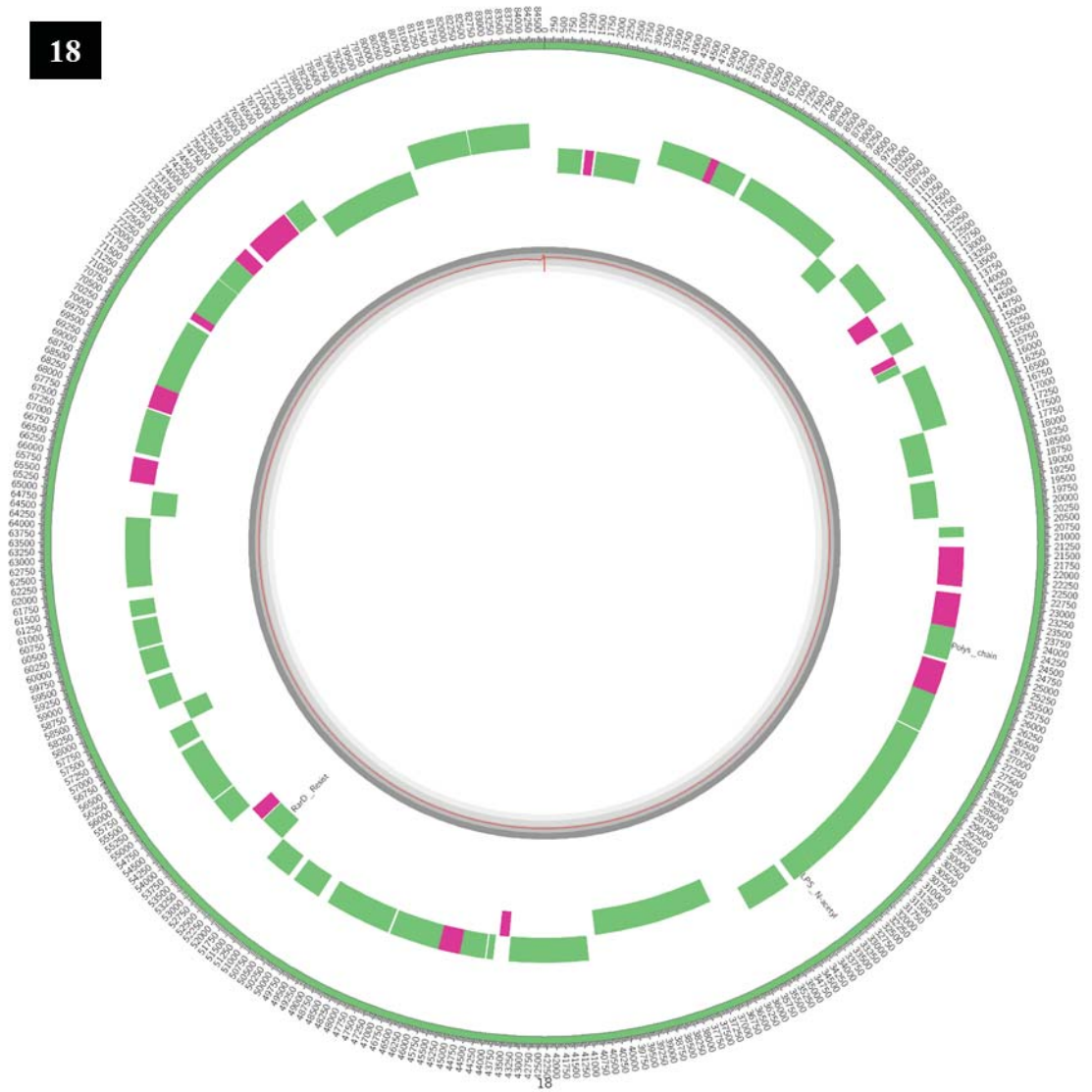


Figure 52. Individual circos plot of node 18. The nucleotide identity is that of *Raoutella* (green). There are scattered non-coding regions, and most genes identify as *Raoutella* (green), or bacterial (pink) in origin. The tagged genes are associated with resistance and polysaccharides. Node ratio 1:1 (1 = 1 bp).

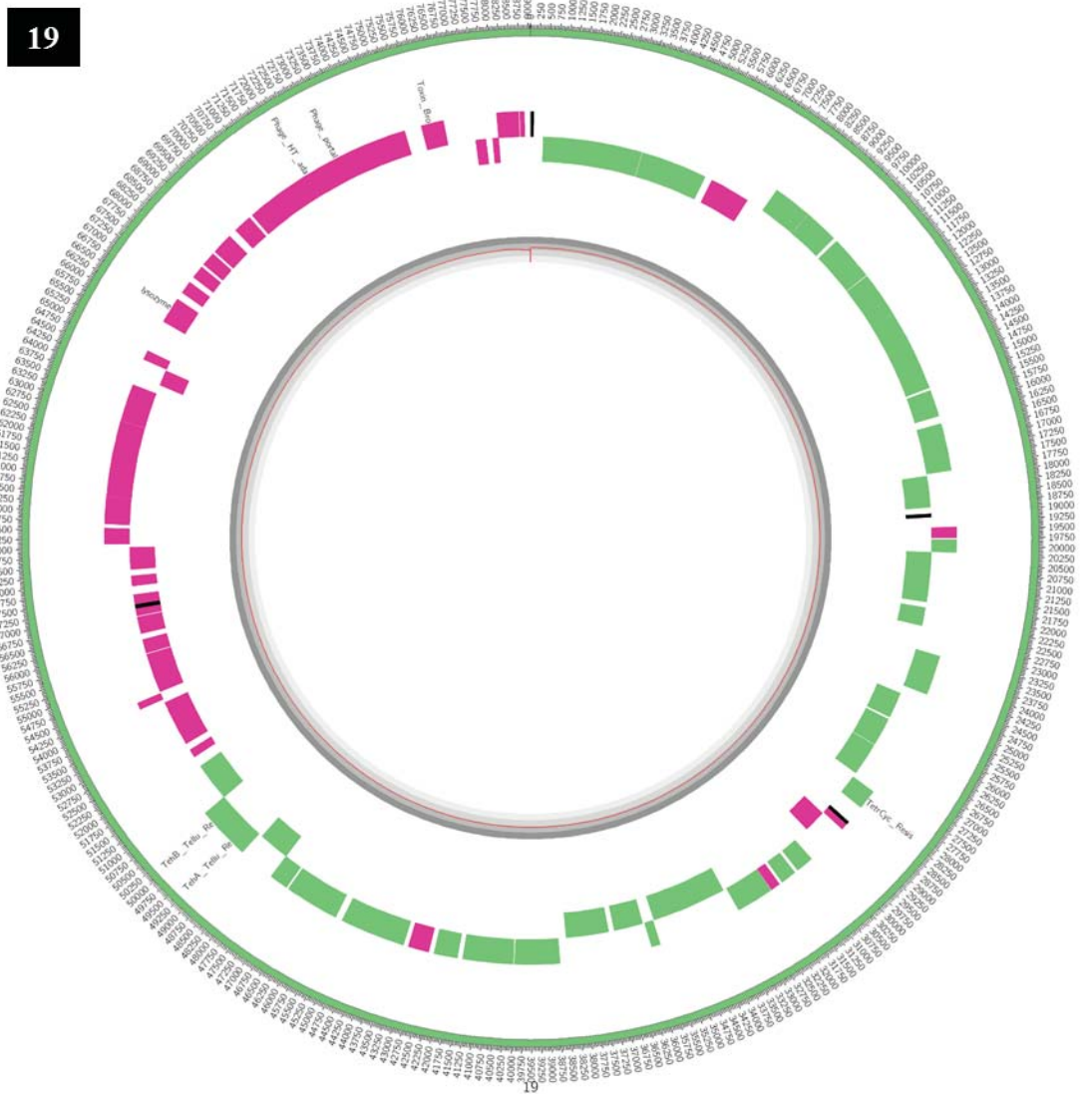


Figure 53. Individual circos plot of node 19. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin with a few uncharacterised genes (black). The tagged genes are associated with resistance and phage. With around a third of only bacterial (pink) gene origin. Node ratio 1:1 (1 = 1 bp).

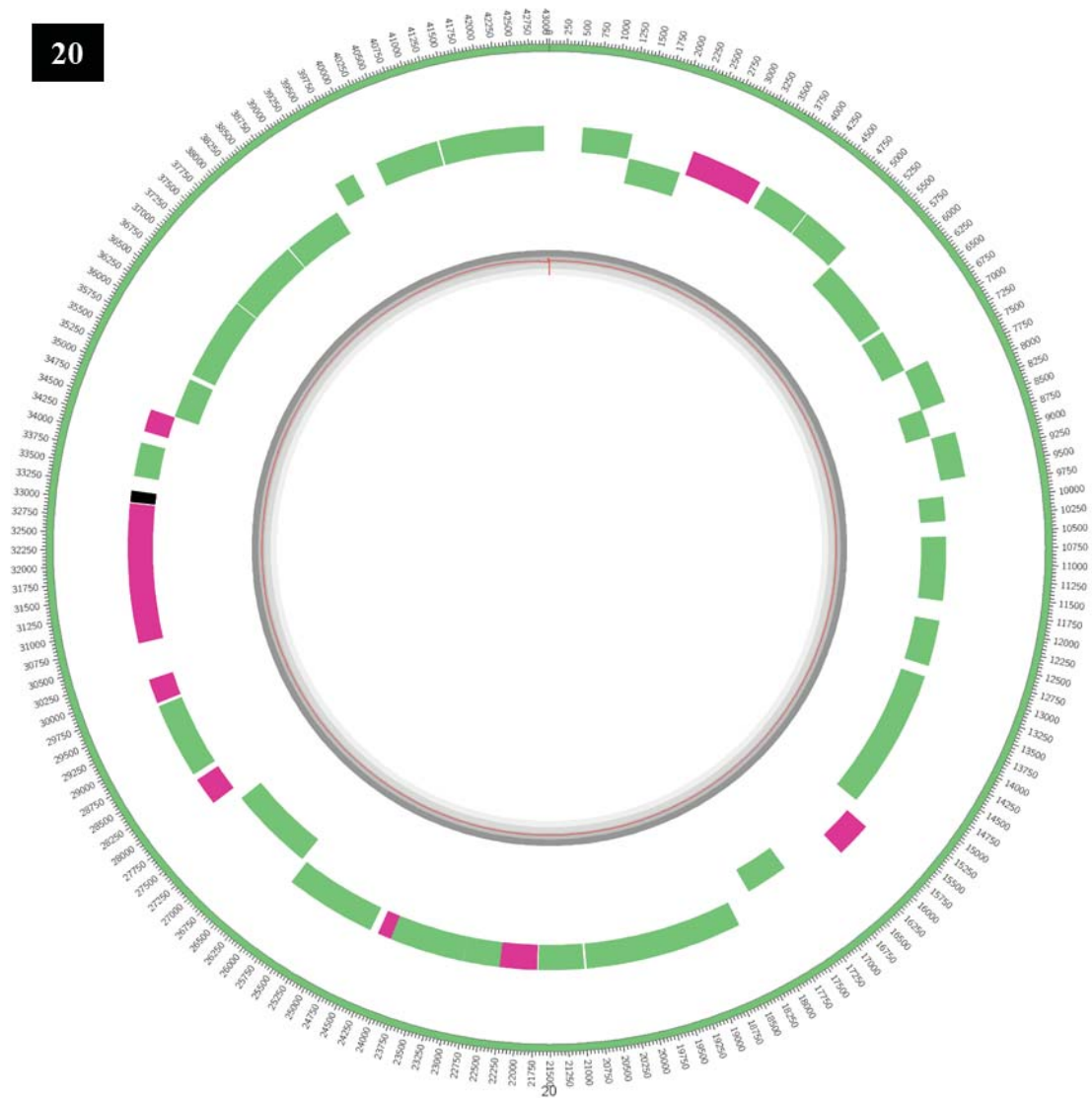


Figure 54. Individual circos plot of node 20. The nucleotide identity is that of *Raoutella* (green). There are scattered non-coding regions, and most genes identify as *Raoutella* (green), or bacterial (pink) in origin with an uncharacterised gene (black). Node ratio 1:1 (1 = 1 bp).

21

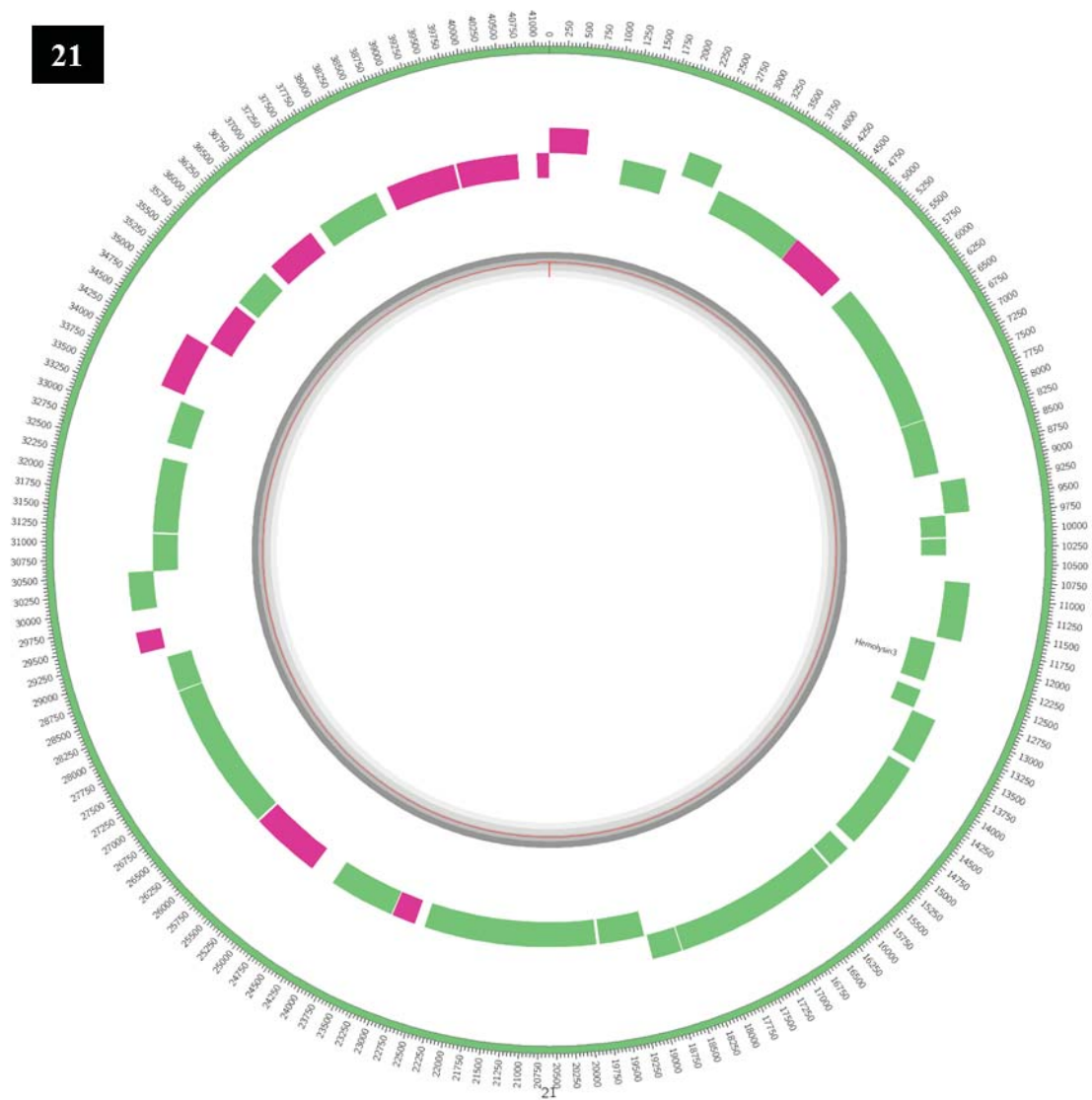


Figure 55. Individual circos plot of node 21. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin. The tagged gene is associated with virulence. Node ratio 1:1 (1 = 1 bp).

22

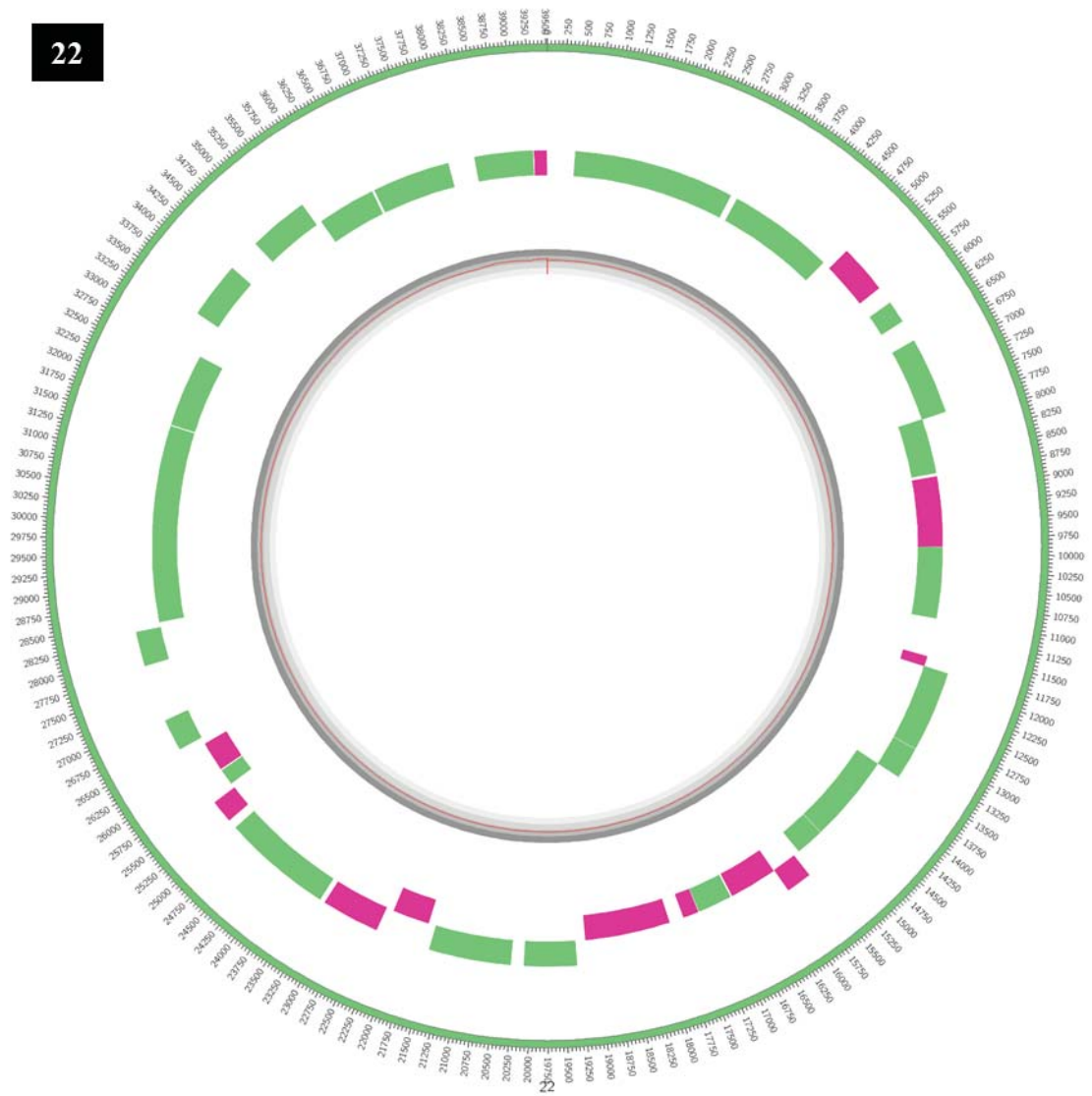


Figure 56. Individual circos plot of node 22. The nucleotide identity is that of *Raoutella* (green). There are scattered non-coding regions, and most genes identify as *Raoutella* (green), or bacterial (pink) in origin. Node ratio 1:1 (1 = 1 bp).

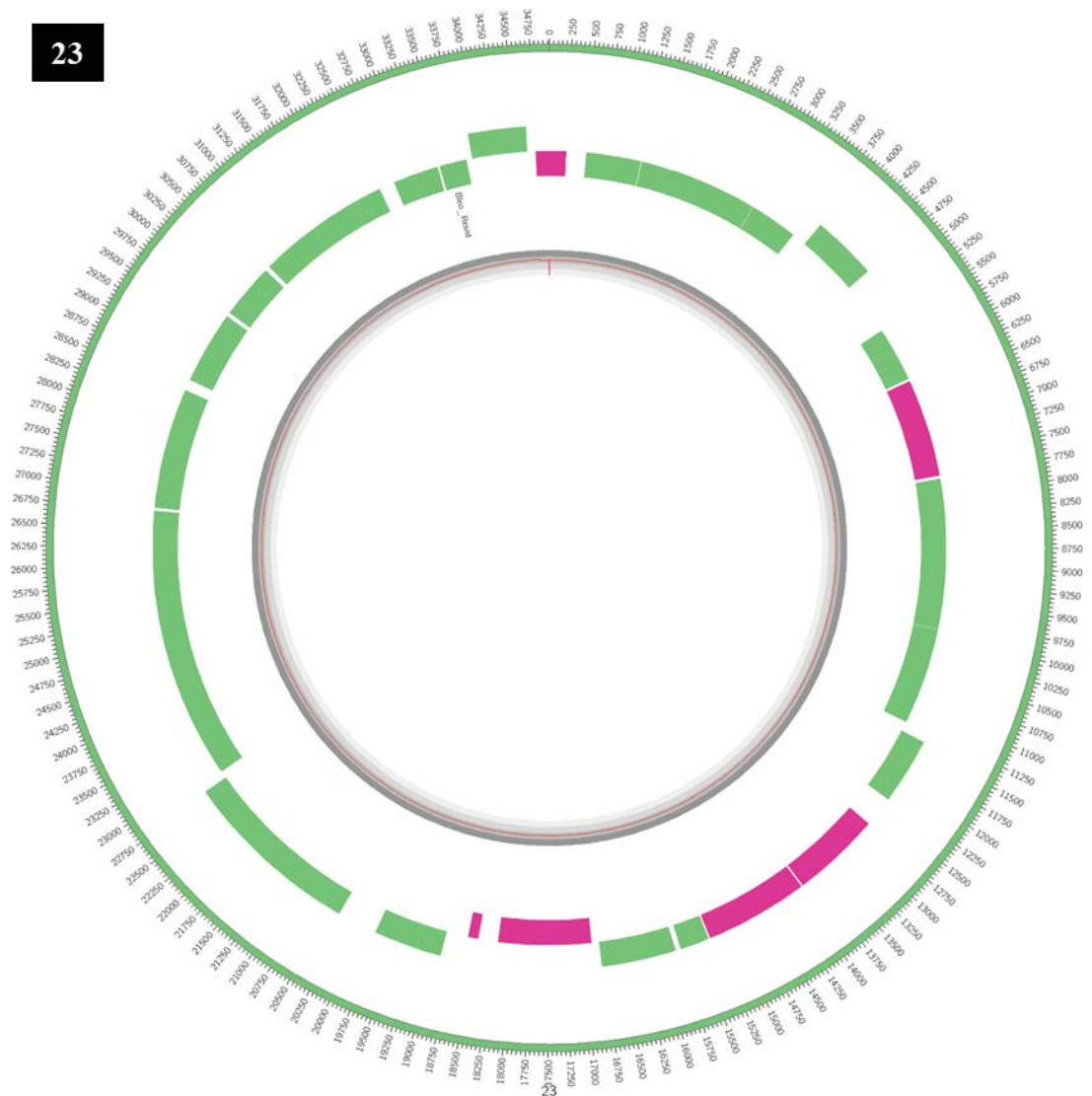


Figure 57. Individual circos plot of node 23. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin. The tagged gene is associated with resistance. Node ratio 1:1 (1 = 1 bp).

24

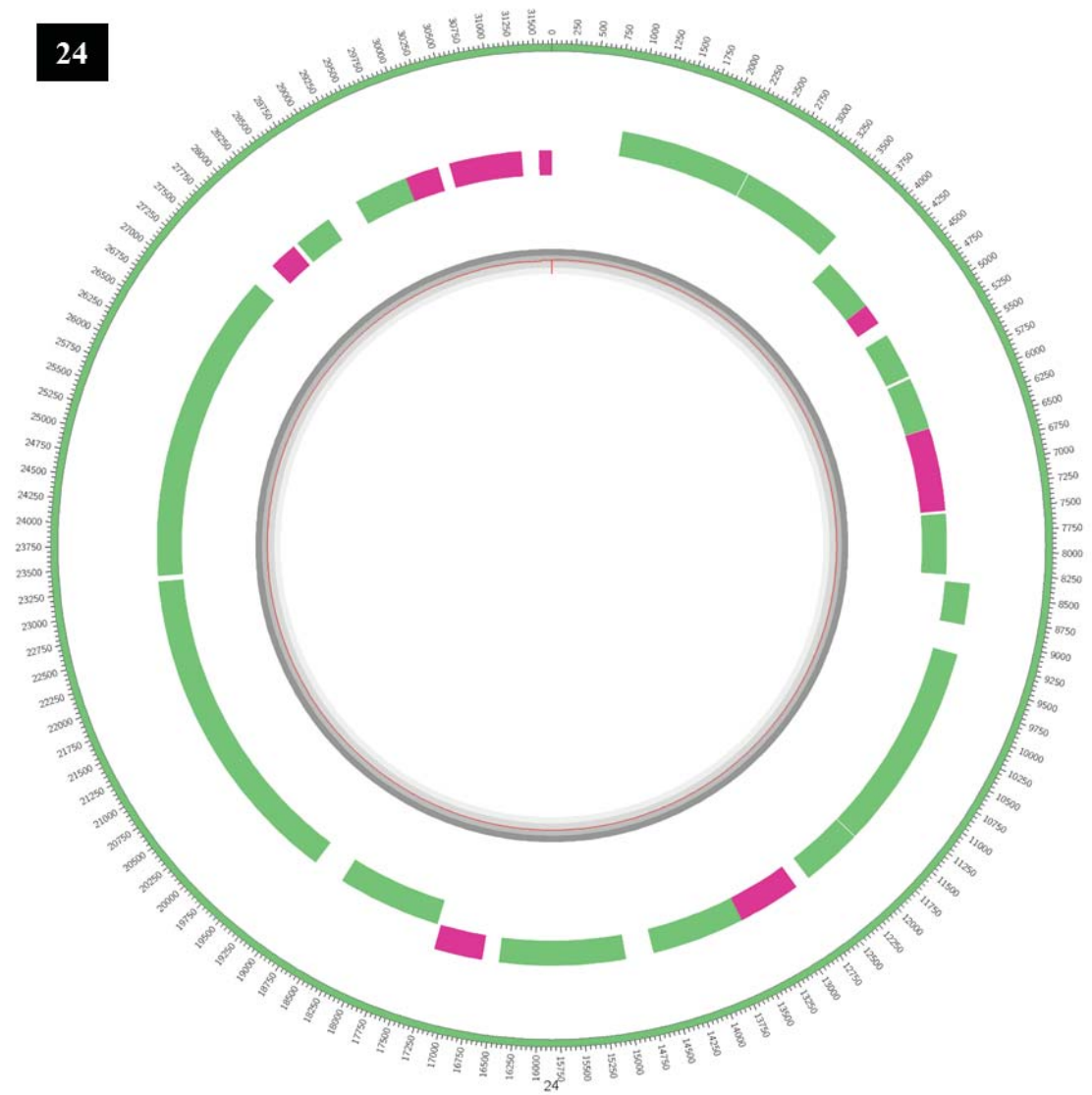


Figure 58. Individual circos plot of node 24. The nucleotide identity is that of *Raoultella* (green). There are scattered non-coding regions, and most genes identify as *Raoultella* (green), or bacterial (pink) in origin. Node ratio 1:1 (1 = 1 bp).

25

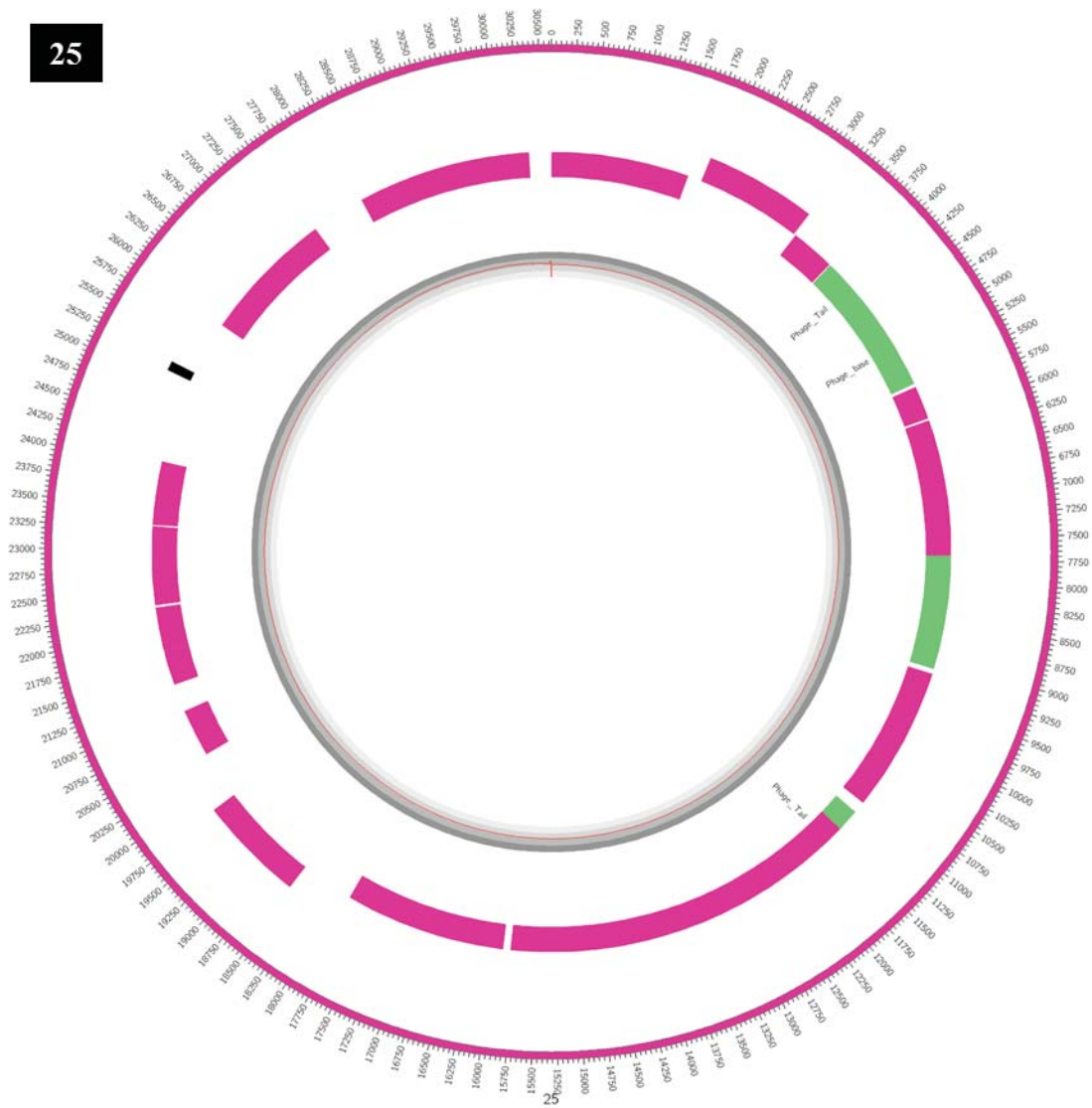


Figure 59. Individual circos plot of node 25. The nucleotide identity is of bacteria (non – *Raoultella*) (pink). There are scattered non-coding regions, and most genes identify as bacterial (pink) in origin with a few *Raoultella* (green), and an uncharacterised (black). The tagged genes are associated with phage. Node ratio 1:1 (1 = 1 bp).

Appendix IV: Gene Tags

This Appendix contains the gene products tagged in Figures (23, 24, and Appendix III) with reference to their gene ID's as found in Appendix V.

Gene ID	Annotation	Full gene product name	Bacteria associated
ID=7	Bleo_Resist	glyoxalase/bleomycin resistance/dioxygenase family protein	<i>Raoultella terrigena</i>
ID=9	Bcr_CfiA_effl	Bcr/CfiA family drug resistance efflux transporter	<i>Enterobacteriaceae</i>
ID=21	TetrCyc_Resis	TetR family transcriptional regulator	<i>Yersinia frederiksenii</i>
ID=30	BhsA_stress_Res	multiple stress resistance protein BhsA	<i>Klebsiella mobilis</i>
ID=101	Antibio_biosyn	MULTISPECIES: antibiotic biosynthesis monooxygenase	<i>Raoultella</i>
ID=131	Stress_Res_chap	oxidative-stress-resistance chaperone	<i>Raoultella ornithinolytica</i>
ID=169	Glycopr-polysac	glycoprotein-polysaccharide metabolism protein	<i>Raoultella ornithinolytica</i>
ID=201	drug_efflux	multidrug efflux RND transporter permease subunit	<i>Raoultella ornithinolytica</i>
ID=202	MexE_drug_effl	MexE family multidrug efflux RND transporter periplasmic adaptor subunit	<i>Raoultella ornithinolytica</i>
ID=271	Phage_HT_con	bacteriophage head to tail connecting protein	<i>Klebsiella pneumoniae</i>
ID=289	lysozyme	lysozyme	<i>Klebsiella oxytoca</i>
ID=295	Hemagglu	filamentous hemagglutinin	<i>Escherichia coli</i>
ID=330	Antibio_trans	antibiotic acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=403	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=517	LPS_LptE	LPS assembly lipoprotein LptE	<i>Raoultella ornithinolytica</i>
ID=525	CorC_metal_eff	MULTISPECIES: magnesium/cobalt efflux protein CorC	<i>Raoultella</i>
ID=596	AcrZ_drug_effl	multidrug efflux pump-associated protein, AcrZ family	<i>Enterobacter cloacae</i>
ID=664	Transpeptidase	L,D-transpeptidase	<i>Raoultella ornithinolytica</i>
ID=671	Glycyl_enzyme	glycyl radical enzyme	<i>Raoultella ornithinolytica</i>
ID=683	Biofil_BssR	biofilm formation regulatory protein BssR	<i>Raoultella terrigena</i>
ID=730	MacB_efflux	MacB family efflux pump subunit	<i>Raoultella ornithinolytica</i>
ID=777	Transpeptidase	L,D-transpeptidase	<i>Raoultella terrigena</i>
ID=843	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=854	TetrCyc_Resis	TetR family transcriptional regulator	<i>Chitiniphilus shinanonensis</i>
ID=857	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=891	Antitoxin	MULTISPECIES: antitoxin	<i>Enterobacteriaceae</i>
ID=956	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=967	Biofil_BssS	MULTISPECIES: biofilm formation regulatory protein BssS	<i>Raoultella</i>
ID=974	MviM_Virul	virulence factor MviM	<i>Raoultella ornithinolytica</i>
ID=1007	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1008	BhsA_stress_Res	MULTISPECIES: multiple stress resistance protein BhsA	<i>Raoultella</i>
ID=1039	RcnA_metal_eff	nickel/cobalt efflux protein RcnA	<i>Raoultella terrigena</i>
ID=1045	Fusaric_Resist	fusaric acid resistance protein	<i>Raoultella terrigena</i>
ID=1082	Leucine_efflux	leucine efflux protein	<i>Raoultella ornithinolytica</i>
ID=1096	Glyco_trans	glycosyl transferase	<i>Raoultella ornithinolytica</i>
ID=1122	Hemolys	hemolysin secretion protein D	<i>Raoultella ornithinolytica</i>
ID=1145	Antibio_biosyn	antibiotic biosynthesis monooxygenase	<i>Raoultella ornithinolytica</i>
ID=1208	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1247	LPS_LapB	lipopolysaccharide assembly protein LapB	<i>Raoultella ornithinolytica</i>
ID=1272	Phage_shock	phage shock protein operon transcriptional activator	<i>Raoultella ornithinolytica</i>
ID=1273	Phage_PspA	MULTISPECIES: phage shock protein PspA	<i>Raoultella</i>
ID=1274	Phage_shock	MULTISPECIES: phage shock protein B	<i>Raoultella</i>
ID=1276	Phage_shock	MULTISPECIES: phage-shock protein	<i>Raoultella</i>
ID=1304	Glyco_trans	glycosyl transferase	<i>Raoultella terrigena</i>
ID=1348	Toxin_RelE	toxin RelE	<i>Raoultella ornithinolytica</i>
ID=1361	Transpeptidase	L,D-transpeptidase	<i>Raoultella ornithinolytica</i>
ID=1367	Antibio_biosyn	antibiotic biosynthesis monooxygenase	<i>Xanthomonas citri</i>
ID=1378	min_T4SC	Minor pilin of type IV secretion complex (VirB5)	<i>Klebsiella varicola</i>
ID=1382	VirB9	P-type conjugative transfer protein VirB9	<i>Klebsiella michiganensis</i>
ID=1383	T4S_protein	type VI secretion protein	<i>Klebsiella michiganensis</i>
ID=1385	VirB11	P-type DNA transfer ATPase VirB11	<i>Pectobacterium carotovorum</i>
ID=1413	Antitoxin	antitoxin	<i>Salmonella enterica</i>
ID=1420	TetrCyc_Resis	MULTISPECIES: TetR family transcriptional regulator	<i>Yersinia</i>
ID=1444	HemolysD	hemolysin D	<i>Raoultella ornithinolytica</i>
ID=1464	Antibio_biosyn	antibiotic biosynthesis monooxygenase	<i>Photobacterium sanctipauli</i>
ID=1498	TetrCyc_Resis	MULTISPECIES: TetR family transcriptional regulator	<i>Enterobacteriaceae</i>
ID=1508	Tellurite_Res	MULTISPECIES: tellurite resistance protein	<i>Raoultella</i>
ID=1541	Glyco_trans	glycosyl transferase	<i>Raoultella ornithinolytica</i>
ID=1551	LPS_biosyn	lipopolysaccharide biosynthesis protein	<i>Klebsiella pneumoniae</i>
ID=1562	Wza_Polysacc	polysaccharide export protein Wza	<i>Klebsiella pneumoniae</i>
ID=1608	T4SEffecter	MULTISPECIES: type VI secretion system effector	<i>Enterobacteriaceae</i>
ID=1637	MdtQ_MDR	multidrug resistance outer membrane protein MdtQ	<i>Raoultella ornithinolytica</i>
ID=1653	Vancomy_exclu	vancomycin high temperature exclusion protein	<i>Raoultella ornithinolytica</i>
ID=1678	Phage_Resist	phage resistance protein	<i>Raoultella ornithinolytica</i>
ID=1684	Bcr_CfiA_effl	Bcr/CfiA family multidrug efflux MFS transporter	<i>Raoultella terrigena</i>
ID=1814	T4S_protein	type VI secretion-associated protein	<i>Enterobacter kobei</i>
ID=1815	T4S_VasK	type VI secretion protein VasK	<i>Raoultella terrigena</i>
ID=1830	TetrCyc_Resis	tetracycline resistance MFS efflux pump	<i>Raoultella terrigena</i>
ID=1831	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella terrigena</i>

Gene ID	Annotation	Full gene product name	Bacteria associated
ID=1833	Qs_LuxR	LuxR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1834	MDR	multidrug resistance transporter	<i>Raoultella ornithinolytica</i>
ID=1870	Hemagglu	filamentous hemagglutinin	<i>Raoultella ornithinolytica</i>
ID=1871	Toxin_RTX	RTX toxin-activating lysine-acyltransferase	<i>Raoultella ornithinolytica</i>
ID=1872	ShlB_FhaC_HecB	ShlB/FhaC/HecB family hemolysin secretion/activation protein	<i>Raoultella terrigena</i>
ID=1873	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=1874	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=1875	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=1876	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=1877	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=1879	fimbrial	fimbrial protein	<i>Raoultella terrigena</i>
ID=1880	T1_fimb	type-1 fimbrial protein subunit A	<i>Raoultella terrigena</i>
ID=1902	Antibio_biosyn	antibiotic biosynthesis monooxygenase	<i>Raoultella ornithinolytica</i>
ID=1907	fimbrial	fimbrial protein	<i>Raoultella terrigena</i>
ID=1908	fimbrial	fimbrial protein	<i>Raoultella terrigena</i>
ID=1909	fimbrial	fimbrial protein	<i>Raoultella terrigena</i>
ID=1912	PilZ	pilus assembly protein PilZ	<i>Raoultella ornithinolytica</i>
ID=1952	prepilin	prepilin-type N-terminal cleavage/methylation domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=1954	prepilin	prepilin-type N-terminal cleavage/methylation domain-containing protein	<i>Raoultella terrigena</i>
ID=1964	CobQ_synthase	cobryic acid synthase CobQ	<i>Raoultella ornithinolytica</i>
ID=2112	EmrB_drug_effl	multidrug efflux MFS transporter subunit EmrB	<i>Raoultella ornithinolytica</i>
ID=2134	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=2135	fimb_ass	fimbrial assembly protein	<i>Raoultella ornithinolytica</i>
ID=2136	T1_fim_usher	export and assembly usher protein of type 1 fimbriae	<i>Raoultella ornithinolytica</i>
ID=2137	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=2138	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=2140	Pil_ass	pilus assembly protein	<i>Raoultella ornithinolytica</i>
ID=2141	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=2191	KefB_efflux	glutathione-regulated potassium-efflux system protein KefB	<i>Raoultella ornithinolytica</i>
ID=2192	KefG_efflux	glutathione-regulated potassium-efflux system ancillary protein KefG	<i>Raoultella ornithinolytica</i>
ID=2218	PilP	pilus assembly protein PilP	<i>Raoultella ornithinolytica</i>
ID=2249	Starch_synth	starch synthase	<i>Raoultella ornithinolytica</i>
ID=2251	Gly_debran_en	glycogen debranching enzyme	<i>Raoultella ornithinolytica</i>
ID=2252	Gly_branch_en	glycogen-branching enzyme	<i>Raoultella ornithinolytica</i>
ID=2355	Cellu_BcsC	cellulose biosynthesis protein BcsC	<i>Raoultella ornithinolytica</i>
ID=2357	Cellu_BcsB	cellulose synthase regulator BcsB	<i>Raoultella ornithinolytica</i>
ID=2358	Cellu_syn	UDP-forming cellulose synthase catalytic subunit	<i>Raoultella ornithinolytica</i>
ID=2361	Cellu_BcsE	cellulose biosynthesis protein BcsE	<i>Raoultella ornithinolytica</i>
ID=2365	Cellu_syn	cellulose synthase	<i>Raoultella terrigena</i>
ID=2366	Cellu_syn	cellulose synthase	<i>Raoultella ornithinolytica</i>
ID=2367	Cellu_BcsB	cellulose synthase regulator BcsB	<i>Raoultella ornithinolytica</i>
ID=2368	Cellu_syn	cellulose synthase catalytic subunit (UDP-forming)	<i>Raoultella terrigena</i>
ID=2369	Cellu_YhjQ	cellulose synthase operon protein YhjQ	<i>Raoultella ornithinolytica</i>
ID=2370	Cellu_BcsO	cellulose biosynthesis protein BcsO	<i>Raoultella ornithinolytica</i>
ID=2422	α -hydroxy_enzy	alpha-hydroxy-acid oxidizing enzyme	<i>Raoultella ornithinolytica</i>
ID=2432	Glyco_trans	family 2 glycosyl transferase	<i>Raoultella ornithinolytica</i>
ID=2436	LPS_heptosyl	ADP-heptose--LPS heptosyltransferase	<i>Raoultella ornithinolytica</i>
ID=2437	LPS_heptosyl1	lipopolysaccharide heptosyltransferase 1	<i>Raoultella ornithinolytica</i>
ID=2440	LPS_1,2-N-acet	LPS 1,2-N-acetylglucosaminetransferase	<i>Raoultella ornithinolytica</i>
ID=2442	LPS_heptosyl3	putative lipopolysaccharide heptosyltransferase III	<i>Raoultella ornithinolytica</i>
ID=2443	Glyco_trans	glycosyl transferase family 1	<i>Raoultella ornithinolytica</i>
ID=2444	Glyco_trans	glycosyl transferase	<i>Raoultella terrigena</i>
ID=2447	LPS_biosyn	LPS biosynthesis protein	<i>Raoultella ornithinolytica</i>
ID=2491	Antibio_biosyn	antibiotic biosynthesis monooxygenase	<i>Raoultella ornithinolytica</i>
ID=2504	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=2506	Acriflavine_Res	acriflavine resistance protein E	<i>Raoultella ornithinolytica</i>
ID=2507	drug_efflux	multidrug efflux RND transporter permease subunit	<i>Raoultella ornithinolytica</i>
ID=2509	Bcr_CfIA_effl	Bcr/CfIA family drug resistance efflux transporter	<i>Raoultella terrigena</i>
ID=2569	Glyco_trans	bifunctional glycosyl transferase/transpeptidase	<i>Raoultella ornithinolytica</i>
ID=2570	pullulanase	pullulanase	<i>Raoultella ornithinolytica</i>
ID=2572	pullulanase	pullulanase	<i>Raoultella ornithinolytica</i>
ID=2573	T2SS_GspC	type II secretion system protein GspC	<i>Raoultella terrigena</i>
ID=2574	T2SS_GspD	type II secretion system protein GspD	<i>Raoultella ornithinolytica</i>
ID=2575	T2SS_GspE	type II secretion system protein GspE	<i>Raoultella ornithinolytica</i>
ID=2576	T2SS_GspF	type II secretion system protein GspF	<i>Raoultella ornithinolytica</i>
ID=2577	T2SS_GspG	MULTISPECIES: type II secretion system protein GspG	<i>Raoultella</i>
ID=2578	T2SS_GspH	type II secretion system protein GspH	<i>Raoultella ornithinolytica</i>
ID=2579	T2SS_GspI	MULTISPECIES: type II secretion system protein GspI	<i>Raoultella</i>
ID=2580	T2SS_GspJ	type II secretion system protein GspJ	<i>Raoultella ornithinolytica</i>

Gene ID	Annotation	Full gene product name	Bacteria associated
ID=2581	pullulanase	pullulanase	<i>Raoultella terrigena</i>
ID=2582	T2SS_GspL	type II secretion system protein GspL	<i>Raoultella ornithinolytica</i>
ID=2584	pullulanase	pullulanase	<i>Raoultella ornithinolytica</i>
ID=2585	prepilin	prepilin peptidase	<i>Raoultella ornithinolytica</i>
ID=2626	prepilin	prepilin peptidase-dependent pilin	<i>Raoultella terrigena</i>
ID=2627	T2SS_GspE	type II secretion system protein GspE	<i>Raoultella ornithinolytica</i>
ID=2628	T4_pilin	type IV pilin biogenesis protein	<i>Raoultella terrigena</i>
ID=2680	LPS_LptD	LPS assembly protein LptD	<i>Raoultella terrigena</i>
ID=2684	ApaG_metal_eff	MULTISPECIES: Co2+/Mg2+ efflux protein ApaG	<i>Raoultella</i>
ID=2687	KefC_efflux	glutathione-regulated potassium-efflux system protein KefC	<i>Raoultella ornithinolytica</i>
ID=2688	Keff_efflux	glutathione-regulated potassium-efflux system ancillary protein Keff	<i>Raoultella ornithinolytica</i>
ID=2714	Riboflavin	MULTISPECIES: bifunctional riboflavin kinase/FMN adenylyltransferase	<i>Raoultella</i>
ID=2797	T4SSeffector	type VI secretion system effector	<i>Raoultella terrigena</i>
ID=2800	T4SSeffector	type VI secretion system effector	<i>Raoultella ornithinolytica</i>
ID=2813	Hemolysin	hemolysin secretion protein D	<i>Raoultella ornithinolytica</i>
ID=2823	FosA_Resist	FosA family fosfomycin resistance glutathione transferase	<i>Raoultella ornithinolytica</i>
ID=2833	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2843	TMA_enzyme	choline TMA-lyase-activating enzyme	<i>Raoultella ornithinolytica</i>
ID=2847	QacE_ammo_eff	QacE family quaternary ammonium compound efflux SMR transporter	<i>Raoultella ornithinolytica</i>
ID=2848	QacE_ammo_eff	MULTISPECIES: QacE family quaternary ammonium compound efflux SMR transporter	<i>Raoultella</i>
ID=2859	drug_efflux	multidrug efflux RND transporter permease subunit	<i>Raoultella ornithinolytica</i>
ID=2883	AaeA_efflux	p-hydroxybenzoic acid efflux subunit AaeA	<i>Raoultella ornithinolytica</i>
ID=2884	AaeB_efflux	p-hydroxybenzoic acid efflux pump subunit AaeB	<i>Raoultella terrigena</i>
ID=2918	LPS_LptA	lipopolysaccharide ABC transporter substrate-binding protein LptA	<i>Raoultella ornithinolytica</i>
ID=2919	LPS_LptC	LPS export ABC transporter periplasmic protein LptC	<i>Raoultella ornithinolytica</i>
ID=3093	ExbB_biopoly	biopolymer transporter ExbB	<i>Raoultella terrigena</i>
ID=3094	ExbD_biopoly	biopolymer transport protein ExbD	<i>Raoultella ornithinolytica</i>
ID=3106	HemolysinD	hemolysin D	<i>Raoultella ornithinolytica</i>
ID=3113	Maj_pilin	major pilin protein fimA	<i>Raoultella ornithinolytica</i>
ID=3127	Pil_PapC	pilus assembly protein PapC	<i>Raoultella ornithinolytica</i>
ID=3128	Pil_PapD	pilus assembly protein PapD	<i>Raoultella terrigena</i>
ID=3129	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=3130	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=3153	YggS_enzyme	YggS family pyridoxal phosphate enzyme	<i>Raoultella ornithinolytica</i>
ID=3154	PilT	MULTISPECIES: twitching motility protein PilT	<i>Raoultella</i>
ID=3211	MATE_efflux	MATE family efflux transporter	<i>Raoultella ornithinolytica</i>
ID=3212	Riboflavin	riboflavin synthase subunit alpha	<i>Raoultella ornithinolytica</i>
ID=3214	Bcr_CflA_effl	Bcr/CflA family multidrug efflux MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3222	Ent_hemoly	enterohemolysin	<i>Klebsiella mobilis</i>
ID=3246	Phage_protein	phage protein	<i>Klebsiella pneumoniae</i>
ID=3251	lysozyme	lysozyme	<i>Klebsiella michiganensis</i>
ID=3260	Phage_Mu_F	phage Mu F like family protein	<i>Raoultella ornithinolytica</i>
ID=3273	Phage_Tail	phage tail protein	<i>Klebsiella pneumoniae</i>
ID=3288	ArsB_metal_eff	arsenical efflux pump membrane protein ArsB	<i>Klebsiella oxytoca</i>
ID=3289	ArsH_Arsenic_R	arsenical resistance protein ArsH	<i>Enterobacter hormaechei</i>
ID=3319	Fusaric_Resist	fusaric acid resistance protein	<i>Raoultella terrigena</i>
ID=3326	lysozyme_inhib	MULTISPECIES: lysozyme inhibitor	<i>Raoultella</i>
ID=3385	HemolysinD	hemolysin D	<i>Raoultella ornithinolytica</i>
ID=3459	lysozyme	lysozyme	<i>Klebsiella pneumoniae</i>
ID=3490	Copper_Resist	copper resistance protein	<i>Raoultella ornithinolytica</i>
ID=3496	T1_fimb	type 1 fimbrial protein	<i>Raoultella terrigena</i>
ID=3497	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=3498	fimb_ass	fimbrial assembly protein	<i>Raoultella ornithinolytica</i>
ID=3525	Tellurite_Res	tellurite resistance protein	<i>Raoultella ornithinolytica</i>
ID=3554	LPS_LptG	LPS export ABC transporter permease LptG	<i>Raoultella ornithinolytica</i>
ID=3555	LPS_LptF	LPS export ABC transporter permease LptF	<i>Raoultella terrigena</i>
ID=3563	Tox-atox_TabA	toxin-antitoxin biofilm protein TabA	<i>Raoultella ornithinolytica</i>
ID=3628	BsmA_Resist	MULTISPECIES: biofilm peroxide resistance protein BsmA	<i>Raoultella</i>
ID=3693	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3741	Qs_LuxR	LuxR family transcriptional regulator	<i>Klebsiella michiganensis</i>
ID=3758	Polys_deacety	polysaccharide deacetylase	<i>Raoultella ornithinolytica</i>
ID=3766	Qs_LuxR	LuxR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3768	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3809	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3811	TetrCyc_Resis	TetR family transcriptional regulator	<i>Methylobium sp.</i>
ID=3845	malic_enzyme	NAD-dependent malic enzyme	<i>Raoultella ornithinolytica</i>
ID=3859	Bleo_Resist	glyoxalase/bleomycin resistance protein/dioxygenase	<i>Raoultella ornithinolytica</i>
ID=3874	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3897	T4S_Rhs	type IV secretion protein Rhs	<i>Citrobacter amalonaticus</i>

Gene ID	Annotation	Full gene product name	Bacteria associated
ID=3923	T4S_protein	type VI secretion protein	<i>Pantoea dispersa</i>
ID=3942	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3948	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=4032	malic_enzyme	NAD-dependent malic enzyme	<i>Raoultella ornithinolytica</i>
ID=4050	fimb_ass	fimbrial assembly protein, partial	<i>Klebsiella michiganensis</i>
ID=4051	fimb_ass	fimbrial assembly protein	<i>Klebsiella mobilis</i>
ID=4052	fimb_chap	fimbrial chaperone protein	<i>Klebsiella mobilis</i>
ID=4056	VirK	virulence factor VirK	<i>Raoultella ornithinolytica</i>
ID=4124	Riboflavin	riboflavin synthase subunit beta	<i>Raoultella ornithinolytica</i>
ID=4137	fimbrial	MULTISPECIES: fimbrial protein	<i>Klebsiella</i>
ID=4138	fimbrial	fimbrial protein	<i>Klebsiella pneumoniae</i>
ID=4139	fimbrial	fimbrial protein	<i>Klebsiella sp. HMSC16C0T</i>
ID=4144	T4S_protein	type VI secretion protein	<i>Raoultella ornithinolytica</i>
ID=4145	T4S_EvpB	type VI secretion protein EvpB	<i>Raoultella ornithinolytica</i>
ID=4146	T4S_protein	type VI secretion protein	<i>Raoultella terrigena</i>
ID=4151	T4S_Rhs	type IV secretion protein Rhs	<i>Raoultella terrigena</i>
ID=4165	T4S_VasK	type VI secretion protein VasK	<i>Raoultella terrigena</i>
ID=4166	T4S_protein	type VI secretion-associated protein	<i>Raoultella terrigena</i>
ID=4167	T4S_ImpG	type VI secretion protein ImpG	<i>Raoultella terrigena</i>
ID=4168	T4S_protein	type VI secretion protein	<i>Raoultella terrigena</i>
ID=4169	T4S_protein	type VI secretion protein	<i>Raoultella terrigena</i>
ID=4170	T4SS	type VI secretion system lysozyme-like protein	<i>Raoultella terrigena</i>
ID=4191	VirG	VirG	<i>Raoultella ornithinolytica</i>
ID=4205	Streptomycin_kin	streptomycin kinase	<i>Citrobacter sp.</i>
ID=4224	TetrCyc_Resis	TetR family transcriptional regulator	<i>Klebsiella mobilis</i>
ID=4256	MarB_MDR	multiple antibiotic resistance regulatory periplasmic protein MarB	<i>Raoultella terrigena</i>
ID=4257	AcrAB_MarA_MDR	MULTISPECIES: MDR efflux pump AcrAB transcriptional activator MarA	<i>Enterobacteriaceae</i>
ID=4321	Riboflavin	riboflavin synthase subunit alpha	<i>Raoultella ornithinolytica</i>
ID=4425	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4429	Transpeptidase	murein transpeptidase	<i>Raoultella ornithinolytica</i>
ID=4534	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=4577	malic_enzyme	malic enzyme	<i>Raoultella ornithinolytica</i>
ID=4582	drug_efflux	multidrug efflux RND transporter permease subunit	<i>Raoultella ornithinolytica</i>
ID=4715	Phage_portal	phage portal protein, partial	<i>Klebsiella pneumoniae</i>
ID=4756	fimbrial	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=4774	Phage_shock	MULTISPECIES: phage-shock protein	<i>Enterobacteriaceae</i>
ID=4779	MATE_efflux	MATE family efflux transporter	<i>Raoultella ornithinolytica</i>
ID=4830	Tox-atox_TisB	type I toxin-antitoxin system toxin TisB	<i>Klebsiella pneumoniae</i>
ID=4953	6-N-HAP_Res	6-N-hydroxylaminopurine resistance protein	<i>Raoultella ornithinolytica</i>
ID=4957	FieF_efflux	cation-efflux pump FieF	<i>Raoultella ornithinolytica</i>
ID=5012	Polys_chain	polysaccharide chain length modulation protein	<i>Raoultella ornithinolytica</i>
ID=5020	LPS_N-acetyl	lipopolysaccharide N-acetylmannosaminouronosyltransferase	<i>Raoultella terrigena</i>
ID=5036	RarD_Resist	chloramphenicol resistance permease RarD	<i>Raoultella ornithinolytica</i>
ID=5041	HS/HSL_efflux	homoserine/homoserine lactone efflux protein	<i>Raoultella ornithinolytica</i>
ID=5092	TetrCyc_Resis	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=5116	TehA_Tellu_Re	dicarboxylate transporter/tellurite-resistance protein TehA	<i>Raoultella ornithinolytica</i>
ID=5117	TehB_Tellu_Re	tellurite resistance methyltransferase TehB	<i>Raoultella ornithinolytica</i>
ID=5145	lysozyme	lysozyme	<i>Klebsiella pneumoniae</i>
ID=5152	Phage_HT_ada	MULTISPECIES: phage head-tail adapter protein	<i>Klebsiella</i>
ID=5153	Phage_portal	MULTISPECIES: phage portal protein	<i>Klebsiella</i>
ID=5155	Toxin_Bro	toxin Bro	<i>Klebsiella variicola</i>
ID=5177	Transpeptidase	transpeptidase	<i>Raoultella ornithinolytica</i>
ID=5214	Hemolys	hemolysin III family protein	<i>Raoultella ornithinolytica</i>
ID=5272	Oqx_B_drug_effl	multidrug efflux RND transporter permease subunit OqxB	<i>Raoultella ornithinolytica</i>
ID=5273	MexE_drug_effl	MexE family multidrug efflux RND transporter periplasmic adaptor subunit	<i>Raoultella terrigena</i>
ID=5310	Bleo_Resist	bleomycin resistance protein	<i>Raoultella ornithinolytica</i>
ID=5343	Phage_Tail	phage tail protein	<i>Raoultella ornithinolytica</i>
ID=5344	Phage_base	phage baseplate protein	<i>Raoultella ornithinolytica</i>
ID=5351	Phage_Tail	MULTISPECIES: phage tail protein	<i>Enterobacteriaceae</i>
ID=5361	Phage_portal	MULTISPECIES: phage portal protein	<i>Klebsiella</i>
ID=5429	Phage_capsid	phage capsid protein, partial	<i>Clostridioides difficile</i>
ID=5430	Phage_capsid	phage capsid protein, partial	<i>Clostridioides difficile</i>

Appendix V: Gene ID

This Appendix contains the entire list of predicted genes (Appendix III) associated with the whole genome sequencing of *Isolate 133 – Raoultella* sp. (section 3.2.3.2.1) including the accession number the gene aligned to using NCBI's database.

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=1	WP_044327380	hypothetical protein	<i>Citrobacter amalonaticus</i>
ID=2	WP_045854115	oxidoreductase	<i>Raoultella terrigena</i>
ID=3	WP_045854116	RbsD/FucU transporter	<i>Raoultella terrigena</i>
ID=4	WP_045854117	LacI family transcriptional regulator	<i>Raoultella terrigena</i>
ID=5	WP_052474609	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=6	WP_045854119	hypothetical protein	<i>Raoultella terrigena</i>
ID=7	WP_045854120	glyoxalase/bleomycin resistance/dioxygenase family protein	<i>Raoultella terrigena</i>
ID=8	WP_041144198	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=9	WP_008815068	Bcr/CflA family drug resistance efflux transporter	<i>Enterobacteriaceae bacterium</i>
ID=11	WP_064367695	alpha/beta hydrolase	<i>Klebsiella oxytoca</i>
ID=12	WP_061797452	aldo/keto reductase	<i>Serratia ficaria</i>
ID=13	WP_045440301	MULTISPECIES: DNA-binding response regulator	<i>Citrobacter</i>
ID=14	WP_045341188	two-component sensor histidine kinase	<i>Enterobacter hormaechei</i>
ID=15	WP_065554733	cupin	<i>Citrobacter freundii</i>
ID=16	WP_046475959	carboxymuconolactone decarboxylase	<i>Citrobacter amalonaticus</i>
ID=17	WP_065906393	flavodoxin	<i>Raoultella ornithinolytica</i>
ID=18	WP_046876686	alpha/beta hydrolase	<i>Klebsiella michiganensis</i>
ID=19	WP_032749296	MULTISPECIES: MFS transporter	<i>Klebsiella</i>
ID=20	WP_043016099	MULTISPECIES: AsnC family transcriptional regulator	<i>Enterobacteriaceae</i>
ID=21	WP_050140755	TetR family transcriptional regulator	<i>Yersinia frederiksenii</i>
ID=22	WP_060682270	arginase	<i>Citrobacter freundii</i>
ID=23	WP_064545918	deoxygluconate dehydrogenase	<i>Kluyvera georgiana</i>
ID=25	WP_045854125	MBL fold metallo-hydrolase	<i>Raoultella terrigena</i>
ID=26	WP_021571240	MULTISPECIES: 2,5-diketo-D-gluconic acid reductase A	<i>Enterobacteriaceae</i>
ID=27	WP_048981575	MULTISPECIES: aldehyde oxidase	<i>Enterobacter cloacae</i>
ID=28	WP_038422977	MULTISPECIES: LysR family transcriptional regulator	<i>Klebsiella</i>
ID=29	WP_061797472	NAD-dependent dehydratase	<i>Serratia ficaria</i>
ID=30	WP_047065362	multiple stress resistance protein BhsA	<i>Klebsiella mobilis</i>
ID=31	WP_049591237	AraC family transcriptional regulator	<i>Klebsiella oxytoca</i>
ID=32	WP_045854127	hypothetical protein	<i>Raoultella terrigena</i>
ID=33	WP_045855402	hypothetical protein	<i>Raoultella terrigena</i>
ID=34	WP_045854130	gamma-glutamyl-phosphate reductase	<i>Raoultella terrigena</i>
ID=35	WP_041144214	MULTISPECIES: glutamate 5-kinase	<i>Raoultella</i>
ID=36	WP_041144215	phosphoprotein PhoE	<i>Raoultella ornithinolytica</i>
ID=37	WP_041144216	MULTISPECIES: lipoprotein nlpC	<i>Raoultella</i>
ID=38	WP_041144217	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=39	WP_041144218	alkanesulfonates-binding protein	<i>Raoultella ornithinolytica</i>
ID=40	WP_045854134	ABC transporter permease	<i>Raoultella terrigena</i>
ID=41	WP_045854135	ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=42	WP_045854135	ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=43	WP_041144221	thioredoxin	<i>Raoultella ornithinolytica</i>
ID=44	WP_041144222	haloacid dehalogenase	<i>Raoultella ornithinolytica</i>
ID=45	WP_041144223	phosphonate ABC transporter, permease protein PhnE	<i>Raoultella ornithinolytica</i>
ID=46	WP_041144224	phosphonate ABC transporter, permease protein PhnE	<i>Raoultella ornithinolytica</i>
ID=47	WP_041144225	phosphonate ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=48	WP_041144226	phosphonate ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=49	WP_045854142	amino acid ABC transporter permease	<i>Raoultella terrigena</i>
ID=50	WP_041144228	membrane protein	<i>Raoultella ornithinolytica</i>
ID=51	WP_041144229	ABC transporter	<i>Raoultella ornithinolytica</i>
ID=52	WP_045854145	cysteine ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=53	WP_045854146	hypothetical protein	<i>Raoultella terrigena</i>
ID=54	WP_041144232	ethanolamine ammonia-lyase	<i>Raoultella ornithinolytica</i>
ID=55	WP_041144233	ethanolamine ammonia-lyase	<i>Raoultella ornithinolytica</i>
ID=56	WP_041144234	ethanolamine permease	<i>Raoultella ornithinolytica</i>
ID=57	WP_041144235	exo-poly-alpha-D-galacturonosidase	<i>Raoultella ornithinolytica</i>
ID=58	WP_041144236	amino acid transporter	<i>Raoultella ornithinolytica</i>
ID=59	WP_041144237	homocysteine S-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=60	WP_041144238	taurine ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=61	WP_041144239	taurine transporter ATP-binding subunit	<i>Raoultella ornithinolytica</i>
ID=62	WP_041144240	taurine transporter subunit	<i>Raoultella ornithinolytica</i>
ID=63	WP_045854156	taurine dioxygenase	<i>Raoultella terrigena</i>
ID=64	WP_041144242	acyltransferase	<i>Raoultella ornithinolytica</i>
ID=65	WP_041144243	MULTISPECIES: delta-aminolevulinic acid dehydratase	<i>Raoultella</i>
ID=66	WP_041144244	outer membrane autotransporter barrel domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=67	WP_041144245	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=68	WP_041144246	D-alanyl-D-alanine-carboxypeptidase/endopeptidase AmpH	<i>Raoultella ornithinolytica</i>
ID=69	WP_041144247	isochorismatase	<i>Raoultella ornithinolytica</i>
ID=70	WP_041144248	microcin B17 transporter	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=71	WP_041144249	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=72	WP_045854164	membrane protein	<i>Raoultella terrigena</i>
ID=73	WP_041144251	membrane protein	<i>Raoultella ornithinolytica</i>
ID=74	WP_045854166	D-alanine--D-alanine ligase A	<i>Raoultella terrigena</i>
ID=75	WP_045854167	MFS transporter	<i>Raoultella terrigena</i>
ID=76	WP_045854168	gluconate 5-dehydrogenase	<i>Raoultella terrigena</i>
ID=77	WP_045854169	MFS transporter	<i>Raoultella terrigena</i>
ID=78	WP_045854170	transcriptional regulator	<i>Raoultella terrigena</i>
ID=79	WP_041144254	anti-adaptor protein IraP	<i>Raoultella ornithinolytica</i>
ID=80	WP_045855405	alkaline phosphatase	<i>Raoultella terrigena</i>
ID=81	WP_041144255	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=82	WP_041144256	pyroline-5-carboxylate reductase	<i>Raoultella ornithinolytica</i>
ID=83	WP_045854174	DUF188 domain-containing protein	<i>Raoultella terrigena</i>
ID=84	WP_041144258	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=85	WP_041144259	shikimate kinase II	<i>Raoultella ornithinolytica</i>
ID=86	WP_041144261	AroM protein	<i>Raoultella ornithinolytica</i>
ID=87	WP_045854179	hypothetical protein	<i>Raoultella terrigena</i>
ID=88	WP_041147534	MULTISPECIES: recombination-associated protein RdgC	<i>Raoultella</i>
ID=89	WP_041144263	fructokinase	<i>Raoultella ornithinolytica</i>
ID=90	WP_041144264	exonuclease subunit SbcC	<i>Raoultella ornithinolytica</i>
ID=91	WP_041144265	exonuclease sbcCD subunit D	<i>Raoultella ornithinolytica</i>
ID=92	WP_004099401	MULTISPECIES: DNA-binding response regulator	<i>Enterobacterales</i>
ID=93	WP_045854184	PAS domain-containing sensor histidine kinase	<i>Raoultella terrigena</i>
ID=95	WP_045854185	branched-chain amino acid ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=96	WP_045854186	proline-specific permease ProY	<i>Raoultella terrigena</i>
ID=97	WP_041144269	alpha-glycosidase	<i>Raoultella ornithinolytica</i>
ID=98	WP_041144270	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=99	WP_041144270	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=100	WP_041144271	MULTISPECIES: hydrolase	<i>Raoultella</i>
ID=101	WP_041144272	MULTISPECIES: antibiotic biosynthesis monooxygenase	<i>Raoultella</i>
ID=102	WP_041144273	amidohydrolase	<i>Raoultella ornithinolytica</i>
ID=103	WP_041144274	fructose-1,6-bisphosphate aldolase, class II	<i>Raoultella ornithinolytica</i>
ID=104	WP_041144275	MULTISPECIES: kinase	<i>Raoultella</i>
ID=105	WP_045854191	PTS ascorbate transporter subunit IIC	<i>Raoultella terrigena</i>
ID=106	WP_041144277	MULTISPECIES: PTS mannose transporter subunit IIA	<i>Raoultella</i>
ID=107	WP_045855406	PTS sugar transporter subunit IIA	<i>Raoultella terrigena</i>
ID=109	WP_004858569	MULTISPECIES: peroxiredoxin	<i>Enterobacteriaceae</i>
ID=110	WP_041144279	ACP phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=111	WP_041144280	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	<i>Raoultella ornithinolytica</i>
ID=112	WP_041144281	MULTISPECIES: tRNA-guanine(34) transglycosylase	<i>Raoultella</i>
ID=113	WP_041144282	MULTISPECIES: preprotein translocase subunit YajC	<i>Raoultella</i>
ID=114	WP_041144283	protein-export membrane protein SecD	<i>Raoultella ornithinolytica</i>
ID=115	WP_041144284	preprotein translocase subunit SecF	<i>Raoultella ornithinolytica</i>
ID=116	WP_041144285	glyoxalase	<i>Raoultella ornithinolytica</i>
ID=117	WP_041144286	DeoR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=118	WP_045854198	nucleoside-specific channel-forming protein Tsx	<i>Raoultella terrigena</i>
ID=119	WP_041144288	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=120	WP_004858609	MULTISPECIES: transcriptional regulator NrdR	<i>Enterobacteriaceae</i>
ID=121	WP_041144289	bifunctional diaminohydroxyphosphoribosylaminopyrimidine.. ..deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase	<i>Raoultella ornithinolytica</i>
ID=122	WP_041144290	MULTISPECIES: 6,7-dimethyl-8-ribityllumazine synthase	<i>Raoultella</i>
ID=123	WP_041144291	N utilization substance protein B	<i>Raoultella ornithinolytica</i>
ID=124	WP_041144292	thiamine-monophosphate kinase	<i>Raoultella ornithinolytica</i>
ID=125	WP_045854203	phosphatidylglycerophosphatase A	<i>Raoultella terrigena</i>
ID=126	WP_041144294	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=127	WP_041144295	1-deoxy-D-xylulose-5-phosphate synthase	<i>Raoultella ornithinolytica</i>
ID=128	WP_045854206	(2E,6E)-farnesyl diphosphate synthase	<i>Raoultella terrigena</i>
ID=129	WP_041144297	MULTISPECIES: exodeoxyribonuclease VII small subunit	<i>Raoultella</i>
ID=130	WP_045854207	tRNA 4-thiouridine(8) synthase Thil	<i>Raoultella terrigena</i>
ID=131	WP_041144299	oxidative-stress-resistance chaperone	<i>Raoultella ornithinolytica</i>
ID=132	WP_045854209	2-dehydropantoate 2-reductase	<i>Raoultella terrigena</i>
ID=133	WP_041144301	MULTISPECIES: YajQ family cyclic di-GMP-binding protein	<i>Raoultella</i>
ID=134	WP_045854210	MFS transporter	<i>Raoultella terrigena</i>
ID=135	WP_041144303	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=136	WP_041144304	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=137	WP_041144305	AP endonuclease	<i>Raoultella ornithinolytica</i>
ID=138	WP_041144306	FAD-binding dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=139	WP_004099512	MULTISPECIES: NIPSNAP family protein	<i>Enterobacteriaceae</i>
ID=140	WP_041144307	3-oxosteroid 1-dehydrogenase	<i>Raoultella ornithinolytica</i>

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ID=141	WP_041144308	shikimate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=142	WP_041144309	IcIR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=143	WP_045854212	protoheme IX farnesyltransferase	<i>Raoultella terrigena</i>
ID=144	WP_004099523	MULTISPECIES: cytochrome o ubiquinol oxidase subunit IV	<i>Enterobacterales</i>
ID=145	WP_041144312	MULTISPECIES: cytochrome o ubiquinol oxidase subunit III	<i>Raoultella</i>
ID=146	WP_041144313	cytochrome ubiquinol oxidase subunit I	<i>Raoultella ornithinolytica</i>
ID=147	WP_041144314	cytochrome ubiquinol oxidase subunit II	<i>Raoultella ornithinolytica</i>
ID=148	WP_041144315	AmpG family muropeptide MFS transporter	<i>Raoultella ornithinolytica</i>
ID=149	WP_045854217	hypothetical protein	<i>Raoultella terrigena</i>
ID=150	WP_041144317	MULTISPECIES: BolA family transcriptional regulator	<i>Raoultella</i>
ID=151	WP_041144318	MULTISPECIES: trigger factor	<i>Raoultella</i>
ID=152	WP_003021624	MULTISPECIES: ATP-dependent Clp protease proteolytic subunit	<i>Enterobacterales</i>
ID=153	WP_045854218	ATP-dependent Clp protease ATP-binding subunit ClpX	<i>Raoultella terrigena</i>
ID=154	WP_041144320	endopeptidase La	<i>Raoultella ornithinolytica</i>
ID=155	WP_002444653	MULTISPECIES: DNA-binding protein HU-beta	<i>Proteobacteria</i>
ID=156	WP_041144321	peptidylprolyl isomerase	<i>Raoultella ornithinolytica</i>
ID=157	WP_041144322	competence protein ComEA	<i>Raoultella ornithinolytica</i>
ID=158	WP_041144323	MULTISPECIES: thioesterase	<i>Raoultella</i>
ID=159	WP_041144324	7-cyano-7-deazaguanine synthase	<i>Raoultella ornithinolytica</i>
ID=160	WP_041144325	peptide ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=161	WP_045854224	thiamin pyrimidine pyrophosphate hydrolase	<i>Raoultella terrigena</i>
ID=162	WP_045854225	cysteine synthase	<i>Raoultella terrigena</i>
ID=163	WP_041144328	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=164	WP_041144329	multidrug ABC transporter permease/ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=165	WP_041144330	multidrug ABC transporter permease/ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=166	WP_004858743	MULTISPECIES: nitrogen regulatory protein P-II 2	<i>Enterobacteriaceae</i>
ID=167	WP_041144331	ammonium transporter	<i>Raoultella ornithinolytica</i>
ID=168	WP_041144332	acyl-CoA thioesterase II	<i>Raoultella ornithinolytica</i>
ID=169	WP_041144333	glycoprotein-polysaccharide metabolism protein	<i>Raoultella ornithinolytica</i>
ID=170	WP_041144334	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=171	WP_045854230	hypothetical protein	<i>Raoultella terrigena</i>
ID=172	WP_045854231	hydrolase	<i>Raoultella terrigena</i>
ID=173	WP_045854232	nucleoside permease	<i>Raoultella terrigena</i>
ID=174	WP_045854233	ribonucleoside hydrolase	<i>Raoultella terrigena</i>
ID=175	WP_045854234	transcriptional regulator YeiL	<i>Raoultella terrigena</i>
ID=176	WP_045854235	hypothetical protein	<i>Raoultella terrigena</i>
ID=177	WP_045854236	hypothetical protein	<i>Raoultella terrigena</i>
ID=178	WP_045854237	DeoR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=180	WP_041144340	membrane protein	<i>Raoultella ornithinolytica</i>
ID=181	WP_041147535	RNA signal recognition particle	<i>Raoultella ornithinolytica</i>
ID=182	WP_041144341	cyclic diguanylate phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=183	WP_045854240	ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=184	WP_041144343	MULTISPECIES: cyclodextrin-binding protein	<i>Raoultella</i>
ID=185	WP_004136032	MULTISPECIES: putative maltodextrin transport permease	<i>Klebsiella</i>
ID=186	WP_041144345	MULTISPECIES: arabinogalactan oligomer ABC transporter permease	<i>Raoultella</i>
ID=187	WP_045854242	galactosidase	<i>Raoultella terrigena</i>
ID=188	WP_041147536	beta-galactosidase	<i>Raoultella ornithinolytica</i>
ID=189	WP_041144347	MULTISPECIES: PTS sugar transporter	<i>Raoultella</i>
ID=190	WP_041144348	maltoporin	<i>Raoultella ornithinolytica</i>
ID=191	WP_041144349	MULTISPECIES: lac repressor	<i>Raoultella</i>
ID=192	WP_045854244	50S ribosomal protein L31	<i>Raoultella terrigena</i>
ID=193	WP_045854245	GNAT family acetyltransferase	<i>Raoultella terrigena</i>
ID=194	WP_041144352	DNA-binding protein	<i>Raoultella ornithinolytica</i>
ID=195	WP_045854247	membrane protein	<i>Raoultella terrigena</i>
ID=196	WP_004858780	MULTISPECIES: membrane protein	<i>Enterobacteriaceae</i>
ID=197	WP_041144354	maltose O-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=198	WP_041144355	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=199	WP_041144356	MULTISPECIES: Hha toxicity attenuator	<i>Raoultella</i>
ID=201	WP_041144357	multidrug efflux RND transporter permease subunit	<i>Raoultella ornithinolytica</i>
ID=202	WP_041144358	MexE family multidrug efflux RND transporter periplasmic adaptor subunit	<i>Raoultella ornithinolytica</i>
ID=203	WP_041144359	DNA-binding transcriptional repressor AcrR	<i>Raoultella ornithinolytica</i>
ID=204	WP_041144360	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=205	WP_004136059	MULTISPECIES: DUF2496 domain-containing protein	<i>Klebsiella</i>
ID=206	WP_041144361	primosomal replication protein N"	<i>Raoultella ornithinolytica</i>
ID=207	WP_041147537	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=208	WP_041144362	MULTISPECIES: adenine phosphoribosyltransferase	<i>Raoultella</i>
ID=209	WP_041144363	DNA polymerase III subunit gamma/tau	<i>Raoultella ornithinolytica</i>
ID=210	WP_013367293	nucleoid-associated protein, YbaB/EbFC family	<i>Enterobacter lignolyticus</i>
ID=211	WP_041144365	MULTISPECIES: recombination protein RecR	<i>Raoultella</i>

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ID=212	WP_041144366	molecular chaperone HtpG	<i>Raoultella ornithinolytica</i>
ID=213	WP_041144367	adenylate kinase	<i>Raoultella ornithinolytica</i>
ID=214	WP_041144368	ferrochelataase	<i>Raoultella ornithinolytica</i>
ID=215	WP_041144369	inosine/guanosine kinase	<i>Raoultella ornithinolytica</i>
ID=216	WP_045854259	Kef family K(+) transporter	<i>Raoultella terrigena</i>
ID=217	WP_045854260	MFS transporter	<i>Raoultella terrigena</i>
ID=218	WP_045854261	bifunctional UDP-sugar hydrolase/5'-nucleotidase	<i>Raoultella terrigena</i>
ID=219	WP_041144373	aminoacyl-tRNA deacylase	<i>Raoultella ornithinolytica</i>
ID=220	WP_015585009	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=221	WP_041144374	conjugal transfer protein TraB	<i>Raoultella ornithinolytica</i>
ID=222	WP_041144375	Cu ⁺ exporting ATPase	<i>Raoultella ornithinolytica</i>
ID=223	WP_041144376	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=224	WP_045854269	heme ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=225	WP_045855411	ABC transporter permease	<i>Raoultella terrigena</i>
ID=226	WP_045854270	hypothetical protein	<i>Raoultella terrigena</i>
ID=227	WP_045854271	heme utilization carrier protein	<i>Raoultella terrigena</i>
ID=228	WP_045854272	putative heme utilization radical SAM enzyme HutW	<i>Raoultella terrigena</i>
ID=229	WP_045855412	hemin ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=230	WP_045854273	ligand-gated channel	<i>Raoultella terrigena</i>
ID=231	WP_041144379	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=232	WP_045854275	membrane protein	<i>Raoultella terrigena</i>
ID=233	WP_041144381	paraslipin	<i>Raoultella ornithinolytica</i>
ID=234	WP_041144382	iron ABC transporter ATP-binding protein FetA	<i>Raoultella ornithinolytica</i>
ID=235	WP_041144383	iron export ABC transporter permease subunit FetB	<i>Raoultella ornithinolytica</i>
ID=236	WP_041144384	MULTISPECIES: co-chaperone YbbN	<i>Raoultella</i>
ID=237	WP_041144385	short-chain dehydrogenase/reductase	<i>Raoultella ornithinolytica</i>
ID=238	WP_041144386	MULTISPECIES: arylesterase	<i>Raoultella</i>
ID=239	WP_041144387	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=240	WP_041144388	sugar ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=241	WP_041144389	monooxygenase	<i>Raoultella ornithinolytica</i>
ID=242	WP_041144390	membrane protein	<i>Raoultella ornithinolytica</i>
ID=243	WP_041144391	selenophosphate-dependent tRNA 2-selenouridine synthase	<i>Raoultella ornithinolytica</i>
ID=244	WP_041144392	5-(carboxyamino)imidazole ribonucleotide synthase	<i>Raoultella ornithinolytica</i>
ID=245	WP_045854285	5-(carboxyamino)imidazole ribonucleotide mutase	<i>Raoultella terrigena</i>
ID=246	WP_041144394	UDP-2,3-diacetylglucosamine diphosphatase	<i>Raoultella ornithinolytica</i>
ID=247	WP_041144395	MULTISPECIES: peptidylprolyl isomerase	<i>Raoultella</i>
ID=248	WP_045854287	cysteine--tRNA ligase	<i>Raoultella terrigena</i>
ID=249	WP_041144397	ribosome-associated protein	<i>Raoultella ornithinolytica</i>
ID=250	WP_041144398	MULTISPECIES: bifunctional 5,10-methylene-tetrahydrofolate.. ..dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase	<i>Raoultella</i>
ID=251	WP_032451772	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=252	WP_004141087	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=253	WP_038782372	transcription elongation protein SprT	<i>Burkholderia pseudomallei</i>
ID=254	WP_047065718	nuclease	<i>Klebsiella mobilis</i>
ID=255	WP_040147827	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=256	WP_040147829	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=257	WP_063444776	DNA polymerase	<i>Klebsiella mobilis</i>
ID=258	WP_032214621	hypothetical protein	<i>Escherichia coli</i>
ID=259	WP_032707214	hypothetical protein	<i>Klebsiella mobilis</i>
ID=260	WP_032707213	hypothetical protein	<i>Klebsiella mobilis</i>
ID=261	WP_045391713	hypothetical protein	<i>Klebsiella mobilis</i>
ID=262	WP_060452353	hypothetical protein	<i>Serratia marcescens</i>
ID=264	WP_058669112	hypothetical protein	<i>Citrobacter koseri</i>
ID=265	WP_032707210	XRE family transcriptional regulator	<i>Klebsiella mobilis</i>
ID=266	WP_000708850	transcriptional regulator	<i>Escherichia coli</i>
ID=267	WP_032707209	replication protein	<i>Klebsiella mobilis</i>
ID=268	WP_047065697	hypothetical protein	<i>Klebsiella mobilis</i>
ID=269	WP_040200587	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=270	WP_040200586	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=271	WP_040200585	bacteriophage head to tail connecting protein	<i>Klebsiella pneumoniae</i>
ID=272	WP_064158774	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=273	WP_064408069	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=274	WP_048275925	hypothetical protein	<i>Pluralibacter gergoviae</i>
ID=275	WP_040200581	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=276	WP_064158778	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=277	WP_041165607	N-acetyltransferase	<i>Klebsiella mobilis</i>
ID=278	WP_032750878	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=279	WP_023316195	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=280	WP_029687389	hypothetical protein	<i>Tatumella saanichensis</i>

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ID=281	WP_064167271	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=282	WP_060435418	hypothetical protein	<i>Serratia marcescens</i>
ID=283	WP_032705971	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=284	WP_064158782	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=285	WP_023282770	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=286	WP_053810469	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=288	WP_040147843	MULTISPECIES: holin	<i>Klebsiella</i>
ID=289	WP_049099746	lysozyme	<i>Klebsiella oxytoca</i>
ID=290	WP_004141014	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=291	WP_004177118	recombinase	<i>Klebsiella pneumoniae</i>
ID=292	WP_046083878	integrase	<i>Escherichia fergusonii</i>
ID=294	WP_045854289	peptide transporter	<i>Raoultella terrigena</i>
ID=295	WP_021515903	filamentous hemagglutinin	<i>Escherichia coli</i>
ID=296	WP_041144402	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=297	WP_041144403	membrane protein	<i>Raoultella ornithinolytica</i>
ID=298	WP_041144404	DUF4810 domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=299	WP_041144405	lipoprotein	<i>Raoultella ornithinolytica</i>
ID=300	WP_041144406	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=301	WP_045854296	serine hydrolase	<i>Raoultella terrigena</i>
ID=302	WP_041144408	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=303	WP_045854298	hypothetical protein	<i>Raoultella terrigena</i>
ID=304	WP_045854299	membrane protein	<i>Raoultella terrigena</i>
ID=305	WP_045854301	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=306	WP_045854302	hypothetical protein	<i>Raoultella terrigena</i>
ID=307	WP_045854303	hypothetical protein	<i>Raoultella terrigena</i>
ID=308	WP_052698700	hypothetical protein	<i>Raoultella terrigena</i>
ID=309	WP_045854304	hypothetical protein	<i>Raoultella terrigena</i>
ID=310	WP_045854305	protein-tyrosine-phosphatase	<i>Raoultella terrigena</i>
ID=311	WP_045854306	PTS mannose transporter subunit IID	<i>Raoultella terrigena</i>
ID=312	WP_045854307	PTS sorbose transporter subunit IIC	<i>Raoultella terrigena</i>
ID=313	WP_045854308	PTS sugar transporter	<i>Raoultella terrigena</i>
ID=314	WP_045854309	PTS mannose transporter subunit IIAB	<i>Raoultella terrigena</i>
ID=315	WP_045854310	RpiR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=316	WP_045854311	AraC family transcriptional regulator	<i>Raoultella terrigena</i>
ID=317	WP_045854312	chloroperoxidase	<i>Raoultella terrigena</i>
ID=318	WP_045854316	DNA-binding response regulator	<i>Raoultella terrigena</i>
ID=319	WP_052698701	two-component sensor histidine kinase	<i>Raoultella terrigena</i>
ID=320	WP_045854313	hypothetical protein	<i>Raoultella terrigena</i>
ID=321	WP_041144410	membrane protein	<i>Raoultella ornithinolytica</i>
ID=322	WP_041144411	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=323	WP_041144412	MULTISPECIES: DUF421 domain-containing protein	<i>Raoultella</i>
ID=324	WP_041144413	competence protein ComA	<i>Raoultella ornithinolytica</i>
ID=325	WP_041144414	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=326	WP_041144415	phosphoadenosine phosphosulfate reductase	<i>Raoultella ornithinolytica</i>
ID=327	WP_041144416	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=328	WP_041144417	GNAT family acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=329	WP_041144418	lipid A biosynthesis lauroyl acyltransferase	<i>Raoultella ornithinolytica</i>
ID=330	WP_041144419	antibiotic acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=331	WP_041144420	transcriptional regulator CadC	<i>Raoultella ornithinolytica</i>
ID=332	WP_041144421	lysine/cadaverine antiporter	<i>Raoultella ornithinolytica</i>
ID=333	WP_041144422	lysine decarboxylase LdcC	<i>Raoultella ornithinolytica</i>
ID=334	WP_041144423	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=335	WP_041144424	lysine--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=336	WP_041144425	deaminase	<i>Raoultella ornithinolytica</i>
ID=337	WP_045854326	carbamate kinase	<i>Raoultella terrigena</i>
ID=338	WP_045854327	hypothetical protein	<i>Raoultella terrigena</i>
ID=339	WP_041144428	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=340	WP_041144429	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=341	WP_041144430	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=342	WP_041144431	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=343	WP_041144432	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=344	WP_041144433	DNA breaking-rejoining protein	<i>Raoultella ornithinolytica</i>
ID=345	WP_041144434	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=345	WP_041144434	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=346	WP_041147543	MULTISPECIES: rhizopine-binding protein	<i>Raoultella</i>
ID=347	WP_041144435	D-ribose transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=348	WP_041144436	ABC transporter	<i>Raoultella ornithinolytica</i>
ID=349	WP_041144437	GGDEF domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=350	WP_041144438	Zn-dependent hydrolase	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=351	WP_041144439	2-amino-thiazoline-4-carboxylic acid hydrolase	<i>Raoultella ornithinolytica</i>
ID=352	WP_041144440	branched chain amino acid ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=353	WP_045854340	ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=354	WP_041144442	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=355	WP_041144443	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=356	WP_041144444	branched-chain amino acid ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=357	WP_041144445	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=358	WP_041144446	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=359	WP_041144447	sucrose operon repressor	<i>Raoultella ornithinolytica</i>
ID=360	WP_041144448	glycosyl hydrolase family 32	<i>Raoultella ornithinolytica</i>
ID=361	WP_045854347	PTS sucrose transporter subunit IIBC	<i>Raoultella terrigena</i>
ID=362	WP_045854348	porin	<i>Raoultella terrigena</i>
ID=363	WP_041144451	aminoimidazole riboside kinase	<i>Raoultella ornithinolytica</i>
ID=364	WP_041144452	Crp/Fnr family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=365	WP_041144453	GTPase	<i>Raoultella ornithinolytica</i>
ID=366	WP_041144454	membrane protein	<i>Raoultella ornithinolytica</i>
ID=367	WP_041144455	iron ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=368	WP_041144456	iron-siderophore ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=369	WP_041144457	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=370	WP_041144458	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=371	WP_041144459	membrane protein	<i>Raoultella ornithinolytica</i>
ID=372	WP_041144460	lipoprotein	<i>Raoultella ornithinolytica</i>
ID=373	WP_041144461	amidohydrolase	<i>Raoultella ornithinolytica</i>
ID=374	WP_041144462	MULTISPECIES: ABC transporter substrate-binding protein	<i>Raoultella</i>
ID=375	WP_041144463	alcohol dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=376	WP_015584964	molybdenum cofactor biosynthesis protein F	<i>Raoultella ornithinolytica</i>
ID=377	WP_064384199	3-oxoacyl-ACP reductase	<i>Klebsiella oxytoca</i>
ID=378	WP_046852991	arylsulfatase	<i>Raoultella ornithinolytica</i>
ID=379	WP_015584961	anaerobic sulfatase maturase	<i>Raoultella ornithinolytica</i>
ID=380	WP_032689061	MULTISPECIES: helix-turn-helix transcriptional regulator	<i>Enterobacteriaceae</i>
ID=381	WP_064384196	MFS transporter	<i>Klebsiella oxytoca</i>
ID=382	WP_047038941	class II histone deacetylase	<i>Klebsiella mobilis</i>
ID=383	WP_032696466	hypothetical protein	<i>Raoultella planticola</i>
ID=384	WP_047049430	APC family amino acid permease	<i>Klebsiella mobilis</i>
ID=385	WP_004859114	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=386	WP_004859120	FAD-dependent oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=387	WP_058676011	NAD-dependent phenylacetaldehyde dehydrogenase	<i>Klebsiella mobilis</i>
ID=388	WP_041144464	NADH dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=389	WP_045854359	periplasmic protein	<i>Raoultella terrigena</i>
ID=390	WP_041144466	TonB-dependent receptor	<i>Raoultella ornithinolytica</i>
ID=391	WP_041144467	phenylalanine transporter	<i>Raoultella ornithinolytica</i>
ID=392	WP_041144468	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=393	WP_045854363	AP endonuclease	<i>Raoultella terrigena</i>
ID=394	WP_041144470	dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=395	WP_045854365	hypothetical protein	<i>Raoultella terrigena</i>
ID=396	WP_041144473	LacI family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=397	WP_045854367	miniconductance mechanosensitive channel	<i>Raoultella terrigena</i>
ID=398	WP_045854368	MFS transporter	<i>Raoultella terrigena</i>
ID=399	WP_045854369	transcriptional regulator	<i>Raoultella terrigena</i>
ID=400	WP_041144477	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=401	WP_045854371	NAD(P)H-dependent oxidoreductase	<i>Raoultella terrigena</i>
ID=402	WP_041144479	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=403	WP_041144480	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=404	WP_045854373	MBL fold metallo-hydrolase	<i>Raoultella terrigena</i>
ID=405	WP_041144482	MULTISPECIES: DNA-binding transcriptional regulator RamA	<i>Raoultella</i>
ID=406	WP_045855418	ferrichrysobactin receptor	<i>Raoultella terrigena</i>
ID=407	WP_041144483	enterochelin esterase	<i>Raoultella ornithinolytica</i>
ID=410	WP_041144485	carbonate dehydratase	<i>Raoultella ornithinolytica</i>
ID=411	WP_041144485	carbonate dehydratase	<i>Raoultella ornithinolytica</i>
ID=412	WP_041144486	RND transporter MFP subunit	<i>Raoultella ornithinolytica</i>
ID=413	WP_041144487	multidrug RND transporter	<i>Raoultella ornithinolytica</i>
ID=414	WP_041144488	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=415	WP_041144489	glutamate--cysteine ligase	<i>Raoultella ornithinolytica</i>
ID=416	WP_041144490	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=417	WP_041144491	ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=418	WP_041144492	ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=419	WP_041144493	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=420	WP_041144494	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=421	WP_041144495	amidase	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=422	WP_041144496	Zn-dependent hydrolase	<i>Raoultella ornithinolytica</i>
ID=423	WP_041144497	GntR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=424	WP_041144498	amino acid ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=425	WP_041144499	ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=426	WP_041144500	MULTISPECIES: ABC transporter permease	<i>Raoultella</i>
ID=427	WP_041144501	glutamate ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=428	WP_041144502	sulfoacetaldehyde reductase	<i>Raoultella ornithinolytica</i>
ID=429	WP_041144503	aspartate aminotransferase family protein	<i>Raoultella ornithinolytica</i>
ID=430	WP_041144504	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=431	WP_045854395	ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=432	WP_041144506	peptide ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=433	WP_045854397	peptide ABC transporter permease	<i>Raoultella terrigena</i>
ID=434	WP_041144508	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=435	WP_041144509	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=436	WP_041144510	short chain dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=437	WP_041144511	SDR family oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=438	WP_045854402	sugar ABC transporter permease	<i>Raoultella terrigena</i>
ID=439	WP_041144513	sugar ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=440	WP_041144514	lipoprotein	<i>Raoultella ornithinolytica</i>
ID=441	WP_041144515	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=442	WP_045854406	carbohydrate kinase	<i>Raoultella terrigena</i>
ID=443	WP_045854407	DeoR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=444	WP_041144518	transketolase	<i>Raoultella ornithinolytica</i>
ID=445	WP_045854409	transketolase	<i>Raoultella terrigena</i>
ID=446	WP_041144520	enterobactin synthase	<i>Raoultella ornithinolytica</i>
ID=447	WP_041144521	outer membrane receptor protein	<i>Raoultella ornithinolytica</i>
ID=448	WP_052474476	enterochelin esterase	<i>Raoultella ornithinolytica</i>
ID=449	WP_045854413	invasin	<i>Raoultella terrigena</i>
ID=450	WP_041144523	enterobactin synthase subunit F	<i>Raoultella ornithinolytica</i>
ID=451	WP_041144524	iron-enterobactin transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=452	WP_041144525	iron-enterobactin transporter permease	<i>Raoultella ornithinolytica</i>
ID=453	WP_041144526	iron-enterobactin transporter membrane protein	<i>Raoultella ornithinolytica</i>
ID=454	WP_045854418	MFS transporter	<i>Raoultella terrigena</i>
ID=455	WP_041144528	Fe ²⁺ -enterobactin ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=456	WP_041144529	isochorismate synthase EntC	<i>Raoultella ornithinolytica</i>
ID=457	WP_045854520	2,3-dihydroxybenzoate-AMP ligase	<i>Raoultella terrigena</i>
ID=458	WP_041144530	isochorismatase	<i>Raoultella ornithinolytica</i>
ID=459	WP_041144531	MULTISPECIES: 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	<i>Raoultella</i>
ID=460	WP_045854421	thioesterase	<i>Raoultella terrigena</i>
ID=461	WP_045854422	carbon starvation protein A	<i>Raoultella terrigena</i>
ID=462	WP_041144534	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=463	WP_043018925	oxidoreductase	<i>Citrobacter freundii</i>
ID=464	WP_041144535	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=465	WP_041144536	ABC transporter	<i>Raoultella ornithinolytica</i>
ID=466	WP_041144537	sugar ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=467	WP_045854426	sugar ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=468	WP_045854427	hypothetical protein	<i>Raoultella terrigena</i>
ID=469	WP_041144540	S-methyl-5-thioribose kinase	<i>Raoultella ornithinolytica</i>
ID=470	WP_041144541	S-methyl-5-thioribose-1-phosphate isomerase	<i>Raoultella ornithinolytica</i>
ID=471	WP_041144542	3-phytase	<i>Raoultella ornithinolytica</i>
ID=472	WP_041144543	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=473	WP_041144544	inositol monophosphatase	<i>Raoultella ornithinolytica</i>
ID=474	WP_041144545	LacI family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=475	WP_041144546	cytosine deaminase	<i>Raoultella ornithinolytica</i>
ID=476	WP_045854431	Fis family transcriptional regulator	<i>Raoultella terrigena</i>
ID=477	WP_045854432	cytosine permease	<i>Raoultella terrigena</i>
ID=478	WP_041144548	methylthioribulose-1-phosphate dehydratase	<i>Raoultella ornithinolytica</i>
ID=479	WP_041144549	carbohydrate kinase	<i>Raoultella ornithinolytica</i>
ID=480	WP_041144550	dihydrofolate reductase	<i>Raoultella ornithinolytica</i>
ID=481	WP_041144551	kinase	<i>Raoultella ornithinolytica</i>
ID=482	WP_045854437	ABC transporter permease	<i>Raoultella terrigena</i>
ID=483	WP_041144553	MULTISPECIES: membrane protein	<i>Raoultella</i>
ID=484	WP_045854438	sugar ABC transporter ATPase	<i>Raoultella terrigena</i>
ID=485	WP_041144555	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=486	WP_041144556	biotin transporter BioY	<i>Raoultella ornithinolytica</i>
ID=487	WP_041144557	acireductone dioxygenase	<i>Raoultella ornithinolytica</i>
ID=488	WP_041144558	2,3-diketo-5-methylthio-1-phosphopentane phosphatase	<i>Raoultella ornithinolytica</i>
ID=489	WP_041144559	methionine aminotransferase	<i>Raoultella ornithinolytica</i>
ID=490	WP_041144560	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=491	WP_041144561	thiol:disulfide interchange protein DsbG	<i>Raoultella ornithinolytica</i>
ID=492	WP_045854446	alkyl hydroperoxide reductase	<i>Raoultella terrigena</i>
ID=493	WP_045854447	alkyl hydroperoxide reductase subunit F	<i>Raoultella terrigena</i>
ID=494	WP_041144564	universal stress protein UspG	<i>Raoultella ornithinolytica</i>
ID=495	WP_041144565	nucleoside diphosphate kinase regulator	<i>Raoultella ornithinolytica</i>
ID=496	WP_041144566	chloroperoxidase	<i>Raoultella ornithinolytica</i>
ID=497	WP_041144567	ribonuclease I	<i>Raoultella ornithinolytica</i>
ID=498	WP_041144568	anaerobic C4-dicarboxylate transporter DcuC	<i>Raoultella ornithinolytica</i>
ID=499	WP_052474478	phospholipid:lipid A palmitoyltransferase	<i>Raoultella ornithinolytica</i>
ID=500	WP_004859511	MULTISPECIES: cold-shock protein	<i>Enterobacteriaceae</i>
ID=501	WP_041144570	fluoride ion transporter CrcB	<i>Raoultella ornithinolytica</i>
ID=502	WP_045854455	hydrolase	<i>Raoultella terrigena</i>
ID=503	WP_041144572	MULTISPECIES: sec-independent protein translocase tatE	<i>Raoultella</i>
ID=504	WP_041144573	lipoyl synthase	<i>Raoultella ornithinolytica</i>
ID=505	WP_041144574	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=506	WP_041144575	octanoyltransferase	<i>Raoultella ornithinolytica</i>
ID=507	WP_041144576	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=508	WP_004147578	serine-type D-Ala-D-Ala carboxypeptidase	<i>Klebsiella pneumoniae</i>
ID=509	WP_041144578	rare lipoprotein A	<i>Raoultella ornithinolytica</i>
ID=510	WP_041144579	cell wall shape-determining protein	<i>Raoultella ornithinolytica</i>
ID=511	WP_041144580	penicillin-binding protein 2	<i>Raoultella ornithinolytica</i>
ID=512	WP_041144581	MULTISPECIES: 23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	<i>Raoultella</i>
ID=513	WP_004859547	MULTISPECIES: ribosome silencing factor RsfS	<i>Enterobacteriaceae</i>
ID=514	WP_041144582	alpha-ribazole phosphatase	<i>Raoultella ornithinolytica</i>
ID=515	WP_041144583	nicotinate-nicotinamide nucleotide adenyllyltransferase	<i>Raoultella ornithinolytica</i>
ID=516	WP_041144584	DNA polymerase III subunit delta	<i>Raoultella ornithinolytica</i>
ID=517	WP_041144585	LPS assembly lipoprotein LptE	<i>Raoultella ornithinolytica</i>
ID=518	WP_047068303	leucine--tRNA ligase	<i>Klebsiella mobilis</i>
ID=519	WP_041147547	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=520	WP_041144587	arginine transporter ATP-binding subunit	<i>Raoultella ornithinolytica</i>
ID=521	WP_041144588	MULTISPECIES: amino acid ABC transporter permease	<i>Raoultella</i>
ID=522	WP_041144589	amino acid ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=523	WP_041144590	glutamate/aspartate ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=524	WP_041144591	apolipoprotein N-acyltransferase	<i>Raoultella ornithinolytica</i>
ID=525	WP_041144592	MULTISPECIES: magnesium/cobalt efflux protein CorC	<i>Raoultella</i>
ID=526	WP_041144593	MULTISPECIES: rRNA maturation RNase YbeY	<i>Raoultella</i>
ID=527	WP_041144594	MULTISPECIES: nucleoside triphosphate hydrolase	<i>Raoultella</i>
ID=528	WP_041144595	MULTISPECIES: tRNA (N6-isopentenyl adenosine(37)-C2)-methylthiotransferase MiaB	<i>Raoultella</i>
ID=530	WP_041144596	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	<i>Raoultella ornithinolytica</i>
ID=531	WP_041144597	asparagine synthase B	<i>Raoultella ornithinolytica</i>
ID=532	WP_041147548	UMP phosphatase	<i>Raoultella ornithinolytica</i>
ID=533	WP_045854474	transcriptional regulator	<i>Raoultella terrigena</i>
ID=534	WP_045854475	N-acetylglucosamine-6-phosphate deacetylase	<i>Raoultella terrigena</i>
ID=535	WP_045854476	glucosamine-6-phosphate deaminase	<i>Raoultella terrigena</i>
ID=536	WP_045854477	PTS N-acetyl glucosamine transporter subunit IIAABC	<i>Raoultella terrigena</i>
ID=537	WP_041144602	glutamine--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=538	WP_041144603	chitoporphin	<i>Raoultella ornithinolytica</i>
ID=539	WP_041144604	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=540	WP_041144605	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=541	WP_041144606	tricarballoylate utilization protein B	<i>Raoultella ornithinolytica</i>
ID=542	WP_041144607	tricarballoylate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=543	WP_041144608	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=544	WP_041144609	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=545	WP_041144610	MULTISPECIES: flavodoxin FldA	<i>Raoultella</i>
ID=546	WP_041144611	MULTISPECIES: LexA regulated protein	<i>Raoultella</i>
ID=547	WP_041144612	acyl-CoA esterase	<i>Raoultella ornithinolytica</i>
ID=548	WP_041144613	replication initiation regulator SeqA	<i>Raoultella ornithinolytica</i>
ID=549	WP_041144614	MULTISPECIES: phosphoglucomutase, alpha-D-glucose phosphate-specific	<i>Raoultella</i>
ID=550	WP_041144615	MULTISPECIES: DNA-binding response regulator	<i>Raoultella</i>
ID=551	WP_041144616	two-component sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=552	WP_041144617	potassium-transporting ATPase subunit C	<i>Raoultella ornithinolytica</i>
ID=553	WP_041144618	K+-transporting ATPase subunit B	<i>Raoultella ornithinolytica</i>
ID=554	WP_045854487	potassium-transporting ATPase subunit KdpA	<i>Raoultella terrigena</i>
ID=555	WP_041144620	K+-transporting ATPase subunit F	<i>Raoultella ornithinolytica</i>
ID=556	WP_004130508	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=557	WP_045854490	deoxyribodipyrimidine photo-lyase	<i>Raoultella terrigena</i>
ID=558	WP_041144623	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=559	WP_041144624	MULTISPECIES: Nif3-like dinuclear metal center hexameric protein	<i>Raoultella</i>
ID=560	WP_041144625	hypothetical protein	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=561	WP_041144626	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=562	WP_041144627	LamB/YcsF family protein	<i>Raoultella ornithinolytica</i>
ID=563	WP_045854495	pyroglutamyl-peptidase I	<i>Raoultella terrigena</i>
ID=564	WP_041144629	endonuclease VIII	<i>Raoultella ornithinolytica</i>
ID=565	WP_041144630	MULTISPECIES: citrate (Si)-synthase	<i>Raoultella</i>
ID=566	WP_045854497	succinate dehydrogenase cytochrome b556 large subunit	<i>Raoultella terrigena</i>
ID=567	WP_041144632	MULTISPECIES: succinate dehydrogenase	<i>Raoultella</i>
ID=568	WP_041144633	succinate dehydrogenase flavoprotein subunit	<i>Raoultella ornithinolytica</i>
ID=569	WP_041144634	succinate dehydrogenase iron-sulfur subunit	<i>Raoultella ornithinolytica</i>
ID=570	WP_041144635	2-oxoglutarate dehydrogenase subunit E1	<i>Raoultella ornithinolytica</i>
ID=571	WP_041144636	dihydrolipoamide succinyltransferase	<i>Raoultella ornithinolytica</i>
ID=572	WP_041144637	succinate--CoA ligase subunit beta	<i>Raoultella ornithinolytica</i>
ID=573	WP_041144638	MULTISPECIES: succinate--CoA ligase subunit alpha	<i>Raoultella</i>
ID=574	WP_041144639	cytochrome bd-I ubiquinol oxidase subunit I	<i>Raoultella ornithinolytica</i>
ID=575	WP_045854504	cytochrome d ubiquinol oxidase subunit 2	<i>Raoultella terrigena</i>
ID=576	WP_041144641	MULTISPECIES: cyd operon protein YbgE	<i>Raoultella</i>
ID=577	WP_041144642	MULTISPECIES: acyl-CoA thioesterase	<i>Raoultella</i>
ID=578	WP_041144643	MULTISPECIES: colicin transporter TolQ	<i>Raoultella</i>
ID=579	WP_065812193	protein TolR	<i>Klebsiella pneumoniae</i>
ID=580	WP_041144644	protein TolA	<i>Raoultella ornithinolytica</i>
ID=580	WP_041144644	protein TolA	<i>Raoultella ornithinolytica</i>
ID=581	WP_041144645	MULTISPECIES: translocation protein TolB	<i>Raoultella</i>
ID=582	WP_004859700	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=583	WP_041144646	cell division protein CpoB	<i>Raoultella ornithinolytica</i>
ID=584	WP_045854508	quinolinate synthetase	<i>Raoultella terrigena</i>
ID=585	WP_045854509	nicotinamide riboside transporter PnuC	<i>Raoultella terrigena</i>
ID=586	WP_045854510	zinc transporter ZitB	<i>Raoultella terrigena</i>
ID=587	WP_041144650	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=588	WP_041144651	3-deoxy-7-phosphoheptulonate synthase	<i>Raoultella ornithinolytica</i>
ID=589	WP_041144652	phosphoglyceromutase	<i>Raoultella ornithinolytica</i>
ID=590	WP_041144653	galactose mutarotase	<i>Raoultella ornithinolytica</i>
ID=591	WP_041144654	galactokinase	<i>Raoultella ornithinolytica</i>
ID=592	WP_041144655	galactose-1-phosphate uridylyltransferase	<i>Raoultella ornithinolytica</i>
ID=593	WP_041144656	MULTISPECIES: UDP-glucose 4-epimerase	<i>Raoultella</i>
ID=594	WP_041144657	molybdate ABC transporter ATP-binding protein ModF	<i>Raoultella ornithinolytica</i>
ID=595	WP_041144658	molybdenum-dependent transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=596	WP_052672099	multidrug efflux pump-associated protein, AcrZ family	<i>Enterobacter cloacae</i>
ID=597	WP_045854519	molybdate ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=598	WP_041144661	MULTISPECIES: molybdate ABC transporter permease	<i>Raoultella</i>
ID=599	WP_041144662	molybdenum ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=600	WP_041144663	pyridoxal phosphatase	<i>Raoultella ornithinolytica</i>
ID=601	WP_041144664	6-phosphogluconolactonase	<i>Raoultella ornithinolytica</i>
ID=602	WP_041144665	membrane protein	<i>Raoultella ornithinolytica</i>
ID=603	WP_041144666	RNA polymerase sigma factor	<i>Raoultella ornithinolytica</i>
ID=604	WP_041144667	tetratricopeptide repeat-containing protein	<i>Raoultella ornithinolytica</i>
ID=605	WP_041144668	acyl-CoA thioesterase	<i>Raoultella ornithinolytica</i>
ID=606	WP_041144669	imidazolonepropionase	<i>Raoultella ornithinolytica</i>
ID=607	WP_041144670	formimidoylglutamase	<i>Raoultella ornithinolytica</i>
ID=608	WP_041147549	histidine utilization repressor	<i>Raoultella ornithinolytica</i>
ID=609	WP_041144671	urocanate hydratase	<i>Raoultella ornithinolytica</i>
ID=610	WP_041144672	histidine ammonia-lyase	<i>Raoultella ornithinolytica</i>
ID=611	WP_041144673	proline-specific permease	<i>Raoultella ornithinolytica</i>
ID=612	WP_041144674	MULTISPECIES: kinase inhibitor	<i>Raoultella</i>
ID=613	WP_041147550	adenosylmethionine--8-amino-7-oxononanoate aminotransferase BioA	<i>Raoultella ornithinolytica</i>
ID=614	WP_041144675	biotin synthase	<i>Raoultella ornithinolytica</i>
ID=615	WP_041144676	8-amino-7-oxononanoate synthase	<i>Raoultella ornithinolytica</i>
ID=616	WP_041144677	malonyl-[acyl-carrier protein] O-methyltransferase BioC	<i>Raoultella ornithinolytica</i>
ID=617	WP_041144678	dethiobiotin synthase	<i>Raoultella ornithinolytica</i>
ID=618	WP_041144679	branched-chain amino acid ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=619	WP_041144680	excinuclease ABC subunit B	<i>Raoultella ornithinolytica</i>
ID=620	WP_041144681	two-component sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=621	WP_045854540	DNA-binding response regulator	<i>Raoultella terrigena</i>
ID=622	WP_041144683	phosphoethanolamine transferase EptA	<i>Raoultella ornithinolytica</i>
ID=623	WP_041144684	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=624	WP_045854543	cyclic pyranopterin phosphate synthase MoaA	<i>Raoultella terrigena</i>
ID=625	WP_041144686	molybdenum cofactor biosynthesis protein	<i>Raoultella ornithinolytica</i>
ID=626	WP_041144687	cyclic pyranopterin monophosphate synthase accessory protein	<i>Raoultella ornithinolytica</i>
ID=627	WP_041147551	molybdopterin synthase sulfur carrier subunit	<i>Raoultella ornithinolytica</i>
ID=628	WP_041144688	MULTISPECIES: molybdopterin guanine dinucleotide biosynthesis protein MoaE	<i>Raoultella</i>

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ID=629	WP_041144689	membrane protein	<i>Raoultella ornithinolytica</i>
ID=630	WP_041144690	membrane protein	<i>Raoultella ornithinolytica</i>
ID=631	WP_041144691	cardiolipin synthase B	<i>Raoultella ornithinolytica</i>
ID=632	WP_041144692	EEP domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=633	WP_041144693	membrane protein	<i>Raoultella ornithinolytica</i>
ID=634	WP_041144694	membrane protein	<i>Raoultella ornithinolytica</i>
ID=635	WP_041144695	membrane protein	<i>Raoultella ornithinolytica</i>
ID=636	WP_045854553	multidrug ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=637	WP_041144697	secretion protein HlyD	<i>Raoultella ornithinolytica</i>
ID=638	WP_041144698	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=639	WP_041144699	ATP-dependent RNA helicase RhlE	<i>Raoultella ornithinolytica</i>
ID=640	WP_041144700	ATP-dependent DNA helicase DinG	<i>Raoultella ornithinolytica</i>
ID=641	WP_041144701	DNA-binding protein YbiB	<i>Raoultella ornithinolytica</i>
ID=642	WP_041144702	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=643	WP_041147552	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=644	WP_041144703	PKHD-type hydroxylase	<i>Raoultella ornithinolytica</i>
ID=645	WP_041147553	catechol siderophore receptor Fiu	<i>Raoultella ornithinolytica</i>
ID=646	WP_041144704	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=647	WP_045854562	Asp/Glu/hydantoin racemase	<i>Raoultella terrigena</i>
ID=648	WP_041144706	23S rRNA (adenine(1618)-N(6))-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=649	WP_045854564	mechanosensitive channel protein	<i>Raoultella terrigena</i>
ID=650	WP_041144707	glutamine ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=651	WP_041144708	glutamine ABC transporter permease GlnP	<i>Raoultella ornithinolytica</i>
ID=652	WP_041144709	amino acid ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=653	WP_041144710	DNA starvation/stationary phase protection protein	<i>Raoultella ornithinolytica</i>
ID=654	WP_041144711	threonine/homoserine exporter RhtA	<i>Raoultella ornithinolytica</i>
ID=655	WP_041144712	membrane protein	<i>Raoultella ornithinolytica</i>
ID=656	WP_041144713	phosphoethanolamine transferase	<i>Raoultella ornithinolytica</i>
ID=657	WP_041144714	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=658	WP_041144715	transcriptional regulator MntR	<i>Raoultella ornithinolytica</i>
ID=659	WP_041144716	anion transporter	<i>Raoultella ornithinolytica</i>
ID=660	WP_041144717	aldo/keto reductase	<i>Raoultella ornithinolytica</i>
ID=661	WP_045854576	6-phospho-beta-glucosidase	<i>Raoultella terrigena</i>
ID=662	WP_045854577	PTS cellobiose transporter subunit IIC	<i>Raoultella terrigena</i>
ID=663	WP_045854578	GntR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=664	WP_052474481	L,D-transpeptidase	<i>Raoultella ornithinolytica</i>
ID=665	WP_041144720	ABC-F family ATPase	<i>Raoultella ornithinolytica</i>
ID=666	WP_045854580	alpha-glucosidase	<i>Raoultella terrigena</i>
ID=667	WP_041144722	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=668	WP_041144723	LacI family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=669	WP_041144724	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=670	WP_041144725	sugar-phosphatase	<i>Raoultella ornithinolytica</i>
ID=671	WP_041147556	glycyl radical enzyme	<i>Raoultella ornithinolytica</i>
ID=672	WP_045854584	pyruvate formate lyase-activating protein	<i>Raoultella terrigena</i>
ID=673	WP_041144726	pyruvate formate lyase-activating protein	<i>Raoultella ornithinolytica</i>
ID=674	WP_041144727	molybdopterin-synthase adenyltransferase MoeB	<i>Raoultella ornithinolytica</i>
ID=675	WP_041144728	molybdopterin molybdenumtransferase MoeA	<i>Raoultella ornithinolytica</i>
ID=676	WP_041144729	beta-aspartyl-peptidase	<i>Raoultella ornithinolytica</i>
ID=677	WP_041144730	glutathione ABC transporter ATP-binding protein GsiA	<i>Raoultella ornithinolytica</i>
ID=678	WP_041144731	glutathione ABC transporter substrate-binding protein GsiB	<i>Raoultella ornithinolytica</i>
ID=679	WP_041144732	glutathione ABC transporter permease GsiC	<i>Raoultella ornithinolytica</i>
ID=680	WP_045854591	glutathione ABC transporter permease GsiD	<i>Raoultella terrigena</i>
ID=681	WP_041144734	ribosomal protein S12 methyltransferase	<i>Raoultella ornithinolytica</i>
ID=682	WP_041144735	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=683	WP_045854597	biofilm formation regulatory protein BssR	<i>Raoultella terrigena</i>
ID=684	WP_041144736	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=685	WP_045854599	glutathione S-transferase	<i>Raoultella terrigena</i>
ID=686	WP_041144738	serine-type D-Ala-D-Ala carboxypeptidase	<i>Raoultella ornithinolytica</i>
ID=687	WP_045854601	DNA-binding transcriptional repressor DeoR	<i>Raoultella terrigena</i>
ID=688	WP_045854602	undecaprenyl-diphosphatase	<i>Raoultella terrigena</i>
ID=689	WP_045854603	multidrug transporter MdfA	<i>Raoultella terrigena</i>
ID=690	WP_041144742	MULTISPECIES: sugar-phosphatase	<i>Raoultella</i>
ID=691	WP_045854604	MFS transporter	<i>Raoultella terrigena</i>
ID=692	WP_041144744	DeoR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=693	WP_041147558	MULTISPECIES: transporter	<i>Raoultella</i>
ID=694	WP_041144745	membrane protein	<i>Raoultella ornithinolytica</i>
ID=695	WP_004859945	MULTISPECIES: glutaredoxin, GrxA family	<i>Enterobacteriaceae</i>
ID=696	WP_041144746	membrane protein	<i>Raoultella ornithinolytica</i>
ID=697	WP_041144747	NADPH-dependent oxidoreductase	<i>Raoultella ornithinolytica</i>

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ID=698	WP_041144748	MULTISPECIES: ribosomal protein S6 modification protein	<i>Raoultella</i>
ID=699	WP_041144749	YbjN domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=700	WP_041144750	MULTISPECIES: spermidine/putrescine ABC transporter substrate-binding protein PotF	<i>Raoultella</i>
ID=701	WP_052474483	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=702	WP_041144751	putrescine ABC transporter permease PotH	<i>Raoultella ornithinolytica</i>
ID=703	WP_041144752	putrescine ABC transporter permease PotI	<i>Raoultella ornithinolytica</i>
ID=704	WP_041144753	membrane protein	<i>Raoultella ornithinolytica</i>
ID=705	WP_045854614	23S rRNA (uracil(747)-C(5))-methyltransferase	<i>Raoultella terrigena</i>
ID=706	WP_041144755	DNA-binding response regulator	<i>Raoultella ornithinolytica</i>
ID=707	WP_041144756	two-component sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=708	WP_045854617	arginine ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=709	WP_045854618	arginine transporter permease subunit ArtM	<i>Raoultella terrigena</i>
ID=710	WP_041144759	arginine transporter permease subunit ArtQ	<i>Raoultella ornithinolytica</i>
ID=711	WP_041147560	arginine ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=712	WP_041144760	MULTISPECIES: arginine ABC transporter ATP-binding protein ArtP	<i>Raoultella</i>
ID=713	WP_041144761	lipoprotein	<i>Raoultella ornithinolytica</i>
ID=714	WP_041147561	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=715	WP_041144762	fatty acid transporter	<i>Raoultella ornithinolytica</i>
ID=716	WP_015704862	hypothetical protein	<i>Enterobacteriaceae</i>
ID=717	WP_041147563	N-acetylmuramoyl-L-alanine amidase	<i>Raoultella ornithinolytica</i>
ID=718	WP_041144763	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=719	WP_041144764	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=720	WP_041144765	low-specificity L-threonine aldolase	<i>Raoultella ornithinolytica</i>
ID=721	WP_041144766	pyruvate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=722	WP_041144767	GntR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=723	WP_041144768	hybrid-cluster NAD(P)-dependent oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=724	WP_041147564	hydroxylamine reductase	<i>Raoultella ornithinolytica</i>
ID=725	WP_041144769	membrane protein	<i>Raoultella ornithinolytica</i>
ID=726	WP_041144770	aquaporin	<i>Raoultella ornithinolytica</i>
ID=727	WP_041144771	ATP-dependent endonuclease	<i>Raoultella ornithinolytica</i>
ID=728	WP_041144771	ATP-dependent endonuclease	<i>Raoultella ornithinolytica</i>
ID=729	WP_041144772	macrolide transporter subunit MacA	<i>Raoultella ornithinolytica</i>
ID=730	WP_041144773	MacB family efflux pump subunit	<i>Raoultella ornithinolytica</i>
ID=731	WP_041144774	stationary phase/starvation inducible regulatory protein CspD	<i>Raoultella ornithinolytica</i>
ID=732	WP_041144775	MULTISPECIES: ATP-dependent Clp protease adaptor ClpS	<i>Raoultella</i>
ID=733	WP_041144776	ATP-dependent Clp protease ATP-binding subunit ClpA	<i>Raoultella ornithinolytica</i>
ID=734	WP_002211347	MULTISPECIES: translation initiation factor IF-1	<i>Proteobacteria</i>
ID=735	WP_041147565	MULTISPECIES: leucyl/phenylalanyl-tRNA--protein transferase	<i>Raoultella</i>
ID=736	WP_041144777	amino acid ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=737	WP_041144778	thiol reductant ABC exporter subunit CydD	<i>Raoultella ornithinolytica</i>
ID=738	WP_041144779	thioredoxin-disulfide reductase	<i>Raoultella ornithinolytica</i>
ID=739	WP_000228469	MULTISPECIES: leucine-responsive regulatory protein	<i>Proteobacteria</i>
ID=740	WP_041144780	DNA translocase FtsK	<i>Raoultella ornithinolytica</i>
ID=741	WP_041144781	MULTISPECIES: outer membrane lipoprotein carrier protein LolA	<i>Raoultella</i>
ID=742	WP_041144782	recombination factor protein RarA	<i>Raoultella ornithinolytica</i>
ID=743	WP_041144783	serine--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=744	WP_041144784	dimethyl sulfoxide reductase subunit A	<i>Raoultella ornithinolytica</i>
ID=745	WP_041144785	MULTISPECIES: dimethylsulfoxide reductase, chain B	<i>Raoultella</i>
ID=746	WP_041144786	dimethyl sulfoxide reductase	<i>Raoultella ornithinolytica</i>
ID=747	WP_041144787	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=748	WP_045854643	PTS sugar transporter subunit IIA	<i>Raoultella terrigena</i>
ID=749	WP_045854644	transketolase	<i>Raoultella terrigena</i>
ID=750	WP_052698704	transketolase	<i>Raoultella terrigena</i>
ID=751	WP_045854645	PTS beta-glucoside transporter subunit IIBC	<i>Raoultella terrigena</i>
ID=752	WP_045854646	PTS ascorbate transporter subunit IIB	<i>Raoultella terrigena</i>
ID=753	WP_045854647	RpiR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=754	WP_045854648	pyruvate formate lyase 1-activating protein	<i>Raoultella terrigena</i>
ID=755	WP_041144789	formate acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=756	WP_041144790	MULTISPECIES: formate transporter FocA	<i>Raoultella</i>
ID=757	WP_041144791	ribosomal protein S12 methylthiotransferase accessory factor YcaO	<i>Raoultella ornithinolytica</i>
ID=758	WP_041144792	DUF421 domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=759	WP_041144793	phosphoserine transaminase	<i>Raoultella ornithinolytica</i>
ID=760	WP_041144794	3-phosphoshikimate 1-carboxyvinyltransferase	<i>Raoultella ornithinolytica</i>
ID=761	WP_004219186	cytidylate kinase	<i>Klebsiella pneumoniae</i>
ID=762	WP_004860074	MULTISPECIES: 30S ribosomal protein S1	<i>Enterobacteriaceae</i>
ID=763	WP_004100704	MULTISPECIES: integration host factor subunit beta	<i>Enterobacteriales</i>
ID=765	WP_045854655	ComEC family protein	<i>Raoultella terrigena</i>
ID=766	WP_041144797	lipid ABC transporter permease/ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=767	WP_041144798	tetraacyldisaccharide 4'-kinase	<i>Raoultella ornithinolytica</i>

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ID=768	WP_045854658	hypothetical protein	<i>Raoultella terrigena</i>
ID=769	WP_041144800	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=770	WP_041144801	3-deoxy-manno-octulosonate cytidyltransferase	<i>Raoultella ornithinolytica</i>
ID=771	WP_041144802	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=772	WP_041144803	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=773	WP_041144804	S-adenosyl-L-methionine-dependent methyltransferase	<i>Raoultella ornithinolytica</i>
ID=774	WP_041144805	chromosome partition protein MukF	<i>Raoultella ornithinolytica</i>
ID=775	WP_041144806	condensin subunit E	<i>Raoultella ornithinolytica</i>
ID=776	WP_041144807	cell division protein MukB	<i>Raoultella ornithinolytica</i>
ID=777	WP_045854666	L,D-transpeptidase	<i>Raoultella terrigena</i>
ID=778	WP_041147566	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=779	WP_041144809	MBL fold metallo-hydrolase	<i>Raoultella ornithinolytica</i>
ID=780	WP_041144810	aromatic amino acid aminotransferase	<i>Raoultella ornithinolytica</i>
ID=781	WP_041144811	membrane protein	<i>Raoultella ornithinolytica</i>
ID=782	WP_041144812	MULTISPECIES: asparagine--tRNA ligase	<i>Raoultella</i>
ID=783	WP_041144813	nicotinate phosphoribosyltransferase	<i>Raoultella ornithinolytica</i>
ID=784	WP_041144814	aminopeptidase N	<i>Raoultella ornithinolytica</i>
ID=785	WP_041144815	aliphatic sulfonates ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=786	WP_041144816	MULTISPECIES: alkanesulfonate transporter permease subunit	<i>Raoultella</i>
ID=787	WP_041144817	alkanesulfonate monooxygenase	<i>Raoultella ornithinolytica</i>
ID=788	WP_045854674	aliphatic sulfonate ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=789	WP_041144819	NAD(P)H-dependent FMN reductase	<i>Raoultella ornithinolytica</i>
ID=790	WP_041144820	MULTISPECIES: dihydroorotate dehydrogenase 2	<i>Raoultella</i>
ID=791	WP_045854676	cell division protein ZapC	<i>Raoultella terrigena</i>
ID=792	WP_041144822	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=793	WP_041144823	23S rRNA (guanine(2445)-N(2))/(guanine(2069)-N(7))-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=794	WP_041144824	ABC transporter ATPase	<i>Raoultella ornithinolytica</i>
ID=795	WP_041144825	paraquat-inducible membrane protein A	<i>Raoultella ornithinolytica</i>
ID=796	WP_041144826	paraquat-inducible protein B	<i>Raoultella ornithinolytica</i>
ID=797	WP_045854682	lipoprotein	<i>Raoultella terrigena</i>
ID=798	WP_041144828	MULTISPECIES: beta-hydroxydecanoyl-ACP dehydratase	<i>Raoultella</i>
ID=799	WP_041144829	Lon protease	<i>Raoultella ornithinolytica</i>
ID=800	WP_041144830	MULTISPECIES: macrodomain Ter protein	<i>Raoultella</i>
ID=801	WP_045855437	porin OmpA	<i>Raoultella terrigena</i>
ID=802	WP_041144831	cell division inhibitor Sula	<i>Raoultella ornithinolytica</i>
ID=803	WP_041144832	competence protein	<i>Raoultella ornithinolytica</i>
ID=804	WP_041144833	membrane protein	<i>Raoultella ornithinolytica</i>
ID=805	WP_041144834	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=806	WP_045854687	DNA helicase IV	<i>Raoultella terrigena</i>
ID=807	WP_041147568	methylglyoxal synthase	<i>Raoultella ornithinolytica</i>
ID=808	WP_041144836	MULTISPECIES: CoA-binding protein	<i>Raoultella</i>
ID=809	WP_041144837	MULTISPECIES: heat-shock protein HspQ	<i>Raoultella</i>
ID=810	WP_041144838	23S rRNA (cytosine(1962)-C(5))-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=811	WP_045854689	kinase inhibitor	<i>Raoultella terrigena</i>
ID=812	WP_041144840	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=813	WP_041144841	MULTISPECIES: acylphosphatase	<i>Raoultella</i>
ID=814	WP_041144842	MULTISPECIES: sulfurtransferase TusE	<i>Raoultella</i>
ID=815	WP_041144843	MULTISPECIES: BAX inhibitor protein	<i>Raoultella</i>
ID=816	WP_045854691	peptide ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=817	WP_036102762	arabinose dehydrogenase	<i>Mangrovibacter sp.</i>
ID=818	WP_051691235	AraC family transcriptional regulator	<i>Mangrovibacter sp.</i>
ID=819	WP_015059223	alcohol dehydrogenase	<i>Escherichia coli</i>
ID=820	WP_007755444	hypothetical protein	<i>Cronobacter dublinensis</i>
ID=821	WP_015059225	hypothetical protein	<i>Escherichia coli</i>
ID=822	WP_007755439	4-carboxymuconolactone decarboxylase	<i>Cronobacter dublinensis</i>
ID=823	WP_007755437	LysR family transcriptional regulator	<i>Cronobacter dublinensis</i>
ID=824	WP_036102758	cystathionine beta-lyase	<i>Mangrovibacter sp.</i>
ID=825	WP_036102905	hypothetical protein	<i>Mangrovibacter sp.</i>
ID=826	WP_023320385	aldo/keto reductase	<i>Klebsiella oxytoca</i>
ID=827	WP_058663466	MULTISPECIES: MdaB protein	<i>Enterobacter cloacae</i>
ID=828	WP_032708034	oxidoreductase	<i>Klebsiella mobilis</i>
ID=829	WP_057616765	hypothetical protein	<i>Yersinia frederiksenii</i>
ID=830	WP_024908511	NAD(P)H dehydrogenase	<i>Enterobacter asburiae</i>
ID=831	WP_012540606	MULTISPECIES: LysR family transcriptional regulator	<i>Klebsiella</i>
ID=832	WP_041144849	membrane protein	<i>Raoultella ornithinolytica</i>
ID=833	WP_041144850	helix-turn-helix-type transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=834	WP_041144851	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=835	WP_041144852	short-chain dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=836	WP_041144853	FAD-dependent oxidoreductase	<i>Raoultella ornithinolytica</i>

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ID=837	WP_041144856	membrane protein	<i>Raoultella ornithinolytica</i>
ID=838	WP_041147569	GGDEF domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=839	WP_041147570	catalase	<i>Raoultella ornithinolytica</i>
ID=840	WP_045854734	cytochrome b	<i>Raoultella terrigena</i>
ID=841	WP_045854735	short-chain dehydrogenase DltE	<i>Raoultella terrigena</i>
ID=842	WP_045854736	hypothetical protein	<i>Raoultella terrigena</i>
ID=843	WP_045854737	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=844	WP_051899380	hypothetical protein	<i>Ewingella americana</i>
ID=845	WP_051899380	hypothetical protein	<i>Ewingella americana</i>
ID=846	WP_045854740	hypothetical protein	<i>Raoultella terrigena</i>
ID=847	WP_058758854	GntR family transcriptional regulator	<i>Pantoea dispersa</i>
ID=848	WP_021509564	GntR family transcriptional regulator	<i>Pantoea dispersa</i>
ID=849	WP_058770506	hypothetical protein	<i>Pantoea dispersa</i>
ID=850	WP_058775106	MFS transporter	<i>Pantoea dispersa</i>
ID=851	WP_038154544	two-component sensor histidine kinase	<i>Trabulsiella guamensis</i>
ID=852	WP_038154543	DNA-binding response regulator	<i>Trabulsiella guamensis</i>
ID=853	WP_054178728	alpha/beta hydrolase	<i>Trabulsiella odontotermitis</i>
ID=854	WP_018748417	TetR family transcriptional regulator	<i>Chitiniphilus shinanonensis</i>
ID=855	WP_002437305	MULTISPECIES: oxidoreductase	<i>Enterobacteriaceae</i>
ID=856	WP_041144861	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=857	WP_041144862	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=858	WP_041144863	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=859	WP_045854742	ethyl tert-butyl ether degradation protein EthD	<i>Raoultella terrigena</i>
ID=860	WP_041144864	alkane 1-monooxygenase	<i>Raoultella ornithinolytica</i>
ID=861	WP_045854744	gamma-glutamylcyclotransferase	<i>Raoultella terrigena</i>
ID=862	WP_045854745	hypothetical protein	<i>Raoultella terrigena</i>
ID=863	WP_045854746	hypothetical protein	<i>Raoultella terrigena</i>
ID=864	WP_045854747	hypothetical protein	<i>Raoultella terrigena</i>
ID=865	WP_045854748	hypothetical protein	<i>Raoultella terrigena</i>
ID=866	WP_041144870	xanthine hydroxylase reductase	<i>Raoultella ornithinolytica</i>
ID=867	WP_041147571	(2Fe-2S)-binding protein	<i>Raoultella ornithinolytica</i>
ID=868	WP_041144871	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=869	WP_041144872	monooxygenase	<i>Raoultella ornithinolytica</i>
ID=870	WP_041144873	OHCu decarboxylase	<i>Raoultella ornithinolytica</i>
ID=871	WP_041144874	hydroxyisourate hydrolase	<i>Raoultella ornithinolytica</i>
ID=872	WP_041144875	guanine deaminase	<i>Raoultella ornithinolytica</i>
ID=873	WP_041144876	nitrate reductase	<i>Raoultella ornithinolytica</i>
ID=874	WP_041144877	GntR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=875	WP_041144878	Asp/Glu racemase	<i>Raoultella ornithinolytica</i>
ID=876	WP_041144879	allantoinase	<i>Raoultella ornithinolytica</i>
ID=877	WP_041144880	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=878	WP_041144881	amidase	<i>Raoultella ornithinolytica</i>
ID=879	WP_041144882	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=880	WP_041144883	gamma-glutamyltransferase	<i>Raoultella ornithinolytica</i>
ID=881	WP_045854762	RpiR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=882	WP_041144885	MULTISPECIES: amino acid ABC transporter substrate-binding protein	<i>Raoultella</i>
ID=883	WP_041144886	polar amino acid ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=884	WP_041147572	amino acid ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=885	WP_041144887	MULTISPECIES: amino acid ABC transporter ATP-binding protein	<i>Raoultella</i>
ID=886	WP_041144888	aminotransferase V	<i>Raoultella ornithinolytica</i>
ID=887	WP_041144889	Zn-dependent hydrolase	<i>Raoultella ornithinolytica</i>
ID=888	WP_041144891	GGDEF domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=889	WP_061154356	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=890	WP_019341462	hypothetical protein	<i>Pseudomonas stutzeri</i>
ID=891	WP_032752108	MULTISPECIES: antitoxin	<i>Enterobacteriaceae</i>
ID=892	WP_032454142	MULTISPECIES: membrane protein	<i>Klebsiella</i>
ID=893	WP_012441311	N-acetyltransferase	<i>Erwinia tasmaniensis</i>
ID=894	WP_034888138	transposase	<i>Erwinia typographi</i>
ID=895	WP_052250260	transposase	<i>Enterobacter sp.</i>
ID=896	WP_041144901	4-aminobutyrate transaminase	<i>Raoultella ornithinolytica</i>
ID=897	WP_041144902	gamma-glutamylputrescine oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=898	WP_041144903	aldehyde dehydrogenase PuuC	<i>Raoultella ornithinolytica</i>
ID=899	WP_041144904	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=900	WP_041144905	gamma-glutamyl-gamma-aminobutyrate hydrolase	<i>Raoultella ornithinolytica</i>
ID=901	WP_041144906	gamma-glutamylputrescine synthetase	<i>Raoultella ornithinolytica</i>
ID=902	WP_045854782	putrescine importer PuuP	<i>Raoultella terrigena</i>
ID=904	WP_045854783	hypothetical protein	<i>Raoultella terrigena</i>
ID=905	WP_045854784	short-chain dehydrogenase	<i>Raoultella terrigena</i>
ID=906	WP_045854785	HxlR family transcriptional regulator	<i>Raoultella terrigena</i>

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ID=907	WP_045854786	bifunctional glucose-1-phosphatase/inositol phosphatase	<i>Raoultella terrigena</i>
ID=908	WP_041144910	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=909	WP_041144911	NAD(P)H:quinone oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=910	WP_041144912	MULTISPECIES: stress-induced protein	<i>Raoultella</i>
ID=911	WP_045854789	membrane protein	<i>Raoultella terrigena</i>
ID=912	WP_045854790	pyrimidine utilization transport protein G	<i>Raoultella terrigena</i>
ID=913	WP_041144915	pyrimidine utilization flavin reductase protein F	<i>Raoultella ornithinolytica</i>
ID=914	WP_041144916	nitroreductase family protein	<i>Raoultella ornithinolytica</i>
ID=915	WP_041144917	pyrimidine utilization protein D	<i>Raoultella ornithinolytica</i>
ID=916	WP_045854794	pyrimidine utilization protein C	<i>Raoultella terrigena</i>
ID=917	WP_045854795	pyrimidine utilization protein B	<i>Raoultella terrigena</i>
ID=918	WP_041147574	pyrimidine utilization protein A	<i>Raoultella ornithinolytica</i>
ID=919	WP_041144920	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=920	WP_041144921	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=921	WP_041144922	trifunctional transcriptional regulator/proline dehydrogenase/..L-glutamate gamma-semialdehyde dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=922	WP_041144923	sodium:proline symporter	<i>Raoultella ornithinolytica</i>
ID=923	WP_045854799	choline dehydrogenase	<i>Raoultella terrigena</i>
ID=924	WP_041144925	nucleoside permease	<i>Raoultella ornithinolytica</i>
ID=925	WP_041144926	iron permease	<i>Raoultella ornithinolytica</i>
ID=926	WP_045855449	iron uptake system component EfeO	<i>Raoultella terrigena</i>
ID=927	WP_041144928	peroxidase	<i>Raoultella ornithinolytica</i>
ID=928	WP_041144929	phosphate starvation protein PhoH	<i>Raoultella ornithinolytica</i>
ID=929	WP_041144930	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=930	WP_024149479	Zn-dependent hydrolase	<i>Salmonella enterica</i>
ID=931	WP_023245875	amidohydrolase	<i>Salmonella enterica</i>
ID=932	WP_023245876	LysR family transcriptional regulator	<i>Salmonella enterica</i>
ID=933	WP_023245877	hypothetical protein	<i>Salmonella enterica</i>
ID=934	WP_023245878	urocanate hydratase	<i>Salmonella enterica</i>
ID=935	WP_023245879	MFS transporter	<i>Salmonella enterica</i>
ID=936	WP_024913284	sugar transporter	<i>Chania multitudinisentens</i>
ID=937	WP_044346893	amino acid ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=938	WP_041144932	nicotinamidase	<i>Raoultella ornithinolytica</i>
ID=939	WP_041144933	quercetin 2,3-dioxygenase	<i>Raoultella ornithinolytica</i>
ID=940	WP_041144934	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=941	WP_024233282	hypothetical protein	<i>Escherichia coli</i>
ID=942	WP_049847314	hypothetical protein	<i>Trabulsiella odontotermis</i>
ID=943	WP_045854808	endoribonuclease	<i>Raoultella terrigena</i>
ID=944	WP_045854809	amino acid ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=945	WP_045854810	amino acid ABC transporter permease	<i>Raoultella terrigena</i>
ID=946	WP_045854811	polar amino acid ABC transporter permease	<i>Raoultella terrigena</i>
ID=947	WP_045854812	hypothetical protein	<i>Raoultella terrigena</i>
ID=948	WP_045854813	amino acid ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=949	WP_052698722	arginase	<i>Raoultella terrigena</i>
ID=950	WP_045854815	RpiR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=951	WP_041144935	glyoxylate/hydroxypyruvate reductase A	<i>Raoultella ornithinolytica</i>
ID=952	WP_045854817	phosphatase	<i>Raoultella terrigena</i>
ID=953	WP_041144937	molecular chaperone	<i>Raoultella ornithinolytica</i>
ID=954	WP_041144938	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=955	WP_041144939	O-acetyl-ADP-ribose deacetylase	<i>Raoultella ornithinolytica</i>
ID=956	WP_045855450	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=957	WP_041144940	glucans biosynthesis protein C	<i>Raoultella ornithinolytica</i>
ID=958	WP_041144941	glucan biosynthesis protein G	<i>Raoultella ornithinolytica</i>
ID=959	WP_045854823	glucan biosynthesis glucosyltransferase H	<i>Raoultella terrigena</i>
ID=960	WP_045854823	glucan biosynthesis glucosyltransferase H	<i>Raoultella terrigena</i>
ID=961	WP_041144943	MULTISPECIES: lipoprotein	<i>Raoultella</i>
ID=962	WP_045854824	secY/secA suppressor protein	<i>Raoultella terrigena</i>
ID=963	WP_041144945	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=964	WP_041144946	lipid A biosynthesis lauroyl acyltransferase	<i>Raoultella ornithinolytica</i>
ID=965	WP_041144947	sulfurtransferase	<i>Raoultella ornithinolytica</i>
ID=966	WP_041144948	N-methyltryptophan oxidase	<i>Raoultella ornithinolytica</i>
ID=967	WP_041144949	MULTISPECIES: biofilm formation regulatory protein BssS	<i>Raoultella</i>
ID=968	WP_041144950	DNA damage-inducible protein I	<i>Raoultella ornithinolytica</i>
ID=969	WP_041144951	dihydroorotase	<i>Raoultella ornithinolytica</i>
ID=970	WP_045854830	lipoprotein	<i>Raoultella terrigena</i>
ID=971	WP_041144953	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=972	WP_041144954	ribosomal protein S5 alanine N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=973	WP_041144955	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=974	WP_041144956	virulence factor MviM	<i>Raoultella ornithinolytica</i>

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ID=975	WP_041144957	lipid II flippase MurJ	<i>Raoultella ornithinolytica</i>
ID=976	WP_041144958	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=977	WP_045855452	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=978	WP_041144959	ribonuclease E	<i>Raoultella ornithinolytica</i>
ID=979	WP_041144959	ribonuclease E	<i>Raoultella ornithinolytica</i>
ID=980	WP_064793002	ribonuclease E	<i>Raoultella planticola</i>
ID=981	WP_000906654	hypothetical protein, partial	<i>Salmonella enterica</i>
ID=982	WP_041144960	MULTISPECIES: 23S rRNA pseudouridine(955/2504/2580) synthase	<i>Raoultella</i>
ID=983	WP_041144961	septum formation inhibitor Maf	<i>Raoultella ornithinolytica</i>
ID=984	WP_041144962	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=985	WP_041144963	phosphate acyltransferase	<i>Raoultella ornithinolytica</i>
ID=986	WP_041144964	3-oxoacyl-ACP synthase	<i>Raoultella ornithinolytica</i>
ID=987	WP_041144965	malonyl CoA-acyl carrier protein transacylase	<i>Raoultella ornithinolytica</i>
ID=988	WP_041144966	MULTISPECIES: beta-ketoacyl-ACP reductase	<i>Raoultella</i>
ID=989	WP_000103754	MULTISPECIES: acyl carrier protein	<i>Proteobacteria</i>
ID=990	WP_041144967	beta-ketoacyl-[acyl-carrier-protein] synthase II	<i>Raoultella ornithinolytica</i>
ID=991	WP_041144968	aminodeoxychorismate lyase	<i>Raoultella ornithinolytica</i>
ID=992	WP_041144969	cell division protein YceG	<i>Raoultella ornithinolytica</i>
ID=993	WP_041144970	dTMP kinase	<i>Raoultella ornithinolytica</i>
ID=994	WP_041144971	DNA polymerase III subunit delta'	<i>Raoultella ornithinolytica</i>
ID=995	WP_045854847	metal-dependent hydrolase	<i>Raoultella terrigena</i>
ID=996	WP_041144973	PTS glucose transporter subunit IIBC	<i>Raoultella ornithinolytica</i>
ID=997	WP_041144974	ferric-rhodotorulic acid/ferric-coprogen receptor FhuE	<i>Raoultella ornithinolytica</i>
ID=998	WP_041144975	MULTISPECIES: histidine triad nucleotide-binding protein	<i>Enterobacteriaceae</i>
ID=999	WP_041144976	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1000	WP_041144977	MULTISPECIES: penicillin-binding protein activator LpoB	<i>Raoultella</i>
ID=1001	WP_041144978	thiamine kinase	<i>Raoultella ornithinolytica</i>
ID=1002	WP_041144979	MULTISPECIES: beta-N-acetylhexosaminidase	<i>Raoultella</i>
ID=1003	WP_041144980	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=1004	WP_041144981	NADH dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1005	WP_052698707	hypothetical protein	<i>Raoultella terrigena</i>
ID=1006	WP_041144983	ligand-gated channel protein	<i>Raoultella ornithinolytica</i>
ID=1007	WP_041144984	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1008	WP_041144985	MULTISPECIES: multiple stress resistance protein BhsA	<i>Raoultella</i>
ID=1009	WP_041144986	peptidoglycan-binding protein LysM	<i>Raoultella ornithinolytica</i>
ID=1010	WP_041144987	transcription-repair coupling factor	<i>Raoultella ornithinolytica</i>
ID=1011	WP_041144988	outer membrane-specific lipoprotein transporter subunit LolC	<i>Raoultella ornithinolytica</i>
ID=1012	WP_041144989	lipoprotein ABC transporter ATP-binding protein LolD	<i>Raoultella ornithinolytica</i>
ID=1013	WP_041144990	lipoprotein transporter subunit LolE	<i>Raoultella ornithinolytica</i>
ID=1014	WP_041144991	N-acetylglucosamine kinase	<i>Raoultella ornithinolytica</i>
ID=1015	WP_041144992	NAD-dependent deacylase	<i>Raoultella ornithinolytica</i>
ID=1016	WP_045854863	hypothetical protein	<i>Raoultella terrigena</i>
ID=1017	WP_041144994	long-chain-fatty-acid--CoA ligase	<i>Raoultella ornithinolytica</i>
ID=1018	WP_041144995	spermidine/putrescine ABC transporter substrate-binding protein PotD	<i>Raoultella ornithinolytica</i>
ID=1019	WP_041144996	spermidine/putrescine ABC transporter permease PotC	<i>Raoultella ornithinolytica</i>
ID=1020	WP_045854867	spermidine/putrescine ABC transporter permease PotB	<i>Raoultella terrigena</i>
ID=1021	WP_041144998	putrescine/spermidine ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=1022	WP_041144998	putrescine/spermidine ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=1023	WP_041144999	peptidase T	<i>Raoultella ornithinolytica</i>
ID=1024	WP_045854870	50S ribosomal protein L16 arginine hydroxylase	<i>Raoultella terrigena</i>
ID=1025	WP_041145005	sensor protein PhoQ	<i>Raoultella ornithinolytica</i>
ID=1026	WP_041145006	DNA-binding response regulator	<i>Raoultella ornithinolytica</i>
ID=1027	WP_041145007	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1028	WP_041145008	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1029	WP_041145009	short-chain dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1030	WP_045854876	hypothetical protein	<i>Raoultella terrigena</i>
ID=1031	WP_045854877	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1032	WP_041145012	adenylosuccinate lyase	<i>Raoultella ornithinolytica</i>
ID=1033	WP_041145013	lysogenization protein HflD	<i>Raoultella ornithinolytica</i>
ID=1034	WP_045854880	tRNA(5-methylaminomethyl-2-thiouridine)-methyltransferase	<i>Raoultella terrigena</i>
ID=1035	WP_041145015	NUDIX hydrolase	<i>Raoultella ornithinolytica</i>
ID=1036	WP_041145016	23S rRNA pseudouridine synthase E	<i>Raoultella ornithinolytica</i>
ID=1037	WP_045854884	isocitrate dehydrogenase (NADP(+))	<i>Raoultella terrigena</i>
ID=1038	WP_015584580	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1039	WP_045854553	nickel/cobalt efflux protein RcnA	<i>Raoultella terrigena</i>
ID=1040	WP_045854885	transcriptional regulator	<i>Raoultella terrigena</i>
ID=1041	WP_045854886	outer membrane receptor protein	<i>Raoultella terrigena</i>
ID=1042	WP_045854887	anti-RssB factor	<i>Raoultella terrigena</i>
ID=1043	WP_041145021	hypothetical protein	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=1044	WP_041145022	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1045	WP_045855454	fusaric acid resistance protein	<i>Raoultella terrigena</i>
ID=1046	WP_041145024	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1047	WP_045854891	5-methyltetrahydropteroyltrimethylglutamate--homocysteine methyltransferase	<i>Raoultella terrigena</i>
ID=1048	WP_045854892	hypothetical protein	<i>Raoultella terrigena</i>
ID=1049	WP_041145027	glyoxalase	<i>Raoultella ornithinolytica</i>
ID=1050	WP_041145028	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1051	WP_041145029	cold-shock protein	<i>Raoultella ornithinolytica</i>
ID=1052	WP_041145030	NAD-dependent dehydratase	<i>Raoultella ornithinolytica</i>
ID=1053	WP_045854897	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1054	WP_007885348	MFS transporter	<i>Pantoea</i> sp.
ID=1055	WP_052465736	hypothetical protein	<i>Phaenobacter</i> sp.
ID=1056	WP_034455908	MFS transporter	<i>Buttiauxella agrestis</i>
ID=1057	WP_058909866	DeoR family transcriptional regulator	<i>Erwinia</i> sp.
ID=1058	WP_012145418	glycerol kinase	<i>Serratia proteamaculans</i>
ID=1059	WP_058909864	ethanolamine utilization protein EutH	<i>Erwinia</i> sp.
ID=1060	WP_061275705	hypothetical protein	<i>Cedecea neteri</i>
ID=1061	WP_012968001	MULTISPECIES: pyridine nucleotide-disulfide oxidoreductase	<i>Klebsiella</i>
ID=1062	WP_040240809	FAD/NAD(P)-binding oxidoreductase	<i>Klebsiella pneumoniae</i>
ID=1063	WP_025123571	MULTISPECIES: cupin	<i>Serratia</i>
ID=1064	WP_049851588	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	<i>Pantoea</i> sp.
ID=1065	WP_064518373	alpha/beta hydrolase	<i>Buttiauxella gaviniae</i>
ID=1066	WP_007885348	MFS transporter	<i>Pantoea</i> sp.
ID=1067	WP_025123574	MULTISPECIES: 3-oxoacyl-ACP reductase	<i>Serratia</i>
ID=1068	WP_045365087	histidinol dehydrogenase	<i>Klebsiella mobilis</i>
ID=1069	WP_032690352	MULTISPECIES: LacI family transcriptional regulator	<i>Enterobacteriaceae</i>
ID=1070	WP_045854898	DeoR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1071	WP_045854899	phosphodiesterase	<i>Raoultella terrigena</i>
ID=1072	WP_045854900	L-asparaginase	<i>Raoultella terrigena</i>
ID=1073	WP_041145035	iron ABC transporter	<i>Raoultella ornithinolytica</i>
ID=1074	WP_041145036	iron-dicitrate transporter subunit FecD	<i>Raoultella ornithinolytica</i>
ID=1075	WP_045854903	iron-dicitrate transporter permease subunit	<i>Raoultella terrigena</i>
ID=1076	WP_045854904	iron-dicitrate transporter substrate-binding subunit	<i>Raoultella terrigena</i>
ID=1077	WP_041145039	transporter	<i>Raoultella ornithinolytica</i>
ID=1078	WP_045854906	iron dicitrate transport regulator FecR	<i>Raoultella terrigena</i>
ID=1079	WP_041145041	RNA polymerase sigma factor FecI	<i>Raoultella ornithinolytica</i>
ID=1080	WP_045854908	SAM-dependent methyltransferase	<i>Raoultella terrigena</i>
ID=1081	WP_041145043	lipid A biosynthesis palmitoleoyl acyltransferase	<i>Raoultella ornithinolytica</i>
ID=1082	WP_041145044	leucine efflux protein	<i>Raoultella ornithinolytica</i>
ID=1083	WP_041145045	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1086	WP_041145047	diguanylate cyclase	<i>Raoultella ornithinolytica</i>
ID=1087	WP_041145049	MarR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1088	WP_045855457	purine-nucleoside phosphorylase	<i>Raoultella terrigena</i>
ID=1089	WP_041145050	HAAAP family serine/threonine permease	<i>Raoultella ornithinolytica</i>
ID=1090	WP_041145051	L-serine ammonia-lyase	<i>Raoultella ornithinolytica</i>
ID=1091	WP_041145052	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1092	WP_041145053	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1093	WP_041145054	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1094	WP_041145055	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1095	WP_041145057	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1096	WP_041147583	glycosyl transferase	<i>Raoultella ornithinolytica</i>
ID=1097	WP_041145058	tetrathionate reductase subunit A	<i>Raoultella ornithinolytica</i>
ID=1098	WP_041145058	tetrathionate reductase subunit A	<i>Raoultella ornithinolytica</i>
ID=1099	WP_041145059	tetrathionate reductase subunit C	<i>Raoultella ornithinolytica</i>
ID=1100	WP_041145060	tetrathionate reductase subunit B	<i>Raoultella ornithinolytica</i>
ID=1101	WP_041145061	sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=1102	WP_041147584	DNA-binding response regulator	<i>Raoultella ornithinolytica</i>
ID=1103	WP_041145062	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1104	WP_041145063	N-acetyl-gamma-glutamyl-phosphate reductase	<i>Raoultella ornithinolytica</i>
ID=1105	WP_041145064	cupin	<i>Raoultella ornithinolytica</i>
ID=1106	WP_041145065	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1107	WP_041145066	peptidase M20	<i>Raoultella ornithinolytica</i>
ID=1108	WP_041145067	beta-galactosidase	<i>Raoultella ornithinolytica</i>
ID=1109	WP_041145068	aryldialkylphosphatase	<i>Raoultella ornithinolytica</i>
ID=1110	WP_041145069	ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=1111	WP_041147585	MULTISPECIES: ABC transporter ATP-binding protein	<i>Raoultella</i>
ID=1112	WP_041145070	cytochrome-c peroxidase	<i>Raoultella ornithinolytica</i>
ID=1113	WP_045854957	sugar ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=1114	WP_041145072	carbohydrate kinase	<i>Raoultella ornithinolytica</i>

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ID=1115	WP_041145073	BtpA family membrane complex biogenesis protein	<i>Raoultella ornithinolytica</i>
ID=1116	WP_041145074	TenA family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1117	WP_041145075	GntR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1118	WP_041145076	PTS glucose transporter subunit IIBC	<i>Raoultella ornithinolytica</i>
ID=1119	WP_041145077	6-phospho-alpha-glucosidase	<i>Raoultella ornithinolytica</i>
ID=1120	WP_052698709	hypothetical protein	<i>Raoultella terrigena</i>
ID=1121	WP_045854968	AcrR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1122	WP_041144207	hemolysin secretion protein D	<i>Raoultella ornithinolytica</i>
ID=1123	WP_045854970	multidrug transporter	<i>Raoultella terrigena</i>
ID=1124	WP_038381485	amidase	<i>Pantoea sp.</i>
ID=1125	WP_058780997	histidinol dehydrogenase	<i>Pantoea dispersa</i>
ID=1126	WP_058780998	ester cyclase	<i>Pantoea dispersa</i>
ID=1127	WP_024965748	polyketide cyclase	<i>Pantoea sp.</i>
ID=1128	WP_024965747	LacI family transcriptional regulator	<i>Pantoea sp.</i>
ID=1129	WP_024965746	MFS transporter	<i>Pantoea sp.</i>
ID=1130	WP_041145086	DNA-binding protein	<i>Raoultella ornithinolytica</i>
ID=1131	WP_041145087	short-chain dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1132	WP_041145088	adenylyl-sulfate kinase	<i>Raoultella ornithinolytica</i>
ID=1133	WP_041145089	cupin	<i>Raoultella ornithinolytica</i>
ID=1134	WP_045854974	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1135	WP_045854963	branched-chain amino acid ABC transporter permease	<i>Raoultella terrigena</i>
ID=1136	WP_045854975	branched-chain amino acid transporter	<i>Raoultella terrigena</i>
ID=1137	WP_045854976	MFS transporter	<i>Raoultella terrigena</i>
ID=1138	WP_041145092	alpha/beta hydrolase	<i>Raoultella ornithinolytica</i>
ID=1139	WP_045854978	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1140	WP_041145094	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1141	WP_045854979	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1142	WP_041145096	CMY/LAT/MOX/ACT/MIR/FOX family class C beta-lactamase	<i>Raoultella ornithinolytica</i>
ID=1143	WP_041145098	cyclic diguanylate phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=1144	WP_041145099	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1145	WP_041145100	antibiotic biosynthesis monooxygenase	<i>Raoultella ornithinolytica</i>
ID=1146	WP_041145101	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1147	WP_041145102	serine protein kinase PrkA	<i>Raoultella ornithinolytica</i>
ID=1148	WP_041145103	MltA-interacting protein MipA	<i>Raoultella ornithinolytica</i>
ID=1149	WP_045855005	hypothetical protein	<i>Raoultella terrigena</i>
ID=1150	WP_041145105	permease	<i>Raoultella ornithinolytica</i>
ID=1151	WP_041145106	D-hexose-6-phosphate mutarotase	<i>Raoultella ornithinolytica</i>
ID=1152	WP_041145107	glycerakdehyde-3-phosphate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1153	WP_041145108	peptide-methionine (R)-S-oxide reductase	<i>Raoultella ornithinolytica</i>
ID=1154	WP_041145109	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1155	WP_041145110	HNH endonuclease	<i>Raoultella ornithinolytica</i>
ID=1156	WP_041145111	chitinase	<i>Raoultella ornithinolytica</i>
ID=1157	WP_041147587	nicotinamidase/pyrazinamidase	<i>Raoultella ornithinolytica</i>
ID=1158	WP_041145112	L-asparaginase I	<i>Raoultella ornithinolytica</i>
ID=1159	WP_041145113	signal peptide peptidase SppA	<i>Raoultella ornithinolytica</i>
ID=1160	WP_041145114	NAD(P)H nitroreductase	<i>Raoultella ornithinolytica</i>
ID=1161	WP_041145115	acid phosphatase	<i>Raoultella ornithinolytica</i>
ID=1162	WP_041145116	selenide, water dikinase	<i>Raoultella ornithinolytica</i>
ID=1163	WP_041145117	DNA topoisomerase III	<i>Raoultella ornithinolytica</i>
ID=1164	WP_045855019	glutamate dehydrogenase	<i>Raoultella terrigena</i>
ID=1165	WP_041147588	pyrimidine (deoxy)nucleoside triphosphate pyrophosphohydrolase	<i>Raoultella ornithinolytica</i>
ID=1166	WP_041145119	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1167	WP_041145120	sulfurtransferase	<i>Raoultella ornithinolytica</i>
ID=1168	WP_041145121	sulfate ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=1169	WP_041145122	thiamine ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=1170	WP_041145123	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=1171	WP_041145124	carboxymuconolactone decarboxylase family protein	<i>Raoultella ornithinolytica</i>
ID=1172	WP_041145125	TVP38/TMEM64 family protein	<i>Raoultella ornithinolytica</i>
ID=1173	WP_052474489	TVP38/TMEM64 family protein	<i>Raoultella ornithinolytica</i>
ID=1175	WP_041145127	exodeoxyribonuclease III	<i>Raoultella ornithinolytica</i>
ID=1176	WP_041145128	acetylornithine aminotransferase	<i>Raoultella ornithinolytica</i>
ID=1177	WP_041145129	arginine N-succinyltransferase	<i>Raoultella ornithinolytica</i>
ID=1178	WP_041145130	N-succinylglutamate 5-semialdehyde dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1179	WP_045855024	succinylarginine dihydrolase	<i>Raoultella terrigena</i>
ID=1180	WP_041145132	succinylglutamate desuccinylase	<i>Raoultella ornithinolytica</i>
ID=1181	WP_041145133	ATP-independent periplasmic protein-refolding chaperone	<i>Raoultella ornithinolytica</i>
ID=1182	WP_041145134	nucleotide excision repair endonuclease	<i>Raoultella ornithinolytica</i>
ID=1183	WP_045855467	NAD(+) synthetase	<i>Raoultella terrigena</i>
ID=1184	WP_041145135	transcriptional regulator	<i>Raoultella ornithinolytica</i>

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ID=1185	WP_041145136	MULTISPECIES: PTS sugar transporter subunit IIB	<i>Raoultella</i>
ID=1186	WP_041145137	MULTISPECIES: PTS N,N'-diacetylchitobiose transporter subunit IIC	<i>Raoultella</i>
ID=1187	WP_041145138	MULTISPECIES: PTS N,N'-diacetylchitobiose transporter subunit IIA	<i>Raoultella</i>
ID=1188	WP_041145139	transcriptional regulator ChbR	<i>Raoultella ornithinolytica</i>
ID=1189	WP_045855030	6-phospho-beta-glucosidase	<i>Raoultella terrigena</i>
ID=1190	WP_041145141	carbohydrate deacetylase	<i>Raoultella ornithinolytica</i>
ID=1191	WP_041145142	catalase	<i>Raoultella ornithinolytica</i>
ID=1192	WP_041145143	cell division modulator	<i>Raoultella ornithinolytica</i>
ID=1193	WP_041145144	L-cystine transporter tcyP	<i>Raoultella ornithinolytica</i>
ID=1194	WP_041145145	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1195	WP_041145146	2-deoxy-D-gluconate 3-dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1196	WP_041145147	2-deoxyglucose-6-phosphatase	<i>Raoultella ornithinolytica</i>
ID=1197	WP_041145148	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1198	WP_041145149	acyl-CoA thioesterase	<i>Raoultella ornithinolytica</i>
ID=1199	WP_041145150	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1200	WP_045855040	intracellular septation protein A	<i>Raoultella terrigena</i>
ID=1201	WP_041145152	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=1202	WP_004190785	outer membrane protein OmpW	<i>Klebsiella pneumoniae</i>
ID=1203	WP_041145154	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1204	WP_041145155	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1205	WP_041145156	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1206	WP_041145157	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1207	WP_041145158	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=1208	WP_041145160	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1209	WP_038990398	DNA polymerase V subunit UmuC	<i>Klebsiella pneumoniae</i>
ID=1210	WP_012016192	hypothetical protein	<i>Enterobacter sp.</i>
ID=1211	WP_015038833	SIR2 family protein	<i>Bordetella parapertussis</i>
ID=1212	WP_064757513	transposase	<i>Klebsiella pneumoniae</i>
ID=1213	WP_064838802	DUF159 family protein	<i>Klebsiella pneumoniae</i>
ID=1214	WP_065697244	outer membrane protein OmpW	<i>Klebsiella pneumoniae</i>
ID=1215	WP_041145163	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1216	WP_045855043	3-oxoacyl-ACP reductase	<i>Raoultella terrigena</i>
ID=1217	WP_041145165	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1218	WP_041145166	alcohol dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1219	WP_041145167	MarR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1220	WP_045855047	tryptophan synthase subunit alpha	<i>Raoultella terrigena</i>
ID=1221	WP_041145169	tryptophan synthase subunit beta	<i>Raoultella ornithinolytica</i>
ID=1222	WP_041145170	bifunctional indole-3-glycerol phosphate synthase/phosphoribosylanthranilate isomerase	<i>Raoultella ornithinolytica</i>
ID=1223	WP_041145171	bifunctional glutamine amidotransferase/anthranilate phosphoribosyltransferase	<i>Raoultella ornithinolytica</i>
ID=1224	WP_041145172	anthranilate synthase component I	<i>Raoultella ornithinolytica</i>
ID=1225	WP_041145173	phosphatase	<i>Raoultella ornithinolytica</i>
ID=1226	WP_041145174	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1227	WP_041145175	GGDEF domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=1228	WP_041145176	GGDEF domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=1229	WP_052474491	diguanylate cyclase	<i>Raoultella ornithinolytica</i>
ID=1230	WP_041145177	MULTISPECIES: 23S rRNA pseudouridylate synthase B	<i>Raoultella</i>
ID=1231	WP_041145178	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1232	WP_045855059	glycosyl hydrolase	<i>Raoultella terrigena</i>
ID=1233	WP_041145180	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1234	WP_045855060	AraC family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1235	WP_041145181	cob(I)yrinic acid a,c-diamide adenosyltransferase	<i>Raoultella ornithinolytica</i>
ID=1236	WP_041145182	NAD(P)-dependent oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=1238	WP_041145183	protease SohB	<i>Raoultella ornithinolytica</i>
ID=1239	WP_041145184	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=1240	WP_041145185	DNA topoisomerase I	<i>Raoultella ornithinolytica</i>
ID=1241	WP_041145186	MULTISPECIES: LysR family transcriptional regulator CysB	<i>Raoultella</i>
ID=1242	WP_065907334	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=1243	WP_041145187	aconitate hydratase I	<i>Raoultella ornithinolytica</i>
ID=1244	WP_041145188	MULTISPECIES: GTP cyclohydrolase II	<i>Raoultella</i>
ID=1245	WP_045855066	phosphatidylglycerophosphatase B	<i>Raoultella terrigena</i>
ID=1246	WP_041145190	MULTISPECIES: membrane protein	<i>Raoultella</i>
ID=1247	WP_041145191	lipopolysaccharide assembly protein LapB	<i>Raoultella ornithinolytica</i>
ID=1248	WP_041145192	orotidine 5'-phosphate decarboxylase	<i>Raoultella ornithinolytica</i>
ID=1249	WP_041145193	translation initiation factor	<i>Raoultella ornithinolytica</i>
ID=1251	WP_041145194	DeoR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1252	WP_041145195	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=1253	WP_041145196	exoribonuclease II	<i>Raoultella ornithinolytica</i>
ID=1254	WP_041145197	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1255	WP_041145198	enoyl-[acyl-carrier-protein] reductase	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=1256	WP_045855074	hutD family protein	<i>Raoultella terrigena</i>
ID=1257	WP_052474493	cytosine permease	<i>Raoultella ornithinolytica</i>
ID=1258	WP_041145205	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=1259	WP_041145206	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=1260	WP_045855078	antimicrobial peptide ABC transporter permease SapC	<i>Raoultella terrigena</i>
ID=1261	WP_041145208	antimicrobial peptide ABC transporter permease SapB	<i>Raoultella ornithinolytica</i>
ID=1262	WP_052474495	peptide ABC transporter substrate-binding protein SapA	<i>Raoultella ornithinolytica</i>
ID=1263	WP_041145209	cyclic diguanylate phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=1264	WP_045855083	PTS cellobiose transporter subunit IIB	<i>Raoultella terrigena</i>
ID=1265	WP_041145211	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1266	WP_041145212	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1267	WP_045855086	NAD-dependent dehydratase	<i>Raoultella terrigena</i>
ID=1268	WP_045855087	transcriptional regulator	<i>Raoultella terrigena</i>
ID=1269	WP_041145215	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1270	WP_041145216	amidohydrolase	<i>Raoultella ornithinolytica</i>
ID=1271	WP_041145217	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1272	WP_041147593	phage shock protein operon transcriptional activator	<i>Raoultella ornithinolytica</i>
ID=1273	WP_041147594	MULTISPECIES: phage shock protein PspA	<i>Raoultella</i>
ID=1274	WP_041145218	MULTISPECIES: phage shock protein B	<i>Raoultella</i>
ID=1275	WP_045855091	DNA-binding transcriptional activator PspC	<i>Raoultella terrigena</i>
ID=1276	WP_041145220	MULTISPECIES: phage-shock protein	<i>Raoultella</i>
ID=1277	WP_041147595	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1278	WP_041145221	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1279	WP_041145222	TyrR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1280	WP_041145223	AbrB family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1281	WP_041145224	2-Cys peroxiredoxin	<i>Raoultella ornithinolytica</i>
ID=1282	WP_041145225	dipeptide epimerase	<i>Raoultella ornithinolytica</i>
ID=1283	WP_045855098	murein peptide amidase A	<i>Raoultella terrigena</i>
ID=1284	WP_041145227	peptide ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=1285	WP_045855100	glutamine amidotransferase	<i>Raoultella terrigena</i>
ID=1289	WP_041145229	MULTISPECIES: DNA damage-inducible protein I	<i>Raoultella</i>
ID=1290	WP_041145231	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1291	WP_045855102	DNA polymerase V subunit UmuD	<i>Raoultella terrigena</i>
ID=1292	WP_045855103	DNA polymerase V subunit UmuC	<i>Raoultella terrigena</i>
ID=1293	WP_048288529	monooxygenase	<i>Pluralibacter gergoviae</i>
ID=1294	WP_045289744	metapyrocatechase	<i>Pluralibacter gergoviae</i>
ID=1295	WP_048282866	5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase	<i>Pluralibacter gergoviae</i>
ID=1296	WP_048282864	GntR family transcriptional regulator	<i>Pluralibacter gergoviae</i>
ID=1297	WP_045855105	oxidoreductase	<i>Raoultella terrigena</i>
ID=1298	WP_045855472	DeoR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1299	WP_045855473	periplasmic protein	<i>Raoultella terrigena</i>
ID=1300	WP_045855106	ferric-rhodotorulic acid transporter	<i>Raoultella terrigena</i>
ID=1301	WP_041145235	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=1302	WP_045855108	microcystin degradation protein MlrC	<i>Raoultella terrigena</i>
ID=1303	WP_045855109	transcriptional regulator	<i>Raoultella terrigena</i>
ID=1304	WP_045855110	glycosyl transferase	<i>Raoultella terrigena</i>
ID=1305	WP_045855111	peptide ABC transporter permease	<i>Raoultella terrigena</i>
ID=1306	WP_041145240	MULTISPECIES: diguanylate cyclase	<i>Raoultella</i>
ID=1307	WP_041145241	ROK family protein	<i>Raoultella ornithinolytica</i>
ID=1308	WP_045855113	zinc transporter ZntB	<i>Raoultella terrigena</i>
ID=1309	WP_041145243	ATP-dependent RNA helicase	<i>Raoultella ornithinolytica</i>
ID=1310	WP_045855115	tRNA 2-thiocytidine(32) synthetase TtcA	<i>Raoultella terrigena</i>
ID=1311	WP_041145245	universal stress protein F	<i>Raoultella ornithinolytica</i>
ID=1312	WP_041145247	porin	<i>Raoultella ornithinolytica</i>
ID=1313	WP_041145248	pyruvate:ferredoxin (flavodoxin) oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=1314	WP_041145249	porin	<i>Raoultella ornithinolytica</i>
ID=1315	WP_041145250	PTS sugar transporter subunit IIA	<i>Raoultella ornithinolytica</i>
ID=1316	WP_041145251	alpha-glucosidase	<i>Raoultella ornithinolytica</i>
ID=1317	WP_041145252	LacI family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1318	WP_041145253	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=1319	WP_041145254	heat-inducible protein	<i>Raoultella ornithinolytica</i>
ID=1320	WP_041145255	lactate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1321	WP_041145256	alkaline phosphatase	<i>Raoultella ornithinolytica</i>
ID=1322	WP_045855126	hypothetical protein	<i>Raoultella terrigena</i>
ID=1323	WP_041147599	lipoprotein	<i>Raoultella ornithinolytica</i>
ID=1324	WP_032700050	hypothetical protein	<i>Raoultella planticola</i>
ID=1325	WP_041145257	transcriptional regulator FeaR	<i>Raoultella ornithinolytica</i>
ID=1326	WP_041145258	aldehyde dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1327	WP_045855130	hypothetical protein	<i>Raoultella terrigena</i>

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ID=1328	WP_045855131	2-dehydropantoate 2-reductase	<i>Raoultella terrigena</i>
ID=1329	WP_045855476	alcohol dehydrogenase	<i>Raoultella terrigena</i>
ID=1330	WP_052474502	CHAP domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=1331	WP_045855133	hypothetical protein	<i>Raoultella terrigena</i>
ID=1332	WP_041145262	tyramine oxidase	<i>Raoultella ornithinolytica</i>
ID=1333	WP_041145263	bifunctional aldehyde dehydrogenase/enoyl-CoA hydratase	<i>Raoultella ornithinolytica</i>
ID=1334	WP_041145264	MULTISPECIES: phenylacetate-CoA oxygenase subunit PaaA	<i>Raoultella</i>
ID=1335	WP_041145265	MULTISPECIES: phenylacetate-CoA oxygenase subunit PaaB	<i>Raoultella</i>
ID=1336	WP_041145266	phenylacetate-CoA oxygenase subunit PaaI	<i>Raoultella ornithinolytica</i>
ID=1337	WP_041145267	phenylacetate-CoA oxygenase subunit PaaJ	<i>Raoultella ornithinolytica</i>
ID=1338	WP_041145268	phenylacetic acid degradation protein	<i>Raoultella ornithinolytica</i>
ID=1339	WP_041145269	2,3-dehydrodipyl-CoA hydratase	<i>Raoultella ornithinolytica</i>
ID=1340	WP_041147602	2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase	<i>Raoultella ornithinolytica</i>
ID=1341	WP_041145270	3-hydroxyacyl-CoA dehydrogenase PaaC	<i>Raoultella ornithinolytica</i>
ID=1342	WP_041145271	phenylacetic acid degradation protein PaaD	<i>Raoultella ornithinolytica</i>
ID=1343	WP_041145272	beta-ketoadipyl CoA thiolase	<i>Raoultella ornithinolytica</i>
ID=1344	WP_041145273	phenylacetate-CoA ligase	<i>Raoultella ornithinolytica</i>
ID=1345	WP_041145274	phenylacetic acid degradation operon negative regulatory protein PaaX	<i>Raoultella ornithinolytica</i>
ID=1346	WP_041145275	phenylacetic acid degradation protein PaaY	<i>Raoultella ornithinolytica</i>
ID=1347	WP_041145276	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=1348	WP_041145277	toxin RelE	<i>Raoultella ornithinolytica</i>
ID=1349	WP_041145278	MULTISPECIES: FMN-dependent NADH-azoreductase	<i>Raoultella</i>
ID=1350	WP_041145279	ATP-dependent helicase	<i>Raoultella ornithinolytica</i>
ID=1351	WP_011815231	MULTISPECIES: transposase	<i>Enterobacterales</i>
ID=1352	WP_049010774	MULTISPECIES: helicase	<i>Klebsiella</i>
ID=1354	WP_041146289	cysteine desulfurase	<i>Raoultella ornithinolytica</i>
ID=1355	WP_041146290	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1356	WP_045859333	molybdenum cofactor biosynthesis protein MoeB	<i>Raoultella terrigena</i>
ID=1357	WP_041146292	MULTISPECIES: molybdopterin synthase sulfur carrier subunit	<i>Raoultella</i>
ID=1358	WP_052698754	hypothetical protein	<i>Raoultella terrigena</i>
ID=1359	WP_045859335	cysteine synthase	<i>Raoultella terrigena</i>
ID=1360	WP_041146294	serine acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=1361	WP_041147688	L,D-transpeptidase	<i>Raoultella ornithinolytica</i>
ID=1362	WP_041146296	transcriptional regulator Cbl	<i>Raoultella ornithinolytica</i>
ID=1363	WP_045859342	nitrogen assimilation transcriptional regulator	<i>Raoultella terrigena</i>
ID=1364	WP_005166191	integrase	<i>Yersinia enterocolitica</i>
ID=1365	WP_048637352	hypothetical protein	<i>Brenneria goodwinii</i>
ID=1367	WP_050545045	antibiotic biosynthesis monooxygenase	<i>Xanthomonas citri</i>
ID=1368	WP_061291259	MFS transporter	<i>Azotobacter vinelandii</i>
ID=1369	WP_008039127	hypothetical protein	<i>Pseudomonas</i> sp.
ID=1370	WP_049264205	MULTISPECIES: IclR family transcriptional regulator	<i>Pseudomonas</i>
ID=1371	WP_039362440	IS630 family transposase	<i>Pectobacterium carotovorum</i>
ID=1372	WP_044206641	IS630 family transposase	<i>Pectobacterium carotovorum</i>
ID=1373	WP_049112359	DUF2857 domain-containing protein	<i>Klebsiella michiganensis</i>
ID=1374	WP_017346461	hypothetical protein	<i>Pantoea</i> sp.
ID=1375	WP_043875035	hypothetical protein	<i>Klebsiella variicola</i>
ID=1376	WP_039356906	TriB protein	<i>Pectobacterium carotovorum</i>
ID=1377	WP_046878104	ATPase	<i>Klebsiella michiganensis</i>
ID=1378	WP_043875032	Minor pilin of type IV secretion complex (VirB5)	<i>Klebsiella variicola</i>
ID=1379	WP_043875031	hypothetical protein	<i>Klebsiella variicola</i>
ID=1380	WP_040000619	conjugal transfer protein TrbL	<i>Dickeya chrysanthemi</i>
ID=1381	WP_046878108	membrane protein	<i>Klebsiella michiganensis</i>
ID=1382	WP_046878109	P-type conjugative transfer protein VirB9	<i>Klebsiella michiganensis</i>
ID=1383	WP_046878110	type VI secretion protein	<i>Klebsiella michiganensis</i>
ID=1384	WP_046878111	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=1385	WP_039356877	P-type DNA transfer ATPase VirB11	<i>Pectobacterium carotovorum</i>
ID=1386	WP_046878113	conjugal transfer protein	<i>Klebsiella michiganensis</i>
ID=1387	WP_039493176	hypothetical protein	<i>Pectobacterium carotovorum</i>
ID=1388	WP_053011070	molybdopterin-guanine dinucleotide biosynthesis protein MobB	<i>Yersinia pseudotuberculosis</i>
ID=1389	WP_053011071	hypothetical protein	<i>Yersinia pseudotuberculosis</i>
ID=1390	WP_057085259	DNA methylase	<i>Dickeya solani</i>
ID=1391	WP_007755429	hypothetical protein	<i>Cronobacter dublinensis</i>
ID=1392	WP_032991515	hypothetical protein	<i>Cronobacter dublinensis</i>
ID=1393	WP_049096991	MULTISPECIES: LysR family transcriptional regulator	<i>Klebsiella</i>
ID=1394	WP_049096989	glutamine amidotransferase	<i>Klebsiella michiganensis</i>
ID=1395	WP_049096987	MULTISPECIES: aspartate racemase	<i>Klebsiella</i>
ID=1396	WP_065793959	arginase	<i>Ensifer</i> sp.
ID=1397	WP_001309681	hypothetical protein	<i>Escherichia coli</i>
ID=1398	WP_069730046	hypothetical protein	<i>Pantoea conspicua</i>

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ID=1399	WP_049613176	MULTISPECIES: hypothetical protein	<i>Yersinia</i>
ID=1400	WP_006053167	hypothetical protein	<i>Paraburkholderia graminis</i>
ID=1402	WP_012541146	DNA primase	<i>Klebsiella pneumoniae</i>
ID=1403	WP_021804867	MULTISPECIES: Mobile element protein	<i>Serratia</i>
ID=1404	WP_042944358	MULTISPECIES: transposase	<i>Klebsiella</i>
ID=1405	WP_016246270	hypothetical protein	<i>Escherichia coli</i>
ID=1407	WP_049848500	hypothetical protein	<i>Trabulsiaella odontotermis</i>
ID=1408	WP_019211389	hypothetical protein	<i>Yersinia massiliensis</i>
ID=1409	WP_019211388	hypothetical protein	<i>Yersinia massiliensis</i>
ID=1411	WP_027911295	hypothetical protein	<i>Pseudomonas sp.</i>
ID=1412	WP_044612975	hypothetical protein	<i>Klebsiella variicola</i>
ID=1413	WP_039520052	antitoxin	<i>Salmonella enterica</i>
ID=1414	WP_062872074	hypothetical protein	<i>Escherichia coli</i>
ID=1415	WP_041146301	thymidylate kinase	<i>Raoultella ornithinolytica</i>
ID=1416	WP_057647853	NADPH:quinone oxidoreductase	<i>Yersinia enterocolitica</i>
ID=1417	WP_057647851	12-oxophytodienoate reductase	<i>Yersinia enterocolitica</i>
ID=1418	WP_057647848	AraC family transcriptional regulator	<i>Yersinia enterocolitica</i>
ID=1419	WP_057647846	oxidoreductase	<i>Yersinia enterocolitica</i>
ID=1420	WP_050292324	MULTISPECIES: TetR family transcriptional regulator	<i>Yersinia</i>
ID=1422	WP_045859352	cytochrome P450	<i>Raoultella terrigena</i>
ID=1423	WP_045859661	ABC transporter	<i>Raoultella terrigena</i>
ID=1424	WP_045859355	hypothetical protein	<i>Raoultella terrigena</i>
ID=1425	WP_052698755	hypothetical protein	<i>Raoultella terrigena</i>
ID=1426	WP_045859357	ABC transporter permease	<i>Raoultella terrigena</i>
ID=1427	WP_045859665	ABC transporter permease	<i>Raoultella terrigena</i>
ID=1428	WP_045859359	hypothetical protein	<i>Raoultella terrigena</i>
ID=1429	WP_045859361	TonB-dependent receptor	<i>Raoultella terrigena</i>
ID=1430	WP_038633962	MULTISPECIES: AraC family transcriptional regulator	<i>Yersinia</i>
ID=1431	WP_045859363	AraC family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1432	WP_045859363	AraC family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1433	WP_045859365	salicylate synthase	<i>Raoultella terrigena</i>
ID=1434	WP_052698761	2,3-dihydroxybenzoate-AMP ligase	<i>Raoultella terrigena</i>
ID=1435	WP_045859370	methyltransferase type 12	<i>Raoultella terrigena</i>
ID=1436	WP_038633975	MULTISPECIES: thioesterase	<i>Yersinia</i>
ID=1437	WP_038633979	MULTISPECIES: thiazolyl imide reductase	<i>Yersinia</i>
ID=1438	WP_038633982	MULTISPECIES: hypothetical protein	<i>Yersinia</i>
ID=1439	WP_038633985	MULTISPECIES: non-ribosomal peptide synthetase	<i>Yersinia</i>
ID=1440	WP_045859383	non-ribosomal peptide synthetase	<i>Raoultella terrigena</i>
ID=1441	WP_045859385	hypothetical protein	<i>Raoultella terrigena</i>
ID=1442	WP_041146303	3-hydroxyisobutyrate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1443	WP_041146304	HxLR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1444	WP_041146305	hemolysin D	<i>Raoultella ornithinolytica</i>
ID=1445	WP_041146306	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1446	WP_041146307	beta-ketoacyl-[acyl-carrier-protein] synthase II	<i>Raoultella ornithinolytica</i>
ID=1447	WP_041146308	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1448	WP_041146309	diaminopimelate decarboxylase	<i>Raoultella ornithinolytica</i>
ID=1449	WP_045859399	carbonate dehydratase	<i>Raoultella terrigena</i>
ID=1450	WP_045859401	universal stress protein UspG	<i>Raoultella terrigena</i>
ID=1451	WP_045859402	membrane protein	<i>Raoultella terrigena</i>
ID=1452	WP_045859404	multidrug transporter AcrB	<i>Raoultella terrigena</i>
ID=1453	WP_041146314	acyltransferase	<i>Raoultella ornithinolytica</i>
ID=1454	WP_045859408	phospholipid:lipid A palmitoyltransferase	<i>Raoultella terrigena</i>
ID=1455	WP_045859410	nucleoside recognition family protein	<i>Raoultella terrigena</i>
ID=1456	WP_045859410	nucleoside recognition family protein	<i>Raoultella terrigena</i>
ID=1457	WP_041147689	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1458	WP_041146317	histidine kinase	<i>Raoultella ornithinolytica</i>
ID=1459	WP_045859415	AMP nucleosidase	<i>Raoultella terrigena</i>
ID=1460	WP_045859417	aldehyde oxidase	<i>Raoultella terrigena</i>
ID=1461	WP_045859420	(2Fe-2S)-binding protein	<i>Raoultella terrigena</i>
ID=1462	WP_052474569	CTP molybdopterin cytidyltransferase	<i>Raoultella ornithinolytica</i>
ID=1463	WP_008076707	oxidoreductase	<i>Vibrio sinoensis</i>
ID=1464	WP_036817535	antibiotic biosynthesis monooxygenase	<i>Photobacterium sanctipauli</i>
ID=1465	WP_000203922	adenosylhomocysteinase	<i>Salmonella enterica</i>
ID=1466	WP_023240251	LacI family transcriptional regulator	<i>Salmonella enterica</i>
ID=1467	WP_052163604	AraC family transcriptional regulator	<i>Pseudomonas aeruginosa</i>
ID=1468	WP_011487955	oxidoreductase	<i>Paraburkholderia xenovorans</i>
ID=1469	WP_034040823	aldo/keto reductase	<i>Pseudomonas aeruginosa</i>
ID=1470	WP_058776086	hypothetical protein	<i>Pantoea dispersa</i>
ID=1471	WP_021508914	hypothetical protein	<i>Pantoea dispersa</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=1472	WP_039297602	cytochrome b	<i>Cedecea neteri</i>
ID=1473	WP_059009276	catalase	<i>Type-C symbiont of Plautia stali</i>
ID=1474	WP_069061898	sulfonate ABC transporter ATP-binding protein	<i>SinoRhizobium sp.</i>
ID=1475	WP_020953136	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	<i>Paracoccus aminophilus</i>
ID=1476	WP_020953135	nitrate ABC transporter permease	<i>Paracoccus aminophilus</i>
ID=1477	WP_061626725	4Fe-4S ferredoxin	<i>Sorangium cellulosum</i>
ID=1478	WP_027025322	oxidoreductase	<i>MesoRhizobium sp.</i>
ID=1479	WP_069061896	hypothetical protein	<i>SinoRhizobium sp.</i>
ID=1480	WP_052698756	hypothetical protein	<i>Raoultella terrigena</i>
ID=1481	WP_045859424	hypothetical protein	<i>Raoultella terrigena</i>
ID=1482	WP_052474570	protease modulator HflK	<i>Raoultella ornithinolytica</i>
ID=1483	WP_052698758	protease	<i>Raoultella terrigena</i>
ID=1484	WP_041146322	protease modulator HflK	<i>Raoultella ornithinolytica</i>
ID=1485	WP_045859430	cadmium ABC transporter ATPase	<i>Raoultella terrigena</i>
ID=1486	WP_041146324	MATE family multidrug exporter	<i>Raoultella ornithinolytica</i>
ID=1487	WP_045859457	hypothetical protein	<i>Raoultella terrigena</i>
ID=1488	WP_044351570	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=1489	WP_032717862	glycerate kinase	<i>Raoultella ornithinolytica</i>
ID=1490	WP_004864443	MULTISPECIES: 3-ketoacyl-ACP reductase	<i>Enterobacteriaceae</i>
ID=1491	WP_004864444	MULTISPECIES: ABC transporter substrate-binding protein	<i>Enterobacteriaceae</i>
ID=1492	WP_049268092	ABC transporter permease	<i>Raoultella planticola</i>
ID=1493	WP_064384372	ABC transporter ATP-binding protein	<i>Klebsiella oxytoca</i>
ID=1494	WP_015583959	sugar ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=1495	WP_032717864	dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1496	WP_032699210	MULTISPECIES: pyridoxal 4-dehydrogenase	<i>Raoultella</i>
ID=1497	WP_032695356	MULTISPECIES: CoA-transferase	<i>Enterobacteriaceae</i>
ID=1498	WP_032686825	MULTISPECIES: TetR family transcriptional regulator	<i>Enterobacteriaceae</i>
ID=1499	WP_032699209	MULTISPECIES: sorbosone dehydrogenase	<i>Raoultella</i>
ID=1500	WP_064384373	alanine-phosphoribitol ligase	<i>Klebsiella oxytoca</i>
ID=1501	WP_004864465	electron transfer flavoprotein subunit beta	<i>Raoultella ornithinolytica</i>
ID=1502	WP_015583955	electron transfer flavoprotein subunit alpha-like protein	<i>Raoultella ornithinolytica</i>
ID=1503	WP_064359038	electron transfer flavoprotein-ubiquinone oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=1504	WP_015583953	acyl-CoA dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1505	WP_049268082	hypothetical protein	<i>Raoultella planticola</i>
ID=1506	WP_049268081	endonuclease	<i>Raoultella planticola</i>
ID=1507	WP_045859459	hypothetical protein	<i>Raoultella terrigena</i>
ID=1508	WP_041146340	MULTISPECIES: tellurite resistance protein	<i>Raoultella</i>
ID=1509	WP_045859461	GGDEF-domain containing protein	<i>Raoultella terrigena</i>
ID=1510	WP_045859463	oxidoreductase	<i>Raoultella terrigena</i>
ID=1511	WP_041146343	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1512	WP_041146344	lipote--protein ligase A	<i>Raoultella ornithinolytica</i>
ID=1513	WP_041146345	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1514	WP_041146346	tautomerase family protein	<i>Raoultella ornithinolytica</i>
ID=1515	WP_041146347	HPP family protein	<i>Raoultella ornithinolytica</i>
ID=1516	WP_041146348	adenosylhomocysteinease	<i>Raoultella ornithinolytica</i>
ID=1517	WP_041146349	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	<i>Raoultella ornithinolytica</i>
ID=1518	WP_045859480	hypothetical protein	<i>Raoultella terrigena</i>
ID=1519	WP_041146351	FUSC family protein	<i>Raoultella ornithinolytica</i>
ID=1520	WP_041146352	DNA gyrase inhibitor	<i>Raoultella ornithinolytica</i>
ID=1521	WP_045859489	membrane protein	<i>Raoultella terrigena</i>
ID=1522	WP_045859491	D-alanyl-D-alanine carboxypeptidase	<i>Raoultella terrigena</i>
ID=1523	WP_045859493	exodeoxyribonuclease I	<i>Raoultella terrigena</i>
ID=1524	WP_045859496	elongation factor G	<i>Raoultella terrigena</i>
ID=1525	WP_024360005	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=1526	WP_041146359	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1527	WP_041146360	putrescine/spermidine ABC transporter	<i>Raoultella ornithinolytica</i>
ID=1528	WP_041146361	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1529	WP_045859504	NAD(P)-dependent oxidoreductase	<i>Raoultella terrigena</i>
ID=1530	WP_041146363	MULTISPECIES: ATP phosphoribosyltransferase	<i>Raoultella</i>
ID=1531	WP_041146364	histidinol dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1532	WP_004864522	MULTISPECIES: histidinol-phosphate transaminase	<i>Enterobacteriaceae</i>
ID=1533	WP_041146366	bifunctional imidazole glycerol-phosphate dehydratase/histidinol phosphatase	<i>Raoultella ornithinolytica</i>
ID=1534	WP_041146367	imidazole glycerol phosphate synthase subunit HisH	<i>Raoultella ornithinolytica</i>
ID=1535	WP_041146368	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)..methyldeneamino]imidazole-4-carboxamide isomerase	<i>Raoultella ornithinolytica</i>
ID=1536	WP_041146369	imidazole glycerol phosphate synthase cyclase subunit	<i>Raoultella ornithinolytica</i>
ID=1537	WP_041146370	bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP diphosphatase	<i>Raoultella ornithinolytica</i>
ID=1538	WP_041146371	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1539	WP_041146372	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>

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ID=1540	WP_041146373	sugar ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=1541	WP_041146374	glycosyl transferase	<i>Raoultella ornithinolytica</i>
ID=1542	WP_041146375	dTDP-4-dehydrorhamnose 3,5-epimerase	<i>Raoultella ornithinolytica</i>
ID=1543	WP_041146376	NAD(P)-dependent oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=1544	WP_041146377	glucose-1-phosphate thymidyltransferase	<i>Raoultella ornithinolytica</i>
ID=1545	WP_041146378	dTDP-glucose 4,6-dehydratase	<i>Raoultella ornithinolytica</i>
ID=1546	WP_041146379	NAD-dependent epimerase	<i>Raoultella ornithinolytica</i>
ID=1547	WP_025422746	acyltransferase	<i>Sodalis praecaptivus</i>
ID=1548	WP_064289988	acyltransferase	<i>Klebsiella oxytoca</i>
ID=1550	WP_045859532	UDP-glucose 6-dehydrogenase	<i>Raoultella terrigena</i>
ID=1551	WP_064323674	lipopolysaccharide biosynthesis protein	<i>Klebsiella pneumoniae</i>
ID=1552	WP_049080029	colanic acid biosynthesis glycosyltransferase WcaL	<i>Klebsiella michiganensis</i>
ID=1553	WP_032699189	colanic acid biosynthesis protein	<i>Raoultella planticola</i>
ID=1554	WP_045859542	phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating)	<i>Raoultella terrigena</i>
ID=1555	WP_064323676	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=1556	WP_021506306	hypothetical protein	<i>Pantoea dispersa</i>
ID=1557	WP_058757645	hypothetical protein	<i>Pantoea dispersa</i>
ID=1558	WP_064323678	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=1559	WP_064323679	undecaprenyl-phosphate glucose phosphotransferase	<i>Klebsiella pneumoniae</i>
ID=1560	WP_064323680	tyrosine-protein kinase	<i>Klebsiella pneumoniae</i>
ID=1561	WP_064170394	protein tyrosine phosphatase	<i>Klebsiella pneumoniae</i>
ID=1562	WP_064323681	polysaccharide export protein Wza	<i>Klebsiella pneumoniae</i>
ID=1563	WP_041146391	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1564	WP_041146392	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1566	WP_041146393	GalU regulator GalF	<i>Raoultella ornithinolytica</i>
ID=1567	WP_041147696	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1569	WP_041146395	outer membrane assembly protein AsmA	<i>Raoultella ornithinolytica</i>
ID=1570	WP_041146396	dCTP deaminase	<i>Raoultella ornithinolytica</i>
ID=1571	WP_041146397	MULTISPECIES: uridine kinase	<i>Raoultella</i>
ID=1572	WP_041146398	3-methyladenine DNA glycosylase 2	<i>Raoultella ornithinolytica</i>
ID=1573	WP_041146399	molecular chaperone	<i>Raoultella ornithinolytica</i>
ID=1574	WP_041147697	histidine kinase	<i>Raoultella ornithinolytica</i>
ID=1575	WP_041146400	chemotaxis protein CheY	<i>Raoultella ornithinolytica</i>
ID=1576	WP_032451537	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=1577	WP_045855753	transcriptional regulator	<i>Raoultella terrigena</i>
ID=1578	WP_041146402	C4-dicarboxylate ABC transporter	<i>Raoultella ornithinolytica</i>
ID=1579	WP_041146404	multidrug transporter subunit MdtA	<i>Raoultella ornithinolytica</i>
ID=1580	WP_041146405	multidrug transporter subunit MdtB	<i>Raoultella ornithinolytica</i>
ID=1581	WP_041146406	multidrug transporter subunit MdtC	<i>Raoultella ornithinolytica</i>
ID=1582	WP_041146407	multidrug transporter subunit MdtD	<i>Raoultella ornithinolytica</i>
ID=1583	WP_041146408	two-component sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=1584	WP_045855766	DNA-binding response regulator	<i>Raoultella terrigena</i>
ID=1585	WP_041146410	U32 family peptidase	<i>Raoultella ornithinolytica</i>
ID=1586	WP_041146411	lipid kinase YegS	<i>Raoultella ornithinolytica</i>
ID=1587	WP_041146412	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=1588	WP_045856425	ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=1589	WP_041146413	D-ala-D-ala transporter subunit	<i>Raoultella ornithinolytica</i>
ID=1590	WP_041146414	MULTISPECIES: ABC transporter permease	<i>Raoultella</i>
ID=1591	WP_041146415	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=1592	WP_041146416	mandelate racemase	<i>Raoultella ornithinolytica</i>
ID=1593	WP_041146417	haloacid dehalogenase	<i>Raoultella ornithinolytica</i>
ID=1594	WP_041146418	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1595	WP_041146419	xylulokinase	<i>Raoultella ornithinolytica</i>
ID=1596	WP_045855788	D-arabinitol 4-dehydrogenase	<i>Raoultella terrigena</i>
ID=1597	WP_045856427	cytochrome c biogenesis protein CcdA	<i>Raoultella terrigena</i>
ID=1598	WP_041146422	LacI family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1599	WP_041146423	glucose dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1600	WP_041146424	ribulokinase	<i>Raoultella ornithinolytica</i>
ID=1601	WP_045855799	fructose-bisphosphate aldolase	<i>Raoultella terrigena</i>
ID=1602	WP_041146426	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1603	WP_041146427	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1604	WP_041146428	sugar kinase	<i>Raoultella ornithinolytica</i>
ID=1605	WP_045855805	GntR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1606	WP_041146430	hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	<i>Raoultella ornithinolytica</i>
ID=1607	WP_041146431	hydroxyethylthiazole kinase	<i>Raoultella ornithinolytica</i>
ID=1608	WP_032717945	MULTISPECIES: type VI secretion system effector	<i>Enterobacteriaceae</i>
ID=1609	WP_045855811	hypothetical protein	<i>Raoultella terrigena</i>
ID=1611	WP_041146438	alkyl/aryl-sulfatase	<i>Raoultella ornithinolytica</i>
ID=1612	WP_041146439	Crp/Fnr family transcriptional regulator	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=1613	WP_041146440	alkyl/aryl-sulfatase	<i>Raoultella ornithinolytica</i>
ID=1614	WP_041146441	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1615	WP_041146442	adenine deaminase	<i>Raoultella ornithinolytica</i>
ID=1616	WP_041146443	permease	<i>Raoultella ornithinolytica</i>
ID=1617	WP_041147699	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1618	WP_041146444	nickel/cobalt homeostasis protein RcnB	<i>Raoultella ornithinolytica</i>
ID=1619	WP_041146445	Fe-S-binding ATPase	<i>Raoultella ornithinolytica</i>
ID=1620	WP_041147700	methionine--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=1621	WP_045855827	lipoprotein	<i>Raoultella terrigena</i>
ID=1622	WP_041146447	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1623	WP_041146448	DNA-binding response regulator	<i>Raoultella ornithinolytica</i>
ID=1624	WP_045855830	DNA-binding response regulator	<i>Raoultella terrigena</i>
ID=1625	WP_041146449	histidine kinase	<i>Raoultella ornithinolytica</i>
ID=1626	WP_041146450	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1627	WP_041146451	osmoprotectant uptake system permease	<i>Raoultella ornithinolytica</i>
ID=1628	WP_045855838	ATP-binding protein	<i>Raoultella terrigena</i>
ID=1629	WP_041147701	MULTISPECIES: osmoprotectant uptake system permease	<i>Raoultella</i>
ID=1630	WP_045855840	ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=1631	WP_041146454	beta-glucosidase	<i>Raoultella ornithinolytica</i>
ID=1632	WP_045855844	D-lactate dehydrogenase	<i>Raoultella terrigena</i>
ID=1633	WP_041146457	MULTISPECIES: GCN5 family acetyltransferase	<i>Raoultella</i>
ID=1634	WP_041147702	D-alanyl-D-alanine endopeptidase	<i>Raoultella ornithinolytica</i>
ID=1635	WP_041146458	YIP1 family protein	<i>Raoultella ornithinolytica</i>
ID=1636	WP_041146459	DedA family protein	<i>Raoultella ornithinolytica</i>
ID=1637	WP_041146460	multidrug resistance outer membrane protein MdtQ	<i>Raoultella ornithinolytica</i>
ID=1638	WP_041146461	SAM-dependent methyltransferase	<i>Raoultella ornithinolytica</i>
ID=1639	WP_041146462	6-phospho-beta-glucosidase	<i>Raoultella ornithinolytica</i>
ID=1640	WP_041146463	PTS beta-glucoside transporter subunit EIIBCA	<i>Raoultella ornithinolytica</i>
ID=1641	WP_041146464	transcription antiterminator LicT	<i>Raoultella ornithinolytica</i>
ID=1642	WP_041146465	porin	<i>Raoultella ornithinolytica</i>
ID=1643	WP_045856435	tRNA dihydrouridine(16) synthase DusC	<i>Raoultella terrigena</i>
ID=1644	WP_041146466	salicylate hydroxylase	<i>Raoultella ornithinolytica</i>
ID=1645	WP_041146467	maleylacetoacetate isomerase	<i>Raoultella ornithinolytica</i>
ID=1646	WP_041146468	5-carboxymethyl-2-hydroxymuconate isomerase	<i>Raoultella ornithinolytica</i>
ID=1647	WP_041146469	gentisate 1,2-dioxygenase	<i>Raoultella ornithinolytica</i>
ID=1648	WP_041146470	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1649	WP_041146471	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1650	WP_041146472	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1651	WP_045855868	CidB/LrgB family autolysis modulator	<i>Raoultella terrigena</i>
ID=1652	WP_041146474	cytidine deaminase	<i>Raoultella ornithinolytica</i>
ID=1653	WP_041146475	vancomycin high temperature exclusion protein	<i>Raoultella ornithinolytica</i>
ID=1654	WP_041146476	GGDEF domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=1655	WP_041146477	galactoside ABC transporter permease MglC	<i>Raoultella ornithinolytica</i>
ID=1656	WP_041146478	galactose/methyl galactoside ABC transporter ATP-binding protein MglA	<i>Raoultella ornithinolytica</i>
ID=1657	WP_045855878	galactose ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=1658	WP_041147704	DNA-binding transcriptional regulator GalS	<i>Raoultella ornithinolytica</i>
ID=1659	WP_041146480	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1660	WP_041146481	MULTISPECIES: GTP cyclohydrolase I	<i>Raoultella</i>
ID=1661	WP_045855882	S-formylglutathione hydrolase	<i>Raoultella terrigena</i>
ID=1662	WP_045855884	ligand-gated channel protein	<i>Raoultella terrigena</i>
ID=1663	WP_045855886	lysine transporter	<i>Raoultella terrigena</i>
ID=1664	WP_045855887	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1665	WP_041146486	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1666	WP_041146487	deoxyribonuclease IV	<i>Raoultella ornithinolytica</i>
ID=1667	WP_041146488	PTS fructose transporter subunit EIIBC	<i>Raoultella ornithinolytica</i>
ID=1668	WP_045855895	1-phosphofructokinase	<i>Raoultella terrigena</i>
ID=1669	WP_041146490	MULTISPECIES: bifunctional PTS fructose transporter subunit IIA/HPr protein	<i>Raoultella</i>
ID=1670	WP_041146491	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1671	WP_041146492	MULTISPECIES: zinc/iron-chelating domain-containing protein	<i>Raoultella</i>
ID=1672	WP_041146493	MULTISPECIES: elongation factor P-like protein YeiP	<i>Raoultella</i>
ID=1673	WP_041146494	mannonate dehydratase	<i>Raoultella ornithinolytica</i>
ID=1674	WP_041146495	D-mannonate oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=1675	WP_041146496	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1676	WP_045855905	membrane protein	<i>Raoultella terrigena</i>
ID=1677	WP_041146498	bifunctional murein DD-endopeptidase/murein LD-carboxypeptidase	<i>Raoultella ornithinolytica</i>
ID=1678	WP_041146499	phage resistance protein	<i>Raoultella ornithinolytica</i>
ID=1679	WP_045855912	ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=1680	WP_041146500	microcin C ABC transporter permease YejB	<i>Raoultella ornithinolytica</i>
ID=1681	WP_041146501	microcin ABC transporter permease	<i>Raoultella ornithinolytica</i>

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ID=1682	WP_041146502	microcin C ABC transporter ATP-binding protein YejF	<i>Raoultella ornithinolytica</i>
ID=1683	WP_041147706	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=1684	WP_045855920	Bcr/CfiA family multidrug efflux MFS transporter	<i>Raoultella terrigena</i>
ID=1685	WP_041146504	16S rRNA pseudouridine(516) synthase	<i>Raoultella ornithinolytica</i>
ID=1686	WP_045855924	ATP-dependent helicase	<i>Raoultella terrigena</i>
ID=1687	WP_041146506	50S ribosomal protein L25	<i>Raoultella ornithinolytica</i>
ID=1688	WP_041146507	MULTISPECIES: LysR family transcriptional regulator	<i>Raoultella</i>
ID=1689	WP_041146508	serine hydrolase	<i>Raoultella ornithinolytica</i>
ID=1690	WP_041146509	GDP-mannose pyrophosphatase	<i>Raoultella ornithinolytica</i>
ID=1691	WP_041146510	DeoR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1692	WP_041146511	nucleoid-associated protein YejK	<i>Raoultella ornithinolytica</i>
ID=1693	WP_015583825	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=1694	WP_041146512	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1695	WP_041146515	AI-2E family transporter	<i>Raoultella ornithinolytica</i>
ID=1696	WP_041146516	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1697	WP_041146517	ecotin	<i>Raoultella ornithinolytica</i>
ID=1698	WP_041146518	malate:quinone oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=1699	WP_045855947	transporter	<i>Raoultella terrigena</i>
ID=1700	WP_041146519	transporter	<i>Raoultella ornithinolytica</i>
ID=1701	WP_041146520	magnesium transporter	<i>Raoultella ornithinolytica</i>
ID=1702	WP_041146521	multidrug ABC transporter permease/ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=1703	WP_045855953	alpha-ketoglutarate-dependent dioxygenase AlkB	<i>Raoultella terrigena</i>
ID=1704	WP_041146523	bifunctional transcriptional regulator/O6-methylguanine-DNA methyltransferase	<i>Raoultella ornithinolytica</i>
ID=1705	WP_045855958	FAD:protein FMN transferase	<i>Raoultella terrigena</i>
ID=1706	WP_047663328	OmpK36 porin	<i>Raoultella planticola</i>
ID=1707	WP_041146526	phosphotransferase RcsD	<i>Raoultella ornithinolytica</i>
ID=1708	WP_041146527	MULTISPECIES: DNA-binding response regulator	<i>Raoultella</i>
ID=1709	WP_041146528	hybrid sensor histidine kinase/response regulator	<i>Raoultella ornithinolytica</i>
ID=1710	WP_041146529	DNA gyrase subunit A	<i>Raoultella ornithinolytica</i>
ID=1711	WP_041146530	MULTISPECIES: bifunctional 3-demethylubiquinone 3-O-methyltransferase/..	<i>Raoultella</i>
		..2-octaprenyl-6-hydroxy phenol methylase	
ID=1712	WP_041146531	ribonucleotide-diphosphate reductase subunit alpha	<i>Raoultella ornithinolytica</i>
ID=1713	WP_041146532	ribonucleotide-diphosphate reductase subunit beta	<i>Raoultella ornithinolytica</i>
ID=1714	WP_041146533	(2Fe-2S) ferredoxin	<i>Raoultella ornithinolytica</i>
ID=1715	WP_041146534	glycerophosphoryl diester phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=1716	WP_041146535	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1717	WP_041146536	sn-glycerol-3-phosphate dehydrogenase subunit A	<i>Raoultella ornithinolytica</i>
ID=1718	WP_045855978	sn-glycerol-3-phosphate dehydrogenase subunit A	<i>Raoultella terrigena</i>
ID=1719	WP_041146537	anaerobic glycerol-3-phosphate dehydrogenase subunit B	<i>Raoultella ornithinolytica</i>
ID=1720	WP_041146538	sn-glycerol-3-phosphate dehydrogenase subunit C	<i>Raoultella ornithinolytica</i>
ID=1721	WP_041146539	2-keto-3-deoxy-L-rhamnonate aldolase	<i>Raoultella ornithinolytica</i>
ID=1722	WP_041146540	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1723	WP_041146541	L-rhamnonate dehydratase	<i>Raoultella ornithinolytica</i>
ID=1724	WP_041146542	IcIR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1725	WP_041146543	competence/damage-inducible protein A	<i>Raoultella ornithinolytica</i>
ID=1726	WP_041146544	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1727	WP_041146545	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1728	WP_041146546	nucleoside triphosphatase	<i>Raoultella ornithinolytica</i>
ID=1729	WP_041146547	2-succinylbenzoate-CoA ligase	<i>Raoultella ornithinolytica</i>
ID=1730	WP_041146548	o-succinylbenzoate synthase	<i>Raoultella ornithinolytica</i>
ID=1731	WP_041146549	MULTISPECIES: 1,4-dihydroxy-2-naphthoyl-CoA synthase	<i>Raoultella</i>
ID=1732	WP_041146550	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	<i>Raoultella ornithinolytica</i>
ID=1733	WP_041146551	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase	<i>Raoultella ornithinolytica</i>
ID=1734	WP_041146552	isochorismate synthase MenF	<i>Raoultella ornithinolytica</i>
ID=1735	WP_041146553	GNAT family N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=1736	WP_041146554	ribonuclease Z	<i>Raoultella ornithinolytica</i>
ID=1737	WP_041146555	NADH-quinone oxidoreductase subunit N	<i>Raoultella ornithinolytica</i>
ID=1738	WP_041146556	NADH-quinone oxidoreductase subunit M	<i>Raoultella ornithinolytica</i>
ID=1739	WP_041146557	NADH-quinone oxidoreductase subunit L	<i>Raoultella ornithinolytica</i>
ID=1740	WP_002913148	MULTISPECIES: NADH-quinone oxidoreductase subunit K	<i>Enterobacterales</i>
ID=1741	WP_041146558	NADH:ubiquinone oxidoreductase subunit J	<i>Raoultella ornithinolytica</i>
ID=1742	WP_015365590	MULTISPECIES: NADH-quinone oxidoreductase subunit I	<i>Enterobacteriaceae</i>
ID=1743	WP_045856041	NADH-quinone oxidoreductase subunit H	<i>Raoultella terrigena</i>
ID=1744	WP_041146560	NADH-quinone oxidoreductase subunit G	<i>Raoultella ornithinolytica</i>
ID=1745	WP_041146561	NADH-quinone oxidoreductase subunit F	<i>Raoultella ornithinolytica</i>
ID=1746	WP_041146562	NADH-quinone oxidoreductase subunit E	<i>Raoultella ornithinolytica</i>
ID=1747	WP_041146563	MULTISPECIES: NADH-quinone oxidoreductase subunit C/D	<i>Raoultella</i>
ID=1748	WP_002913178	MULTISPECIES: NADH-quinone oxidoreductase subunit B	<i>Enterobacterales</i>
ID=1749	WP_004865103	MULTISPECIES: NADH-quinone oxidoreductase subunit A	<i>Enterobacteriaceae</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=1750	WP_041146564	transcriptional regulator LrhA	<i>Raoultella ornithinolytica</i>
ID=1751	WP_041146565	aminotransferase	<i>Raoultella ornithinolytica</i>
ID=1752	WP_041146566	5'-deoxynucleotidase	<i>Raoultella ornithinolytica</i>
ID=1753	WP_041146567	citrate transporter	<i>Raoultella ornithinolytica</i>
ID=1754	WP_045856442	sugar phosphatase	<i>Raoultella terrigena</i>
ID=1755	WP_041146568	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=1756	WP_041146569	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=1757	WP_041146570	acetate kinase	<i>Raoultella ornithinolytica</i>
ID=1758	WP_041146571	phosphate acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=1759	WP_041146571	phosphate acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=1760	WP_041146572	transketolase	<i>Raoultella ornithinolytica</i>
ID=1761	WP_045856064	carbohydrate degradation protein	<i>Raoultella terrigena</i>
ID=1762	WP_045856066	PTS ascorbate transporter subunit IIC	<i>Raoultella terrigena</i>
ID=1763	WP_041146575	MULTISPECIES: PTS mannitol transporter subunit IIB	<i>Enterobacteriaceae</i>
ID=1764	WP_041146576	PTS ascorbate transporter subunit IIA	<i>Raoultella ornithinolytica</i>
ID=1765	WP_041146577	MULTISPECIES: LacI family transcriptional regulator	<i>Raoultella</i>
ID=1766	WP_041146578	NUDIX hydrolase	<i>Raoultella ornithinolytica</i>
ID=1767	WP_041147708	phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=1768	WP_041146579	glutathione S-transferase	<i>Raoultella ornithinolytica</i>
ID=1769	WP_041146580	aldehyde dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1770	WP_041146581	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1771	WP_041146582	thiol:disulfide oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=1772	WP_041146583	MULTISPECIES: dihydroneopterin triphosphate 2'-epimerase	<i>Raoultella</i>
ID=1773	WP_045856080	epimerase	<i>Raoultella terrigena</i>
ID=1774	WP_041146585	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1775	WP_041146586	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1776	WP_041146588	MULTISPECIES: histidine/lysine/arginine/ornithine ABC transporter ATP-binding protein	<i>Raoultella</i>
ID=1777	WP_041146589	amino acid ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=1778	WP_041146590	MULTISPECIES: amino acid ABC transporter permease	<i>Raoultella</i>
ID=1779	WP_041146591	MULTISPECIES: histidine ABC transporter substrate-binding protein HisJ	<i>Raoultella</i>
ID=1780	WP_041146592	histidine ABC transporter substrate-binding protein HisJ	<i>Raoultella ornithinolytica</i>
ID=1781	WP_041146593	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	<i>Raoultella ornithinolytica</i>
ID=1782	WP_041146594	amidophosphoribosyltransferase	<i>Raoultella ornithinolytica</i>
ID=1783	WP_041147709	MULTISPECIES: colicin V production protein	<i>Raoultella</i>
ID=1784	WP_045856097	cell division protein DedD	<i>Raoultella terrigena</i>
ID=1785	WP_045856100	bifunctional tetrahydrofolate synthase/dihydrofolate synthase	<i>Raoultella terrigena</i>
ID=1786	WP_023290526	MULTISPECIES: acetyl-CoA carboxylase subunit beta	<i>Klebsiella</i>
ID=1787	WP_041146598	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1788	WP_041146599	tRNA pseudouridine(38-40) synthase	<i>Raoultella ornithinolytica</i>
ID=1789	WP_041146600	aspartate-semialdehyde dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1790	WP_045856108	erythronate-4-phosphate dehydrogenase	<i>Raoultella terrigena</i>
ID=1791	WP_041146602	flagella biosynthesis regulator	<i>Raoultella ornithinolytica</i>
ID=1792	WP_004865226	carbohydrate porin	<i>Raoultella ornithinolytica</i>
ID=1793	WP_032695487	MULTISPECIES: PTS cellobiose transporter subunit IIC	<i>Enterobacteriaceae</i>
ID=1794	WP_064794182	PTS sugar transporter subunit IIB	<i>Raoultella planticola</i>
ID=1795	WP_032686630	MULTISPECIES: GntR family transcriptional regulator	<i>Enterobacteriaceae</i>
ID=1796	WP_041146603	arabinose transporter	<i>Raoultella ornithinolytica</i>
ID=1797	WP_041146604	beta-ketoacyl-[acyl-carrier-protein] synthase I	<i>Raoultella ornithinolytica</i>
ID=1798	WP_041146605	bifunctional tRNA (5-methylaminomethyl-2-thiouridine)(34)-methyltransferase MnmD/..FAD-dependent 5-carboxymethylaminomethyl-2-thiouridine(34) oxidoreductase MnmC	<i>Raoultella ornithinolytica</i>
ID=1799	WP_041146606	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1800	WP_041146607	elongation factor P hydroxylase	<i>Raoultella ornithinolytica</i>
ID=1801	WP_041146608	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1802	WP_041146609	penicillin-insensitive murein endopeptidase	<i>Raoultella ornithinolytica</i>
ID=1803	WP_041146610	MULTISPECIES: chorismate synthase	<i>Raoultella</i>
ID=1804	WP_041146611	ribosomal protein L3 N(5)-glutamine methyltransferase	<i>Raoultella ornithinolytica</i>
ID=1805	WP_045856128	hypothetical protein	<i>Raoultella terrigena</i>
ID=1806	WP_045856130	phosphohistidine phosphatase	<i>Raoultella terrigena</i>
ID=1807	WP_041146614	multifunctional fatty acid oxidation complex subunit alpha	<i>Raoultella ornithinolytica</i>
ID=1808	WP_045856133	3-ketoacyl-CoA thiolase	<i>Raoultella terrigena</i>
ID=1809	WP_041146616	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=1810	WP_041146617	long-chain fatty acid transporter	<i>Raoultella ornithinolytica</i>
ID=1811	WP_041146618	phospholipid-binding lipoprotein MlaA	<i>Raoultella ornithinolytica</i>
ID=1812	WP_041146619	membrane protein	<i>Raoultella ornithinolytica</i>
ID=1813	WP_052698725	hypothetical protein	<i>Raoultella terrigena</i>
ID=1814	WP_045269251	type VI secretion-associated protein	<i>Enterobacter kobei</i>
ID=1815	WP_045859622	type VI secretion protein VasK	<i>Raoultella terrigena</i>
ID=1816	WP_062743040	hypothetical protein	<i>Erwinia persicina</i>
ID=1817	WP_049853079	hypothetical protein	<i>Pantoea</i> sp.

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=1818	WP_016154471	hypothetical protein	<i>Citrobacter</i> sp.
ID=1819	WP_044597851	MULTISPECIES: hypothetical protein	<i>Enterobacter cloacae</i>
ID=1820	WP_016154474	hypothetical protein	<i>Citrobacter</i> sp.
ID=1822	WP_041146621	maltoporin	<i>Raoultella ornithinolytica</i>
ID=1823	WP_011815231	MULTISPECIES: transposase	<i>Enterobacterales</i>
ID=1824	WP_045857172	hypothetical protein	<i>Raoultella terrigena</i>
ID=1825	WP_045857176	Hcp family T6SS protein CtsH1	<i>Raoultella terrigena</i>
ID=1826	WP_041147133	NIPSNAP family containing protein	<i>Raoultella ornithinolytica</i>
ID=1827	WP_045857916	N-acetyltransferase	<i>Raoultella terrigena</i>
ID=1828	WP_041147131	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1829	WP_045857215	MFS transporter	<i>Raoultella terrigena</i>
ID=1830	WP_045857217	tetracycline resistance MFS efflux pump	<i>Raoultella terrigena</i>
ID=1831	WP_045857218	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1832	WP_041147129	diacetyl reductase	<i>Raoultella ornithinolytica</i>
ID=1833	WP_045857223	LuxR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1834	WP_041147127	multidrug resistance transporter	<i>Raoultella ornithinolytica</i>
ID=1835	WP_041147126	multidrug transporter	<i>Raoultella ornithinolytica</i>
ID=1836	WP_041147125	multidrug transporter subunit MdtN	<i>Raoultella ornithinolytica</i>
ID=1837	WP_039188419	MULTISPECIES: hypothetical protein	<i>Hafnia paralvei</i>
ID=1838	WP_041147123	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1839	WP_041147122	MULTISPECIES: N-acetyltransferase	<i>Raoultella</i>
ID=1840	WP_045857237	MFS transporter	<i>Raoultella terrigena</i>
ID=1841	WP_041147120	L-alanine exporter AlaE	<i>Raoultella ornithinolytica</i>
ID=1842	WP_021508844	SDR family oxidoreductase	<i>Pantoea dispersa</i>
ID=1843	WP_031279961	ArsR family transcriptional regulator	<i>Pantoea dispersa</i>
ID=1844	WP_017346503	hypothetical protein	<i>Pantoea</i> sp.
ID=1845	WP_041659362	hypothetical protein	<i>Acaryochloris marina</i>
ID=1846	WP_007151964	hypothetical protein	<i>Marinobacter algicola</i>
ID=1847	WP_059457643	Short chain oxidoreductase	<i>Burkholderia vietnamiensis</i>
ID=1848	WP_059621903	alcohol dehydrogenase	<i>Burkholderia vietnamiensis</i>
ID=1849	WP_041147119	ester cyclase	<i>Raoultella ornithinolytica</i>
ID=1850	WP_041147118	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1851	WP_049268274	LysR family transcriptional regulator	<i>Raoultella planticola</i>
ID=1852	WP_049268273	MBL fold hydrolase	<i>Raoultella planticola</i>
ID=1853	WP_041147117	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1854	WP_045857271	N-acetyltransferase	<i>Raoultella terrigena</i>
ID=1855	WP_045857272	hypothetical protein	<i>Raoultella terrigena</i>
ID=1856	WP_035606760	hypothetical protein	<i>Edwardsiella tarda</i>
ID=1857	WP_045854122	membrane protein	<i>Raoultella terrigena</i>
ID=1858	WP_045855401	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1859	WP_045855401	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1860	WP_032967625	hypothetical protein	<i>Cronobacter dublinensis</i>
ID=1861	WP_055317780	hypothetical protein	<i>Serratia marcescens</i>
ID=1862	WP_047664296	adhesin	<i>Escherichia coli</i>
ID=1863	WP_050659931	hypothetical protein	<i>Gallaecimonas pentaromativoran.</i>
ID=1864	WP_050659930	EVE domain-containing protein	<i>Gallaecimonas pentaromativoran.</i>
ID=1865	WP_018646703	hypothetical protein	<i>Bradyrhizobium japonicum</i>
ID=1867	WP_045857921	hypothetical protein	<i>Raoultella terrigena</i>
ID=1868	WP_050539008	hypothetical protein	<i>Yersinia mollaretii</i>
ID=1869	WP_034864095	hypothetical protein	<i>Enterobacteriaceae bacterium</i>
ID=1870	WP_052474593	filamentous hemagglutinin	<i>Raoultella ornithinolytica</i>
ID=1871	WP_041147100	RTX toxin-activating lysine-acyltransferase	<i>Raoultella ornithinolytica</i>
ID=1872	WP_045857299	ShlB/FhaC/HecB family hemolysin secretion/activation protein	<i>Raoultella terrigena</i>
ID=1873	WP_041147099	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=1874	WP_041147098	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=1875	WP_041147097	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=1876	WP_041147737	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=1877	WP_041147096	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=1878	WP_052474591	molecular chaperone FimC	<i>Raoultella ornithinolytica</i>
ID=1879	WP_045857310	fimbrial protein	<i>Raoultella terrigena</i>
ID=1880	WP_045857312	type-1 fimbrial protein subunit A	<i>Raoultella terrigena</i>
ID=1881	WP_045857315	tyrosine recombinase	<i>Raoultella terrigena</i>
ID=1883	WP_041147093	integrase	<i>Raoultella ornithinolytica</i>
ID=1884	WP_041147092	lysine transporter LysE	<i>Raoultella ornithinolytica</i>
ID=1885	WP_041147735	AsnC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1886	WP_041147091	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1887	WP_041147090	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1888	WP_045857321	flavin reductase	<i>Raoultella terrigena</i>
ID=1889	WP_041147088	Vanillate O-demethylase oxidoreductase	<i>Raoultella ornithinolytica</i>

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ID=1890	WP_041147087	3-oxoacyl-ACP reductase	<i>Raoultella ornithinolytica</i>
ID=1891	WP_041147086	aromatic-ring-hydroxylating dioxygenase	<i>Raoultella ornithinolytica</i>
ID=1892	WP_041147085	(2Fe-2S)-binding protein	<i>Raoultella ornithinolytica</i>
ID=1893	WP_041147084	polyketide cyclase	<i>Raoultella ornithinolytica</i>
ID=1894	WP_041147083	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1895	WP_052474589	acyl-CoA dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1896	WP_041147082	amidase	<i>Raoultella ornithinolytica</i>
ID=1897	WP_045857930	MarR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1898	WP_045857340	nickel transporter	<i>Raoultella terrigena</i>
ID=1899	WP_045857341	MarR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1900	WP_045857343	ABC transporter permease	<i>Raoultella terrigena</i>
ID=1901	WP_015585822	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=1902	WP_041147078	antibiotic biosynthesis monooxygenase	<i>Raoultella ornithinolytica</i>
ID=1903	WP_045857353	amino acid-binding protein	<i>Raoultella terrigena</i>
ID=1904	WP_045857355	transcriptional regulator	<i>Raoultella terrigena</i>
ID=1905	WP_045857357	ferrous iron transporter B	<i>Raoultella terrigena</i>
ID=1906	WP_041147074	MULTISPECIES: molecular chaperone	<i>Enterobacteriaceae</i>
ID=1907	WP_045857360	fimbrial protein	<i>Raoultella terrigena</i>
ID=1908	WP_045857361	fimbrial protein	<i>Raoultella terrigena</i>
ID=1909	WP_045857363	fimbrial protein	<i>Raoultella terrigena</i>
ID=1910	WP_041147070	diguanylate phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=1911	WP_045857367	helix-turn-helix transcriptional regulator	<i>Raoultella terrigena</i>
ID=1912	WP_041147068	pilus assembly protein PilZ	<i>Raoultella ornithinolytica</i>
ID=1913	WP_045857371	oxidoreductase	<i>Raoultella terrigena</i>
ID=1914	WP_045857373	transporter	<i>Raoultella terrigena</i>
ID=1915	WP_041147065	Na ⁺ -translocating NADH-quinone reductase subunit E	<i>Raoultella ornithinolytica</i>
ID=1916	WP_041147064	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1917	WP_045857382	acetyl-CoA acetyltransferase	<i>Raoultella terrigena</i>
ID=1918	WP_041147062	porin	<i>Raoultella ornithinolytica</i>
ID=1919	WP_041147061	oligogalacturonate lyase	<i>Raoultella ornithinolytica</i>
ID=1920	WP_041147060	2-deoxy-D-gluconate 3-dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=1921	WP_045857390	MFS transporter	<i>Raoultella terrigena</i>
ID=1922	WP_045857392	sucrose operon repressor	<i>Raoultella terrigena</i>
ID=1923	WP_045857395	MFS transporter	<i>Raoultella terrigena</i>
ID=1924	WP_041147056	glycosyl hydrolase family 32	<i>Raoultella ornithinolytica</i>
ID=1925	WP_041147055	porin	<i>Raoultella ornithinolytica</i>
ID=1926	WP_041147054	sugar ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=1927	WP_041147053	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=1928	WP_041147052	sugar ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=1929	WP_041147051	MULTISPECIES: sugar ABC transporter permease	<i>Raoultella</i>
ID=1930	WP_045857407	cupin	<i>Raoultella terrigena</i>
ID=1931	WP_041147049	aspartate/glutamate racemase	<i>Raoultella ornithinolytica</i>
ID=1932	WP_041147048	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1933	WP_014226671	MULTISPECIES: LysR family transcriptional regulator	<i>Klebsiella</i>
ID=1934	WP_041147047	diaminopimelate decarboxylase	<i>Raoultella ornithinolytica</i>
ID=1935	WP_045857411	LacI family transcriptional regulator	<i>Raoultella terrigena</i>
ID=1936	WP_041147045	PTS lactose transporter subunit IIC	<i>Raoultella ornithinolytica</i>
ID=1937	WP_041147732	6-phospho-beta-glucosidase	<i>Raoultella ornithinolytica</i>
ID=1938	WP_041147044	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1939	WP_041147043	GNAT family acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=1940	WP_041147042	MULTISPECIES: transcriptional regulator GalR	<i>Raoultella</i>
ID=1941	WP_045857418	acyl-[ACP]-phospholipid O-acyltransferase	<i>Raoultella terrigena</i>
ID=1942	WP_045857420	lysophospholipid transporter LpIT	<i>Raoultella terrigena</i>
ID=1943	WP_041147039	NADP(H)-dependent aldo-keto reductase	<i>Raoultella ornithinolytica</i>
ID=1944	WP_004867116	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=1945	WP_045857424	membrane protein	<i>Raoultella terrigena</i>
ID=1946	WP_045857426	DNA mismatch repair protein MutH	<i>Raoultella terrigena</i>
ID=1947	WP_041147036	MULTISPECIES: RNA pyrophosphohydrolase	<i>Raoultella</i>
ID=1948	WP_041147035	phosphoenolpyruvate--protein phosphotransferase PtsP	<i>Raoultella ornithinolytica</i>
ID=1949	WP_041147034	prolipoprotein diacylglycerol transferase	<i>Raoultella ornithinolytica</i>
ID=1950	WP_045857434	thymidylate synthase	<i>Raoultella terrigena</i>
ID=1951	WP_041147031	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1952	WP_041147030	prepilin-type N-terminal cleavage/methylation domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=1953	WP_041147029	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1954	WP_045857442	prepilin-type N-terminal cleavage/methylation domain-containing protein	<i>Raoultella terrigena</i>
ID=1955	WP_045857444	exonuclease V subunit gamma	<i>Raoultella terrigena</i>
ID=1956	WP_041147026	pitriysin	<i>Raoultella ornithinolytica</i>
ID=1957	WP_045857448	exodeoxyribonuclease V subunit beta	<i>Raoultella terrigena</i>
ID=1958	WP_041147024	exonuclease V subunit alpha	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=1959	WP_041147023	MULTISPECIES: amino-acid N-acetyltransferase	<i>Raoultella</i>
ID=1960	WP_041147022	N-acetylmutamoyl-L-alanine amidase	<i>Raoultella ornithinolytica</i>
ID=1961	WP_041147021	threonine-phosphate decarboxylase	<i>Raoultella ornithinolytica</i>
ID=1963	WP_041147020	adenosylcobinamide-phosphate synthase	<i>Raoultella ornithinolytica</i>
ID=1964	WP_041147019	cobyrinic acid synthase CobQ	<i>Raoultella ornithinolytica</i>
ID=1965	WP_045857459	adenosylcobinamide kinase/adenosylcobinamide phosphate guanylttransferase	<i>Raoultella terrigena</i>
ID=1966	WP_041147017	adenosylcobinamide-GDP ribazoletransferase	<i>Raoultella ornithinolytica</i>
ID=1967	WP_041147016	MULTISPECIES: murein transglycosylase A	<i>Raoultella</i>
ID=1968	WP_045857463	tRNA threonylcarbamoyladenine dehydratase	<i>Raoultella terrigena</i>
ID=1969	WP_045857465	cysteine desulfurase, sulfur acceptor subunit CsdE	<i>Raoultella terrigena</i>
ID=1970	WP_041147013	cysteine sulfinatase desulfinase	<i>Raoultella ornithinolytica</i>
ID=1971	WP_041147012	transcriptional regulator GcvA	<i>Raoultella ornithinolytica</i>
ID=1972	WP_041147011	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=1973	WP_041147010	23S rRNA (cytidine(2498)-2'-O)-methyltransferase RlmM	<i>Raoultella ornithinolytica</i>
ID=1974	WP_041147009	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=1975	WP_041147008	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=1976	WP_041147007	L-fuculokinase	<i>Raoultella ornithinolytica</i>
ID=1977	WP_041147006	L-fucose isomerase	<i>Raoultella ornithinolytica</i>
ID=1978	WP_041147005	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=1979	WP_041147004	MULTISPECIES: fucose phosphate aldolase	<i>Raoultella</i>
ID=1980	WP_045857484	lactaldehyde reductase	<i>Raoultella terrigena</i>
ID=1981	WP_045857486	flap endonuclease Xni	<i>Raoultella terrigena</i>
ID=1982	WP_045857489	ATPase AAA	<i>Raoultella terrigena</i>
ID=1983	WP_041147000	alkanesulfonate monooxygenase	<i>Raoultella ornithinolytica</i>
ID=1984	WP_041146999	FAD-dependent oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=1985	WP_045857492	5,10-methylenetetrahydromethanopterin reductase	<i>Raoultella terrigena</i>
ID=1986	WP_045857495	methionine ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=1987	WP_041146996	MULTISPECIES: ABC transporter permease	<i>Raoultella</i>
ID=1988	WP_045857497	metal ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=1989	WP_041146994	MULTISPECIES: MFS transporter	<i>Raoultella</i>
ID=1990	WP_045857500	monooxygenase	<i>Raoultella terrigena</i>
ID=1991	WP_045857502	sulfonate ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=1992	WP_045857502	sulfonate ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=1993	WP_041146991	L-serine ammonia-lyase	<i>Raoultella ornithinolytica</i>
ID=1994	WP_045857508	HAAAP family serine/threonine permease	<i>Raoultella terrigena</i>
ID=1995	WP_041146988	LOG family protein	<i>Raoultella ornithinolytica</i>
ID=1996	WP_045857513	preQ(1) synthase	<i>Raoultella terrigena</i>
ID=1997	WP_045857514	SecY-interacting protein	<i>Raoultella terrigena</i>
ID=1998	WP_004137275	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=1999	WP_041146985	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2000	WP_045857518	tRNA pseudouridine synthase TruC	<i>Raoultella terrigena</i>
ID=2001	WP_041146983	MULTISPECIES: flavodoxin	<i>Raoultella</i>
ID=2002	WP_041146982	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2003	WP_041146981	glucarate dehydratase	<i>Raoultella ornithinolytica</i>
ID=2004	WP_041146980	glucarate dehydratase	<i>Raoultella ornithinolytica</i>
ID=2005	WP_041146979	glycerate kinase	<i>Raoultella ornithinolytica</i>
ID=2006	WP_041146978	hybrid sensor histidine kinase/response regulator	<i>Raoultella ornithinolytica</i>
ID=2007	WP_041146977	23S rRNA (uracil(1939)-C(5))-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=2008	WP_041146976	GTP diphosphokinase	<i>Raoultella ornithinolytica</i>
ID=2009	WP_041146975	nucleoside triphosphate pyrophosphohydrolase	<i>Raoultella ornithinolytica</i>
ID=2010	WP_041146974	CTP synthetase	<i>Raoultella ornithinolytica</i>
ID=2011	WP_041146973	phosphopyruvate hydratase	<i>Raoultella ornithinolytica</i>
ID=2012	WP_041146972	thiamine biosynthesis protein ThiF	<i>Raoultella ornithinolytica</i>
ID=2013	WP_041147731	MULTISPECIES: 7-carboxy-7-deazaguanine synthase QueE	<i>Raoultella</i>
ID=2014	WP_041146961	6-carboxy-5,6,7,8-tetrahydropterin synthase	<i>Raoultella ornithinolytica</i>
ID=2015	WP_041146960	sulfite reductase subunit alpha	<i>Raoultella ornithinolytica</i>
ID=2016	WP_045857559	sulfite reductase subunit beta	<i>Raoultella terrigena</i>
ID=2017	WP_041146958	MULTISPECIES: phosphoadenosine phosphosulfate reductase	<i>Raoultella</i>
ID=2018	WP_058111104	CRISPR-associated protein Cas3	<i>Salmonella enterica</i>
ID=2019	WP_041146950	Zn-dependent exopeptidase M28	<i>Raoultella ornithinolytica</i>
ID=2020	WP_041147730	siroheme synthase	<i>Raoultella ornithinolytica</i>
ID=2021	WP_041146949	MULTISPECIES: sulfate adenylyltransferase subunit 2	<i>Raoultella</i>
ID=2022	WP_041146948	sulfate adenylyltransferase	<i>Raoultella ornithinolytica</i>
ID=2023	WP_041146947	adenylyl-sulfate kinase	<i>Raoultella ornithinolytica</i>
ID=2024	WP_041146946	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2025	WP_045857570	cell division protein FtsB	<i>Raoultella terrigena</i>
ID=2026	WP_045857574	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	<i>Raoultella terrigena</i>
ID=2027	WP_001219254	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	<i>Salmonella bongori</i>
ID=2028	WP_041146942	MULTISPECIES: tRNA pseudouridine(13) synthase TruD	<i>Raoultella</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=2029	WP_041146941	MULTISPECIES: 5'/3'-nucleotidase SurE	<i>Raoultella</i>
ID=2030	WP_041146940	MULTISPECIES: protein-L-isoaspartate O-methyltransferase	<i>Raoultella</i>
ID=2031	WP_041146939	lipoprotein NlpD	<i>Raoultella ornithinolytica</i>
ID=2032	WP_004866938	MULTISPECIES: RNA polymerase sigma factor RpoS	<i>Enterobacteriaceae</i>
ID=2033	WP_045857578	hypothetical protein	<i>Raoultella terrigena</i>
ID=2034	WP_041146937	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2035	WP_045857583	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=2036	WP_045857584	DNA mismatch repair protein MutS	<i>Raoultella terrigena</i>
ID=2037	WP_045857586	heme ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=2038	WP_045857589	iron ABC transporter	<i>Raoultella terrigena</i>
ID=2039	WP_041146926	hemin ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=2040	WP_041146925	hemin-degrading factor	<i>Raoultella ornithinolytica</i>
ID=2041	WP_045857596	TonB-dependent receptor	<i>Raoultella terrigena</i>
ID=2042	WP_041146923	MULTISPECIES: selenoprotein W-related protein	<i>Raoultella</i>
ID=2043	WP_041146922	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2044	WP_041146921	iron ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=2045	WP_041146920	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2046	WP_041146919	manganese/iron transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2047	WP_041146918	metal ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=2048	WP_041146917	LacI family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2049	WP_041146916	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2050	WP_045857609	molecular chaperone TorD	<i>Raoultella terrigena</i>
ID=2051	WP_041146914	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2052	WP_041146913	PTS sugar transporter subunit IIB	<i>Raoultella ornithinolytica</i>
ID=2053	WP_041146912	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2054	WP_041146911	malto porin	<i>Raoultella ornithinolytica</i>
ID=2055	WP_041146910	beta-1,4 mannanase	<i>Raoultella ornithinolytica</i>
ID=2056	WP_041146909	6-phospho-beta-glucosidase	<i>Raoultella ornithinolytica</i>
ID=2057	WP_041146908	pectin acetylase	<i>Raoultella ornithinolytica</i>
ID=2058	WP_045857624	transporter	<i>Raoultella terrigena</i>
ID=2058	WP_045857624	transporter	<i>Raoultella terrigena</i>
ID=2059	WP_041146907	transcriptional regulator FhlA	<i>Raoultella ornithinolytica</i>
ID=2060	WP_041146906	hydrogenase expression/formation protein HypE	<i>Raoultella ornithinolytica</i>
ID=2061	WP_041146905	hydrogenase formation protein HypD	<i>Raoultella ornithinolytica</i>
ID=2062	WP_041146904	hydrogenase assembly chaperone	<i>Raoultella ornithinolytica</i>
ID=2063	WP_041146903	hydrogenase nickel incorporation protein HypB	<i>Raoultella ornithinolytica</i>
ID=2064	WP_041146902	hydrogenase maturation nickel metallochaperone HypA	<i>Raoultella ornithinolytica</i>
ID=2065	WP_041146901	formate hydrogenlyase regulatory protein HycA	<i>Raoultella ornithinolytica</i>
ID=2066	WP_041146900	formate hydrogenlyase	<i>Raoultella ornithinolytica</i>
ID=2067	WP_041146899	formate hydrogenlyase subunit 3	<i>Raoultella ornithinolytica</i>
ID=2068	WP_041146898	hydrogenase 3 membrane subunit	<i>Raoultella ornithinolytica</i>
ID=2069	WP_045857645	hydrogenase 3 large subunit	<i>Raoultella terrigena</i>
ID=2070	WP_041146896	formate hydrogenlyase complex iron-sulfur subunit	<i>Raoultella ornithinolytica</i>
ID=2071	WP_041146895	formate hydrogenlyase	<i>Raoultella ornithinolytica</i>
ID=2072	WP_041146894	formate hydrogenlyase maturation protein HycH	<i>Raoultella ornithinolytica</i>
ID=2073	WP_046877488	hydrogenase 3 maturation endopeptidase HyCI	<i>Klebsiella michiganensis</i>
ID=2074	WP_041146892	6-phospho-beta-glucosidase	<i>Raoultella ornithinolytica</i>
ID=2075	WP_041146891	PTS cellobiose/arbutin/salicin transporter subunit IIBC	<i>Raoultella ornithinolytica</i>
ID=2076	WP_041146889	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2077	WP_045857662	formate dehydrogenase	<i>Raoultella terrigena</i>
ID=2078	WP_041146887	carbamoyltransferase HypF	<i>Raoultella ornithinolytica</i>
ID=2079	WP_045857666	nickel transporter	<i>Raoultella terrigena</i>
ID=2080	WP_052474626	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2082	WP_032705085	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=2083	WP_013357519	hypothetical protein	<i>Pantoea vagans</i>
ID=2084	WP_041146882	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2085	WP_041146881	NADH:flavoredoxin oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=2086	WP_041146880	anaerobic nitric oxide reductase flavoredoxin	<i>Raoultella ornithinolytica</i>
ID=2087	WP_041146879	nitric oxide reductase transcription regulator	<i>Raoultella ornithinolytica</i>
ID=2088	WP_041146878	arabinose-5-phosphate isomerase	<i>Raoultella ornithinolytica</i>
ID=2089	WP_045857684	transcriptional regulator	<i>Raoultella terrigena</i>
ID=2090	WP_045857686	transcriptional regulator GutM	<i>Raoultella terrigena</i>
ID=2091	WP_045857688	sorbitol 6-phosphate dehydrogenase	<i>Raoultella terrigena</i>
ID=2092	WP_045857690	PTS glucitol/sorbitol transporter subunit IIA	<i>Raoultella terrigena</i>
ID=2093	WP_041146873	PTS glucitol/sorbitol transporter subunit IIB	<i>Raoultella ornithinolytica</i>
ID=2094	WP_041146872	PTS glucitol/sorbitol transporter subunit IIC	<i>Raoultella ornithinolytica</i>
ID=2095	WP_052698739	murein transglycosylase B	<i>Raoultella terrigena</i>
ID=2097	WP_045857698	ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=2098	WP_041146869	iron ABC transporter	<i>Raoultella ornithinolytica</i>

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ID=2099	WP_045857701	metal ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=2100	WP_041146867	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2101	WP_041146866	DNA recombination/repair protein RecA	<i>Raoultella ornithinolytica</i>
ID=2102	WP_041147727	recombination regulator RecX	<i>Raoultella ornithinolytica</i>
ID=2103	WP_041146865	alanine--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=2104	WP_000906486	MULTISPECIES: carbon storage regulator	<i>Proteobacteria</i>
ID=2105	WP_041146864	BON domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=2106	WP_045857711	fructose-1-phosphate/6-phosphogluconate phosphatase	<i>Raoultella terrigena</i>
ID=2107	WP_041146862	MULTISPECIES: membrane protein	<i>Raoultella</i>
ID=2108	WP_041146861	glutamate--cysteine ligase	<i>Raoultella ornithinolytica</i>
ID=2109	WP_041146860	S-ribosylhomocysteine lyase	<i>Raoultella ornithinolytica</i>
ID=2110	WP_041146859	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2111	WP_041146858	2-isopropylmalate synthase	<i>Raoultella ornithinolytica</i>
ID=2112	WP_041146857	multidrug efflux MFS transporter subunit EmrB	<i>Raoultella ornithinolytica</i>
ID=2113	WP_041146856	multidrug export protein EmrA	<i>Raoultella ornithinolytica</i>
ID=2115	WP_041146855	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=2116	WP_041146854	glycine betaine ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=2117	WP_041146853	proline/betaine ABC transporter permease ProW	<i>Raoultella ornithinolytica</i>
ID=2118	WP_041146852	glycine betaine/L-proline ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2119	WP_041146851	ribonucleotide-diphosphate reductase subunit beta	<i>Raoultella ornithinolytica</i>
ID=2120	WP_045857735	ribonucleotide-diphosphate reductase	<i>Raoultella terrigena</i>
ID=2121	WP_045857737	ribonucleotide reductase assembly protein NrdI	<i>Raoultella terrigena</i>
ID=2122	WP_041146848	NrdH-redoxin	<i>Raoultella ornithinolytica</i>
ID=2123	WP_045857742	alkylhydroperoxidase	<i>Raoultella terrigena</i>
ID=2124	WP_045857744	DeoR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=2125	WP_041146846	MULTISPECIES: membrane protein	<i>Raoultella</i>
ID=2126	WP_041146845	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2127	WP_041146844	L-alanine exporter AlaE	<i>Raoultella ornithinolytica</i>
ID=2128	WP_041146843	DNA-binding protein	<i>Raoultella ornithinolytica</i>
ID=2129	WP_045857751	hypothetical protein	<i>Raoultella terrigena</i>
ID=2130	WP_041146841	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2131	WP_041146840	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2132	WP_041146838	sigma-54-dependent Fis family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2133	WP_045857758	aldehyde dehydrogenase	<i>Raoultella terrigena</i>
ID=2134	WP_041146836	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=2135	WP_041147725	fimbrial assembly protein	<i>Raoultella ornithinolytica</i>
ID=2136	WP_052474624	export and assembly usher protein of type 1 fimbriae	<i>Raoultella ornithinolytica</i>
ID=2137	WP_041146835	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=2138	WP_041146834	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=2139	WP_041146833	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2140	WP_041146832	pilus assembly protein	<i>Raoultella ornithinolytica</i>
ID=2141	WP_041146831	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=2142	WP_041146830	helix-turn-helix transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2143	WP_041146829	peptide ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2144	WP_041146828	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2145	WP_041146827	D-ala-D-ala transporter subunit	<i>Raoultella ornithinolytica</i>
ID=2146	WP_045857765	peptide ABC transporter permease	<i>Raoultella terrigena</i>
ID=2147	WP_045857938	peptide ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=2148	WP_041146825	D-alanyl-D-alanine dipeptidase	<i>Raoultella ornithinolytica</i>
ID=2149	WP_041146824	RpiR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2150	WP_041146823	amino acid ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=2151	WP_045857774	MFS transporter	<i>Raoultella terrigena</i>
ID=2152	WP_045857776	cyclic peptide transporter	<i>Raoultella terrigena</i>
ID=2153	WP_045857778	fecCD transport family protein	<i>Raoultella terrigena</i>
ID=2154	WP_045857780	ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=2155	WP_045857782	TonB-dependent receptor	<i>Raoultella terrigena</i>
ID=2156	WP_045857784	AraC family transcriptional regulator	<i>Raoultella terrigena</i>
ID=2157	WP_045857786	PTS galactitol transporter subunit IIB	<i>Raoultella terrigena</i>
ID=2158	WP_045857789	DNA mismatch repair protein MutT	<i>Raoultella terrigena</i>
ID=2159	WP_045857791	PTS glucose transporter subunit IIA	<i>Raoultella terrigena</i>
ID=2160	WP_045857792	hypothetical protein	<i>Raoultella terrigena</i>
ID=2161	WP_045857794	oxidoreductase	<i>Raoultella terrigena</i>
ID=2162	WP_045857796	glyoxylate/hydroxypyruvate reductase A	<i>Raoultella terrigena</i>
ID=2163	WP_045857798	class II aldolase	<i>Raoultella terrigena</i>
ID=2164	WP_041146818	amino acid ABC transporter ATPase	<i>Raoultella ornithinolytica</i>
ID=2165	WP_041146817	amino acid ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=2166	WP_041146816	2OG-Fe(II) oxygenase	<i>Raoultella ornithinolytica</i>
ID=2167	WP_041147722	xylose isomerase	<i>Raoultella ornithinolytica</i>
ID=2168	WP_041146815	agmatinase	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=2169	WP_041146814	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2170	WP_045857810	hypothetical protein	<i>Raoultella terrigena</i>
ID=2171	WP_041146813	5'/3'-nucleotidase SurE	<i>Raoultella ornithinolytica</i>
ID=2172	WP_045857814	phosphoglycerate mutase	<i>Raoultella terrigena</i>
ID=2173	WP_045857817	porin	<i>Raoultella terrigena</i>
ID=2174	WP_045857819	transcriptional regulator	<i>Raoultella terrigena</i>
ID=2175	WP_045857822	triose-phosphate isomerase	<i>Raoultella terrigena</i>
ID=2176	WP_045857823	dihydroxyacetone kinase	<i>Raoultella terrigena</i>
ID=2177	WP_045857825	ribose-5-phosphate isomerase	<i>Raoultella terrigena</i>
ID=2178	WP_045857827	transaldolase	<i>Raoultella terrigena</i>
ID=2179	WP_052537438	hypothetical protein	<i>Cronobacter sakazakii</i>
ID=2180	WP_041142973	elongation factor G	<i>Raoultella ornithinolytica</i>
ID=2181	WP_004106370	MULTISPECIES: 30S ribosomal protein S7	<i>Enterobacterales</i>
ID=2182	WP_003023654	MULTISPECIES: 30S ribosomal protein S12	<i>Enterobacteriaceae</i>
ID=2183	WP_041142974	MULTISPECIES: tRNA 2-thiouridine(34) synthase TusB	<i>Raoultella</i>
ID=2184	WP_041142975	sulfurtransferase	<i>Raoultella ornithinolytica</i>
ID=2185	WP_041142976	sulfurtransferase	<i>Raoultella ornithinolytica</i>
ID=2186	WP_004868391	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=2187	WP_041142977	peptidylprolyl isomerase	<i>Raoultella ornithinolytica</i>
ID=2188	WP_041142978	MULTISPECIES: phi X174 lysis protein	<i>Raoultella</i>
ID=2189	WP_041142979	MULTISPECIES: peptidylprolyl isomerase	<i>Raoultella</i>
ID=2190	WP_013364433	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=2191	WP_041142980	glutathione-regulated potassium-efflux system protein KefB	<i>Raoultella ornithinolytica</i>
ID=2192	WP_041142981	glutathione-regulated potassium-efflux system ancillary protein KefG	<i>Raoultella ornithinolytica</i>
ID=2193	WP_041142982	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2194	WP_041142983	hydrolase	<i>Raoultella ornithinolytica</i>
ID=2195	WP_041142984	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2196	WP_041142985	MULTISPECIES: phosphoribulokinase	<i>Raoultella</i>
ID=2197	WP_041142986	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2198	WP_000242758	MULTISPECIES: cAMP-activated global transcriptional regulator CRP	<i>Proteobacteria</i>
ID=2199	WP_041142987	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2200	WP_041142988	MULTISPECIES: acetylornithine aminotransferase	<i>Raoultella</i>
ID=2201	WP_041142988	MULTISPECIES: acetylornithine aminotransferase	<i>Raoultella</i>
ID=2202	WP_045854054	glutamine amidotransferase	<i>Raoultella terrigena</i>
ID=2203	WP_041142990	cell filamentation protein Fic	<i>Raoultella ornithinolytica</i>
ID=2204	WP_045854052	peptidylprolyl isomerase A	<i>Raoultella terrigena</i>
ID=2205	WP_041142992	MFS transporter TsgA	<i>Raoultella ornithinolytica</i>
ID=2206	WP_041142993	cytosine deaminase	<i>Raoultella ornithinolytica</i>
ID=2207	WP_045854049	nitrite reductase large subunit	<i>Raoultella terrigena</i>
ID=2208	WP_045854048	nitrite reductase small subunit	<i>Raoultella terrigena</i>
ID=2209	WP_045854047	siroheme synthase	<i>Raoultella terrigena</i>
ID=2210	WP_045854046	tryptophan--tRNA ligase	<i>Raoultella terrigena</i>
ID=2211	WP_041142998	phosphoglycolate phosphatase	<i>Raoultella ornithinolytica</i>
ID=2212	WP_041142999	MULTISPECIES: ribulose-phosphate 3-epimerase	<i>Raoultella</i>
ID=2213	WP_041143000	DNA adenine methylase	<i>Raoultella ornithinolytica</i>
ID=2214	WP_004115986	cell division protein DamX	<i>Klebsiella oxytoca</i>
ID=2215	WP_041143002	MULTISPECIES: 3-dehydroquinate synthase	<i>Raoultella</i>
ID=2216	WP_004868452	MULTISPECIES: shikimate kinase	<i>Enterobacteriaceae</i>
ID=2217	WP_041143003	DNA transporter HofQ	<i>Raoultella ornithinolytica</i>
ID=2218	WP_041143004	pilus assembly protein PilP	<i>Raoultella ornithinolytica</i>
ID=2219	WP_041143005	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2220	WP_041143006	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2221	WP_045854038	hypothetical protein	<i>Raoultella terrigena</i>
ID=2222	WP_041143008	carboxypeptidase/penicillin-binding protein 1A	<i>Raoultella ornithinolytica</i>
ID=2223	WP_041147478	ADP compounds hydrolase NudE	<i>Raoultella ornithinolytica</i>
ID=2224	WP_045854036	intracellular growth attenuator protein IgaA	<i>Raoultella terrigena</i>
ID=2225	WP_041143010	nucleotidase	<i>Raoultella ornithinolytica</i>
ID=2226	WP_041143011	MULTISPECIES: heat-shock protein Hsp15	<i>Raoultella</i>
ID=2227	WP_041143012	molecular chaperone Hsp33	<i>Raoultella ornithinolytica</i>
ID=2228	WP_041143013	phosphoenolpyruvate carboxykinase (ATP)	<i>Raoultella ornithinolytica</i>
ID=2229	WP_041143014	two-component sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=2230	WP_001157751	MULTISPECIES: DNA-binding response regulator	<i>Proteobacteria</i>
ID=2231	WP_045854031	transcription elongation factor GreB	<i>Raoultella terrigena</i>
ID=2232	WP_045854030	transcription accessory protein	<i>Raoultella terrigena</i>
ID=2233	WP_004868486	MULTISPECIES: iron transporter	<i>Enterobacteriaceae</i>
ID=2234	WP_041143017	ferrous iron transport protein B	<i>Raoultella ornithinolytica</i>
ID=2235	WP_041143018	ferrous iron transporter C	<i>Raoultella ornithinolytica</i>
ID=2236	WP_041143019	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2237	WP_041143020	pimeloyl-[acyl-carrier protein] methyl ester esterase	<i>Raoultella ornithinolytica</i>

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ID=2169	WP_041146814	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2170	WP_045857810	hypothetical protein	<i>Raoultella terrigena</i>
ID=2171	WP_041146813	5'/3'-nucleotidase SurE	<i>Raoultella ornithinolytica</i>
ID=2172	WP_045857814	phosphoglycerate mutase	<i>Raoultella terrigena</i>
ID=2173	WP_045857817	porin	<i>Raoultella terrigena</i>
ID=2174	WP_045857819	transcriptional regulator	<i>Raoultella terrigena</i>
ID=2175	WP_045857822	triose-phosphate isomerase	<i>Raoultella terrigena</i>
ID=2176	WP_045857823	dihydroxyacetone kinase	<i>Raoultella terrigena</i>
ID=2177	WP_045857825	ribose-5-phosphate isomerase	<i>Raoultella terrigena</i>
ID=2178	WP_045857827	transaldolase	<i>Raoultella terrigena</i>
ID=2179	WP_052537438	hypothetical protein	<i>Cronobacter sakazakii</i>
ID=2180	WP_041142973	elongation factor G	<i>Raoultella ornithinolytica</i>
ID=2181	WP_004106370	MULTISPECIES: 30S ribosomal protein S7	<i>Enterobacterales</i>
ID=2182	WP_003023654	MULTISPECIES: 30S ribosomal protein S12	<i>Enterobacteriaceae</i>
ID=2183	WP_041142974	MULTISPECIES: tRNA 2-thiouridine(34) synthase TusB	<i>Raoultella</i>
ID=2184	WP_041142975	sulfurtransferase	<i>Raoultella ornithinolytica</i>
ID=2185	WP_041142976	sulfurtransferase	<i>Raoultella ornithinolytica</i>
ID=2186	WP_004868391	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=2187	WP_041142977	peptidylprolyl isomerase	<i>Raoultella ornithinolytica</i>
ID=2188	WP_041142978	MULTISPECIES: phi X174 lysis protein	<i>Raoultella</i>
ID=2189	WP_041142979	MULTISPECIES: peptidylprolyl isomerase	<i>Raoultella</i>
ID=2190	WP_013364433	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=2191	WP_041142980	glutathione-regulated potassium-efflux system protein KefB	<i>Raoultella ornithinolytica</i>
ID=2192	WP_041142981	glutathione-regulated potassium-efflux system ancillary protein KefG	<i>Raoultella ornithinolytica</i>
ID=2193	WP_041142982	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2194	WP_041142983	hydrolase	<i>Raoultella ornithinolytica</i>
ID=2195	WP_041142984	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2196	WP_041142985	MULTISPECIES: phosphoribulokinase	<i>Raoultella</i>
ID=2197	WP_041142986	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2198	WP_000242758	MULTISPECIES: cAMP-activated global transcriptional regulator CRP	<i>Proteobacteria</i>
ID=2199	WP_041142987	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2200	WP_041142988	MULTISPECIES: acetylornithine aminotransferase	<i>Raoultella</i>
ID=2201	WP_041142988	MULTISPECIES: acetylornithine aminotransferase	<i>Raoultella</i>
ID=2202	WP_045854054	glutamine amidotransferase	<i>Raoultella terrigena</i>
ID=2203	WP_041142990	cell filamentation protein Fic	<i>Raoultella ornithinolytica</i>
ID=2204	WP_045854052	peptidylprolyl isomerase A	<i>Raoultella terrigena</i>
ID=2205	WP_041142992	MFS transporter TsgA	<i>Raoultella ornithinolytica</i>
ID=2206	WP_041142993	cytosine deaminase	<i>Raoultella ornithinolytica</i>
ID=2207	WP_045854049	nitrite reductase large subunit	<i>Raoultella terrigena</i>
ID=2208	WP_045854048	nitrite reductase small subunit	<i>Raoultella terrigena</i>
ID=2209	WP_045854047	siroheme synthase	<i>Raoultella terrigena</i>
ID=2210	WP_045854046	tryptophan--tRNA ligase	<i>Raoultella terrigena</i>
ID=2211	WP_041142998	phosphoglycolate phosphatase	<i>Raoultella ornithinolytica</i>
ID=2212	WP_041142999	MULTISPECIES: ribulose-phosphate 3-epimerase	<i>Raoultella</i>
ID=2213	WP_041143000	DNA adenine methylase	<i>Raoultella ornithinolytica</i>
ID=2214	WP_004115986	cell division protein DamX	<i>Klebsiella oxytoca</i>
ID=2215	WP_041143002	MULTISPECIES: 3-dehydroquinate synthase	<i>Raoultella</i>
ID=2216	WP_004868452	MULTISPECIES: shikimate kinase	<i>Enterobacteriaceae</i>
ID=2217	WP_041143003	DNA transporter HofQ	<i>Raoultella ornithinolytica</i>
ID=2218	WP_041143004	pilus assembly protein PilP	<i>Raoultella ornithinolytica</i>
ID=2219	WP_041143005	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2220	WP_041143006	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2221	WP_045854038	hypothetical protein	<i>Raoultella terrigena</i>
ID=2222	WP_041143008	carboxypeptidase/penicillin-binding protein 1A	<i>Raoultella ornithinolytica</i>
ID=2223	WP_041147478	ADP compounds hydrolase NudE	<i>Raoultella ornithinolytica</i>
ID=2224	WP_045854036	intracellular growth attenuator protein IgaA	<i>Raoultella terrigena</i>
ID=2225	WP_041143010	nucleotidase	<i>Raoultella ornithinolytica</i>
ID=2226	WP_041143011	MULTISPECIES: heat-shock protein Hsp15	<i>Raoultella</i>
ID=2227	WP_041143012	molecular chaperone Hsp33	<i>Raoultella ornithinolytica</i>
ID=2228	WP_041143013	phosphoenolpyruvate carboxykinase (ATP)	<i>Raoultella ornithinolytica</i>
ID=2229	WP_041143014	two-component sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=2230	WP_001157751	MULTISPECIES: DNA-binding response regulator	<i>Proteobacteria</i>
ID=2231	WP_045854031	transcription elongation factor GreB	<i>Raoultella terrigena</i>
ID=2232	WP_045854030	transcription accessory protein	<i>Raoultella terrigena</i>
ID=2233	WP_004868486	MULTISPECIES: iron transporter	<i>Enterobacteriaceae</i>
ID=2234	WP_041143017	ferrous iron transport protein B	<i>Raoultella ornithinolytica</i>
ID=2235	WP_041143018	ferrous iron transporter C	<i>Raoultella ornithinolytica</i>
ID=2236	WP_041143019	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2237	WP_041143020	pimeloyl-[acyl-carrier protein] methyl ester esterase	<i>Raoultella ornithinolytica</i>

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ID=2238	WP_041143021	DNA utilization protein GntX	<i>Raoultella ornithinolytica</i>
ID=2239	WP_045854024	Fe-S biogenesis protein NfuA	<i>Raoultella terrigena</i>
ID=2240	WP_045854023	gluconate transporter	<i>Raoultella terrigena</i>
ID=2241	WP_041143024	4-alpha-glucanotransferase	<i>Raoultella ornithinolytica</i>
ID=2242	WP_041143025	maltodextrin phosphorylase	<i>Raoultella ornithinolytica</i>
ID=2243	WP_045854020	transcriptional regulator MaIT	<i>Raoultella terrigena</i>
ID=2244	WP_041143027	DeoR/GlpR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2245	WP_041143028	rhomboid family intramembrane serine protease GlpG	<i>Raoultella ornithinolytica</i>
ID=2246	WP_041143029	MULTISPECIES: thiosulfate sulfurtransferase	<i>Raoultella</i>
ID=2247	WP_041143030	glycerol-3-phosphate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=2248	WP_041143031	glycogen phosphorylase	<i>Raoultella ornithinolytica</i>
ID=2249	WP_041143032	starch synthase	<i>Raoultella ornithinolytica</i>
ID=2250	WP_041143033	MULTISPECIES: glucose-1-phosphate adenylyltransferase	<i>Raoultella</i>
ID=2251	WP_041143034	glycogen debranching enzyme	<i>Raoultella ornithinolytica</i>
ID=2252	WP_041143035	glycogen-branching enzyme	<i>Raoultella ornithinolytica</i>
ID=2253	WP_041143036	MULTISPECIES: aspartate-semialdehyde dehydrogenase	<i>Raoultella</i>
ID=2254	WP_041143037	gluconate transporter	<i>Raoultella ornithinolytica</i>
ID=2255	WP_045854011	gluconokinase	<i>Raoultella terrigena</i>
ID=2256	WP_044644046	gluconokinase, partial	<i>Klebsiella variicola</i>
ID=2257	WP_041143038	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=2259	WP_041143039	MULTISPECIES: quercetin 2,3-dioxygenase	<i>Raoultella</i>
ID=2260	WP_041143040	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=2261	WP_041143041	acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=2262	WP_045854008	gamma-glutamyltransferase	<i>Raoultella terrigena</i>
ID=2263	WP_041143043	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2264	WP_041143044	glycerophosphoryl diester phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=2265	WP_041143045	glycerol-3-phosphate transporter ATP-binding subunit	<i>Raoultella ornithinolytica</i>
ID=2266	WP_041143046	glycerol-3-phosphate transporter membrane protein	<i>Raoultella ornithinolytica</i>
ID=2267	WP_041147479	glycerol-3-phosphate transporter permease	<i>Raoultella ornithinolytica</i>
ID=2268	WP_041143047	sn-glycerol-3-phosphate ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=2269	WP_032718455	MULTISPECIES: ABC transporter ATP-binding protein	<i>Raoultella</i>
ID=2270	WP_041143048	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2271	WP_041143049	branched-chain amino acid ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=2272	WP_041143050	MULTISPECIES: branched-chain amino acid ABC transporter permease LivH	<i>Raoultella</i>
ID=2273	WP_041143051	MULTISPECIES: branched chain amino acid ABC transporter substrate-binding protein	<i>Raoultella</i>
ID=2274	WP_042322249	hypothetical protein	<i>Enterobacter cancerogenus</i>
ID=2275	WP_041143053	acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=2276	WP_041143054	MULTISPECIES: branched chain amino acid ABC transporter substrate-binding protein	<i>Raoultella</i>
ID=2277	WP_041143055	aspartate aminotransferase family protein	<i>Raoultella ornithinolytica</i>
ID=2278	WP_041143056	MULTISPECIES: RNA polymerase factor sigma-32	<i>Raoultella</i>
ID=2280	WP_041143057	cell division protein FtsX	<i>Raoultella ornithinolytica</i>
ID=2281	WP_004868565	MULTISPECIES: cell division protein FtsE	<i>Enterobacteriaceae</i>
ID=2282	WP_041143058	signal recognition particle-docking protein FtsY	<i>Raoultella ornithinolytica</i>
ID=2283	WP_041143059	16S rRNA (guanine(966)-N(2))-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=2284	WP_041143060	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2285	WP_041143061	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2286	WP_041143062	lysoplasmalogenase	<i>Raoultella ornithinolytica</i>
ID=2287	WP_041143063	zinc/cadmium/mercury/lead-transporting ATPase	<i>Raoultella ornithinolytica</i>
ID=2288	WP_041147480	MULTISPECIES: sulfurtransferase TusA	<i>Raoultella</i>
ID=2289	WP_041143064	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2290	WP_041143065	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2291	WP_045853988	hypothetical protein	<i>Raoultella terrigena</i>
ID=2292	WP_041143066	MULTISPECIES: lipoprotein	<i>Raoultella</i>
ID=2293	WP_041143067	beta-ketoacyl synthase	<i>Raoultella ornithinolytica</i>
ID=2294	WP_045853986	1-acyl-sn-glycerol-3-phosphate acyltransferase	<i>Raoultella terrigena</i>
ID=2295	WP_041143069	MULTISPECIES: acyl carrier protein	<i>Raoultella</i>
ID=2296	WP_045853985	acyl carrier protein	<i>Raoultella terrigena</i>
ID=2297	WP_041143071	DNA gyrase subunit B	<i>Raoultella ornithinolytica</i>
ID=2298	WP_045853983	AMP-dependent synthetase	<i>Raoultella terrigena</i>
ID=2299	WP_041143073	hydroxymyristoyl-ACP dehydratase	<i>Raoultella ornithinolytica</i>
ID=2300	WP_041143074	acyltransferase	<i>Raoultella ornithinolytica</i>
ID=2301	WP_041143075	4-hydroxybenzoyl-CoA thioesterase	<i>Raoultella ornithinolytica</i>
ID=2302	WP_041143076	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2303	WP_041143077	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2304	WP_041143078	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2305	WP_041143079	beta-ketoacyl-[acyl-carrier-protein] synthase II	<i>Raoultella ornithinolytica</i>
ID=2306	WP_045853975	3-hydroxy-fatty acyl-ACP dehydratase	<i>Raoultella terrigena</i>
ID=2307	WP_041143081	beta-ketoacyl-ACP reductase	<i>Raoultella ornithinolytica</i>
ID=2308	WP_041143082	beta-ketoacyl-ACP synthase II	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=2309	WP_041143083	ACP synthase	<i>Raoultella ornithinolytica</i>
ID=2310	WP_045853971	4-amino-4-deoxy-L-arabinose-phospho-UDP flippase	<i>Raoultella terrigena</i>
ID=2311	WP_041143085	4-amino-4-deoxy-L-arabinose-phospho-UDP flippase	<i>Raoultella ornithinolytica</i>
ID=2312	WP_045853969	4-amino-4-deoxy-L-arabinose lipid A transferase	<i>Raoultella terrigena</i>
ID=2313	WP_045853968	4-deoxy-4-formamido-L-arabinose-phosphoundecaprenol deformylase	<i>Raoultella terrigena</i>
ID=2314	WP_045853967	bifunctional UDP-glucuronic acid oxidase/UDP-4-amino-4-deoxy-..	<i>Raoultella terrigena</i>
		..L-arabinose formyltransferase	
ID=2315	WP_041143089	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase	<i>Raoultella ornithinolytica</i>
ID=2316	WP_041143090	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	<i>Raoultella ornithinolytica</i>
ID=2317	WP_041143091	phenolic acid decarboxylase	<i>Raoultella ornithinolytica</i>
ID=2318	WP_041143092	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2319	WP_045853990	nickel ABC transporter, nickel/metallophore periplasmic binding protein	<i>Raoultella terrigena</i>
ID=2320	WP_041143093	nickel ABC transporter permease subunit NikB	<i>Raoultella ornithinolytica</i>
ID=2321	WP_041143094	nickel ABC transporter permease subunit NikC	<i>Raoultella ornithinolytica</i>
ID=2322	WP_041143095	nickel import ATP-binding protein NikD	<i>Raoultella ornithinolytica</i>
ID=2323	WP_041143096	nickel import ATP-binding protein NikE	<i>Raoultella ornithinolytica</i>
ID=2324	WP_041143097	nickel responsive regulator	<i>Raoultella ornithinolytica</i>
ID=2325	WP_041143098	magnesium transporter	<i>Raoultella ornithinolytica</i>
ID=2326	WP_064559335	hypothetical protein	<i>Buttiauxella brennerae</i>
ID=2327	WP_025120590	MULTISPECIES: LysR family transcriptional regulator	<i>Serratia</i>
ID=2328	WP_041143099	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2329	WP_045853955	anion permease	<i>Raoultella terrigena</i>
ID=2330	WP_004868669	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2331	WP_041143101	universal stress protein UspB	<i>Raoultella ornithinolytica</i>
ID=2332	WP_041143102	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=2333	WP_041143103	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2334	WP_045853952	transcriptional regulator	<i>Raoultella terrigena</i>
ID=2335	WP_045853951	pyridine nucleotide-disulfide oxidoreductase	<i>Raoultella terrigena</i>
ID=2336	WP_041143104	16S rRNA (guanine(1516)-N(2))-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=2337	WP_041143105	oligopeptidase A	<i>Raoultella ornithinolytica</i>
ID=2338	WP_045853948	phosphoesterase PA-phosphatase	<i>Raoultella terrigena</i>
ID=2339	WP_041143107	23S rRNA (adenine(2030)-N(6))-methyltransferase RlmJ	<i>Raoultella ornithinolytica</i>
ID=2340	WP_041143108	glutathione-disulfide reductase	<i>Raoultella ornithinolytica</i>
ID=2341	WP_045853945	serine hydrolase	<i>Raoultella terrigena</i>
ID=2342	WP_041143110	glutathione S-transferase	<i>Raoultella ornithinolytica</i>
ID=2343	WP_041143111	alcohol dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=2344	WP_041143112	alpha, alpha-trehalase	<i>Raoultella ornithinolytica</i>
ID=2345	WP_041143113	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=2346	WP_041143114	short-chain dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=2347	WP_041143115	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2348	WP_041143116	inner membrane protein YhjD	<i>Raoultella ornithinolytica</i>
ID=2349	WP_045853937	MFS transporter	<i>Raoultella terrigena</i>
ID=2350	WP_041143118	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2351	WP_041143119	ketodeoxygluconokinase	<i>Raoultella ornithinolytica</i>
ID=2352	WP_041143120	peptidase M16	<i>Raoultella ornithinolytica</i>
ID=2353	WP_045853933	C4-dicarboxylate transporter	<i>Raoultella terrigena</i>
ID=2354	WP_045853932	phosphodiesterase	<i>Raoultella terrigena</i>
ID=2355	WP_041143123	cellulose biosynthesis protein BcsC	<i>Raoultella ornithinolytica</i>
ID=2356	WP_041143124	endoglucanase	<i>Raoultella ornithinolytica</i>
ID=2357	WP_041143125	cellulose synthase regulator BcsB	<i>Raoultella ornithinolytica</i>
ID=2358	WP_041143126	UDP-forming cellulose synthase catalytic subunit	<i>Raoultella ornithinolytica</i>
ID=2359	WP_045853927	cell division protein	<i>Raoultella terrigena</i>
ID=2360	WP_004868728	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=2361	WP_041143128	cellulose biosynthesis protein BcsE	<i>Raoultella ornithinolytica</i>
ID=2362	WP_041143129	MULTISPECIES: membrane protein	<i>Raoultella</i>
ID=2363	WP_041143130	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2364	WP_045853924	endoglucanase	<i>Raoultella terrigena</i>
ID=2365	WP_045853923	cellulose synthase	<i>Raoultella terrigena</i>
ID=2366	WP_041143133	cellulose synthase	<i>Raoultella ornithinolytica</i>
ID=2367	WP_041143134	cellulose synthase regulator BcsB	<i>Raoultella ornithinolytica</i>
ID=2368	WP_052698696	cellulose synthase catalytic subunit (UDP-forming)	<i>Raoultella terrigena</i>
ID=2369	WP_041143135	cellulose synthase operon protein YhjQ	<i>Raoultella ornithinolytica</i>
ID=2370	WP_041143136	cellulose biosynthesis protein BcsO	<i>Raoultella ornithinolytica</i>
ID=2371	WP_041143137	dipeptide ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2372	WP_041143138	dipeptide ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2373	WP_041143139	peptide transporter	<i>Raoultella ornithinolytica</i>
ID=2374	WP_041143140	MULTISPECIES: peptide transporter	<i>Raoultella</i>
ID=2375	WP_041143141	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=2376	WP_041143142	phosphoethanolamine transferase	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=2377	WP_041143143	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2378	WP_041143144	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2379	WP_041143145	DNA-3-methyladenine glycosylase I	<i>Raoultella ornithinolytica</i>
ID=2380	WP_041143147	trimethylamine N-oxide reductase I catalytic subunit	<i>Raoultella ornithinolytica</i>
ID=2381	WP_041143148	OmpA family lipoprotein	<i>Raoultella ornithinolytica</i>
ID=2382	WP_041143149	MULTISPECIES: LacI family transcriptional regulator	<i>Raoultella</i>
ID=2383	WP_041143150	xylose isomerase	<i>Raoultella ornithinolytica</i>
ID=2384	WP_041143151	2-dehydro-3-deoxygluconokinase	<i>Raoultella ornithinolytica</i>
ID=2385	WP_041143152	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2386	WP_041143152	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2387	WP_041143153	D-glycerate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=2388	WP_041143154	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2389	WP_041143155	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2390	WP_041143156	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2391	WP_004868803	MULTISPECIES: cold-shock protein	<i>Enterobacteriaceae</i>
ID=2392	WP_041143157	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2393	WP_041143158	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2394	WP_041143159	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2395	WP_041143160	glycine--tRNA ligase subunit beta	<i>Raoultella ornithinolytica</i>
ID=2396	WP_041143161	MULTISPECIES: glycine--tRNA ligase subunit alpha	<i>Raoultella</i>
ID=2397	WP_041143162	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2398	WP_041143163	acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=2399	WP_041143164	xylokkinase	<i>Raoultella ornithinolytica</i>
ID=2400	WP_041143165	xylose isomerase	<i>Raoultella ornithinolytica</i>
ID=2401	WP_045359263	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=2402	WP_045853894	D-xylose transporter subunit XylF	<i>Raoultella terrigena</i>
ID=2403	WP_041143167	D-xylose ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2404	WP_045853892	sugar ABC transporter permease	<i>Raoultella terrigena</i>
ID=2405	WP_041143169	XylR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2406	WP_045853890	mannosyl-glycoprotein endo-beta-N-acetylglucosamidase	<i>Raoultella terrigena</i>
ID=2407	WP_041143171	alpha-amylase	<i>Raoultella ornithinolytica</i>
ID=2408	WP_041143172	valine--pyruvate transaminase	<i>Raoultella ornithinolytica</i>
ID=2409	WP_041143173	effector protein	<i>Raoultella ornithinolytica</i>
ID=2410	WP_041143186	selenocysteine-specific translation factor	<i>Raoultella ornithinolytica</i>
ID=2411	WP_041143187	L-selenocysteinyl-tRNA(Sec) synthase	<i>Raoultella ornithinolytica</i>
ID=2412	WP_041143188	glutathione S-transferase	<i>Raoultella ornithinolytica</i>
ID=2413	WP_041143189	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2414	WP_041143190	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2415	WP_041143191	PTS mannitol transporter subunit IICBA	<i>Raoultella ornithinolytica</i>
ID=2416	WP_041143192	mannitol-1-phosphate 5-dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=2417	WP_041143193	mannitol operon repressor	<i>Raoultella ornithinolytica</i>
ID=2418	WP_041143194	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2419	WP_041143195	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2420	WP_041147484	L-lactate permease	<i>Raoultella ornithinolytica</i>
ID=2421	WP_041143196	transcriptional regulator LldR	<i>Raoultella ornithinolytica</i>
ID=2422	WP_041143197	alpha-hydroxy-acid oxidizing enzyme	<i>Raoultella ornithinolytica</i>
ID=2423	WP_041143198	tRNA (cytidine(34)-2'-O)-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=2424	WP_041143199	serine O-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=2425	WP_041143200	glycerol-3-phosphate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=2426	WP_041143201	MULTISPECIES: protein-export chaperone SecB	<i>Raoultella</i>
ID=2427	WP_041143202	MULTISPECIES: glutaredoxin 3	<i>Raoultella</i>
ID=2428	WP_041143203	rhodanese-like domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=2429	WP_041143204	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	<i>Raoultella ornithinolytica</i>
ID=2430	WP_041143205	murein hydrolase activator EnvC	<i>Raoultella ornithinolytica</i>
ID=2431	WP_041143206	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2432	WP_041143207	family 2 glycosyl transferase	<i>Raoultella ornithinolytica</i>
ID=2433	WP_041143208	MULTISPECIES: L-threonine 3-dehydrogenase	<i>Raoultella</i>
ID=2434	WP_041143209	glycine C-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=2435	WP_041143210	ADP-L-glycero-D-mannoheptose-6-epimerase	<i>Raoultella ornithinolytica</i>
ID=2436	WP_041143211	ADP-heptose--LPS heptosyltransferase	<i>Raoultella ornithinolytica</i>
ID=2437	WP_041143212	lipopolysaccharide heptosyltransferase I	<i>Raoultella ornithinolytica</i>
ID=2438	WP_041143213	sugar glycosyltransferase	<i>Raoultella ornithinolytica</i>
ID=2439	WP_041143214	polymerase	<i>Raoultella ornithinolytica</i>
ID=2440	WP_041143215	LPS 1,2-N-acetylglucosamintransferase	<i>Raoultella ornithinolytica</i>
ID=2441	WP_041143216	deacetylase	<i>Raoultella ornithinolytica</i>
ID=2442	WP_041143217	putative lipopolysaccharide heptosyltransferase III	<i>Raoultella ornithinolytica</i>
ID=2443	WP_041143218	glycosyl transferase family I	<i>Raoultella ornithinolytica</i>
ID=2444	WP_045853841	glycosyl transferase	<i>Raoultella terrigena</i>
ID=2445	WP_041143220	MULTISPECIES: glycosyltransferase	<i>Raoultella</i>

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ID=2446	WP_041143221	3-deoxy-D-manno-octulosonic acid transferase	<i>Raoultella ornithinolytica</i>
ID=2447	WP_041143222	LPS biosynthesis protein	<i>Raoultella ornithinolytica</i>
ID=2448	WP_041143223	MULTISPECIES: pantetheine-phosphate adenylyltransferase	<i>Raoultella</i>
ID=2449	WP_045853838	DNA-formamidopyrimidine glycosylase	<i>Raoultella terrigena</i>
ID=2450	WP_003024094	MULTISPECIES: 50S ribosomal protein L33	<i>GammaProteobacteria</i>
ID=2451	WP_041143225	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2452	WP_041143226	phosphopantothienoylcysteine decarboxylase	<i>Raoultella ornithinolytica</i>
ID=2453	WP_041143227	deoxyuridine 5'-triphosphate nucleotidohydrolase	<i>Raoultella ornithinolytica</i>
ID=2454	WP_041143228	nucleoid occlusion factor SlmA	<i>Raoultella ornithinolytica</i>
ID=2455	WP_041143229	orotate phosphoribosyltransferase	<i>Raoultella ornithinolytica</i>
ID=2456	WP_041143230	ribonuclease PH	<i>Raoultella ornithinolytica</i>
ID=2457	WP_041143231	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2458	WP_041143232	chloride channel protein	<i>Raoultella ornithinolytica</i>
ID=2459	WP_041143233	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2460	WP_041147485	DNA ligase B	<i>Raoultella ornithinolytica</i>
ID=2461	WP_041143234	MULTISPECIES: guanylate kinase	<i>Raoultella</i>
ID=2462	WP_006817787	MULTISPECIES: DNA-directed RNA polymerase subunit omega	<i>Enterobacteriaceae</i>
ID=2463	WP_041143235	(p)ppGpp synthetase	<i>Raoultella ornithinolytica</i>
ID=2464	WP_041143236	tRNA (guanosine(18)-2'-O)-methyltransferase TrmH	<i>Raoultella ornithinolytica</i>
ID=2465	WP_041143237	ATP-dependent DNA helicase RecG	<i>Raoultella ornithinolytica</i>
ID=2466	WP_041143238	fructose-1,6-bisphosphatase, class II	<i>Raoultella ornithinolytica</i>
ID=2467	WP_041143239	ferredoxin--NADP(+) reductase	<i>Raoultella ornithinolytica</i>
ID=2468	WP_041143240	MULTISPECIES: DUF805 domain-containing protein	<i>Raoultella</i>
ID=2469	WP_041143241	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2470	WP_041143242	MULTISPECIES: triose-phosphate isomerase	<i>Raoultella</i>
ID=2471	WP_041143243	citrate transporter	<i>Raoultella ornithinolytica</i>
ID=2472	WP_041143244	GntR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2473	WP_041143245	ADP-ribosylglycohydrolase	<i>Raoultella ornithinolytica</i>
ID=2474	WP_045853820	aminoimidazole riboside kinase	<i>Raoultella terrigena</i>
ID=2475	WP_045853819	sodium:galactoside symporter	<i>Raoultella terrigena</i>
ID=2476	WP_041143248	CDP-diacylglycerol diphosphatase	<i>Raoultella ornithinolytica</i>
ID=2477	WP_041143249	sulfate transporter subunit	<i>Raoultella ornithinolytica</i>
ID=2478	WP_041147486	septal ring assembly protein ZapB	<i>Raoultella ornithinolytica</i>
ID=2479	WP_041143250	aquaporin	<i>Raoultella ornithinolytica</i>
ID=2480	WP_041143251	glycerol kinase	<i>Raoultella ornithinolytica</i>
ID=2481	WP_041143252	sodium:glutamate symporter	<i>Raoultella ornithinolytica</i>
ID=2482	WP_041143253	xanthine permease XanP	<i>Raoultella ornithinolytica</i>
ID=2483	WP_045853813	hypothetical protein	<i>Raoultella terrigena</i>
ID=2484	WP_041143255	PTS glucose transporter subunit IIBC	<i>Raoultella ornithinolytica</i>
ID=2485	WP_041143256	glycoside hydrolase	<i>Raoultella ornithinolytica</i>
ID=2486	WP_045853810	sugar isomerase	<i>Raoultella terrigena</i>
ID=2487	WP_032615667	sensor domain-containing protein	<i>Leclercia adecarboxylata</i>
ID=2488	WP_059215313	hydroxyacid dehydrogenase	<i>Escherichia albertii</i>
ID=2489	WP_041143268	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2490	WP_041143269	NADPH:quinone reductase	<i>Raoultella ornithinolytica</i>
ID=2491	WP_041143270	antibiotic biosynthesis monooxygenase	<i>Raoultella ornithinolytica</i>
ID=2492	WP_045853804	zinc-binding dehydrogenase	<i>Raoultella terrigena</i>
ID=2493	WP_041143272	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2494	WP_041143273	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2495	WP_041143275	EamA family transporter	<i>Raoultella ornithinolytica</i>
ID=2496	WP_041143276	lipoprotein NlpA	<i>Raoultella ornithinolytica</i>
ID=2497	WP_041143277	XRE family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2498	WP_045853797	AraC family transcriptional regulator	<i>Raoultella terrigena</i>
ID=2499	WP_041143279	alkylhydroperoxidase	<i>Raoultella ornithinolytica</i>
ID=2500	WP_045853795	50S ribosomal protein L21	<i>Raoultella terrigena</i>
ID=2501	WP_045853794	phosphatase	<i>Raoultella terrigena</i>
ID=2502	WP_041143282	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2503	WP_045853792	MFS transporter	<i>Raoultella terrigena</i>
ID=2504	WP_045853791	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=2505	WP_041143285	blasticidin S-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=2506	WP_041143286	acriflavine resistance protein E	<i>Raoultella ornithinolytica</i>
ID=2507	WP_041143287	multidrug efflux RND transporter permease subunit	<i>Raoultella ornithinolytica</i>
ID=2508	WP_041143288	multidrug transporter	<i>Raoultella ornithinolytica</i>
ID=2509	WP_045853786	Bcr/CflA family drug resistance efflux transporter	<i>Raoultella terrigena</i>
ID=2510	WP_041143289	N-acetylmuramic acid 6-phosphate etherase	<i>Raoultella ornithinolytica</i>
ID=2511	WP_041143290	PTS N-acetylmuramic acid transporter subunits IIBC	<i>Raoultella ornithinolytica</i>
ID=2512	WP_041143291	MULTISPECIES: EamA family transporter	<i>Raoultella</i>
ID=2513	WP_041143292	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2514	WP_041143293	MULTISPECIES: LacI family transcriptional regulator	<i>Raoultella</i>

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ID=2515	WP_041143294	MULTISPECIES: PTS sugar transporter subunit IIB	<i>Raoultella</i>
ID=2516	WP_041143295	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2517	WP_041143296	MULTISPECIES: molecular chaperone TorD	<i>Raoultella</i>
ID=2518	WP_058674293	hypothetical protein, partial	<i>Klebsiella mobilis</i>
ID=2519	WP_041144156	MULTISPECIES: D-glycero-beta-D-manno-heptose 1,7-bisphosphate 7-phosphatase	<i>Raoultella</i>
ID=2520	WP_041144155	D-methionine ABC transporter, ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2521	WP_041144154	MULTISPECIES: methionine ABC transporter permease	<i>Raoultella</i>
ID=2522	WP_041144153	methionine ABC transporter substrate-binding protein MetQ	<i>Raoultella ornithinolytica</i>
ID=2523	WP_041144151	tRNA (N6-threonylcarbamoyladenine(37)-N6)-methyltransferase TrmO	<i>Raoultella ornithinolytica</i>
ID=2524	WP_041144150	proline--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=2525	WP_045859723	copper homeostasis/adhesion lipoprotein NlpE	<i>Raoultella terrigena</i>
ID=2526	WP_041144148	aminoacyl-tRNA hydrolase	<i>Raoultella ornithinolytica</i>
ID=2527	WP_045859726	hypothetical protein	<i>Raoultella terrigena</i>
ID=2528	WP_045859728	Rho-binding antiterminator	<i>Raoultella terrigena</i>
ID=2529	WP_045860306	tRNA (Ile)-lysine synthetase	<i>Raoultella terrigena</i>
ID=2530	WP_041144144	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2531	WP_041144143	lysine decarboxylase LdcC	<i>Raoultella ornithinolytica</i>
ID=2532	WP_041144142	acetyl-CoA carboxylase carboxyltransferase subunit alpha	<i>Raoultella ornithinolytica</i>
ID=2533	WP_041144141	DNA polymerase III subunit alpha	<i>Raoultella ornithinolytica</i>
ID=2534	WP_041144140	ribonuclease HII	<i>Raoultella ornithinolytica</i>
ID=2535	WP_041144139	lipid-A-disaccharide synthase	<i>Raoultella ornithinolytica</i>
ID=2536	WP_041144138	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase	<i>Raoultella ornithinolytica</i>
ID=2538	WP_034949603	beta-hydroxyacyl-ACP dehydratase	<i>Erwinia oleae</i>
ID=2539	WP_061797011	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	<i>Serratia ficaria</i>
ID=2540	WP_041144137	MULTISPECIES: UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase	<i>Raoultella</i>
ID=2541	WP_041144136	MULTISPECIES: molecular chaperone	<i>Raoultella</i>
ID=2542	WP_041144135	outer membrane protein assembly factor BamA	<i>Raoultella ornithinolytica</i>
ID=2543	WP_041144134	MULTISPECIES: zinc metalloproteinase RseP	<i>Raoultella</i>
ID=2544	WP_041144133	MULTISPECIES: phosphatidate cytidyltransferase	<i>Raoultella</i>
ID=2545	WP_041147522	MULTISPECIES: (2E,6E)-farnesyl- diphosphate-specific ..	<i>Raoultella</i>
		..ditrans.polycis-undecaprenyl-diphosphate synthase	
ID=2546	WP_041144132	1-deoxy-D-xylulose-5-phosphate reductoisomerase	<i>Raoultella ornithinolytica</i>
ID=2547	WP_041144131	MULTISPECIES: ribosome-recycling factor	<i>Raoultella</i>
ID=2548	WP_041144130	MULTISPECIES: UMP kinase	<i>Raoultella</i>
ID=2549	WP_041144129	elongation factor Ts	<i>Raoultella ornithinolytica</i>
ID=2550	WP_041144128	30S ribosomal protein S2	<i>Raoultella ornithinolytica</i>
ID=2551	WP_041144127	MULTISPECIES: type I methionyl aminopeptidase	<i>Raoultella</i>
ID=2552	WP_064357490	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2552	WP_064357490	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2553	WP_041144126	bifunctional uridylyltransferase/uridylyl-removing protein	<i>Raoultella ornithinolytica</i>
ID=2554	WP_004872026	MULTISPECIES: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	<i>Enterobacteriaceae</i>
ID=2555	WP_004858100	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=2556	WP_041144125	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=2557	WP_041144124	serine endoprotease	<i>Raoultella ornithinolytica</i>
ID=2558	WP_041144123	dGTPase	<i>Raoultella ornithinolytica</i>
ID=2559	WP_045376578	MULTISPECIES: 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	<i>Enterobacteriaceae</i>
ID=2560	WP_041144121	cobalamin-binding protein	<i>Raoultella ornithinolytica</i>
ID=2561	WP_041144120	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2562	WP_041144119	MULTISPECIES: iron-sulfur cluster insertion protein ErpA	<i>Raoultella</i>
ID=2563	WP_045859764	CIC family H(+)/Cl(-) exchange transporter	<i>Raoultella terrigena</i>
ID=2564	WP_041144117	aspartate aminotransferase family protein	<i>Raoultella ornithinolytica</i>
ID=2565	WP_041144116	Fe3+-hydroxamate ABC transporter permease FhuB	<i>Raoultella ornithinolytica</i>
ID=2566	WP_041144115	iron-hydroxamate transporter substrate-binding subunit	<i>Raoultella ornithinolytica</i>
ID=2567	WP_041144114	iron-hydroxamate transporter ATP-binding subunit	<i>Raoultella ornithinolytica</i>
ID=2568	WP_041144113	ferrichrome porin FhuA	<i>Raoultella ornithinolytica</i>
ID=2569	WP_041144112	bifunctional glycosyl transferase/transpeptidase	<i>Raoultella ornithinolytica</i>
ID=2570	WP_041144111	pullulanase	<i>Raoultella ornithinolytica</i>
ID=2571	WP_041144110	general secretion pathway protein GspB	<i>Raoultella ornithinolytica</i>
ID=2572	WP_041144109	pullulanase	<i>Raoultella ornithinolytica</i>
ID=2573	WP_045860314	type II secretion system protein GspC	<i>Raoultella terrigena</i>
ID=2574	WP_041147521	type II secretion system protein GspD	<i>Raoultella ornithinolytica</i>
ID=2575	WP_041144107	type II secretion system protein GspE	<i>Raoultella ornithinolytica</i>
ID=2576	WP_041144106	type II secretion system protein GspF	<i>Raoultella ornithinolytica</i>
ID=2577	WP_041144105	MULTISPECIES: type II secretion system protein GspG	<i>Raoultella</i>
ID=2578	WP_041144104	type II secretion system protein GspH	<i>Raoultella ornithinolytica</i>
ID=2579	WP_041144103	MULTISPECIES: type II secretion system protein GspI	<i>Raoultella</i>
ID=2580	WP_041144102	type II secretion system protein GspJ	<i>Raoultella ornithinolytica</i>
ID=2581	WP_045859792	pullulanase	<i>Raoultella terrigena</i>
ID=2582	WP_041144100	type II secretion system protein GspL	<i>Raoultella ornithinolytica</i>

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ID=2583	WP_041144099	general secretion pathway protein GspM	<i>Raoultella ornithinolytica</i>
ID=2584	WP_041144098	pullulanase	<i>Raoultella ornithinolytica</i>
ID=2585	WP_041144097	prepilin peptidase	<i>Raoultella ornithinolytica</i>
ID=2586	WP_041144096	ATP-dependent helicase HrpB	<i>Raoultella ornithinolytica</i>
ID=2587	WP_045859802	2'-5' RNA ligase	<i>Raoultella terrigena</i>
ID=2588	WP_041144094	sugar fermentation stimulation protein SfsA	<i>Raoultella ornithinolytica</i>
ID=2589	WP_007373199	MULTISPECIES: transcriptional regulator	<i>Enterobacteriaceae</i>
ID=2590	WP_045859809	tRNA glutamyl-Q synthetase	<i>Raoultella terrigena</i>
ID=2591	WP_004858013	MULTISPECIES: polynucleotide adenyltransferase PcnB	<i>Enterobacteriaceae</i>
ID=2592	WP_045859811	polynucleotide adenyltransferase PcnB	<i>Raoultella terrigena</i>
ID=2593	WP_041144091	MULTISPECIES: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	<i>Raoultella</i>
ID=2594	WP_041144090	3-methyl-2-oxobutanoate hydroxymethyltransferase	<i>Raoultella ornithinolytica</i>
ID=2595	WP_045859816	pantoate--beta-alanine ligase	<i>Raoultella terrigena</i>
ID=2596	WP_041144088	MULTISPECIES: aspartate 1-decarboxylase	<i>Raoultella</i>
ID=2597	WP_045859818	hypothetical protein	<i>Raoultella terrigena</i>
ID=2598	WP_045859822	hypothetical protein	<i>Raoultella terrigena</i>
ID=2599	WP_045859823	PTS sugar transporter subunit IIA	<i>Raoultella terrigena</i>
ID=2600	WP_041144086	ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=2601	WP_041144085	MULTISPECIES: multidrug ABC transporter ATP-binding protein	<i>Raoultella</i>
ID=2602	WP_045859826	carbonate dehydratase	<i>Raoultella terrigena</i>
ID=2603	WP_041147520	MULTISPECIES: hypoxanthine phosphoribosyltransferase	<i>Raoultella</i>
ID=2604	WP_041144083	glucose dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=2605	WP_041144082	multicopper oxidase	<i>Raoultella ornithinolytica</i>
ID=2606	WP_041144081	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2607	WP_041144080	spermidine synthase	<i>Raoultella ornithinolytica</i>
ID=2608	WP_041144079	S-adenosylmethionine decarboxylase	<i>Raoultella ornithinolytica</i>
ID=2609	WP_041144078	UPF0231 family protein	<i>Raoultella ornithinolytica</i>
ID=2610	WP_044349235	aconitate hydratase B	<i>Raoultella ornithinolytica</i>
ID=2611	WP_041144076	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2612	WP_041144075	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2613	WP_041144074	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2614	WP_041147519	dihydrolipoyl dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=2615	WP_045859856	pyruvate dehydrogenase complex dihydrolipoyllysine-residue acetyltransferase	<i>Raoultella terrigena</i>
ID=2616	WP_041144072	pyruvate dehydrogenase (acetyl-transferring), homodimeric type	<i>Raoultella ornithinolytica</i>
ID=2617	WP_004857919	MULTISPECIES: transcriptional regulator PdhR	<i>Enterobacteriaceae</i>
ID=2618	WP_004857919	MULTISPECIES: transcriptional regulator PdhR	<i>Enterobacteriaceae</i>
ID=2619	WP_041144070	aromatic amino acid transporter AroP	<i>Raoultella ornithinolytica</i>
ID=2621	WP_041144069	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2622	WP_041144068	alpha-N-arabinofuranosidase	<i>Raoultella ornithinolytica</i>
ID=2623	WP_045859866	regulatory protein AmpE	<i>Raoultella terrigena</i>
ID=2624	WP_041144066	N-acetylmuramoyl-L-alanine amidase	<i>Raoultella ornithinolytica</i>
ID=2625	WP_045859870	nicotinate-nucleotide diphosphorylase	<i>Raoultella terrigena</i>
ID=2626	WP_045859871	prepilin peptidase-dependent pilin	<i>Raoultella terrigena</i>
ID=2627	WP_041144063	type II secretion system protein GspE	<i>Raoultella ornithinolytica</i>
ID=2628	WP_045859875	type IV pilin biogenesis protein	<i>Raoultella terrigena</i>
ID=2629	WP_041144061	guanosine monophosphate reductase	<i>Raoultella ornithinolytica</i>
ID=2630	WP_041144060	dephospho-CoA kinase	<i>Raoultella ornithinolytica</i>
ID=2631	WP_041144059	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2632	WP_041144057	8-oxo-dGTP diphosphatase	<i>Raoultella ornithinolytica</i>
ID=2633	WP_041144056	preprotein translocase subunit SecA	<i>Raoultella ornithinolytica</i>
ID=2634	WP_045859891	SecA regulator SecM	<i>Raoultella terrigena</i>
ID=2635	WP_041144054	MULTISPECIES: UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	<i>Raoultella</i>
ID=2636	WP_041144053	MULTISPECIES: cell division protein FtsZ	<i>Raoultella</i>
ID=2637	WP_004857881	MULTISPECIES: cell division protein FtsA	<i>Enterobacteriaceae</i>
ID=2638	WP_041144052	cell division protein FtsQ	<i>Raoultella ornithinolytica</i>
ID=2639	WP_041144051	D-alanine--D-alanine ligase	<i>Raoultella ornithinolytica</i>
ID=2640	WP_041144050	UDP-N-acetylmuramate--L-alanine ligase	<i>Raoultella ornithinolytica</i>
ID=2641	WP_041144049	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	<i>Raoultella ornithinolytica</i>
ID=2642	WP_041144048	cell division protein FtsW	<i>Raoultella ornithinolytica</i>
ID=2643	WP_041144047	UDP-N-acetylmuramoylalanine--D-glutamate ligase	<i>Raoultella ornithinolytica</i>
ID=2644	WP_041144046	phospho-N-acetylmuramoyl-pentapeptide-transferase	<i>Raoultella ornithinolytica</i>
ID=2645	WP_041144045	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	<i>Raoultella ornithinolytica</i>
ID=2646	WP_041144044	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase	<i>Raoultella ornithinolytica</i>
ID=2647	WP_041144043	MULTISPECIES: peptidoglycan glycosyltransferase FtsI	<i>Raoultella</i>
ID=2648	WP_004857854	MULTISPECIES: cell division protein FtsL	<i>Enterobacteriaceae</i>
ID=2649	WP_041144042	16S rRNA (cytosine(1402)-N(4))-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=2650	WP_041144041	MULTISPECIES: division/cell wall cluster transcriptional repressor MraZ	<i>Raoultella</i>
ID=2651	WP_041144040	MULTISPECIES: DNA-binding transcriptional regulator FruR	<i>Raoultella</i>

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ID=2652	WP_041144039	MULTISPECIES: acetolactate synthase small subunit	<i>Raoultella</i>
ID=2653	WP_041144038	acetolactate synthase 3 large subunit	<i>Raoultella ornithinolytica</i>
ID=2654	WP_041147518	transcriptional regulator LeuO	<i>Raoultella ornithinolytica</i>
ID=2655	WP_041144037	2-isopropylmalate synthase	<i>Raoultella ornithinolytica</i>
ID=2656	WP_041144036	MULTISPECIES: 3-isopropylmalate dehydrogenase	<i>Raoultella</i>
ID=2657	WP_041144035	3-isopropylmalate dehydratase large subunit	<i>Raoultella ornithinolytica</i>
ID=2658	WP_041144034	3-isopropylmalate dehydratase small subunit	<i>Raoultella ornithinolytica</i>
ID=2659	WP_041144033	3-dehydroquinase	<i>Raoultella ornithinolytica</i>
ID=2660	WP_041144032	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2661	WP_004204309	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=2662	WP_041144031	transcriptional regulator SgrR	<i>Raoultella ornithinolytica</i>
ID=2663	WP_041144030	MULTISPECIES: thiamine transporter substrate binding subunit	<i>Raoultella</i>
ID=2664	WP_041144029	thiamine/thiamine pyrophosphate ABC transporter permease ThiP	<i>Raoultella ornithinolytica</i>
ID=2665	WP_041144028	thiamine ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2666	WP_041144027	DedA family protein	<i>Raoultella ornithinolytica</i>
ID=2667	WP_041144026	DNA-binding transcriptional regulator AraC	<i>Raoultella ornithinolytica</i>
ID=2668	WP_041144025	ribulokinase	<i>Raoultella ornithinolytica</i>
ID=2669	WP_041144024	L-arabinose isomerase	<i>Raoultella ornithinolytica</i>
ID=2670	WP_041144023	ribulose 5-phosphate epimerase	<i>Raoultella ornithinolytica</i>
ID=2671	WP_041144022	DNA polymerase II	<i>Raoultella ornithinolytica</i>
ID=2672	WP_041144022	DNA polymerase II	<i>Raoultella ornithinolytica</i>
ID=2673	WP_041144021	RNA polymerase-associated protein RapA	<i>Raoultella ornithinolytica</i>
ID=2674	WP_041144020	RNA pseudouridine synthase	<i>Raoultella ornithinolytica</i>
ID=2675	WP_041144019	holo-ACP synthase CitX	<i>Raoultella ornithinolytica</i>
ID=2676	WP_041144018	malate permease	<i>Raoultella ornithinolytica</i>
ID=2677	WP_045859956	histidine kinase	<i>Raoultella terrigena</i>
ID=2678	WP_041144016	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2679	WP_041144015	MULTISPECIES: molecular chaperone DjlA	<i>Raoultella</i>
ID=2680	WP_045859960	LPS assembly protein LptD	<i>Raoultella terrigena</i>
ID=2681	WP_041144013	peptidylprolyl isomerase SurA	<i>Raoultella ornithinolytica</i>
ID=2682	WP_041144012	MULTISPECIES: 4-hydroxythreonine-4-phosphate dehydrogenase PdxA	<i>Raoultella</i>
ID=2683	WP_041144011	MULTISPECIES: 16S rRNA (adenine(1518)-N(6)/..adenine(1519)-N(6))-dimethyltransferase	<i>Raoultella</i>
ID=2684	WP_041144010	MULTISPECIES: Co2+/Mg2+ efflux protein ApaG	<i>Raoultella</i>
ID=2685	WP_045859964	bis(5'-nucleosyl)-tetraphosphatase (symmetrical)	<i>Raoultella terrigena</i>
ID=2686	WP_041144008	dihydrofolate reductase	<i>Raoultella ornithinolytica</i>
ID=2687	WP_041144007	glutathione-regulated potassium-efflux system protein KefC	<i>Raoultella ornithinolytica</i>
ID=2688	WP_041144006	glutathione-regulated potassium-efflux system ancillary protein KefF	<i>Raoultella ornithinolytica</i>
ID=2689	WP_041144005	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2690	WP_045859974	dihydrofolate reductase	<i>Raoultella terrigena</i>
ID=2691	WP_045859976	transcriptional regulator	<i>Raoultella terrigena</i>
ID=2692	WP_041144002	gluconate 5-dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=2693	WP_041144001	gluconate kinase	<i>Raoultella ornithinolytica</i>
ID=2694	WP_041144000	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2695	WP_041143999	MULTISPECIES: lipoprotein	<i>Raoultella</i>
ID=2696	WP_041143998	carbamoyl phosphate synthase large subunit	<i>Raoultella ornithinolytica</i>
ID=2697	WP_041143997	MULTISPECIES: carbamoyl-phosphate synthase small subunit	<i>Raoultella</i>
ID=2698	WP_041143996	4-hydroxy-tetrahydrodipicolinate reductase	<i>Raoultella ornithinolytica</i>
ID=2699	WP_041143995	LacI family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2700	WP_041143994	mannose-6-phosphate isomerase	<i>Raoultella ornithinolytica</i>
ID=2701	WP_041143993	PTS fructose transporter subunit IIA	<i>Raoultella ornithinolytica</i>
ID=2702	WP_041143992	PTS N-acetylgalactosamine transporter subunit IID	<i>Raoultella ornithinolytica</i>
ID=2703	WP_041143991	PTS sorbose transporter subunit IIC	<i>Raoultella ornithinolytica</i>
ID=2704	WP_041143990	PTS fructose transporter subunit IID	<i>Raoultella ornithinolytica</i>
ID=2705	WP_041143989	glucose-6-phosphate isomerase	<i>Raoultella ornithinolytica</i>
ID=2706	WP_041143988	glucose-6-phosphate isomerase	<i>Raoultella ornithinolytica</i>
ID=2707	WP_045860007	serine-tRNA(Ala) deacylase AlaX	<i>Raoultella terrigena</i>
ID=2708	WP_041143986	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2709	WP_041143985	ribonucleoside hydrolase RihC	<i>Raoultella ornithinolytica</i>
ID=2710	WP_041143984	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	<i>Raoultella ornithinolytica</i>
ID=2711	WP_041143983	peptidylprolyl isomerase	<i>Raoultella ornithinolytica</i>
ID=2712	WP_041143982	signal peptidase II	<i>Raoultella ornithinolytica</i>
ID=2713	WP_041147517	isoleucine--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=2714	WP_041143981	MULTISPECIES: bifunctional riboflavin kinase/FMN adenylyltransferase	<i>Raoultella</i>
ID=2715	WP_003018940	MULTISPECIES: 30S ribosomal protein S20	<i>GammaProteobacteria</i>
ID=2716	WP_041143980	MULTISPECIES: transcriptional activator NhaR	<i>Raoultella</i>
ID=2717	WP_041143979	Na+/H+ antiporter NhaA	<i>Raoultella ornithinolytica</i>
ID=2718	WP_041143978	molecular chaperone DnaJ	<i>Raoultella ornithinolytica</i>
ID=2719	WP_041143977	molecular chaperone DnaK	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=2720	WP_041143976	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2721	WP_041143975	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2722	WP_041143974	MULTISPECIES: molybdopterin adenylyltransferase	<i>Raoultella</i>
ID=2723	WP_045860032	transaldolase	<i>Raoultella terrigena</i>
ID=2724	WP_041143972	sodium:alanine symporter	<i>Raoultella ornithinolytica</i>
ID=2725	WP_041143971	peroxide stress protein YaaA	<i>Raoultella ornithinolytica</i>
ID=2726	WP_041143970	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2727	WP_045860040	threonine synthase	<i>Raoultella terrigena</i>
ID=2728	WP_041143968	homoserine kinase	<i>Raoultella ornithinolytica</i>
ID=2729	WP_041143967	bifunctional aspartokinase I/homoserine dehydrogenase I	<i>Raoultella ornithinolytica</i>
ID=2730	WP_041143966	tRNA/rRNA methyltransferase	<i>Raoultella ornithinolytica</i>
ID=2731	WP_002887843	MULTISPECIES: DNA-binding response regulator	<i>Enterobacterales</i>
ID=2732	WP_041143965	cell envelope integrity protein CreD	<i>Raoultella ornithinolytica</i>
ID=2733	WP_045860051	two-component sensor histidine kinase	<i>Raoultella terrigena</i>
ID=2734	WP_045860053	DNA-binding response regulator	<i>Raoultella terrigena</i>
ID=2735	WP_041143962	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2736	WP_041143961	right oriC-binding transcriptional activator	<i>Raoultella ornithinolytica</i>
ID=2737	WP_045860058	phosphoglycerate mutase	<i>Raoultella terrigena</i>
ID=2738	WP_045860061	non-canonical purine NTP phosphatase	<i>Raoultella terrigena</i>
ID=2739	WP_045860062	murein transglycosylase	<i>Raoultella terrigena</i>
ID=2740	WP_045860064	MULTISPECIES: energy-dependent translational throttle protein EttA	<i>Raoultella</i>
ID=2741	WP_045860065	trifunctional nicotinamide-nucleotide adenylyltransferase/..	<i>Raoultella terrigena</i>
		..ribosylnicotinamide kinase/transcriptional regulator NadR	
ID=2742	WP_041143954	DNA repair protein RadA	<i>Raoultella ornithinolytica</i>
ID=2743	WP_045860068	phosphoserine phosphatase	<i>Raoultella terrigena</i>
ID=2744	WP_041143952	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2745	WP_041143951	lipoate--protein ligase	<i>Raoultella ornithinolytica</i>
ID=2746	WP_004857662	MULTISPECIES: purine-nucleoside phosphorylase	<i>Enterobacteriaceae</i>
ID=2747	WP_041143949	phosphopentomutase	<i>Raoultella ornithinolytica</i>
ID=2748	WP_041143948	thymidine phosphorylase	<i>Raoultella ornithinolytica</i>
ID=2749	WP_047663983	2-deoxyribose-5-phosphate aldolase	<i>Raoultella planticola</i>
ID=2750	WP_041143946	deoxyribonuclease YjjV	<i>Raoultella ornithinolytica</i>
ID=2751	WP_041143945	patatin family protein	<i>Raoultella ornithinolytica</i>
ID=2753	WP_041143944	BON domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=2754	WP_041143943	peptide chain release factor 3	<i>Raoultella ornithinolytica</i>
ID=2755	WP_041143942	dUMP phosphatase	<i>Raoultella ornithinolytica</i>
ID=2756	WP_041143941	ribosomal-protein-alanine N-acetyltransferase RimI	<i>Raoultella ornithinolytica</i>
ID=2757	WP_041143940	DNA polymerase III subunit psi	<i>Raoultella ornithinolytica</i>
ID=2758	WP_041143939	16S rRNA (guanine(1207)-N(2))-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=2759	WP_004233707	membrane protein	<i>Klebsiella pneumoniae</i>
ID=2760	WP_041143938	GGDEF domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=2761	WP_045860098	hydroxamate siderophore iron reductase FhuF	<i>Raoultella terrigena</i>
ID=2762	WP_041143936	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2763	WP_041143935	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2764	WP_052474464	helix-turn-helix transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2765	WP_041143934	helix-turn-helix transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2766	WP_041143933	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2767	WP_041143932	4-hydroxybenzoate 3-monoxygenase	<i>Raoultella ornithinolytica</i>
ID=2768	WP_045860110	membrane protein	<i>Raoultella terrigena</i>
ID=2769	WP_041143930	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2770	WP_041143929	MULTISPECIES: primosomal protein DnaI	<i>Raoultella</i>
ID=2771	WP_041143928	DNA replication protein DnaC	<i>Raoultella ornithinolytica</i>
ID=2772	WP_041143927	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2773	WP_045860112	phosphoglycerol transferase I	<i>Raoultella terrigena</i>
ID=2774	WP_041143925	GCN5 family acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=2775	WP_045860116	N-acetyltransferase	<i>Raoultella terrigena</i>
ID=2776	WP_041143923	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2777	WP_041143921	2-oxo-3-deoxygalactonate kinase	<i>Raoultella ornithinolytica</i>
ID=2778	WP_045860124	sodium:proline symporter	<i>Raoultella terrigena</i>
ID=2779	WP_041143919	endoribonuclease L-PSP	<i>Raoultella ornithinolytica</i>
ID=2780	WP_041143918	D-aminoacylase	<i>Raoultella ornithinolytica</i>
ID=2781	WP_041143917	aldolase	<i>Raoultella ornithinolytica</i>
ID=2782	WP_041143916	homoprotocatechuate degradation operon regulator, HpaR	<i>Raoultella ornithinolytica</i>
ID=2783	WP_041143915	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	<i>Raoultella ornithinolytica</i>
ID=2784	WP_041143914	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	<i>Raoultella ornithinolytica</i>
ID=2785	WP_041143913	5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=2786	WP_041143912	3,4-dihydroxyphenylacetate 2,3-dioxygenase	<i>Raoultella ornithinolytica</i>
ID=2787	WP_045860162	5-carboxymethyl-2-hydroxymuconate Delta-isomerase	<i>Raoultella terrigena</i>
ID=2788	WP_041143910	2-oxo-hepta-3-ene-1,7-dioic acid hydratase	<i>Raoultella ornithinolytica</i>

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ID=2789	WP_041143909	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	<i>Raoultella ornithinolytica</i>
ID=2790	WP_041143908	4-hydroxyphenylacetate permease	<i>Raoultella ornithinolytica</i>
ID=2791	WP_045860170	4-hydroxyphenylacetate catabolism regulatory protein HpaA	<i>Raoultella terrigena</i>
ID=2792	WP_041143906	4-hydroxyphenylacetate 3-monooxygenase, oxygenase component	<i>Raoultella ornithinolytica</i>
ID=2793	WP_041143905	4-hydroxyphenylacetate 3-monooxygenase	<i>Raoultella ornithinolytica</i>
ID=2794	WP_041143904	carbon starvation protein A	<i>Raoultella ornithinolytica</i>
ID=2795	WP_045860179	hypothetical protein	<i>Raoultella terrigena</i>
ID=2796	WP_045860181	GTPase	<i>Raoultella terrigena</i>
ID=2797	WP_045860182	type VI secretion system effector	<i>Raoultella terrigena</i>
ID=2798	WP_045860184	hypothetical protein	<i>Raoultella terrigena</i>
ID=2799	WP_045860186	porin	<i>Raoultella terrigena</i>
ID=2800	WP_041143900	type VI secretion system effector	<i>Raoultella ornithinolytica</i>
ID=2801	WP_052474463	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2802	WP_037035402	hypothetical protein	<i>Rahnella sp.</i>
ID=2803	WP_041143898	succinate-semialdehyde dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=2804	WP_041143897	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2805	WP_041143896	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2806	WP_041143895	threonine transporter RhtB	<i>Raoultella ornithinolytica</i>
ID=2807	WP_041143894	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2808	WP_041143893	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2809	WP_045860203	hypothetical protein	<i>Raoultella terrigena</i>
ID=2810	WP_041143891	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2811	WP_041143890	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2812	WP_041143889	1,4-alpha-glucan-branching protein	<i>Raoultella ornithinolytica</i>
ID=2813	WP_041143888	hemolysin secretion protein D	<i>Raoultella ornithinolytica</i>
ID=2814	WP_041143887	MarR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2815	WP_064497381	MULTISPECIES: DUF1127 domain-containing protein	<i>Enterobacteriaceae</i>
ID=2816	WP_045860214	GntR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=2817	WP_046853159	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2818	WP_046853136	ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=2819	WP_046853140	type I restriction endonuclease	<i>Raoultella ornithinolytica</i>
ID=2820	WP_064359610	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2821	WP_015585222	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2822	WP_045860220	hypothetical protein	<i>Raoultella terrigena</i>
ID=2823	WP_064359613	FosA family fosfomycin resistance glutathione transferase	<i>Raoultella ornithinolytica</i>
ID=2824	WP_045860224	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=2825	WP_045860226	NAD(P)H dehydrogenase	<i>Raoultella terrigena</i>
ID=2826	WP_045860227	transcriptional regulator	<i>Raoultella terrigena</i>
ID=2827	WP_045860230	MULTISPECIES: PTS fructose transporter subunit IIA	<i>Enterobacteriaceae</i>
ID=2828	WP_045860231	PTS sugar transporter	<i>Raoultella terrigena</i>
ID=2829	WP_045860234	PTS sorbose transporter subunit IIC	<i>Raoultella terrigena</i>
ID=2830	WP_045860236	PTS fructose transporter subunit IID	<i>Raoultella terrigena</i>
ID=2831	WP_045860238	selenocysteine synthase	<i>Raoultella terrigena</i>
ID=2832	WP_045860240	4-hydroxy-2-ketovalerate aldolase	<i>Raoultella terrigena</i>
ID=2833	WP_041143880	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2834	WP_045860245	transcriptional regulator	<i>Raoultella terrigena</i>
ID=2835	WP_045860247	hypothetical protein	<i>Raoultella terrigena</i>
ID=2836	WP_010634659	MULTISPECIES: microcompartments family protein	<i>GammaProteobacteria</i>
ID=2837	WP_041143877	MULTISPECIES: bacterial microcompartment protein	<i>Raoultella</i>
ID=2838	WP_015585230	MULTISPECIES: ethanolamine utilization polyhedral-body-like protein EutM	<i>Enterobacteriaceae</i>
ID=2839	WP_052474460	acetaldehyde dehydrogenase (acetylating)	<i>Raoultella ornithinolytica</i>
ID=2840	WP_041143876	ethanolamine utilization protein EutN	<i>Raoultella ornithinolytica</i>
ID=2841	WP_045860278	alcohol dehydrogenase	<i>Raoultella terrigena</i>
ID=2842	WP_045860280	choline trimethylamine-lyase	<i>Raoultella terrigena</i>
ID=2843	WP_041147513	choline TMA-lyase-activating enzyme	<i>Raoultella ornithinolytica</i>
ID=2844	WP_041143873	BMC domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=2845	WP_041143872	phosphate propanoyltransferase	<i>Raoultella ornithinolytica</i>
ID=2846	WP_041143871	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2847	WP_041143870	QacE family quaternary ammonium compound efflux SMR transporter	<i>Raoultella ornithinolytica</i>
ID=2848	WP_041143869	MULTISPECIES: QacE family quaternary ammonium compound efflux SMR transporter	<i>Raoultella</i>
ID=2849	WP_041143868	tryptophan--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=2850	WP_041143867	diguanylate cyclase	<i>Raoultella ornithinolytica</i>
ID=2851	WP_041143866	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2852	WP_041143865	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2853	WP_041143864	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2854	WP_041143863	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2856	XP_011503954	PREDICTED: probable sulfate/thiosulfate import ATP-binding protein CysA	<i>Ceratosolen solmsi marchali</i>
ID=2857	WP_041147475	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2859	WP_041147474	multidrug efflux RND transporter permease subunit	<i>Raoultella ornithinolytica</i>

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ID=2860	WP_041147473	multidrug transporter	<i>Raoultella ornithinolytica</i>
ID=2861	WP_041147472	acrEF/envCD operon transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2862	WP_003855228	MULTISPECIES: Fis family transcriptional regulator	<i>Enterobacterales</i>
ID=2863	WP_041147471	MULTISPECIES: tRNA dihydrouridine synthase DusB	<i>Raoultella</i>
ID=2864	WP_041147470	ribosomal protein L11 methyltransferase	<i>Raoultella ornithinolytica</i>
ID=2865	WP_045856501	sodiumpantothenate symporter	<i>Raoultella terrigena</i>
ID=2866	WP_041147468	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2867	WP_041147467	MULTISPECIES: acetyl-CoA carboxylase biotin carboxylase subunit	<i>Raoultella</i>
ID=2868	WP_041147466	MULTISPECIES: acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	<i>Raoultella</i>
ID=2869	WP_041147465	MULTISPECIES: 3-dehydroquinase dehydratase	<i>Raoultella</i>
ID=2870	WP_045856504	sulfoxide reductase heme-binding subunit YedZ	<i>Raoultella terrigena</i>
ID=2871	WP_041147463	sulfoxide reductase	<i>Raoultella ornithinolytica</i>
ID=2872	WP_045856507	quinone oxidoreductase	<i>Raoultella terrigena</i>
ID=2873	WP_041147461	RNase E specificity factor CsrD	<i>Raoultella ornithinolytica</i>
ID=2874	WP_002918653	MULTISPECIES: rod shape-determining protein	<i>Enterobacterales</i>
ID=2875	WP_041147460	MULTISPECIES: rod shape-determining protein MreC	<i>Raoultella</i>
ID=2876	WP_041147459	MULTISPECIES: rod shape-determining protein MreD	<i>Raoultella</i>
ID=2877	WP_045856513	septum formation protein Maf	<i>Raoultella terrigena</i>
ID=2878	WP_041147457	MULTISPECIES: ribonuclease G	<i>Raoultella</i>
ID=2879	WP_041147456	TIGR02099 family protein	<i>Raoultella ornithinolytica</i>
ID=2880	WP_045856518	metalloprotease TldD	<i>Raoultella terrigena</i>
ID=2881	WP_041147454	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2882	WP_004868260	MULTISPECIES: protein AaeX	<i>Enterobacteriaceae</i>
ID=2883	WP_041147452	p-hydroxybenzoic acid efflux subunit AaeA	<i>Raoultella ornithinolytica</i>
ID=2884	WP_045856525	p-hydroxybenzoic acid efflux pump subunit AaeB	<i>Raoultella terrigena</i>
ID=2885	WP_041147450	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2886	WP_045857851	membrane protein	<i>Raoultella terrigena</i>
ID=2887	WP_041147449	membrane protein	<i>Raoultella ornithinolytica</i>
ID=2889	WP_041147448	MULTISPECIES: arginine repressor	<i>Raoultella</i>
ID=2890	WP_041147447	MULTISPECIES: malate dehydrogenase	<i>Raoultella</i>
ID=2891	WP_041147441	MULTISPECIES: outer membrane-stress sensor serine endopeptidase DegS	<i>Raoultella</i>
ID=2892	WP_041147440	serine endoprotease DegQ	<i>Raoultella ornithinolytica</i>
ID=2893	WP_041147439	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2894	WP_041147438	cell division protein ZapE	<i>Raoultella ornithinolytica</i>
ID=2895	WP_041147438	cell division protein ZapE	<i>Raoultella ornithinolytica</i>
ID=2896	WP_004106200	MULTISPECIES: 50S ribosomal protein L13	<i>Enterobacterales</i>
ID=2897	WP_003025138	MULTISPECIES: 30S ribosomal protein S9	<i>Enterobacterales</i>
ID=2898	WP_041147437	MULTISPECIES: stringent starvation protein A	<i>Raoultella</i>
ID=2899	WP_041147436	stringent starvation protein B	<i>Raoultella ornithinolytica</i>
ID=2900	WP_041147435	transcriptional regulator NanR	<i>Raoultella ornithinolytica</i>
ID=2901	WP_041147434	N-acetylneuraminase lyase	<i>Raoultella ornithinolytica</i>
ID=2902	WP_041147433	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2903	WP_041147432	N-acetylmannosamine-6-phosphate 2-epimerase	<i>Raoultella ornithinolytica</i>
ID=2904	WP_041147431	N-acetylmannosamine kinase	<i>Raoultella ornithinolytica</i>
ID=2905	WP_041147430	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2906	WP_041147429	glutamate synthase	<i>Raoultella ornithinolytica</i>
ID=2907	WP_015703611	glutamate synthase large subunit	<i>Enterobacteriaceae</i>
ID=2908	WP_041147427	TIGR01212 family radical SAM protein	<i>Raoultella ornithinolytica</i>
ID=2909	WP_041147426	hybrid sensor histidine kinase/response regulator	<i>Raoultella ornithinolytica</i>
ID=2910	WP_045856567	glutamine amidotransferase	<i>Raoultella terrigena</i>
ID=2911	WP_045856569	monofunctional biosynthetic peptidoglycan transglycosylase	<i>Raoultella terrigena</i>
ID=2912	WP_041147423	MULTISPECIES: phosphohistidinoprotein-hexose phosphotransferase	<i>Raoultella</i>
ID=2913	WP_041147422	MULTISPECIES: glmZ(sRNA)-inactivating NTPase	<i>Raoultella</i>
ID=2914	WP_041147421	PTS IIA-like nitrogen regulatory protein PtsN	<i>Raoultella ornithinolytica</i>
ID=2915	WP_004868168	MULTISPECIES: ribosome hibernation promoting factor HPF	<i>Enterobacteriaceae</i>
ID=2916	WP_045856573	RNA polymerase sigma-54 factor	<i>Raoultella terrigena</i>
ID=2917	WP_004206203	MULTISPECIES: ABC transporter ATP-binding protein	<i>Enterobacteriaceae</i>
ID=2918	WP_041147419	lipopolysaccharide ABC transporter substrate-binding protein LptA	<i>Raoultella ornithinolytica</i>
ID=2919	WP_041147418	LPS export ABC transporter periplasmic protein LptC	<i>Raoultella ornithinolytica</i>
ID=2920	WP_041147417	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	<i>Raoultella ornithinolytica</i>
ID=2921	WP_045857853	D-arabinose 5-phosphate isomerase	<i>Raoultella terrigena</i>
ID=2922	WP_045856583	calcium/sodium antiporter	<i>Raoultella terrigena</i>
ID=2923	WP_041147415	MULTISPECIES: phospholipid ABC transporter ATP-binding protein MlaF	<i>Raoultella</i>
ID=2924	WP_041147414	ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=2925	WP_045857854	outer membrane lipid asymmetry maintenance protein MlaD	<i>Raoultella terrigena</i>
ID=2926	WP_045856587	phospholipid-binding protein MlaC	<i>Raoultella terrigena</i>
ID=2927	WP_045856589	phospholipid ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=2928	WP_000900133	hypothetical protein	<i>Salmonella enterica</i>
ID=2929	WP_041147410	MULTISPECIES: UDP-N-acetylglucosamine 1-carboxyvinyltransferase	<i>Raoultella</i>

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ID=2930	WP_041147409	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=2931	WP_041147408	octaprenyl diphosphate synthase	<i>Raoultella ornithinolytica</i>
ID=2932	WP_041147407	MULTISPECIES: 50S ribosomal protein L21	<i>Raoultella</i>
ID=2933	WP_041147406	MULTISPECIES: 50S ribosomal protein L27	<i>Raoultella</i>
ID=2934	WP_041147405	EamA family transporter	<i>Raoultella ornithinolytica</i>
ID=2935	WP_041147404	Obg family GTPase CgtA	<i>Raoultella ornithinolytica</i>
ID=2936	WP_041147403	serine-type D-Ala-D-Ala carboxypeptidase	<i>Raoultella ornithinolytica</i>
ID=2938	WP_041147402	transcription elongation factor GreA	<i>Raoultella ornithinolytica</i>
ID=2939	WP_013098922	RNA-binding protein	<i>Enterobacter cloacae</i>
ID=2940	WP_041147401	MULTISPECIES: 23S rRNA (uridine(2552)-2'-O)-methyltransferase	<i>Raoultella</i>
ID=2941	WP_041147400	ATP-dependent metalloprotease	<i>Raoultella ornithinolytica</i>
ID=2942	WP_041147399	dihydropteroate synthase	<i>Raoultella ornithinolytica</i>
ID=2943	WP_041147398	phosphoglucosamine mutase	<i>Raoultella ornithinolytica</i>
ID=2944	WP_041147397	MULTISPECIES: preprotein translocase subunit SecG	<i>Raoultella</i>
ID=2945	WP_041147396	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2946	WP_041147395	porin	<i>Raoultella ornithinolytica</i>
ID=2948	WP_041147394	Crp/Fnr family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2949	WP_041147393	argininosuccinate synthase	<i>Raoultella ornithinolytica</i>
ID=2950	WP_041147392	ribosome maturation factor	<i>Raoultella ornithinolytica</i>
ID=2951	WP_041147391	transcription termination protein NusA	<i>Raoultella ornithinolytica</i>
ID=2952	WP_041147390	translation initiation factor IF-2	<i>Raoultella ornithinolytica</i>
ID=2953	WP_041147389	MULTISPECIES: ribosome-binding factor A	<i>Raoultella</i>
ID=2954	WP_045856618	tRNA pseudouridine(55) synthase	<i>Raoultella terrigena</i>
ID=2955	WP_004868066	MULTISPECIES: 30S ribosomal protein S15	<i>Enterobacteriaceae</i>
ID=2956	WP_041147387	polyribonucleotide nucleotidyltransferase	<i>Raoultella ornithinolytica</i>
ID=2957	WP_041147386	lipoprotein NlpI	<i>Raoultella ornithinolytica</i>
ID=2958	WP_045856627	DEAD/DEAH family ATP-dependent RNA helicase	<i>Raoultella terrigena</i>
ID=2960	WP_041147384	tryptophan permease	<i>Raoultella ornithinolytica</i>
ID=2961	WP_041147383	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=2962	WP_041147382	U32 family peptidase	<i>Raoultella ornithinolytica</i>
ID=2963	WP_041147381	protease	<i>Raoultella ornithinolytica</i>
ID=2964	WP_041147380	MULTISPECIES: SCP2 domain-containing protein	<i>Raoultella</i>
ID=2965	WP_041147379	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=2966	WP_041147377	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2967	WP_045856641	hypothetical protein	<i>Raoultella terrigena</i>
ID=2968	WP_045856644	membrane protein	<i>Raoultella terrigena</i>
ID=2969	WP_041147374	BON domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=2970	WP_041147373	MULTISPECIES: DnaA initiator-associating protein DiaA	<i>Raoultella</i>
ID=2971	WP_041147372	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2972	WP_041147371	penicillin-binding protein activator	<i>Raoultella ornithinolytica</i>
ID=2973	WP_045856650	rRNA (cytidine-2'-O-)-methyltransferase	<i>Raoultella terrigena</i>
ID=2974	WP_015960566	galactosamine-6-phosphate isomerase	<i>Enterobacter sp.</i>
ID=2975	WP_045856657	PTS N-acetylglactosamine transporter subunit IID	<i>Raoultella terrigena</i>
ID=2976	WP_045856660	PTS N-acetylglactosamine transporter subunit IIC	<i>Raoultella terrigena</i>
ID=2977	WP_045856662	PTS N-acetylglactosamine transporter subunit IIB	<i>Raoultella terrigena</i>
ID=2978	WP_045856665	tagatose-bisphosphate aldolase	<i>Raoultella terrigena</i>
ID=2979	WP_041147367	aldose isomerase	<i>Raoultella ornithinolytica</i>
ID=2980	WP_041147366	N-acetylglucosamine-6-phosphate deacetylase	<i>Raoultella ornithinolytica</i>
ID=2981	WP_045856672	hypothetical protein	<i>Raoultella terrigena</i>
ID=2982	WP_041147364	PTS N-acetylglactosamine transporter subunit IID	<i>Raoultella ornithinolytica</i>
ID=2983	WP_045856676	PTS N-acetylglactosamine transporter subunit IIC	<i>Raoultella terrigena</i>
ID=2984	WP_041147362	PTS N-acetylglactosamine transporter subunit IIB	<i>Raoultella ornithinolytica</i>
ID=2985	WP_041147361	tagatose-bisphosphate aldolase subunit KbaZ	<i>Raoultella ornithinolytica</i>
ID=2986	WP_045856682	DeoR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=2987	WP_041147359	galactarate dehydratase	<i>Raoultella ornithinolytica</i>
ID=2988	WP_041147358	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=2989	WP_045856688	5-keto-4-deoxy-D-glucarate aldolase	<i>Raoultella terrigena</i>
ID=2990	WP_041147356	2-hydroxy-3-oxopropionate reductase	<i>Raoultella ornithinolytica</i>
ID=2991	WP_041147355	glycerate 2-kinase	<i>Raoultella ornithinolytica</i>
ID=2992	WP_041147354	mechanosensitive ion channel protein MscS	<i>Raoultella ornithinolytica</i>
ID=2993	WP_049003122	hypothetical protein	<i>Klebsiella quasipneumoniae</i>
ID=2994	WP_041147353	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=2995	WP_041147352	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=2996	WP_041147351	DUF805 domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=2997	WP_041147350	glutathione-dependent reductase	<i>Raoultella ornithinolytica</i>
ID=2998	WP_006818186	membrane protein	<i>Yokenella regensburgei</i>
ID=2999	WP_045856702	membrane protein	<i>Raoultella terrigena</i>
ID=3000	WP_041147348	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3001	WP_041147347	MULTISPECIES: hypothetical protein	<i>Raoultella</i>

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ID=3002	WP_041147346	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3003	WP_041147756	EnvZ/OmpR regulon moderator	<i>Raoultella ornithinolytica</i>
ID=3004	WP_041147345	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3005	WP_041147344	transcriptional regulator ExuR	<i>Raoultella ornithinolytica</i>
ID=3006	WP_041147343	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3007	WP_041147342	uronate isomerase	<i>Raoultella ornithinolytica</i>
ID=3008	WP_041147341	altronate hydrolase	<i>Raoultella ornithinolytica</i>
ID=3009	WP_041147340	serine/threonine transporter SstT	<i>Raoultella ornithinolytica</i>
ID=3010	WP_045856722	membrane protein	<i>Raoultella terrigena</i>
ID=3011	WP_041147338	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3012	WP_041147337	MULTISPECIES: metal-dependent hydrolase	<i>Raoultella</i>
ID=3013	WP_041147336	23S rRNA (guanine(1835)-N(2))-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=3014	WP_041147335	NADPH-dependent 2,4-dienoyl-CoA reductase	<i>Raoultella ornithinolytica</i>
ID=3015	WP_041147334	autoinducer-2 kinase	<i>Raoultella ornithinolytica</i>
ID=3016	WP_045856735	LsrR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3017	WP_041147332	autoinducer 2 ABC transporter ATP-binding protein LsrA	<i>Raoultella ornithinolytica</i>
ID=3018	WP_041147331	autoinducer 2 ABC transporter permease LsrC	<i>Raoultella ornithinolytica</i>
ID=3019	WP_041147330	autoinducer 2 import system permease LsrD	<i>Raoultella ornithinolytica</i>
ID=3020	WP_041147329	autoinducer 2 ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3021	WP_041147328	autoinducer 2 aldolase	<i>Raoultella ornithinolytica</i>
ID=3022	WP_041147327	autoinducer-2 (AI-2) modifying protein LsrG	<i>Raoultella ornithinolytica</i>
ID=3024	WP_045856750	putrescine aminotransferase	<i>Raoultella terrigena</i>
ID=3025	WP_045856752	PadR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3026	WP_041147755	siderophore-interacting protein	<i>Raoultella ornithinolytica</i>
ID=3027	WP_041147322	dihydroxyacetone kinase	<i>Raoultella ornithinolytica</i>
ID=3028	WP_041147321	dihydroxyacetone kinase subunit DhaM	<i>Raoultella ornithinolytica</i>
ID=3029	WP_041147320	dihydroxyacetone kinase subunit L	<i>Raoultella ornithinolytica</i>
ID=3030	WP_041147319	dihydroxyacetone kinase subunit DhaK	<i>Raoultella ornithinolytica</i>
ID=3031	WP_041147318	glycerol dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3032	WP_041147317	sigma-54-dependent Fis family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3033	WP_041147316	arylsulfatase	<i>Raoultella ornithinolytica</i>
ID=3034	WP_041147315	anaerobic sulfatase maturase	<i>Raoultella ornithinolytica</i>
ID=3035	WP_041147314	haloacid dehalogenase	<i>Raoultella ornithinolytica</i>
ID=3036	WP_041147313	oxygen tolerance domain protein	<i>Raoultella ornithinolytica</i>
ID=3037	WP_041147312	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3038	WP_041147311	VWA domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=3039	WP_041147310	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3040	WP_041147309	ATPase	<i>Raoultella ornithinolytica</i>
ID=3041	WP_041147308	ATPase AAA	<i>Raoultella ornithinolytica</i>
ID=3042	WP_041147307	anaerobic sulfatase maturase	<i>Raoultella ornithinolytica</i>
ID=3043	WP_041147306	arylsulfatase	<i>Raoultella ornithinolytica</i>
ID=3044	WP_041147305	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3045	WP_041147304	mismatch-specific DNA-glycosylase	<i>Raoultella ornithinolytica</i>
ID=3046	WP_041147303	RNA polymerase sigma factor RpoD	<i>Raoultella ornithinolytica</i>
ID=3047	WP_041147302	DNA primase	<i>Raoultella ornithinolytica</i>
ID=3048	WP_041147301	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase..	<i>Raoultella ornithinolytica</i>
		.. complex transferase subunit TsaD	
ID=3049	WP_041147300	allantoin permease	<i>Raoultella ornithinolytica</i>
ID=3050	WP_041147299	MULTISPECIES: urease accessory protein UreG	<i>Raoultella</i>
ID=3051	WP_041147298	urease accessory protein UreF	<i>Raoultella ornithinolytica</i>
ID=3052	WP_045856818	urease accessory protein UreE	<i>Raoultella terrigena</i>
ID=3053	WP_041147296	urease subunit alpha	<i>Raoultella ornithinolytica</i>
ID=3054	WP_041147295	urease subunit beta	<i>Raoultella ornithinolytica</i>
ID=3055	WP_041147294	MULTISPECIES: urease subunit gamma	<i>Raoultella</i>
ID=3056	WP_041147293	urease accessory protein	<i>Raoultella ornithinolytica</i>
ID=3057	WP_045856825	MFS transporter	<i>Raoultella terrigena</i>
ID=3058	WP_041147754	glycerol-3-phosphate acyltransferase	<i>Raoultella ornithinolytica</i>
ID=3059	WP_041147291	bifunctional dihydroneopterin aldolase/7,8-dihydroneopterin epimerase	<i>Raoultella ornithinolytica</i>
ID=3060	WP_045856829	undecaprenyl-diphosphatase	<i>Raoultella terrigena</i>
ID=3061	WP_041147289	multifunctional CCA tRNA nucleotidyl transferase/..	<i>Raoultella ornithinolytica</i>
		..2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase	
ID=3062	WP_041147288	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=3063	WP_045856832	adenylate cyclase	<i>Raoultella terrigena</i>
ID=3064	WP_045856834	glutamine-synthetase adenyltransferase	<i>Raoultella terrigena</i>
ID=3065	WP_041147285	bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenyltransferase	<i>Raoultella ornithinolytica</i>
ID=3066	WP_041147284	glycogen synthase	<i>Raoultella ornithinolytica</i>
ID=3067	WP_041147283	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3068	WP_045856843	3,4-dihydroxy-2-butanone-4-phosphate synthase	<i>Raoultella terrigena</i>
ID=3069	WP_041147281	MULTISPECIES: zinc transporter ZupT	<i>Raoultella</i>

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ID=3070	WP_045856844	4,5-DOPA dioxygenase extradiol	<i>Raoultella terrigena</i>
ID=3071	WP_045856846	hypothetical protein	<i>Raoultella terrigena</i>
ID=3072	WP_041147278	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3073	WP_041147277	outer membrane channel protein TolC	<i>Raoultella ornithinolytica</i>
ID=3074	WP_041147276	ADP-ribose diphosphatase	<i>Raoultella ornithinolytica</i>
ID=3075	WP_041147275	MULTISPECIES: dehydrogenase	<i>Raoultella</i>
ID=3076	WP_041147274	phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=3077	WP_045856855	esterase YqiA	<i>Raoultella terrigena</i>
ID=3078	WP_041147272	DNA topoisomerase IV subunit B	<i>Raoultella ornithinolytica</i>
ID=3079	WP_041147271	quinol monooxygenase	<i>Raoultella ornithinolytica</i>
ID=3080	WP_041147270	NADPH quinone reductase MdaB	<i>Raoultella ornithinolytica</i>
ID=3081	WP_041147269	two-component sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=3082	WP_045856864	DNA-binding response regulator	<i>Raoultella terrigena</i>
ID=3083	WP_041147267	TIGR00156 family protein	<i>Raoultella ornithinolytica</i>
ID=3084	WP_041147266	DNA topoisomerase IV subunit A	<i>Raoultella ornithinolytica</i>
ID=3085	WP_041147265	MULTISPECIES: 1-acyl-sn-glycerol-3-phosphate acyltransferase	<i>Raoultella</i>
ID=3086	WP_041147264	cell division protein FtsP	<i>Raoultella ornithinolytica</i>
ID=3087	WP_041147263	YgiQ family radical SAM protein	<i>Raoultella ornithinolytica</i>
ID=3088	WP_041147262	MULTISPECIES: 2,5-didehydrogluconate reductase A	<i>Raoultella</i>
ID=3089	WP_041147261	NADH-dependent alcohol dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3090	WP_041147260	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3091	WP_041147259	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3092	WP_045856879	cystathionine beta-lyase	<i>Raoultella terrigena</i>
ID=3093	WP_045856881	biopolymer transporter ExbB	<i>Raoultella terrigena</i>
ID=3094	WP_041147256	biopolymer transport protein ExbD	<i>Raoultella ornithinolytica</i>
ID=3095	WP_041147753	TIGR00645 family protein	<i>Raoultella ornithinolytica</i>
ID=3096	WP_045856886	dienelactone hydrolase	<i>Raoultella terrigena</i>
ID=3097	WP_045856888	hypothetical protein	<i>Raoultella terrigena</i>
ID=3098	WP_041147752	thiol:disulfide oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3099	WP_041147254	MULTISPECIES: thioredoxin	<i>Raoultella</i>
ID=3100	WP_041147253	bifunctional glutathionylspermidine amidase/glutathionylspermidine synthase	<i>Raoultella ornithinolytica</i>
ID=3101	WP_045856892	GntR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3102	WP_045856893	hypothetical protein	<i>Raoultella terrigena</i>
ID=3103	WP_041147250	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3104	WP_052474604	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3105	WP_052474601	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3106	WP_041147249	hemolysin D	<i>Raoultella ornithinolytica</i>
ID=3107	WP_041147248	aspartate aminotransferase family protein	<i>Raoultella ornithinolytica</i>
ID=3108	WP_045856897	aldehyde dehydrogenase	<i>Raoultella terrigena</i>
ID=3110	WP_041147246	MULTISPECIES: LysR family transcriptional regulator	<i>Raoultella</i>
ID=3111	WP_041147245	FAD-dependent oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3112	WP_041147244	MULTISPECIES: endoribonuclease	<i>Raoultella</i>
ID=3113	WP_041147243	major pilin protein fimA	<i>Raoultella ornithinolytica</i>
ID=3114	WP_041147242	acetylornithine deacetylase	<i>Raoultella ornithinolytica</i>
ID=3115	WP_041147241	allantoin permease	<i>Raoultella ornithinolytica</i>
ID=3116	WP_041147240	short chain dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3117	WP_041147239	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3118	WP_041147238	MULTISPECIES: peptidoglycan-binding protein LysM	<i>Raoultella</i>
ID=3119	WP_041147237	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3120	WP_041147236	cystathionine beta-lyase	<i>Raoultella ornithinolytica</i>
ID=3121	WP_041147235	cystathionine beta-synthase	<i>Raoultella ornithinolytica</i>
ID=3122	WP_052474600	cysteine ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=3123	WP_041147233	ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=3124	WP_041147232	amino acid ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3125	WP_041147231	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3126	WP_041147230	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3127	WP_041147229	pilus assembly protein PapC	<i>Raoultella ornithinolytica</i>
ID=3128	WP_045856931	pilus assembly protein PapD	<i>Raoultella terrigena</i>
ID=3129	WP_041147227	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=3130	WP_041147749	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=3131	WP_041147226	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3132	WP_041147225	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3133	WP_041147224	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3134	WP_045856948	DNA-binding response regulator	<i>Raoultella terrigena</i>
ID=3135	WP_045856949	hypothetical protein	<i>Raoultella terrigena</i>
ID=3136	WP_045856950	hypothetical protein	<i>Raoultella terrigena</i>
ID=3137	WP_041147219	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3138	WP_045857039	ornithine decarboxylase	<i>Raoultella terrigena</i>
ID=3139	WP_041147217	nucleoside permease	<i>Raoultella ornithinolytica</i>

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ID=3140	WP_041147216	lytic murein transglycosylase	<i>Raoultella ornithinolytica</i>
ID=3141	WP_041147215	Fe(2+)-trafficking protein	<i>Raoultella ornithinolytica</i>
ID=3142	WP_041147214	A/G-specific adenine glycosylase	<i>Raoultella ornithinolytica</i>
ID=3143	WP_041147213	MULTISPECIES: tRNA (guanine(46)-N(7))-methyltransferase	<i>Raoultella</i>
ID=3144	WP_041147212	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=3145	WP_041147211	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3146	WP_041147210	MULTISPECIES: ABC transporter permease	<i>Raoultella</i>
ID=3147	WP_041147209	sugar ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=3148	WP_045857055	ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=3149	WP_041147207	YggW family oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3150	WP_041147206	non-canonical purine NTP pyrophosphatase	<i>Raoultella ornithinolytica</i>
ID=3151	WP_041147205	MULTISPECIES: YggU family protein	<i>Raoultella</i>
ID=3152	WP_041147204	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=3153	WP_041147203	YggS family pyridoxal phosphate enzyme	<i>Raoultella ornithinolytica</i>
ID=3154	WP_041147202	MULTISPECIES: twitching motility protein PilT	<i>Raoultella</i>
ID=3155	WP_045857066	helix-turn-helix transcriptional regulator	<i>Raoultella terrigena</i>
ID=3156	WP_041147200	MULTISPECIES: crossover junction endodeoxyribonuclease RuvA	<i>Raoultella</i>
ID=3157	WP_041147199	MULTISPECIES: DUF179 domain-containing protein	<i>Raoultella</i>
ID=3158	WP_041147198	glutathione synthase	<i>Raoultella ornithinolytica</i>
ID=3159	WP_041147197	16S rRNA (uracil(1498)-N(3))-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=3160	WP_041147196	deoxyribonuclease I	<i>Raoultella ornithinolytica</i>
ID=3161	WP_041147195	SprT family protein	<i>Raoultella ornithinolytica</i>
ID=3162	WP_041147194	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3163	WP_041147193	methionine adenosyltransferase	<i>Raoultella ornithinolytica</i>
ID=3164	WP_041147192	arginine decarboxylase	<i>Raoultella ornithinolytica</i>
ID=3165	WP_045857086	agmatinase	<i>Raoultella terrigena</i>
ID=3166	WP_041147190	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3167	WP_041147189	naphthalene 1,2-dioxygenase	<i>Raoultella ornithinolytica</i>
ID=3168	WP_041147188	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3169	WP_041147187	3-phenylpropionate dioxygenase	<i>Raoultella ornithinolytica</i>
ID=3170	WP_041147186	short-chain dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3171	WP_045857098	IcLR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3172	WP_041147184	glyoxalase	<i>Raoultella ornithinolytica</i>
ID=3173	WP_041147183	pyridine nucleotide-disulfide oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3174	WP_041147182	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3175	WP_041147181	MULTISPECIES: cupin	<i>Raoultella</i>
ID=3176	WP_041147180	hydrolase	<i>Raoultella ornithinolytica</i>
ID=3177	WP_041147179	short chain dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3178	WP_041147178	aspartate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3179	WP_045857111	aldehyde dehydrogenase	<i>Raoultella terrigena</i>
ID=3180	WP_041147176	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3181	WP_041147175	metalloprotease	<i>Raoultella ornithinolytica</i>
ID=3182	WP_041145947	spermidine/putrescine ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3184	WP_041145946	purine permease	<i>Raoultella ornithinolytica</i>
ID=3185	WP_041145945	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3186	WP_041145944	(Fe-S)-binding protein	<i>Raoultella ornithinolytica</i>
ID=3187	WP_041145944	(Fe-S)-binding protein	<i>Raoultella ornithinolytica</i>
ID=3188	WP_041145943	effector protein	<i>Raoultella ornithinolytica</i>
ID=3189	WP_049153132	hypothetical protein	<i>Klebsiella variicola</i>
ID=3189	WP_049153132	hypothetical protein	<i>Klebsiella variicola</i>
ID=3190	WP_041145942	chlorohydrolase	<i>Raoultella ornithinolytica</i>
ID=3191	WP_041145941	putative selenate reductase subunit YgkK	<i>Raoultella ornithinolytica</i>
ID=3192	WP_047050061	hypothetical protein	<i>Klebsiella mobilis</i>
ID=3193	WP_041145940	carbamate kinase	<i>Raoultella ornithinolytica</i>
ID=3194	WP_041145939	dihydropyrimidinase	<i>Raoultella ornithinolytica</i>
ID=3195	WP_041145938	selenium metabolism hydrolase	<i>Raoultella ornithinolytica</i>
ID=3196	WP_041145937	PLP-dependent lyase/thiolase	<i>Raoultella ornithinolytica</i>
ID=3197	WP_041145936	knotted carbamoyltransferase YgeW	<i>Raoultella ornithinolytica</i>
ID=3198	WP_041145935	sigma-54-dependent Fis family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3199	WP_041145934	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3200	WP_045858634	carbonic anhydrase	<i>Raoultella terrigena</i>
ID=3201	WP_052474544	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3202	WP_041145933	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3203	WP_045858628	hypothetical protein	<i>Raoultella terrigena</i>
ID=3204	WP_041145929	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3206	WP_045858624	outer membrane receptor protein	<i>Raoultella terrigena</i>
ID=3207	WP_052474542	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3208	WP_041145926	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3209	WP_041145925	NADP oxidoreductase	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=3210	WP_045858620	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3211	WP_041145923	MATE family efflux transporter	<i>Raoultella ornithinolytica</i>
ID=3212	WP_041145922	riboflavin synthase subunit alpha	<i>Raoultella ornithinolytica</i>
ID=3213	WP_041145921	cyclopropane-fatty-acyl-phospholipid synthase	<i>Raoultella ornithinolytica</i>
ID=3214	WP_041145920	Bcr/CflA family multidrug efflux MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3215	WP_041145919	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3216	WP_041145918	transcriptional repressor PurR	<i>Raoultella ornithinolytica</i>
ID=3217	WP_061708935	hypothetical protein	<i>Enterobacter</i> sp.
ID=3218	WP_041145916	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3219	WP_041145915	superoxide dismutase	<i>Raoultella ornithinolytica</i>
ID=3220	WP_041145914	endopeptidase	<i>Raoultella ornithinolytica</i>
ID=3221	WP_049082743	integrase	<i>Klebsiella michiganensis</i>
ID=3222	WP_063414245	enterohemolysin	<i>Klebsiella mobilis</i>
ID=3223	WP_046852401	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3224	WP_041147664	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3225	WP_041145908	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3226	WP_046876615	transcriptional regulator	<i>Klebsiella michiganensis</i>
ID=3227	WP_049124971	transcriptional regulator	<i>Klebsiella pneumoniae</i>
ID=3228	WP_048262111	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=3229	WP_046852410	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3230	WP_041145902	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3231	WP_041145901	Replication protein P	<i>Raoultella ornithinolytica</i>
ID=3232	WP_065365959	hypothetical protein, partial	<i>Klebsiella michiganensis</i>
ID=3233	WP_064411668	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=3234	WP_046852398	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3235	WP_047359560	hypothetical protein	<i>Enterobacter hormaechei</i>
ID=3237	WP_038207904	N-6 DNA methylase	<i>Vibrio tubiashii</i>
ID=3238	WP_062758199	ATP-binding protein	<i>Pantoea agglomerans</i>
ID=3239	WP_062758197	response regulator	<i>Pantoea agglomerans</i>
ID=3241	WP_058646353	XRE family transcriptional regulator	<i>Enterobacter hormaechei</i>
ID=3242	WP_041145893	XRE family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3243	WP_039270098	MULTISPECIES: hypothetical protein	<i>Enterobacter cloacae</i>
ID=3244	WP_049101119	DUF1367 domain-containing protein	<i>Klebsiella oxytoca</i>
ID=3245	WP_041145891	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3246	WP_032755722	phage protein	<i>Klebsiella pneumoniae</i>
ID=3247	WP_049079672	endodeoxyribonuclease RusA	<i>Klebsiella michiganensis</i>
ID=3248	WP_048997853	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3249	WP_064407162	antitermination protein	<i>Klebsiella oxytoca</i>
ID=3250	WP_004151282	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=3251	WP_049088202	lysozyme	<i>Klebsiella michiganensis</i>
ID=3252	WP_065953944	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3253	WP_064793851	hypothetical protein	<i>Raoultella planticola</i>
ID=3254	WP_041145884	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3255	WP_032687546	MULTISPECIES: membrane protein	<i>Enterobacteriaceae</i>
ID=3256	WP_047058610	hypothetical protein	<i>Klebsiella mobilis</i>
ID=3257	WP_064162822	terminase small subunit	<i>Klebsiella pneumoniae</i>
ID=3258	WP_049079661	terminase	<i>Klebsiella michiganensis</i>
ID=3259	WP_041145881	DNA-binding protein	<i>Raoultella ornithinolytica</i>
ID=3260	WP_041145880	phage Mu F like family protein	<i>Raoultella ornithinolytica</i>
ID=3261	WP_041145879	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3262	WP_041145878	coat protein	<i>Raoultella ornithinolytica</i>
ID=3263	WP_015705695	hypothetical protein	<i>Klebsiella mobilis</i>
ID=3264	WP_004139360	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=3265	WP_064360281	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=3266	WP_064360282	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=3267	WP_064360283	electron transfer flavoprotein subunit beta	<i>Klebsiella oxytoca</i>
ID=3268	WP_064360284	Ig domain-containing protein	<i>Klebsiella oxytoca</i>
ID=3269	WP_041145871	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3270	WP_004139348	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=3271	WP_047058596	lipoprotein	<i>Klebsiella mobilis</i>
ID=3272	WP_049083470	membrane protein	<i>Klebsiella michiganensis</i>
ID=3273	WP_064173565	phage tail protein	<i>Klebsiella pneumoniae</i>
ID=3274	WP_042896389	hypothetical protein	<i>Klebsiella mobilis</i>
ID=3275	WP_041145866	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3276	WP_041145865	ArsR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3277	WP_041145864	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3278	WP_041145863	kinase	<i>Raoultella ornithinolytica</i>
ID=3279	WP_064161126	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3280	WP_049001092	hypothetical protein	<i>Klebsiella pneumoniae</i>

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ID=3281	WP_047053431	hypothetical protein	<i>Klebsiella mobilis</i>
ID=3282	WP_039104017	hypothetical protein	<i>Klebsiella variicola</i>
ID=3283	WP_041147658	DNA-invertase	<i>Raoultella ornithinolytica</i>
ID=3284	WP_042934076	DNA polymerase V subunit UmuD	<i>Klebsiella oxytoca</i>
ID=3285	WP_049182665	DNA polymerase V subunit UmuC	<i>Klebsiella pneumoniae</i>
ID=3286	WP_004118128	MULTISPECIES: IS30 family transposase	<i>Klebsiella</i>
ID=3287	WP_070558872	arsenate reductase (glutaredoxin)	<i>Serratia sp.</i>
ID=3288	WP_064349939	arsenical efflux pump membrane protein ArsB	<i>Klebsiella oxytoca</i>
ID=3289	WP_047735665	arsenical resistance protein ArsH	<i>Enterobacter hormaechei</i>
ID=3290	WP_049265065	AraC family transcriptional regulator	<i>Raoultella planticola</i>
ID=3291	WP_049265108	MFS transporter	<i>Raoultella planticola</i>
ID=3292	WP_049265067	LysR family transcriptional regulator	<i>Raoultella planticola</i>
ID=3293	WP_049265069	amidohydrolase	<i>Raoultella planticola</i>
ID=3294	WP_049265072	integral membrane protein	<i>Raoultella planticola</i>
ID=3295	WP_049265078	gluconolactonase	<i>Raoultella planticola</i>
ID=3296	WP_041145852	DUF159 family protein	<i>Raoultella ornithinolytica</i>
ID=3297	WP_064793827	hypothetical protein	<i>Raoultella planticola</i>
ID=3298	WP_041145851	MULTISPECIES: glutaredoxin	<i>Raoultella</i>
ID=3299	WP_041145850	ribonuclease T	<i>Raoultella ornithinolytica</i>
ID=3300	WP_041147656	MULTISPECIES: lactoylglutathione lyase	<i>Raoultella</i>
ID=3301	WP_041145849	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3302	WP_041145848	TonB-dependent receptor	<i>Raoultella ornithinolytica</i>
ID=3303	WP_045859596	colicin Js sensitivity protein CjxB	<i>Raoultella terrigena</i>
ID=3304	WP_045858592	iron-regulated protein	<i>Raoultella terrigena</i>
ID=3306	WP_045858590	short-chain dehydrogenase/reductase	<i>Raoultella terrigena</i>
ID=3307	WP_041145845	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3308	WP_045858586	transcriptional regulator	<i>Raoultella terrigena</i>
ID=3309	WP_045858586	transcriptional regulator	<i>Raoultella terrigena</i>
ID=3310	WP_045859595	hydrolase	<i>Raoultella terrigena</i>
ID=3311	WP_045858584	peptidase C45	<i>Raoultella terrigena</i>
ID=3312	WP_045858581	peptide ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=3313	WP_045858579	peptide ABC transporter	<i>Raoultella terrigena</i>
ID=3314	WP_045858577	peptide ABC transporter permease	<i>Raoultella terrigena</i>
ID=3315	WP_045858575	ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=3316	WP_041145843	alkene reductase	<i>Raoultella ornithinolytica</i>
ID=3317	WP_045858571	transcriptional regulator	<i>Raoultella terrigena</i>
ID=3318	WP_041145840	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3319	WP_045858563	fusaric acid resistance protein	<i>Raoultella terrigena</i>
ID=3320	WP_041145838	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3321	WP_045858559	DUF1656 domain-containing protein	<i>Raoultella terrigena</i>
ID=3322	WP_041145836	MULTISPECIES: SlyA family transcriptional regulator	<i>Raoultella</i>
ID=3323	WP_041145835	GGDEF domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=3324	WP_041145834	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3325	WP_041145833	anhydro-N-acetylmuramic acid kinase	<i>Raoultella ornithinolytica</i>
ID=3326	WP_041145832	MULTISPECIES: lysozyme inhibitor	<i>Raoultella</i>
ID=3327	WP_041147654	pyridoxamine 5'-phosphate oxidase	<i>Raoultella ornithinolytica</i>
ID=3328	WP_045858552	tyrosine--tRNA ligase	<i>Raoultella terrigena</i>
ID=3329	WP_041145830	pyridoxal kinase	<i>Raoultella ornithinolytica</i>
ID=3330	WP_041145829	glutathione S-transferase	<i>Raoultella ornithinolytica</i>
ID=3331	WP_041145828	dipeptide/tripeptide permease A	<i>Raoultella ornithinolytica</i>
ID=3332	WP_041145827	endonuclease III	<i>Raoultella ornithinolytica</i>
ID=3333	WP_041145826	electron transport complex subunit RxsE	<i>Raoultella ornithinolytica</i>
ID=3334	WP_041145825	electron transport complex subunit G	<i>Raoultella ornithinolytica</i>
ID=3335	WP_041145824	electron transport complex subunit D	<i>Raoultella ornithinolytica</i>
ID=3336	WP_045858536	electron transport complex subunit RxsC	<i>Raoultella terrigena</i>
ID=3337	WP_041145822	electron transport complex subunit RxsB	<i>Raoultella ornithinolytica</i>
ID=3338	WP_025710820	MULTISPECIES: electron transport complex subunit A	<i>Enterobacteriaceae</i>
ID=3339	WP_045858531	membrane protein	<i>Raoultella terrigena</i>
ID=3340	WP_004148584	nucleoid-associated protein	<i>Klebsiella pneumoniae</i>
ID=3341	WP_041145820	aryl-phospho-beta-D-glucosidase	<i>Raoultella ornithinolytica</i>
ID=3342	WP_041145819	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3343	WP_041145818	adenosine deaminase	<i>Raoultella ornithinolytica</i>
ID=3344	WP_041145817	MarR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3345	WP_041145816	MULTISPECIES: cold-shock protein	<i>Raoultella</i>
ID=3346	WP_041145815	methionine ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3347	WP_041145814	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=3348	WP_041145813	MULTISPECIES: SirA-like protein	<i>Raoultella</i>
ID=3349	WP_041145812	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3351	WP_041145811	magnesium transporter CorA	<i>Raoultella ornithinolytica</i>

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ID=3352	WP_052474533	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3353	WP_041145810	bifunctional beta-cystathionase/maltose regulon regulatory protein	<i>Raoultella ornithinolytica</i>
ID=3354	WP_041145809	bifunctional PTS system maltose and glucose-specific transporter subunits IICB	<i>Raoultella ornithinolytica</i>
ID=3355	WP_041145808	Mal regulon transcriptional regulator Mall	<i>Raoultella ornithinolytica</i>
ID=3356	WP_041145807	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3357	WP_041145806	mannose-6-phosphate isomerase	<i>Raoultella ornithinolytica</i>
ID=3358	WP_045858504	fumarate hydratase	<i>Raoultella terrigena</i>
ID=3359	WP_041145804	class II fumarate hydratase	<i>Raoultella ornithinolytica</i>
ID=3360	WP_045858500	DNA replication terminus site-binding protein	<i>Raoultella terrigena</i>
ID=3361	WP_041145802	two-component sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=3362	WP_041145801	DNA-binding response regulator	<i>Raoultella ornithinolytica</i>
ID=3363	WP_045858494	membrane protein	<i>Raoultella terrigena</i>
ID=3364	WP_045858492	dihydromonapterin reductase	<i>Raoultella terrigena</i>
ID=3365	WP_045858490	arginine:ornithine antiporter	<i>Raoultella terrigena</i>
ID=3366	WP_045858488	hypothetical protein	<i>Raoultella terrigena</i>
ID=3367	WP_045858486	NAD(P) transhydrogenase subunit alpha	<i>Raoultella terrigena</i>
ID=3368	WP_041145795	NAD(P) transhydrogenase subunit beta	<i>Raoultella ornithinolytica</i>
ID=3369	WP_041145794	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3370	WP_041145793	universal stress protein UspE	<i>Raoultella ornithinolytica</i>
ID=3371	WP_002903394	MULTISPECIES: transcriptional regulator FNR	<i>Enterobacterales</i>
ID=3372	WP_045858476	methylated-DNA--protein-cysteine methyltransferase	<i>Raoultella terrigena</i>
ID=3373	WP_041147651	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3375	WP_045858472	DNA endonuclease SmrA	<i>Raoultella terrigena</i>
ID=3376	WP_045859586	IcIR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3377	WP_041145789	3-oxoadipate CoA-transferase	<i>Raoultella ornithinolytica</i>
ID=3378	WP_045858467	3-oxoadipate CoA-transferase	<i>Raoultella terrigena</i>
ID=3379	WP_041145787	beta-ketoadipyl CoA thiolase	<i>Raoultella ornithinolytica</i>
ID=3380	WP_041145786	3-carboxy-cis,cis-muconate cycloisomerase	<i>Raoultella ornithinolytica</i>
ID=3381	WP_041145785	3-oxoadipate enol-lactonase	<i>Raoultella ornithinolytica</i>
ID=3382	WP_041145784	4-carboxymuconolactone decarboxylase	<i>Raoultella ornithinolytica</i>
ID=3383	WP_041145783	mechanosensitive ion channel protein MscS	<i>Raoultella ornithinolytica</i>
ID=3384	WP_041145782	MarR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3385	WP_041145781	hemolysin D	<i>Raoultella ornithinolytica</i>
ID=3386	WP_041145780	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3387	WP_041145779	fumarate hydratase	<i>Raoultella ornithinolytica</i>
ID=3388	WP_041145778	citrate:succinate antiporter	<i>Raoultella ornithinolytica</i>
ID=3389	WP_041145777	flavocytochrome c	<i>Raoultella ornithinolytica</i>
ID=3390	WP_045858445	thiamine biosynthesis protein ApbE	<i>Raoultella terrigena</i>
ID=3391	WP_041145775	response regulator	<i>Raoultella ornithinolytica</i>
ID=3392	WP_041145774	two-component system sensor histidine kinase DcuS	<i>Raoultella ornithinolytica</i>
ID=3393	WP_045859584	N-acetylmuramic acid 6-phosphate etherase	<i>Raoultella terrigena</i>
ID=3394	WP_045859582	malate:quinone oxidoreductase	<i>Raoultella terrigena</i>
ID=3395	WP_041145773	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3396	WP_041145771	malonate decarboxylase holo-ACP synthase	<i>Raoultella ornithinolytica</i>
ID=3397	WP_041145770	transporter	<i>Raoultella ornithinolytica</i>
ID=3398	WP_041147648	biotin-independent malonate decarboxylase subunit gamma	<i>Raoultella ornithinolytica</i>
ID=3399	WP_041145769	biotin-independent malonate decarboxylase subunit beta	<i>Raoultella ornithinolytica</i>
ID=3400	WP_041145768	malonate decarboxylase acyl carrier protein	<i>Raoultella ornithinolytica</i>
ID=3401	WP_045858429	triphosphoribosyl-dephospho-CoA synthase	<i>Raoultella terrigena</i>
ID=3402	WP_045858428	malonate decarboxylase subunit alpha	<i>Raoultella terrigena</i>
ID=3403	WP_045858426	pheromone autoinducer 2 transporter	<i>Raoultella terrigena</i>
ID=3404	WP_041145764	multidrug transporter subunit MdtJ	<i>Raoultella ornithinolytica</i>
ID=3405	WP_041145763	multidrug transporter subunit MdtI	<i>Raoultella ornithinolytica</i>
ID=3406	WP_045858419	bifunctional diguanylate cyclase/phosphodiesterase	<i>Raoultella terrigena</i>
ID=3407	WP_045858417	serine protease	<i>Raoultella terrigena</i>
ID=3408	WP_045859577	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3409	WP_045858415	translocator protein, LysE family	<i>Raoultella terrigena</i>
ID=3410	WP_052474620	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3411	WP_041147647	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3412	WP_041145757	carboxypeptidase M32	<i>Raoultella ornithinolytica</i>
ID=3413	WP_045858409	AraC family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3414	WP_041145755	lysine transporter LysE	<i>Raoultella ornithinolytica</i>
ID=3415	WP_041145754	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3416	WP_041145753	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3417	WP_041145752	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3418	WP_045858399	dethiobiotin synthase	<i>Raoultella terrigena</i>
ID=3419	WP_045858398	voltage-gated ClC-type chloride channel ClcB	<i>Raoultella terrigena</i>
ID=3420	WP_041145749	DMSO reductase maturation protein DsmD	<i>Raoultella ornithinolytica</i>
ID=3421	WP_041145748	dimethylsulfoxide reductase	<i>Raoultella ornithinolytica</i>

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ID=3422	WP_041145747	dimethyl sulfoxide reductase subunit A	<i>Raoultella ornithinolytica</i>
ID=3423	WP_041145746	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3424	WP_041145745	lipoprotein	<i>Raoultella ornithinolytica</i>
ID=3425	WP_041145744	MULTISPECIES: spermidine acetyltransferase	<i>Raoultella</i>
ID=3426	WP_041145743	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3427	WP_045858382	hypothetical protein	<i>Raoultella terrigena</i>
ID=3428	WP_041145741	starvation-sensing protein RspA	<i>Raoultella ornithinolytica</i>
ID=3429	WP_041145740	Zn-dependent oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3430	WP_046852396	integrase	<i>Raoultella ornithinolytica</i>
ID=3431	WP_046852397	DNA-binding protein	<i>Raoultella ornithinolytica</i>
ID=3432	WP_041145911	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3433	WP_032723534	hypothetical protein	<i>Klebsiella mobilis</i>
ID=3434	WP_040217352	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3435	WP_032453666	MULTISPECIES: morphogenetic protein	<i>Klebsiella</i>
ID=3436	WP_049100473	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=3437	WP_064385627	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=3438	WP_000344964	hypothetical protein	<i>Escherichia coli</i>
ID=3439	WP_048266105	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3440	WP_064392176	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=3441	WP_064392090	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=3442	WP_065782090	XRE family transcriptional regulator	<i>Klebsiella pneumoniae</i>
ID=3443	WP_064794122	Rha family transcriptional regulator	<i>Raoultella planticola</i>
ID=3444	WP_064385628	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=3445	WP_064794118	hypothetical protein	<i>Raoultella planticola</i>
ID=3446	WP_064794116	hypothetical protein	<i>Raoultella planticola</i>
ID=3447	WP_049109373	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3448	WP_032693337	site-specific DNA-methyltransferase	<i>Klebsiella sp.</i>
ID=3449	WP_052626769	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3450	WP_065802909	HNH endonuclease	<i>Klebsiella pneumoniae</i>
ID=3451	WP_053087478	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=3452	WP_049099384	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=3453	WP_064794107	hypothetical protein	<i>Raoultella planticola</i>
ID=3454	WP_064164282	methyltransferase	<i>Klebsiella pneumoniae</i>
ID=3455	WP_048257892	MULTISPECIES: DNA methyltransferase	<i>Klebsiella</i>
ID=3456	WP_064375011	MULTISPECIES: hypothetical protein	<i>Enterobacteriales</i>
ID=3457	WP_047684265	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=3458	WP_032428647	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3459	WP_023343145	lysozyme	<i>Klebsiella pneumoniae</i>
ID=3460	WP_040239919	endopeptidase	<i>Klebsiella pneumoniae</i>
ID=3461	WP_057393647	terminase small subunit	<i>Salmonella enterica</i>
ID=3462	WP_057523589	terminase	<i>Serratia marcescens</i>
ID=3463	WP_060656983	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3464	WP_043001707	hypothetical protein	<i>Citrobacter sp.</i>
ID=3465	WP_032700392	NUDIX hydrolase	<i>Raoultella planticola</i>
ID=3466	WP_003833610	hypothetical protein	<i>Citrobacter freundii</i>
ID=3467	WP_048321450	MULTISPECIES: hypothetical protein	<i>Enterobacteriales</i>
ID=3468	WP_050072751	hypothetical protein	<i>Yersinia intermedia</i>
ID=3469	WP_047048767	hypothetical protein	<i>Klebsiella mobilis</i>
ID=3470	WP_023283949	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3471	WP_004884180	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3472	WP_064174995	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3473	WP_019704134	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3474	WP_047935517	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=3475	WP_064148551	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3476	WP_064148550	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3477	WP_047684905	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=3478	WP_047935521	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=3479	WP_064148547	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3480	WP_047935524	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=3481	WP_004884185	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=3482	WP_032700371	baseplate J-like family protein	<i>Raoultella planticola</i>
ID=3483	WP_000883217	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=3484	WP_051975543	hypothetical protein	<i>Klebsiella variicola</i>
ID=3485	WP_041143862	50S ribosomal protein L16 arginine hydroxylase	<i>Raoultella ornithinolytica</i>
ID=3486	WP_045853223	two-component sensor histidine kinase	<i>Raoultella terrigena</i>
ID=3487	WP_041143860	DNA-binding response regulator	<i>Raoultella ornithinolytica</i>
ID=3488	WP_041143859	copper transporter	<i>Raoultella ornithinolytica</i>
ID=3489	WP_041143858	copper-binding protein	<i>Raoultella ornithinolytica</i>
ID=3490	WP_041143857	copper resistance protein	<i>Raoultella ornithinolytica</i>

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ID=3491	WP_041143856	cation transporter	<i>Raoultella ornithinolytica</i>
ID=3492	WP_041143855	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3493	WP_041143854	colicin V biosynthesis protein	<i>Raoultella ornithinolytica</i>
ID=3494	WP_041143853	ATPase	<i>Raoultella ornithinolytica</i>
ID=3495	WP_015585248	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=3496	WP_045853232	type 1 fimbrial protein	<i>Raoultella terrigena</i>
ID=3497	WP_041143850	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=3498	WP_041143849	fimbrial assembly protein	<i>Raoultella ornithinolytica</i>
ID=3499	WP_052474458	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3500	WP_052474457	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3501	WP_032725073	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=3502	WP_041143847	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3503	WP_041143846	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3504	WP_052474454	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3506	WP_015585265	MULTISPECIES: proteolipid membrane potential modulator	<i>Enterobacteriaceae</i>
ID=3507	WP_046853174	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=3508	WP_041143842	PTS sorbitol transporter subunit IIC	<i>Raoultella ornithinolytica</i>
ID=3509	WP_041143841	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3510	WP_041143840	PTS sorbitol transporter subunit IIB	<i>Raoultella ornithinolytica</i>
ID=3511	WP_041143839	dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3512	WP_041143832	endoribonuclease SymE	<i>Raoultella ornithinolytica</i>
ID=3513	WP_041143837	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3514	WP_041143836	HNH endonuclease	<i>Raoultella ornithinolytica</i>
ID=3515	WP_041143835	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3516	WP_041143834	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3517	WP_041143833	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3518	WP_048268184	MULTISPECIES: hypothetical protein	<i>Enterobacterales</i>
ID=3519	WP_012907487	restriction endonuclease subunit M	<i>Citrobacter rodentium</i>
ID=3520	WP_064362549	MULTISPECIES: hypothetical protein	<i>Enterobacterales</i>
ID=3521	WP_038162494	type I restriction endonuclease subunit R	<i>Trabulsiella guamensis</i>
ID=3522	WP_048268187	MULTISPECIES: ATPase	<i>Enterobacterales</i>
ID=3523	WP_058841603	restriction endonuclease	<i>Enterobacter asburiae</i>
ID=3524	WP_041143819	HNH endonuclease	<i>Raoultella ornithinolytica</i>
ID=3525	WP_041143818	tellurite resistance protein	<i>Raoultella ornithinolytica</i>
ID=3526	WP_041143817	alcohol dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3527	WP_045853265	sugar ABC transporter permease	<i>Raoultella terrigena</i>
ID=3528	WP_041143815	ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=3529	WP_041143814	phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=3530	WP_041143813	ABC transporter	<i>Raoultella ornithinolytica</i>
ID=3531	WP_041143812	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3532	WP_041143811	IcIR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3533	WP_041143810	beta-xylosidase	<i>Raoultella ornithinolytica</i>
ID=3534	WP_041143809	symporter YagG	<i>Raoultella ornithinolytica</i>
ID=3535	WP_041143808	dehydratase	<i>Raoultella ornithinolytica</i>
ID=3536	WP_041143807	dihydrodipicolinate synthase family protein	<i>Raoultella ornithinolytica</i>
ID=3537	WP_041143806	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3538	WP_041143805	myo-inosose-2 dehydratase	<i>Raoultella ornithinolytica</i>
ID=3539	WP_045853277	protein iolH	<i>Raoultella terrigena</i>
ID=3540	WP_041143803	inositol 2-dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3541	WP_041143802	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione acylhydrolase (decyclizing)	<i>Raoultella ornithinolytica</i>
ID=3542	WP_041143801	5-dehydro-2-deoxygluconokinase	<i>Raoultella ornithinolytica</i>
ID=3543	WP_045853281	Fe-S cluster assembly protein HesB	<i>Raoultella terrigena</i>
ID=3544	WP_041143799	5-deoxy-glucuronate isomerase	<i>Raoultella ornithinolytica</i>
ID=3545	WP_041143798	methylmalonate-semialdehyde dehydrogenase (acylating)	<i>Raoultella ornithinolytica</i>
ID=3546	WP_041143797	inosose isomerase	<i>Raoultella ornithinolytica</i>
ID=3547	WP_041143796	ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=3548	WP_032718605	carbamate kinase	<i>Raoultella ornithinolytica</i>
ID=3549	WP_004857332	MULTISPECIES: MFS transporter	<i>Enterobacteriaceae</i>
ID=3550	WP_032718604	acyl-CoA synthetase FdrA	<i>Raoultella ornithinolytica</i>
ID=3551	WP_004857327	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3552	WP_004857324	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3553	WP_004857321	MULTISPECIES: LysR family transcriptional regulator	<i>Enterobacteriaceae</i>
ID=3554	WP_041143795	LPS export ABC transporter permease LptG	<i>Raoultella ornithinolytica</i>
ID=3555	WP_045853287	LPS export ABC transporter permease LptF	<i>Raoultella terrigena</i>
ID=3556	WP_041143793	MULTISPECIES: leucyl aminopeptidase	<i>Raoultella</i>
ID=3557	WP_041143792	MULTISPECIES: DNA polymerase III subunit chi	<i>Raoultella</i>
ID=3558	WP_041143791	valine--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=3559	WP_045853289	N-acetyltransferase	<i>Raoultella terrigena</i>
ID=3560	WP_045853290	hypothetical protein	<i>Raoultella terrigena</i>

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ID=3561	WP_045853291	RNase E inhibitor protein	<i>Raoultella terrigena</i>
ID=3562	WP_041143787	ornithine carbamoyltransferase	<i>Raoultella ornithinolytica</i>
ID=3563	WP_041143786	toxin-antitoxin biofilm protein TabA	<i>Raoultella ornithinolytica</i>
ID=3564	WP_065805915	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3565	WP_045853294	aspartate carbamoyltransferase	<i>Raoultella terrigena</i>
ID=3566	WP_045853295	aspartate carbamoyltransferase regulatory subunit	<i>Raoultella terrigena</i>
ID=3567	WP_041143783	MULTISPECIES: endoribonuclease L-PSP	<i>Raoultella</i>
ID=3568	WP_041143779	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3569	WP_041143778	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3570	WP_041143777	beta-N-acetylhexosaminidase	<i>Raoultella ornithinolytica</i>
ID=3571	WP_045853308	magnesium-translocating P-type ATPase	<i>Raoultella terrigena</i>
ID=3572	WP_045853309	trehalose operon repressor	<i>Raoultella terrigena</i>
ID=3573	WP_041143774	PTS trehalose transporter subunit IIBC	<i>Raoultella ornithinolytica</i>
ID=3574	WP_045853311	glucohydrolase	<i>Raoultella terrigena</i>
ID=3575	WP_041143772	PTS system, cellobiose-specific IIC component	<i>Raoultella ornithinolytica</i>
ID=3576	WP_045853500	6-phospho-beta-glucosidase	<i>Raoultella terrigena</i>
ID=3577	WP_041143771	MULTISPECIES: PTS sugar transporter subunit IIB	<i>Raoultella</i>
ID=3578	WP_045853313	RpiR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3579	WP_041143769	anaerobic ribonucleoside triphosphate reductase	<i>Raoultella ornithinolytica</i>
ID=3580	WP_041143768	anaerobic ribonucleoside-triphosphate reductase activating protein	<i>Raoultella ornithinolytica</i>
ID=3581	WP_041143767	transcription antiterminator BglG	<i>Raoultella ornithinolytica</i>
ID=3582	WP_045853317	6-phosphogluconolactonase	<i>Raoultella terrigena</i>
ID=3583	WP_041143765	MULTISPECIES: 2-dehydro-3-deoxyphosphooctonate aldolase	<i>Raoultella</i>
ID=3584	WP_041143764	L-seryl-tRNA selenium transferase	<i>Raoultella ornithinolytica</i>
ID=3585	WP_041143763	dihydroorotase	<i>Raoultella ornithinolytica</i>
ID=3586	WP_032689791	MULTISPECIES: membrane protein	<i>Enterobacteriaceae</i>
ID=3587	WP_041143762	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3588	WP_041143761	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=3589	WP_041143760	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3590	WP_041143759	MULTISPECIES: glycine dehydrogenase	<i>Raoultella</i>
ID=3591	WP_041143758	cytochrome b562	<i>Raoultella ornithinolytica</i>
ID=3592	WP_041143757	metalloprotease PmbA	<i>Raoultella ornithinolytica</i>
ID=3593	WP_041143756	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3594	WP_041143755	DUF4432 domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=3595	WP_041143754	acyltransferase	<i>Raoultella ornithinolytica</i>
ID=3596	WP_041143753	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	<i>Raoultella ornithinolytica</i>
ID=3597	WP_041143752	fructose-bisphosphatase	<i>Raoultella ornithinolytica</i>
ID=3598	WP_041143751	sugar ABC transporter permease Yjff	<i>Raoultella ornithinolytica</i>
ID=3599	WP_041143750	sugar ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=3600	WP_041143749	sugar ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=3601	WP_041143748	MULTISPECIES: sugar ABC transporter substrate-binding protein	<i>Raoultella</i>
ID=3602	WP_061075418	inorganic pyrophosphatase	<i>Citrobacter amalonaticus</i>
ID=3603	WP_041143746	receptor	<i>Raoultella ornithinolytica</i>
ID=3604	WP_041143745	TonB-dependent receptor	<i>Raoultella ornithinolytica</i>
ID=3605	WP_041143744	MULTISPECIES: gamma-glutamylcyclotransferase	<i>Raoultella</i>
ID=3606	WP_041143743	translocation and assembly module TamB	<i>Raoultella ornithinolytica</i>
ID=3607	WP_041143742	outer membrane protein assembly factor	<i>Raoultella ornithinolytica</i>
ID=3608	WP_045853335	peptide-methionine (S)-S-oxide reductase	<i>Raoultella terrigena</i>
ID=3609	WP_041143740	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3610	WP_041143739	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=3611	WP_041143738	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3612	WP_041143737	3'(2'),5'-bisphosphate nucleotidase CysQ	<i>Raoultella ornithinolytica</i>
ID=3613	WP_041143736	2',3'-cyclic-nucleotide 2'-phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=3614	WP_041143735	HxIR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3615	WP_041143734	NAD(P)-dependent oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3616	WP_045853342	AraC family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3617	WP_041143732	EamA family transporter	<i>Raoultella ornithinolytica</i>
ID=3618	WP_045853343	iron-sulfur cluster repair di-iron protein	<i>Raoultella terrigena</i>
ID=3619	WP_041143730	D-serine/D-alanine/glycine transporter	<i>Raoultella ornithinolytica</i>
ID=3620	WP_041143729	MULTISPECIES: peptidylprolyl isomerase	<i>Raoultella</i>
ID=3621	WP_045853345	hypothetical protein	<i>Raoultella terrigena</i>
ID=3622	WP_033754882	MULTISPECIES: 50S ribosomal protein L9	<i>Pantoea</i>
ID=3623	WP_002210155	MULTISPECIES: 30S ribosomal protein S18	<i>Enterobacterales</i>
ID=3624	WP_041143726	MULTISPECIES: primosomal replication protein N	<i>Raoultella</i>
ID=3625	WP_004098001	MULTISPECIES: 30S ribosomal protein S6	<i>Enterobacterales</i>
ID=3626	WP_041143725	MULTISPECIES: membrane protein	<i>Raoultella</i>
ID=3627	WP_041143724	esterase	<i>Raoultella ornithinolytica</i>
ID=3628	WP_041143723	MULTISPECIES: biofilm peroxide resistance protein BsmA	<i>Raoultella</i>
ID=3629	WP_041143722	isovaleryl-CoA dehydrogenase	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=3630	WP_045853348	MFS transporter	<i>Raoultella terrigena</i>
ID=3631	WP_041143720	23S rRNA (guanosine(2251)-2'-O)-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=3632	WP_041143719	exoribonuclease R	<i>Raoultella ornithinolytica</i>
ID=3633	WP_041143718	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3634	WP_041143717	adenylosuccinate synthase	<i>Raoultella ornithinolytica</i>
ID=3635	WP_041143716	MULTISPECIES: membrane protein	<i>Raoultella</i>
ID=3636	WP_041143715	protease modulator HflC	<i>Raoultella ornithinolytica</i>
ID=3637	WP_041143714	protease modulator HflK	<i>Raoultella ornithinolytica</i>
ID=3638	WP_041143713	GTPase HflX	<i>Raoultella ornithinolytica</i>
ID=3639	WP_041143712	MULTISPECIES: RNA-binding protein Hfq	<i>Raoultella</i>
ID=3640	WP_045853364	tRNA dimethylallyltransferase	<i>Raoultella terrigena</i>
ID=3641	WP_041143710	DNA mismatch repair protein MutL	<i>Raoultella ornithinolytica</i>
ID=3642	WP_041143709	N-acetylmuramoyl-L-alanine amidase AmiB	<i>Raoultella ornithinolytica</i>
ID=3643	WP_041143708	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase..	<i>Raoultella ornithinolytica</i>
		..complex ATPase subunit type 1 TsaE	
ID=3644	WP_041143707	bifunctional ADP-dependent (S)-NAD(P)H-hydrate dehydratase/..	<i>Raoultella ornithinolytica</i>
		..NAD(P)H-hydrate epimerase	
ID=3645	WP_041143706	epoxyqueuosine reductase	<i>Raoultella ornithinolytica</i>
ID=3647	WP_041143705	arginine ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3648	WP_000520890	oligoribonuclease	<i>Shigella flexneri</i>
ID=3649	WP_063887853	ribosome biogenesis GTPase RsgA, partial	<i>Salmonella enterica</i>
ID=3650	WP_041143703	ribosome small subunit-dependent GTPase	<i>Raoultella ornithinolytica</i>
ID=3651	WP_041143702	phosphatidylserine decarboxylase	<i>Raoultella ornithinolytica</i>
ID=3652	WP_041143701	miniconductance mechanosensitive channel MscM	<i>Raoultella ornithinolytica</i>
ID=3653	WP_045853374	elongation factor P lysine(34) lysyltransferase	<i>Raoultella terrigena</i>
ID=3654	WP_041143699	fumarate reductase flavoprotein subunit	<i>Raoultella ornithinolytica</i>
ID=3655	WP_041143698	succinate dehydrogenase/fumarate reductase iron-sulfur subunit	<i>Raoultella ornithinolytica</i>
ID=3656	WP_041143697	fumarate reductase subunit C	<i>Raoultella ornithinolytica</i>
ID=3657	WP_041143696	fumarate reductase	<i>Raoultella ornithinolytica</i>
ID=3658	WP_041143695	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3659	WP_041143694	MULTISPECIES: multidrug transporter	<i>Raoultella</i>
ID=3661	WP_041143692	MULTISPECIES: elongation factor P	<i>Raoultella</i>
ID=3662	WP_041143691	EF-P beta-lysylation protein EpmB	<i>Raoultella ornithinolytica</i>
ID=3663	WP_041143690	MULTISPECIES: membrane protein	<i>Raoultella</i>
ID=3664	WP_041143689	molecular chaperone GroEL	<i>Raoultella ornithinolytica</i>
ID=3665	WP_041143688	molecular chaperone GroES	<i>Raoultella ornithinolytica</i>
ID=3666	WP_041143687	L-methionine/branched-chain amino acid transporter	<i>Raoultella ornithinolytica</i>
ID=3667	WP_064164219	membrane protein FxsA	<i>Klebsiella pneumoniae</i>
ID=3668	WP_041143685	aspartate ammonia-lyase	<i>Raoultella ornithinolytica</i>
ID=3669	WP_045853385	C4-dicarboxylate ABC transporter	<i>Raoultella terrigena</i>
ID=3670	WP_041143683	MULTISPECIES: cation tolerance protein CutA	<i>Raoultella</i>
ID=3671	WP_041143682	protein-disulfide reductase DsbD	<i>Raoultella ornithinolytica</i>
ID=3672	WP_041143681	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3673	WP_041143680	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3674	WP_057067565	integrase	<i>Citrobacter freundii</i>
ID=3675	WP_047734841	MULTISPECIES: transcriptional regulator	<i>Enterobacteriaceae</i>
ID=3676	WP_047734842	MULTISPECIES: PTS sorbitol transporter subunit IIC	<i>Enterobacteriaceae</i>
ID=3678	WP_047734844	MULTISPECIES: PTS sorbitol transporter subunit IIB	<i>Enterobacteriaceae</i>
ID=3679	WP_047734845	MFS transporter	<i>Enterobacter hormaechei</i>
ID=3680	WP_057067568	hypothetical protein	<i>Citrobacter freundii</i>
ID=3682	WP_045307701	baseplate assembly protein, partial	<i>Enterobacter kobei</i>
ID=3683	WP_045352366	MULTISPECIES: hypothetical protein	<i>Enterobacter cloacae</i>
ID=3684	WP_029392161	serine/threonine protein kinase	<i>Escherichia coli</i>
ID=3685	WP_029392160	hypothetical protein	<i>Escherichia coli</i>
ID=3686	WP_000944486	hypothetical protein	<i>Salmonella enterica</i>
ID=3687	WP_052899573	hypothetical protein	<i>Escherichia coli</i>
ID=3688	WP_000957732	hypothetical protein	<i>Escherichia coli</i>
ID=3689	WP_001254976	MULTISPECIES: hypothetical protein	<i>Enterobacterales</i>
ID=3690	WP_069203114	hypothetical protein	<i>Aeromonas veronii</i>
ID=3691	WP_061063842	hypothetical protein	<i>Providencia stuartii</i>
ID=3692	WP_041143679	NAD(P)H dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3693	WP_041143678	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3694	WP_041143677	DSBA oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3695	WP_041143676	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3696	WP_041143675	DNA-binding protein	<i>Raoultella ornithinolytica</i>
ID=3697	WP_041143674	chaperone-modulator protein CbpM	<i>Raoultella ornithinolytica</i>
ID=3698	WP_045853400	alpha-glucosidase/alpha-galactosidase	<i>Raoultella terrigena</i>
ID=3699	WP_041143672	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3700	WP_041143671	hypothetical protein	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=3701	WP_041143670	transcriptional regulator MeIR	<i>Raoultella ornithinolytica</i>
ID=3702	WP_041143669	proline/betaine transporter	<i>Raoultella ornithinolytica</i>
ID=3703	WP_041143668	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=3704	WP_041147506	VOC family protein	<i>Raoultella ornithinolytica</i>
ID=3705	WP_041143667	MULTISPECIES: phosphonate metabolism transcriptional regulator PhnF	<i>Raoultella</i>
ID=3706	WP_045853406	phosphonate C-P lyase system protein PhnG	<i>Raoultella terrigena</i>
ID=3707	WP_041143665	MULTISPECIES: carbon-phosphorus lyase subunit PhnH	<i>Raoultella</i>
ID=3708	WP_041143664	carbon-phosphorus lyase complex subunit PhnI	<i>Raoultella ornithinolytica</i>
ID=3709	WP_041143663	MULTISPECIES: carbon-phosphorus lyase complex subunit PhnJ	<i>Raoultella</i>
ID=3710	WP_041143662	MULTISPECIES: phosphonate C-P lyase system protein PhnK	<i>Raoultella</i>
ID=3711	WP_041143661	phosphonate C-P lyase system protein PhnL	<i>Raoultella ornithinolytica</i>
ID=3712	WP_045853409	phosphonate metabolism protein PhnM	<i>Raoultella terrigena</i>
ID=3713	WP_041143659	ribose 1,5-bisphosphokinase	<i>Raoultella ornithinolytica</i>
ID=3714	WP_045853412	phosphonate metabolism protein PhnP	<i>Raoultella terrigena</i>
ID=3715	WP_041143658	phosphonate metabolism protein PhnP	<i>Raoultella ornithinolytica</i>
ID=3716	WP_048025186	MULTISPECIES: membrane protein	<i>Enterobacteriaceae</i>
ID=3717	WP_045853414	hybrid sensor histidine kinase/response regulator	<i>Raoultella terrigena</i>
ID=3719	WP_041143648	D-ribose transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=3720	WP_041143647	MULTISPECIES: ribose ABC transporter permease	<i>Raoultella</i>
ID=3721	WP_041143646	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3722	WP_041143645	DNA-binding response regulator	<i>Raoultella ornithinolytica</i>
ID=3723	WP_041143644	spermidine/putrescine ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3724	WP_032710320	hypothetical protein	<i>Klebsiella mobilis</i>
ID=3725	WP_018981203	hypothetical protein	<i>Saccharibacter floricola</i>
ID=3726	WP_003617554	2,5-diketo-D-gluconic acid reductase	<i>Komagataeibacter hansenii</i>
ID=3727	WP_003617561	FMN reductase	<i>Komagataeibacter hansenii</i>
ID=3728	WP_013207632	alcohol dehydrogenase	<i>Ralstonia solanacearum</i>
ID=3729	WP_049034096	oxidoreductase	<i>Klebsiella mobilis</i>
ID=3730	WP_001312830	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=3731	WP_000974326	MULTISPECIES: transposase	<i>Enterobacteriaceae</i>
ID=3732	WP_017372674	transposase	<i>Enterobacteriaceae</i>
ID=3733	WP_045427728	MULTISPECIES: hypothetical protein	<i>Edwardsiella</i>
ID=3734	WP_046622877	N-acetyltransferase	<i>Klebsiella pneumoniae</i>
ID=3735	WP_003026799	MULTISPECIES: hypothetical protein	<i>Enterobacterales</i>
ID=3736	WP_041145530	transglutaminase	<i>Raoultella ornithinolytica</i>
ID=3737	WP_041145529	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3738	WP_041145528	IMP dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3739	WP_041147626	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3740	WP_041147625	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3741	WP_049112097	LuxR family transcriptional regulator	<i>Klebsiella michiganensis</i>
ID=3742	WP_041145527	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3743	WP_041145526	pyruvate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3744	WP_041145525	diaminohydroxyphosphoribosylaminopyrimidine deaminase	<i>Raoultella ornithinolytica</i>
ID=3745	WP_041145524	dihydrolipoyl dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3746	WP_041147624	alpha/beta hydrolase	<i>Raoultella ornithinolytica</i>
ID=3747	WP_041145523	GntR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3748	WP_041145522	deaminase	<i>Raoultella ornithinolytica</i>
ID=3749	WP_041145521	ethylamine chlorohydrolase	<i>Raoultella ornithinolytica</i>
ID=3750	WP_041145520	cytosine deaminase	<i>Raoultella ornithinolytica</i>
ID=3751	WP_041145520	cytosine deaminase	<i>Raoultella ornithinolytica</i>
ID=3752	WP_041145519	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=3753	WP_041145518	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=3754	WP_041145517	ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=3755	WP_041145516	ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=3756	WP_041145515	peptide ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3757	WP_041145514	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3758	WP_041145513	polysaccharide deacetylase	<i>Raoultella ornithinolytica</i>
ID=3759	WP_012907273	MFS transporter	<i>Citrobacter rodentium</i>
ID=3760	WP_004113000	protocatechuate 4,5-dioxygenase subunit alpha	<i>Klebsiella oxytoca</i>
ID=3761	WP_012907275	LysR family transcriptional regulator	<i>Citrobacter rodentium</i>
ID=3762	WP_004137116	MULTISPECIES: DNA-binding protein	<i>Klebsiella</i>
ID=3763	WP_049129493	4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate decarboxylase	<i>Klebsiella oxytoca</i>
ID=3764	WP_004137121	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=3765	WP_049129492	6-phosphogluconate dehydrogenase	<i>Klebsiella oxytoca</i>
ID=3766	WP_041145504	LuxR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3767	WP_041145503	major royal jelly protein	<i>Raoultella ornithinolytica</i>
ID=3768	WP_041145502	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3769	WP_041145501	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3770	WP_045855354	hypothetical protein	<i>Raoultella terrigena</i>

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ID=3771	WP_045855353	RES domain protein	<i>Raoultella terrigena</i>
ID=3772	WP_045855352	hypothetical protein	<i>Raoultella terrigena</i>
ID=3773	WP_045855351	N-acetyltransferase	<i>Raoultella terrigena</i>
ID=3774	WP_041145497	amino acid ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3775	WP_052698715	pyrophosphatase	<i>Raoultella terrigena</i>
ID=3776	WP_041145496	citrate (Si)-synthase	<i>Raoultella ornithinolytica</i>
ID=3777	WP_041145495	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=3778	WP_045855347	ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=3779	WP_041145493	branched-chain amino acid ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=3780	WP_041145492	branched-chain amino acid ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=3781	WP_045855344	branched chain amino acid ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=3782	WP_045855493	hypothetical protein	<i>Raoultella terrigena</i>
ID=3783	WP_041145490	MULTISPECIES: peroxiredoxin	<i>Raoultella</i>
ID=3784	WP_041145489	cytochrome c biogenesis protein	<i>Raoultella ornithinolytica</i>
ID=3785	WP_041145488	DNA-directed RNA polymerase sigma-70 factor	<i>Raoultella ornithinolytica</i>
ID=3786	WP_041145487	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3787	WP_041145486	serine/threonine protein kinase	<i>Raoultella ornithinolytica</i>
ID=3788	WP_045855339	transcriptional regulator	<i>Raoultella terrigena</i>
ID=3789	WP_041147618	RNA polymerase subunit sigma-24	<i>Raoultella ornithinolytica</i>
ID=3790	WP_041145484	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3791	WP_041145483	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3792	WP_045855491	diguanylate cyclase	<i>Raoultella terrigena</i>
ID=3793	WP_041145482	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3794	WP_041147617	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3795	WP_041145481	glyceraldehyde-3-phosphate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3796	WP_045855337	thiaminase	<i>Raoultella terrigena</i>
ID=3797	WP_041145479	ABC transporter ATPase	<i>Raoultella ornithinolytica</i>
ID=3798	WP_041145478	MULTISPECIES: ABC transporter permease	<i>Raoultella</i>
ID=3799	WP_041145477	thiamine biosynthesis protein	<i>Raoultella ornithinolytica</i>
ID=3800	WP_041145476	aspartate aminotransferase family protein	<i>Raoultella ornithinolytica</i>
ID=3801	WP_041145475	2,4-diaminobutyrate decarboxylase	<i>Raoultella ornithinolytica</i>
ID=3802	WP_041145474	DUF4865 domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=3803	WP_045855490	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3804	WP_041145473	cytochrome c biogenesis protein	<i>Raoultella ornithinolytica</i>
ID=3805	WP_041145472	two-component sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=3806	WP_041145471	DNA-binding response regulator	<i>Raoultella ornithinolytica</i>
ID=3807	WP_041145470	alpha/beta hydrolase	<i>Raoultella ornithinolytica</i>
ID=3808	WP_041145469	SDR family oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=3809	WP_041145468	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3810	WP_045855329	glutamine amidotransferase	<i>Raoultella terrigena</i>
ID=3811	WP_047587517	TetR family transcriptional regulator	<i>Methylibium sp.</i>
ID=3812	WP_015963556	dehydrogenase of unknown specificity, short-chain alcohol dehydrogenase like protein	<i>Enterobacteriaceae bacterium</i>
ID=3813	WP_045855328	penicillin-binding protein 2	<i>Raoultella terrigena</i>
ID=3814	WP_041145465	allophanate hydrolase	<i>Raoultella ornithinolytica</i>
ID=3815	WP_041145464	urea carboxylase	<i>Raoultella ornithinolytica</i>
ID=3816	WP_041145463	MULTISPECIES: urea carboxylase	<i>Raoultella</i>
ID=3817	WP_041145462	urea carboxylase	<i>Raoultella ornithinolytica</i>
ID=3818	WP_041145461	lauroyl acyltransferase	<i>Raoultella ornithinolytica</i>
ID=3819	WP_041145460	lipid kinase	<i>Raoultella ornithinolytica</i>
ID=3820	WP_041145459	lipid kinase	<i>Raoultella ornithinolytica</i>
ID=3821	WP_041145458	lysine transporter LysE	<i>Raoultella ornithinolytica</i>
ID=3822	WP_041145457	catalase/peroxidase HPI	<i>Raoultella ornithinolytica</i>
ID=3823	WP_041145456	cell division protein ZapE	<i>Raoultella ornithinolytica</i>
ID=3824	WP_041145455	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3826	WP_041145454	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3827	WP_041145453	MBL fold metallo-hydrolase	<i>Raoultella ornithinolytica</i>
ID=3828	WP_045855315	TonB-dependent receptor	<i>Raoultella terrigena</i>
ID=3829	WP_045855314	ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=3830	WP_041145452	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3831	WP_041145451	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3832	WP_041145450	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3833	WP_052698714	hypothetical protein	<i>Raoultella terrigena</i>
ID=3834	WP_041145449	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3835	WP_041145448	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3836	WP_041147615	lysine transporter LysE	<i>Raoultella ornithinolytica</i>
ID=3837	WP_041145447	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3838	WP_045855308	bestrophin	<i>Raoultella terrigena</i>
ID=3839	WP_045855307	histidine kinase	<i>Raoultella terrigena</i>
ID=3840	WP_041145444	peroxiredoxin OsmC	<i>Raoultella ornithinolytica</i>

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ID=3841	WP_045855305	N-acetyltransferase	<i>Raoultella terrigena</i>
ID=3842	WP_041145442	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3843	WP_041145441	MBL fold metallo-hydrolase	<i>Raoultella ornithinolytica</i>
ID=3844	WP_004861775	MULTISPECIES: 30S ribosomal protein S22	<i>Enterobacteriaceae</i>
ID=3845	WP_041145440	NAD-dependent malic enzyme	<i>Raoultella ornithinolytica</i>
ID=3846	WP_041145439	ABC transporter	<i>Raoultella ornithinolytica</i>
ID=3847	WP_041145437	potassium ABC transporter ATPase	<i>Raoultella ornithinolytica</i>
ID=3848	WP_041145436	zinc-dependent alcohol dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3849	WP_045855299	zinc-dependent alcohol dehydrogenase	<i>Raoultella terrigena</i>
ID=3850	WP_041145435	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3851	WP_045855297	ABC transporter substrate binding protein	<i>Raoultella terrigena</i>
ID=3852	WP_045855296	peptide ABC transporter permease	<i>Raoultella terrigena</i>
ID=3853	WP_045855295	ABC transporter permease	<i>Raoultella terrigena</i>
ID=3854	WP_041145431	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=3855	WP_041145430	luciferase	<i>Raoultella ornithinolytica</i>
ID=3856	WP_045855292	alkylhydroperoxidase domain protein	<i>Raoultella terrigena</i>
ID=3857	WP_041145428	MFS transporter AraJ	<i>Raoultella ornithinolytica</i>
ID=3858	WP_041145427	polyphosphate kinase 2	<i>Raoultella ornithinolytica</i>
ID=3859	WP_041145426	glyoxalase/bleomycin resistance protein/dioxygenase	<i>Raoultella ornithinolytica</i>
ID=3860	WP_041145425	formate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3861	WP_041145424	formate dehydrogenase subunit beta	<i>Raoultella ornithinolytica</i>
ID=3862	WP_045855286	formate dehydrogenase-N subunit alpha	<i>Raoultella terrigena</i>
ID=3863	WP_041145422	MULTISPECIES: sulfate ABC transporter substrate-binding protein	<i>Raoultella</i>
ID=3864	WP_041145421	aromatic amino acid exporter	<i>Raoultella ornithinolytica</i>
ID=3865	WP_041145420	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=3866	WP_041145419	NADH oxidase	<i>Raoultella ornithinolytica</i>
ID=3867	WP_041145418	benzoate 1,2-dioxygenase small subunit	<i>Raoultella ornithinolytica</i>
ID=3868	WP_041145417	benzene 1,2-dioxygenase	<i>Raoultella ornithinolytica</i>
ID=3869	WP_041145416	catechol 1,2-dioxygenase	<i>Raoultella ornithinolytica</i>
ID=3870	WP_041145415	MULTISPECIES: muconolactone delta-isomerase	<i>Raoultella</i>
ID=3871	WP_041145414	muconate cycloisomerase	<i>Raoultella ornithinolytica</i>
ID=3872	WP_041145413	MULTISPECIES: IclR family transcriptional regulator	<i>Raoultella</i>
ID=3873	WP_041145412	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3874	WP_041147612	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3875	WP_041145411	nitrate/nitrite transporter NarU	<i>Raoultella ornithinolytica</i>
ID=3876	WP_041145410	nitrate reductase subunit alpha	<i>Raoultella ornithinolytica</i>
ID=3877	WP_041145409	nitrate reductase subunit beta	<i>Raoultella ornithinolytica</i>
ID=3878	WP_045855276	nitrate reductase molybdenum cofactor assembly chaperone	<i>Raoultella terrigena</i>
ID=3879	WP_041145407	MULTISPECIES: respiratory nitrate reductase subunit gamma	<i>Raoultella</i>
ID=3880	WP_049009760	helicase IV	<i>Klebsiella variicola</i>
ID=3881	WP_045855274	N-hydroxyarylamine O-acetyltransferase	<i>Raoultella terrigena</i>
ID=3882	WP_045855273	ABC transporter permease	<i>Raoultella terrigena</i>
ID=3883	WP_041145392	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3884	WP_041145391	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3885	WP_041145390	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3886	WP_041145389	MarR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3887	WP_041145388	DNA alkylation repair protein	<i>Raoultella ornithinolytica</i>
ID=3888	WP_041145387	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3889	WP_041145386	sugar hydrolase	<i>Raoultella ornithinolytica</i>
ID=3890	WP_041145385	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3891	WP_041145384	porin	<i>Raoultella ornithinolytica</i>
ID=3892	WP_045855267	hypothetical protein	<i>Raoultella terrigena</i>
ID=3893	WP_063216465	hypothetical protein	<i>Enterobacter cloacae</i>
ID=3894	WP_044209841	hypothetical protein	<i>Pectobacterium carotovorum</i>
ID=3895	WP_064356802	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3896	WP_032675276	MULTISPECIES: hypothetical protein	<i>Enterobacter cloacae</i>
ID=3897	WP_046275244	type IV secretion protein RhS	<i>Citrobacter amalonaticus</i>
ID=3899	WP_045855266	hypothetical protein	<i>Raoultella terrigena</i>
ID=3900	WP_041145381	GntR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3901	WP_041145380	mandelate racemase	<i>Raoultella ornithinolytica</i>
ID=3902	WP_041145379	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=3903	WP_045855263	MFS transporter	<i>Raoultella terrigena</i>
ID=3904	WP_041145378	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3905	WP_041145377	arginine ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=3906	WP_041145376	MULTISPECIES: amino acid ABC transporter permease	<i>Raoultella</i>
ID=3907	WP_045855260	N-acetyltransferase	<i>Raoultella terrigena</i>
ID=3908	WP_041145374	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3909	WP_041145373	monooxygenase	<i>Raoultella ornithinolytica</i>
ID=3910	WP_045855257	hydrolase	<i>Raoultella terrigena</i>

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ID=3911	WP_041145371	alkane 1-monoxygenase	<i>Raoultella ornithinolytica</i>
ID=3912	WP_041145370	adenylate kinase	<i>Raoultella ornithinolytica</i>
ID=3913	WP_045855254	germin	<i>Raoultella terrigena</i>
ID=3914	WP_041145368	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3915	WP_041145367	amino acid permease	<i>Raoultella ornithinolytica</i>
ID=3916	WP_041145366	MULTISPECIES: membrane protein	<i>Raoultella</i>
ID=3917	WP_041145365	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3918	WP_045855484	TonB-dependent receptor	<i>Raoultella terrigena</i>
ID=3919	WP_041145364	pyrimidine-specific ribonucleoside hydrolase RihA	<i>Raoultella ornithinolytica</i>
ID=3920	WP_025759515	hypothetical protein	<i>Enterobacter cloacae</i>
ID=3921	WP_063411562	hypothetical protein	<i>Enterobacter cloacae</i>
ID=3922	WP_063923991	hypothetical protein	<i>Enterobacter cloacae</i>
ID=3923	WP_058770792	type VI secretion protein	<i>Pantoea dispersa</i>
ID=3924	WP_064384984	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=3925	WP_045855241	NADP-dependent oxidoreductase	<i>Raoultella terrigena</i>
ID=3926	WP_041145362	LacI family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3927	WP_041145361	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=3928	WP_041145360	membrane protein	<i>Raoultella ornithinolytica</i>
ID=3929	WP_041145359	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3930	WP_041145358	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3931	WP_045855235	salicylaldehyde dehydrogenase	<i>Raoultella terrigena</i>
ID=3932	WP_045855234	alpha/beta hydrolase	<i>Raoultella terrigena</i>
ID=3933	WP_004850604	MULTISPECIES: DUF2566 domain-containing protein	<i>Enterobacteriales</i>
ID=3934	WP_045855483	hypothetical protein	<i>Raoultella terrigena</i>
ID=3935	WP_041145355	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3936	WP_045855233	1-pyrroline dehydrogenase	<i>Raoultella terrigena</i>
ID=3937	WP_014838385	spermidine/putrescine ABC transporter permease	<i>Klebsiella oxytoca</i>
ID=3938	WP_041145352	spermidine/putrescine ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=3939	WP_041145351	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=3940	WP_041145350	spermidine/putrescine ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3941	WP_041145349	GntR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3942	WP_045855227	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3943	WP_045855226	DUF3313 domain-containing protein	<i>Raoultella terrigena</i>
ID=3944	WP_045855225	paraquat-inducible membrane protein A	<i>Raoultella terrigena</i>
ID=3945	WP_045855224	paraquat-inducible protein A	<i>Raoultella terrigena</i>
ID=3946	WP_045855223	mammalian cell entry protein	<i>Raoultella terrigena</i>
ID=3947	WP_045855222	hypothetical protein	<i>Raoultella terrigena</i>
ID=3948	WP_045855221	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3949	WP_045855220	cytochrome ubiquinol oxidase subunit I	<i>Raoultella terrigena</i>
ID=3950	WP_045855219	ubiquinol oxidase subunit II	<i>Raoultella terrigena</i>
ID=3951	WP_004112746	MULTISPECIES: DUF2474 domain-containing protein	<i>Enterobacteriaceae</i>
ID=3952	WP_045855218	hypothetical protein	<i>Raoultella terrigena</i>
ID=3953	WP_041145345	protease	<i>Raoultella ornithinolytica</i>
ID=3954	WP_045855216	XRE family transcriptional regulator	<i>Raoultella terrigena</i>
ID=3955	WP_045855215	DNA-binding transcriptional regulator AraC	<i>Raoultella terrigena</i>
ID=3956	WP_045855214	MFS transporter	<i>Raoultella terrigena</i>
ID=3957	WP_045855213	beta-galactosidase	<i>Raoultella terrigena</i>
ID=3958	WP_041145343	benzoate transporter	<i>Raoultella ornithinolytica</i>
ID=3959	WP_041145342	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3960	WP_041145341	multidrug DMT transporter permease	<i>Raoultella ornithinolytica</i>
ID=3961	WP_041145340	DUF3313 domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=3962	WP_041145339	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=3963	WP_064386212	integrase	<i>Klebsiella oxytoca</i>
ID=3964	WP_047664942	hypothetical protein	<i>Raoultella planticola</i>
ID=3965	WP_064386216	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=3966	WP_064323901	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=3967	WP_032710320	hypothetical protein	<i>Klebsiella mobilis</i>
ID=3968	WP_041146288	DgsA anti-repressor MtfA	<i>Raoultella ornithinolytica</i>
ID=3969	WP_045859316	membrane protein	<i>Raoultella terrigena</i>
ID=3970	WP_041146287	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3971	WP_041146286	phosphohydrolase	<i>Raoultella ornithinolytica</i>
ID=3972	WP_041147686	DNA cytosine methyltransferase	<i>Raoultella ornithinolytica</i>
ID=3973	WP_041147685	very short patch repair endonuclease	<i>Raoultella ornithinolytica</i>
ID=3974	WP_041146285	drug/metabolite exporter YedA	<i>Raoultella ornithinolytica</i>
ID=3975	WP_041146284	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3976	WP_004852220	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=3977	WP_041146283	diguanylate cyclase	<i>Raoultella ornithinolytica</i>
ID=3978	WP_045859646	hypothetical protein	<i>Raoultella terrigena</i>
ID=3979	WP_041146281	hypothetical protein	<i>Raoultella ornithinolytica</i>

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ID=3980	WP_041146280	helix-turn-helix transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=3981	WP_045859296	lipoprotein	<i>Raoultella terrigena</i>
ID=3982	WP_045859294	alpha-amylase	<i>Raoultella terrigena</i>
ID=3983	WP_041146277	MULTISPECIES: cystine ABC transporter substrate-binding protein	<i>Raoultella</i>
ID=3984	WP_045859292	aminocyclopropane-1-carboxylate deaminase/D-cysteine desulphydrase family protein	<i>Raoultella terrigena</i>
ID=3985	WP_045859290	amino acid ABC transporter permease	<i>Raoultella terrigena</i>
ID=3986	WP_041146274	L-cystine ABC transporter ATP-binding protein YecC	<i>Raoultella ornithinolytica</i>
ID=3987	WP_041146273	transcriptional regulator SdiA	<i>Raoultella ornithinolytica</i>
ID=3988	WP_041146272	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=3989	WP_041146271	MULTISPECIES: DNA-binding response regulator	<i>Raoultella</i>
ID=3990	WP_041146270	excinuclease ABC subunit C	<i>Raoultella ornithinolytica</i>
ID=3991	WP_041146269	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	<i>Raoultella ornithinolytica</i>
ID=3992	WP_045859280	hypothetical protein	<i>Raoultella terrigena</i>
ID=3993	WP_052474565	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=3994	WP_041146268	integral membrane protein	<i>Raoultella ornithinolytica</i>
ID=3995	WP_045859644	hypothetical protein	<i>Raoultella terrigena</i>
ID=3996	WP_045859275	tyrosine transporter TyrP	<i>Raoultella terrigena</i>
ID=3997	WP_045859273	hypothetical protein	<i>Raoultella terrigena</i>
ID=3998	WP_045859271	ferritin	<i>Raoultella terrigena</i>
ID=3999	WP_041146264	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4000	WP_041146263	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4001	WP_041146262	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=4002	WP_052474562	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4003	WP_045859263	ferritin	<i>Raoultella terrigena</i>
ID=4004	WP_041146259	MULTISPECIES: arabinose ABC transporter substrate-binding protein	<i>Raoultella</i>
ID=4005	WP_045859261	L-arabinose transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=4006	WP_045859259	L-arabinose ABC transporter permease AraH	<i>Raoultella terrigena</i>
ID=4007	WP_045859257	trehalose-phosphatase	<i>Raoultella terrigena</i>
ID=4008	WP_041146255	trehalose-6-phosphate synthase	<i>Raoultella ornithinolytica</i>
ID=4009	WP_045859253	universal stress protein UspC	<i>Raoultella terrigena</i>
ID=4010	WP_041146253	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4011	WP_041146252	glycosyl hydrolase family 88	<i>Raoultella ornithinolytica</i>
ID=4012	WP_041146251	arginine--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=4013	WP_041146250	VOC family protein	<i>Raoultella ornithinolytica</i>
ID=4014	WP_041146249	copper homeostasis protein CutC	<i>Raoultella ornithinolytica</i>
ID=4015	WP_041146248	MULTISPECIES: tRNA (mo5U34)-methyltransferase	<i>Raoultella</i>
ID=4016	WP_045859241	tRNA (cmo5U34)-methyltransferase	<i>Raoultella terrigena</i>
ID=4017	WP_041146246	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4018	WP_045859237	hypothetical protein	<i>Raoultella terrigena</i>
ID=4019	WP_041146244	MULTISPECIES: hydrolase	<i>Raoultella</i>
ID=4020	WP_041146243	aspartate--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=4021	WP_041146242	NUDIX pyrophosphatase	<i>Raoultella ornithinolytica</i>
ID=4022	WP_041146241	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4023	WP_041146240	MULTISPECIES: crossover junction endodeoxyribonuclease RuvC	<i>Raoultella</i>
ID=4024	WP_041146239	Holliday junction ATP-dependent DNA helicase RuvA	<i>Raoultella ornithinolytica</i>
ID=4025	WP_041146238	Holliday junction DNA helicase RuvB	<i>Raoultella ornithinolytica</i>
ID=4026	WP_045859226	zinc ABC transporter permease	<i>Raoultella terrigena</i>
ID=4027	WP_041146236	MULTISPECIES: zinc ABC transporter ATP-binding protein ZnuC	<i>Raoultella</i>
ID=4028	WP_045859224	zinc ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=4029	WP_041146234	murein DD-endopeptidase MepM	<i>Raoultella ornithinolytica</i>
ID=4030	WP_041146233	lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase	<i>Raoultella ornithinolytica</i>
ID=4031	WP_041146232	two-component system response regulator DcuR	<i>Raoultella ornithinolytica</i>
ID=4032	WP_041146231	NAD-dependent malic enzyme	<i>Raoultella ornithinolytica</i>
ID=4033	WP_045859216	transporter	<i>Raoultella terrigena</i>
ID=4034	WP_041146229	malate permease	<i>Raoultella ornithinolytica</i>
ID=4035	WP_041146228	pyruvate kinase	<i>Raoultella ornithinolytica</i>
ID=4036	WP_041147682	transcriptional regulator HexR	<i>Raoultella ornithinolytica</i>
ID=4037	WP_041146227	MULTISPECIES: glucose-6-phosphate dehydrogenase	<i>Raoultella</i>
ID=4038	WP_041146226	phosphogluconate dehydratase	<i>Raoultella ornithinolytica</i>
ID=4039	WP_041146225	MULTISPECIES: keto-deoxy-phosphogluconate aldolase	<i>Raoultella</i>
ID=4040	WP_041146224	phosphoribosylglycinamide formyltransferase 2	<i>Raoultella ornithinolytica</i>
ID=4041	WP_041146223	LexA family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4042	WP_045859203	protein YebE	<i>Raoultella terrigena</i>
ID=4043	WP_041146221	oligopeptidase B	<i>Raoultella ornithinolytica</i>
ID=4044	WP_041146220	MULTISPECIES: DNA polymerase III subunit epsilon	<i>Raoultella</i>
ID=4045	WP_041146219	MULTISPECIES: DNA polymerase III subunit theta	<i>Raoultella</i>
ID=4046	WP_041146218	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4047	WP_041146217	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4048	WP_041146216	hypothetical protein	<i>Raoultella ornithinolytica</i>

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ID=4049	WP_049060939	spore coat protein U	<i>Klebsiella mobilis</i>
ID=4050	WP_049082450	fimbrial assembly protein, partial	<i>Klebsiella michiganensis</i>
ID=4051	WP_047066869	fimbrial assembly protein	<i>Klebsiella mobilis</i>
ID=4052	WP_063446401	fimbrial chaperone protein	<i>Klebsiella mobilis</i>
ID=4053	WP_047077758	spore coat protein U	<i>Klebsiella mobilis</i>
ID=4054	WP_047045315	spore coat U domain-containing protein	<i>Klebsiella mobilis</i>
ID=4055	WP_045859193	hypothetical protein	<i>Raoultella terrigena</i>
ID=4056	WP_041146215	virulence factor VirK	<i>Raoultella ornithinolytica</i>
ID=4057	WP_041146214	serine/threonine-protein phosphatase	<i>Raoultella ornithinolytica</i>
ID=4058	WP_041146213	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4059	WP_041146212	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4060	WP_045859183	16S rRNA (cytosine(1407)-C(5))-methyltransferase RsmF	<i>Raoultella terrigena</i>
ID=4061	WP_041146210	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4062	WP_045859179	paraquat-inducible membrane protein A	<i>Raoultella terrigena</i>
ID=4063	WP_041146208	methionine-R-sulfoxide reductase	<i>Raoultella ornithinolytica</i>
ID=4064	WP_041146207	RNA chaperone ProQ	<i>Raoultella ornithinolytica</i>
ID=4065	WP_041146206	tail-specific protease	<i>Raoultella ornithinolytica</i>
ID=4066	WP_041146205	MULTISPECIES: zinc metalloprotease HtpX	<i>Raoultella</i>
ID=4067	WP_041146204	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4068	WP_041146203	DNA-binding transcriptional regulator KdgR	<i>Raoultella ornithinolytica</i>
ID=4069	WP_041146202	MULTISPECIES: membrane protein	<i>Raoultella</i>
ID=4070	WP_041146201	MULTISPECIES: PhoP regulon feedback inhibition membrane protein MgrB	<i>Raoultella</i>
ID=4071	WP_045859168	hypothetical protein	<i>Raoultella terrigena</i>
ID=4072	WP_001062678	MULTISPECIES: cold-shock protein CspC	<i>Proteobacteria</i>
ID=4073	WP_041146199	peptidoglycan synthase	<i>Raoultella ornithinolytica</i>
ID=4074	WP_041146198	23S rRNA (guanine(745)-N(1))-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=4075	WP_041146197	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4076	WP_041146196	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4077	WP_041146195	MULTISPECIES: PTS mannose transporter subunit IID	<i>Raoultella</i>
ID=4078	WP_041146194	PTS mannose/fructose/sorbose transporter subunit IIC	<i>Raoultella ornithinolytica</i>
ID=4079	WP_041146193	PTS mannose transporter subunit EIIB	<i>Raoultella ornithinolytica</i>
ID=4080	WP_045859153	hypothetical protein	<i>Raoultella terrigena</i>
ID=4081	WP_041146191	c-di-GMP phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=4082	WP_041147681	L-serine ammonia-lyase	<i>Raoultella ornithinolytica</i>
ID=4083	WP_045859150	coenzyme A pyrophosphatase	<i>Raoultella terrigena</i>
ID=4084	WP_041146189	aminodeoxychorismate synthase subunit I	<i>Raoultella ornithinolytica</i>
ID=4085	WP_045859145	hypothetical protein	<i>Raoultella terrigena</i>
ID=4086	WP_041146187	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4087	WP_045859142	ATP-dependent helicase	<i>Raoultella terrigena</i>
ID=4088	WP_041146185	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase..	<i>Raoultella ornithinolytica</i>
		..complex dimerization subunit type 1 TsaB	
ID=4089	WP_041146184	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4090	WP_041146183	long-chain-fatty-acid--CoA ligase	<i>Raoultella ornithinolytica</i>
ID=4091	WP_045859133	ribonuclease D	<i>Raoultella terrigena</i>
ID=4092	WP_041146181	MULTISPECIES: cell division topological specificity factor MinE	<i>Raoultella</i>
ID=4093	WP_041146180	MULTISPECIES: septum site-determining protein MinD	<i>Raoultella</i>
ID=4094	WP_045859131	septum formation inhibitor	<i>Raoultella terrigena</i>
ID=4095	WP_041146178	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4096	WP_041146177	isomerase/hydrolase	<i>Raoultella ornithinolytica</i>
ID=4097	WP_041146176	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=4098	WP_041146175	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4099	WP_041146174	MULTISPECIES: disulfide bond formation protein B	<i>Raoultella</i>
ID=4100	WP_041146173	Na ⁺ /H ⁺ antiporter NhaB	<i>Raoultella ornithinolytica</i>
ID=4101	WP_041146172	fatty acid metabolism regulator	<i>Raoultella ornithinolytica</i>
ID=4102	WP_041146171	MULTISPECIES: SpoVR family protein	<i>Raoultella</i>
ID=4103	WP_045859119	D-amino acid dehydrogenase small subunit	<i>Raoultella terrigena</i>
ID=4104	WP_041146169	alanine racemase	<i>Raoultella ornithinolytica</i>
ID=4105	WP_041146168	K ⁺ /H ⁺ antiporter	<i>Raoultella ornithinolytica</i>
ID=4106	WP_041146167	muramoyltetrapeptide carboxypeptidase	<i>Raoultella ornithinolytica</i>
ID=4107	WP_041146166	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=4108	WP_041146165	ferrioxamine B receptor	<i>Raoultella ornithinolytica</i>
ID=4110	WP_041146164	alpha, alpha-trehalase	<i>Raoultella ornithinolytica</i>
ID=4111	WP_041146163	hydrolase	<i>Raoultella ornithinolytica</i>
ID=4112	WP_041146162	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4113	WP_041146161	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4114	WP_041146160	transglutaminase	<i>Raoultella ornithinolytica</i>
ID=4115	WP_041146159	peptidase	<i>Raoultella ornithinolytica</i>
ID=4116	WP_045859089	AraC family transcriptional regulator	<i>Raoultella terrigena</i>
ID=4117	WP_041146157	MFS transporter	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=4118	WP_041146156	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=4119	WP_041146155	ribokinase	<i>Raoultella ornithinolytica</i>
ID=4120	WP_041146154	sugar ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=4121	WP_041146153	ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=4122	WP_045859074	ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=4123	WP_041146151	ROK family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4124	WP_041146150	riboflavin synthase subunit beta	<i>Raoultella ornithinolytica</i>
ID=4125	WP_041146149	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4126	WP_041146148	fatty acid desaturase	<i>Raoultella ornithinolytica</i>
ID=4127	WP_041146147	phosphate ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4128	WP_041146146	monooxygenase	<i>Raoultella ornithinolytica</i>
ID=4129	WP_041146145	quaternary ammonium transporter	<i>Raoultella ornithinolytica</i>
ID=4130	WP_041146144	ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=4131	WP_041146143	quaternary ammonium transporter	<i>Raoultella ornithinolytica</i>
ID=4132	WP_041146142	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=4133	WP_041146141	branched-chain amino acid ABC transporter	<i>Raoultella ornithinolytica</i>
ID=4134	WP_045859037	branched-chain amino acid permease	<i>Raoultella terrigena</i>
ID=4135	WP_041147680	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4136	WP_052698752	cupin	<i>Raoultella terrigena</i>
ID=4137	WP_002904802	MULTISPECIES: fimbrial protein	<i>Klebsiella</i>
ID=4138	WP_032423497	fimbrial protein	<i>Klebsiella pneumoniae</i>
ID=4139	WP_070611643	fimbrial protein	<i>Klebsiella</i> sp.
ID=4140	WP_016161011	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=4141	WP_041146138	RNA pseudouridine synthase	<i>Raoultella ornithinolytica</i>
ID=4142	WP_041146137	MULTISPECIES: cell density-dependent motility repressor	<i>Raoultella</i>
ID=4143	WP_041146136	phosphoenolpyruvate carboxykinase (ATP)	<i>Raoultella ornithinolytica</i>
ID=4144	WP_041146135	type VI secretion protein	<i>Raoultella ornithinolytica</i>
ID=4145	WP_041146134	type VI secretion protein EvpB	<i>Raoultella ornithinolytica</i>
ID=4146	WP_045859025	type VI secretion protein	<i>Raoultella terrigena</i>
ID=4147	WP_045859022	membrane protein	<i>Raoultella terrigena</i>
ID=4148	WP_045859020	membrane protein	<i>Raoultella terrigena</i>
ID=4149	WP_041146130	MULTISPECIES: Hcp family T6SS protein CtsH1	<i>Raoultella</i>
ID=4150	WP_045859018	ClpV1 family T6SS ATPase	<i>Raoultella terrigena</i>
ID=4151	WP_045859017	type IV secretion protein Rhc	<i>Raoultella terrigena</i>
ID=4152	WP_045859014	hypothetical protein	<i>Raoultella terrigena</i>
ID=4153	WP_052119560	hypothetical protein	<i>Enterobacter</i> sp.
ID=4154	WP_048029643	MULTISPECIES: hypothetical protein	<i>Leclercia</i>
ID=4155	WP_063617133	hypothetical protein	<i>Enterobacter cloacae</i>
ID=4156	WP_029571284	acetyltransferase	<i>Pantoea ananatis</i>
ID=4157	WP_039495218	hypothetical protein	<i>Pectobacterium carotovorum</i>
ID=4158	WP_029742079	hypothetical protein, partial	<i>Enterobacter asburiae</i>
ID=4159	WP_063617132	hypothetical protein	<i>Enterobacter cloacae</i>
ID=4160	WP_064356805	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=4161	WP_048994606	hypothetical protein, partial	<i>Enterobacter cloacae</i>
ID=4162	WP_045859009	hypothetical protein	<i>Raoultella terrigena</i>
ID=4163	WP_063957693	hypothetical protein	<i>Enterobacter cloacae</i>
ID=4164	WP_039495150	hypothetical protein	<i>Pectobacterium carotovorum</i>
ID=4165	WP_045859622	type VI secretion protein VasK	<i>Raoultella terrigena</i>
ID=4166	WP_045859005	type VI secretion-associated protein	<i>Raoultella terrigena</i>
ID=4167	WP_045859002	type VI secretion protein ImpG	<i>Raoultella terrigena</i>
ID=4168	WP_045859000	type VI secretion protein	<i>Raoultella terrigena</i>
ID=4169	WP_045858998	type VI secretion protein	<i>Raoultella terrigena</i>
ID=4170	WP_045858996	type VI secretion system lysozyme-like protein	<i>Raoultella terrigena</i>
ID=4171	WP_045858994	hypothetical protein	<i>Raoultella terrigena</i>
ID=4172	WP_064323901	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4173	WP_060619942	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4174	WP_047664942	hypothetical protein	<i>Raoultella planticola</i>
ID=4175	WP_019704145	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4176	WP_041145739	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4177	WP_050592516	MFS transporter	<i>Citrobacter freundii</i>
ID=4178	WP_041145736	D-mannonate oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=4179	WP_045858368	universal stress protein UspG	<i>Raoultella terrigena</i>
ID=4180	WP_041145734	MULTISPECIES: GntR family transcriptional regulator	<i>Raoultella</i>
ID=4181	WP_045858366	NAD(P)-dependent oxidoreductase	<i>Raoultella terrigena</i>
ID=4182	WP_041145732	dipeptidyl carboxypeptidase II	<i>Raoultella ornithinolytica</i>
ID=4183	WP_045330309	MULTISPECIES: hypothetical protein	<i>Enterobacter cloacae</i>
ID=4184	WP_058675488	hypothetical protein	<i>Klebsiella mobilis</i>
ID=4185	WP_063865146	class A beta-lactamase TER-2	<i>Raoultella terrigena</i>
ID=4186	WP_041145728	hypothetical protein	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=4187	WP_041145727	DNA recombination protein RecF	<i>Raoultella ornithinolytica</i>
ID=4188	WP_041145726	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4189	WP_041145725	beta-D-galactosidase	<i>Raoultella ornithinolytica</i>
ID=4190	WP_041145724	LacI family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4191	WP_052474531	VirG	<i>Raoultella ornithinolytica</i>
ID=4192	WP_041145723	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4193	WP_041145722	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=4194	WP_045858326	type I methionyl aminopeptidase	<i>Raoultella terrigena</i>
ID=4195	WP_045858324	transcriptional regulator	<i>Raoultella terrigena</i>
ID=4196	WP_041145719	glutathione S-transferase	<i>Raoultella ornithinolytica</i>
ID=4197	WP_041145718	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4198	WP_038502269	hypothetical protein	<i>Hafnia paralveia alvei</i>
ID=4199	WP_041145717	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4200	WP_052474529	acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=4201	WP_045858314	diguanylate phosphodiesterase	<i>Raoultella terrigena</i>
ID=4202	WP_045858312	S-transferase	<i>Raoultella terrigena</i>
ID=4203	WP_041145715	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=4204	WP_045858308	GntR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=4205	WP_045442613	streptomycin kinase	<i>Citrobacter</i> sp.
ID=4206	WP_041145707	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4207	WP_041145706	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4208	WP_041145705	YciE/YciF family protein	<i>Raoultella ornithinolytica</i>
ID=4209	WP_041145704	periplasmic protein	<i>Raoultella ornithinolytica</i>
ID=4210	WP_041909709	2'-hydroxyisoflavone reductase	<i>Enterobacter</i> sp.
ID=4211	WP_024561298	LysR family transcriptional regulator	<i>Franconibacter pulveris</i>
ID=4212	WP_007373408	phosphohydrolase	<i>Kosakonia radicincitans</i>
ID=4213	WP_007373407	AraC family transcriptional regulator	<i>Kosakonia radicincitans</i>
ID=4214	WP_041145703	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4215	WP_045858296	acetyltransferase	<i>Raoultella terrigena</i>
ID=4216	WP_041145701	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4217	WP_045858292	DeoR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=4218	WP_045858290	Xaa-Pro aminopeptidase	<i>Raoultella terrigena</i>
ID=4219	WP_012968013	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=4220	WP_049162570	membrane protein	<i>Klebsiella variicola</i>
ID=4221	WP_049591242	MFS transporter	<i>Klebsiella oxytoca</i>
ID=4222	WP_004110842	MULTISPECIES: oxidoreductase	<i>Klebsiella</i>
ID=4223	WP_023340281	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=4224	WP_047050208	TetR family transcriptional regulator	<i>Klebsiella mobilis</i>
ID=4225	WP_012968007	LysR family transcriptional regulator	<i>Klebsiella variicola</i>
ID=4226	WP_041145691	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4227	WP_062778463	hypothetical protein	<i>Kluyvera intermedia</i>
ID=4228	WP_045858285	LacI family transcriptional regulator	<i>Raoultella terrigena</i>
ID=4229	WP_045858283	inositol monophosphatase	<i>Raoultella terrigena</i>
ID=4230	WP_045858281	ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=4231	WP_045858279	MULTISPECIES: ABC transporter ATP-binding protein	<i>Enterobacteriaceae</i>
ID=4232	WP_048335675	ABC transporter permease	<i>Klebsiella pneumoniae</i>
ID=4233	WP_065954220	acid phosphatase	<i>Klebsiella pneumoniae</i>
ID=4234	WP_045858275	membrane protein	<i>Raoultella terrigena</i>
ID=4235	WP_045858270	type I glyceraldehyde-3-phosphate dehydrogenase	<i>Raoultella terrigena</i>
ID=4236	WP_041145677	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4237	WP_045858268	chorismate mutase	<i>Raoultella terrigena</i>
ID=4238	WP_045858267	glutathione peroxidase	<i>Raoultella terrigena</i>
ID=4239	WP_041145665	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4240	WP_041145664	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4241	WP_045858263	cytochrome b	<i>Raoultella terrigena</i>
ID=4242	WP_041145653	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=4243	WP_041145651	MULTISPECIES: DUF4177 domain-containing protein	<i>Raoultella</i>
ID=4244	WP_045858260	transcriptional regulator FtrA	<i>Raoultella terrigena</i>
ID=4245	WP_041145649	rhodanese	<i>Raoultella ornithinolytica</i>
ID=4246	WP_041145648	5-methyltetrahydropteroylglutamate--homocysteine S-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=4247	WP_041145647	urea ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4248	WP_041145646	branched-chain amino acid ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=4249	WP_045858252	urea ABC transporter permease subunit UrtC	<i>Raoultella terrigena</i>
ID=4250	WP_045858251	ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=4251	WP_041145643	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=4252	WP_041145642	DNA-binding protein	<i>Raoultella ornithinolytica</i>
ID=4253	WP_041145641	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4254	WP_064357026	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4255	WP_041145640	O-acetylserine/cysteine exporter	<i>Raoultella ornithinolytica</i>

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ID=4256	WP_045858245	multiple antibiotic resistance regulatory periplasmic protein MarB	<i>Raoultella terrigena</i>
ID=4257	WP_004862191	MULTISPECIES: MDR efflux pump AcrAB transcriptional activator MarA	<i>Enterobacteriaceae</i>
ID=4258	WP_041145638	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=4259	WP_041145637	stress protection protein MarC	<i>Raoultella ornithinolytica</i>
ID=4260	WP_041145636	sugar transporter	<i>Raoultella ornithinolytica</i>
ID=4261	WP_041145635	isomerase	<i>Raoultella ornithinolytica</i>
ID=4262	WP_041145634	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=4263	WP_045858233	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=4264	WP_041145632	succinate-semialdehyde dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=4265	WP_045858230	glutaminase	<i>Raoultella terrigena</i>
ID=4266	WP_041145630	DUF4186 domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=4267	WP_041145629	GGDEF domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=4268	WP_041145628	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=4269	WP_041145627	altronate oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=4270	WP_045858219	hypothetical protein	<i>Raoultella terrigena</i>
ID=4271	WP_041147639	lipoprotein signal peptide	<i>Raoultella ornithinolytica</i>
ID=4272	WP_041145626	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4273	WP_041147638	LacI family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4274	WP_041145625	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=4275	WP_041145624	decarboxylase	<i>Raoultella ornithinolytica</i>
ID=4276	WP_041145623	MULTISPECIES: carboxymuconolactone decarboxylase	<i>Raoultella</i>
ID=4277	WP_041145622	trans-aconitate 2-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=4278	WP_041145621	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=4279	WP_041145620	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4280	WP_045858206	lysine transporter LysE	<i>Raoultella terrigena</i>
ID=4281	WP_041145618	glyoxalase	<i>Raoultella ornithinolytica</i>
ID=4282	WP_041145617	sugar transporter	<i>Raoultella ornithinolytica</i>
ID=4283	WP_041145616	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4284	WP_041145615	2-nitropropane dioxygenase	<i>Raoultella ornithinolytica</i>
ID=4285	WP_041147637	metal ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=4286	WP_053094803	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=4287	WP_041145614	metal ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4288	WP_041145613	2-oxobutyrate oxidase	<i>Raoultella ornithinolytica</i>
ID=4289	WP_045858189	hypothetical protein	<i>Raoultella terrigena</i>
ID=4290	WP_045858188	hypothetical protein	<i>Raoultella terrigena</i>
ID=4291	WP_052698746	hypothetical protein	<i>Raoultella terrigena</i>
ID=4292	WP_041145611	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4293	WP_041145610	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4294	WP_045858182	MerR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=4295	WP_041145608	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4296	WP_041145607	dihydrodipicolinate synthase family protein	<i>Raoultella ornithinolytica</i>
ID=4297	WP_041145606	EamA family transporter	<i>Raoultella ornithinolytica</i>
ID=4298	WP_041145605	GntR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4299	WP_041145604	deaminase/reductase	<i>Raoultella ornithinolytica</i>
ID=4300	WP_041145603	iron-molybdenum cofactor biosynthesis protein NifQ	<i>Raoultella ornithinolytica</i>
ID=4301	WP_041145602	nitrogenase cofactor biosynthesis protein NifB	<i>Raoultella ornithinolytica</i>
ID=4302	WP_041145601	nif-specific transcriptional activator NifA	<i>Raoultella ornithinolytica</i>
ID=4303	WP_041145600	nitrogen fixation negative regulator NifL	<i>Raoultella ornithinolytica</i>
ID=4304	WP_041145599	flavodoxin	<i>Raoultella ornithinolytica</i>
ID=4305	WP_041145598	nitrogen fixation protein NifM	<i>Raoultella ornithinolytica</i>
ID=4306	WP_041145597	MULTISPECIES: protein NifZ	<i>Raoultella</i>
ID=4307	WP_041145596	nitrogen fixation protein NifW	<i>Raoultella ornithinolytica</i>
ID=4308	WP_041145595	homocitrate synthase	<i>Raoultella ornithinolytica</i>
ID=4309	WP_045858151	cysteine desulfurase NifS	<i>Raoultella terrigena</i>
ID=4310	WP_045858149	iron-sulfur cluster assembly scaffold protein NifU	<i>Raoultella terrigena</i>
ID=4312	WP_045858147	nitrogen fixation protein NifX	<i>Raoultella terrigena</i>
ID=4313	WP_041145591	nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	<i>Raoultella ornithinolytica</i>
ID=4314	WP_041145590	nitrogenase iron-molybdenum cofactor biosynthesis protein NifE	<i>Raoultella ornithinolytica</i>
ID=4315	WP_041145589	protein NifY	<i>Raoultella ornithinolytica</i>
ID=4316	WP_041145588	protein NifT	<i>Raoultella ornithinolytica</i>
ID=4317	WP_041145587	nitrogenase molybdenum-iron protein subunit beta	<i>Raoultella ornithinolytica</i>
ID=4318	WP_041145586	nitrogenase molybdenum-iron protein alpha chain	<i>Raoultella ornithinolytica</i>
ID=4319	WP_041145585	nitrogenase iron protein	<i>Raoultella ornithinolytica</i>
ID=4320	WP_041145584	pyruvate:ferredoxin (flavodoxin) oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=4321	WP_041145583	riboflavin synthase subunit alpha	<i>Raoultella ornithinolytica</i>
ID=4322	WP_041145582	NAD(P)H-quinone oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=4323	WP_041145581	MULTISPECIES: ABC transporter ATP-binding protein	<i>Raoultella</i>
ID=4324	WP_045858116	amino acid ABC transporter permease	<i>Raoultella terrigena</i>
ID=4325	WP_041145579	amino acid ABC transporter permease	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=4326	WP_045858111	amino acid ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=4327	WP_045858109	thiamine biosynthesis protein ThiJ	<i>Raoultella terrigena</i>
ID=4328	WP_032611697	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=4329	WP_041145576	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=4330	WP_045858108	amino acid ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=4331	WP_045858106	amino acid ABC transporter permease	<i>Raoultella terrigena</i>
ID=4332	WP_045858104	amino acid ABC transporter permease	<i>Raoultella terrigena</i>
ID=4333	WP_041145572	amino acid ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4334	WP_041145571	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4335	WP_041145570	glyoxalase-like domain protein	<i>Raoultella ornithinolytica</i>
ID=4336	WP_041145569	pyrroline-5-carboxylate reductase	<i>Raoultella ornithinolytica</i>
ID=4337	WP_045858093	alpha/beta hydrolase	<i>Raoultella terrigena</i>
ID=4338	WP_052474618	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4339	WP_045858091	hypothetical protein	<i>Raoultella terrigena</i>
ID=4340	WP_064371620	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=4341	WP_061800769	hypothetical protein	<i>Serratia ficaria</i>
ID=4342	WP_064171701	pyocin	<i>Klebsiella pneumoniae</i>
ID=4343	WP_049295977	hypothetical protein	<i>Serratia marcescens</i>
ID=4344	WP_015705899	klebicin D activity protein	<i>Klebsiella mobilis</i>
ID=4345	WP_049593937	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=4346	WP_057394178	hypothetical protein	<i>Salmonella enterica</i>
ID=4347	WP_064177723	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4348	WP_064794664	6-phospho-beta-glucosidase	<i>Klebsiella quasipneumoniae</i>
ID=4349	WP_049004055	MULTISPECIES: 6-phospho-beta-glucosidase	<i>Klebsiella</i>
ID=4350	WP_040241336	6-phospho-beta-glucosidase	<i>Klebsiella pneumoniae</i>
ID=4351	WP_065696977	PTS beta-glucoside transporter subunit EIIBCA	<i>Klebsiella pneumoniae</i>
ID=4352	WP_049004057	hypothetical protein	<i>Klebsiella quasipneumoniae</i>
ID=4353	WP_064352064	transposase	<i>Klebsiella oxytoca</i>
ID=4354	WP_064155836	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4356	WP_008373006	hypothetical protein	<i>Pseudomonas</i> sp.
ID=4357	WP_023158405	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4358	WP_010259423	2,5-diketo-D-gluconic acid reductase	<i>Alistipes timonensis</i>
ID=4359	WP_052752447	AraC family transcriptional regulator	<i>Tatumella morbirosei</i>
ID=4360	WP_052752446	MFS transporter	<i>Tatumella morbirosei</i>
ID=4361	WP_040510403	short-chain dehydrogenase	<i>Komagataeibacter hansenii</i>
ID=4362	WP_064802155	MULTISPECIES: LysR family transcriptional regulator	<i>Rhizobium</i>
ID=4363	WP_041145975	c-type cytochrome biogenesis protein CcmI	<i>Raoultella ornithinolytica</i>
ID=4364	WP_041145976	cytochrome c-type biogenesis protein CcmH	<i>Raoultella ornithinolytica</i>
ID=4365	WP_041145977	thiol:disulfide interchange protein DsbE	<i>Raoultella ornithinolytica</i>
ID=4366	WP_041145978	c-type cytochrome biogenesis protein CcmF	<i>Raoultella ornithinolytica</i>
ID=4367	WP_041145979	cytochrome c biogenesis protein CcmE	<i>Raoultella ornithinolytica</i>
ID=4369	WP_041145981	heme ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=4370	WP_045858734	heme exporter protein CcmB	<i>Raoultella terrigena</i>
ID=4371	WP_041145983	heme ABC exporter ATP-binding protein CcmA	<i>Raoultella ornithinolytica</i>
ID=4372	WP_041147667	alcohol dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=4373	WP_041145984	GMC family oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=4374	WP_041145985	gluconate 2-dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=4375	WP_045858742	lipase	<i>Raoultella terrigena</i>
ID=4376	WP_041145987	MULTISPECIES: spermidine/putrescine ABC transporter permease	<i>Raoultella</i>
ID=4377	WP_041145988	iron ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4378	WP_045858748	phytanoyl-CoA dioxygenase	<i>Raoultella terrigena</i>
ID=4379	WP_041145990	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4380	WP_041145991	amino acid ABC transporter ATPase	<i>Raoultella ornithinolytica</i>
ID=4381	WP_041145992	restriction endonuclease subunit S	<i>Raoultella ornithinolytica</i>
ID=4382	WP_045858758	flagellar motor switch protein FliY	<i>Raoultella terrigena</i>
ID=4383	WP_041145994	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4384	WP_045858760	thioredoxin	<i>Raoultella terrigena</i>
ID=4385	WP_045858762	ABC transporter ATP-binding protein	<i>Raoultella terrigena</i>
ID=4386	WP_045858764	ABC transporter permease	<i>Raoultella terrigena</i>
ID=4387	WP_045858766	ABC transporter permease	<i>Raoultella terrigena</i>
ID=4388	WP_045858768	membrane protein	<i>Raoultella terrigena</i>
ID=4389	WP_045858770	iron transporter	<i>Raoultella terrigena</i>
ID=4390	WP_045858772	iron permease	<i>Raoultella terrigena</i>
ID=4391	WP_045858773	NADH:ubiquinone reductase (Na(+)-transporting) subunit C	<i>Raoultella terrigena</i>
ID=4392	WP_045858775	hypothetical protein	<i>Raoultella terrigena</i>
ID=4394	WP_045858777	malate/lactate/ureidoglycolate dehydrogenase	<i>Raoultella terrigena</i>
ID=4395	WP_045858777	malate/lactate/ureidoglycolate dehydrogenase	<i>Raoultella terrigena</i>
ID=4396	WP_041145998	formate dehydrogenase subunit alpha	<i>Raoultella ornithinolytica</i>
ID=4397	WP_045858781	peptidase M20	<i>Raoultella terrigena</i>

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ID=4398	WP_041147668	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4399	WP_041147669	amino acid ABC transporter ATPase	<i>Raoultella ornithinolytica</i>
ID=4400	WP_041146000	MULTISPECIES: amino acid ABC transporter permease	<i>Raoultella</i>
ID=4401	WP_041146001	basic amino acid ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4402	WP_041146002	RpiR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4403	WP_045858787	protein translocase component YidC	<i>Raoultella terrigena</i>
ID=4404	WP_045858789	iron ABC transporter	<i>Raoultella terrigena</i>
ID=4405	WP_045858790	heme ABC transporter	<i>Raoultella terrigena</i>
ID=4406	WP_041146006	ABC transporter	<i>Raoultella ornithinolytica</i>
ID=4407	WP_041146007	TonB-dependent receptor	<i>Raoultella ornithinolytica</i>
ID=4408	WP_041146008	ABC transporter	<i>Raoultella ornithinolytica</i>
ID=4409	WP_041146009	sulfonate ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=4410	WP_041146010	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4411	WP_041146011	sulfonate ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4412	WP_052474622	acyl-CoA dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=4413	WP_041146013	alkanesulfonate monooxygenase	<i>Raoultella ornithinolytica</i>
ID=4414	WP_041146014	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4415	WP_041146015	cysteine dioxygenase	<i>Raoultella ornithinolytica</i>
ID=4416	WP_041146016	sulfurtransferase	<i>Raoultella ornithinolytica</i>
ID=4417	WP_041146017	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4418	WP_045858814	hypothetical protein	<i>Raoultella terrigena</i>
ID=4419	WP_045858816	ABC transporter permease	<i>Raoultella terrigena</i>
ID=4420	WP_045858819	ABC transporter	<i>Raoultella terrigena</i>
ID=4421	WP_041146018	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4422	WP_041146019	shikimate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=4423	WP_045858825	MFS transporter	<i>Raoultella terrigena</i>
ID=4424	WP_041146021	4-hydroxyphenylpyruvate dioxygenase	<i>Raoultella ornithinolytica</i>
ID=4425	WP_041146022	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4426	WP_041146023	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=4427	WP_045858833	pyruvate kinase	<i>Raoultella terrigena</i>
ID=4428	WP_001082307	MULTISPECIES: hypothetical protein	<i>Proteobacteria</i>
ID=4429	WP_041146025	murein transpeptidase	<i>Raoultella ornithinolytica</i>
ID=4430	WP_041146026	MULTISPECIES: cysteine desulfuration protein SufE	<i>Raoultella</i>
ID=4431	WP_041146027	bifunctional cysteine desulfurase/selenocysteine lyase	<i>Raoultella ornithinolytica</i>
ID=4432	WP_045858843	Fe-S cluster assembly protein SufD	<i>Raoultella terrigena</i>
ID=4433	WP_041146029	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=4434	WP_045858848	Fe-S cluster assembly protein SufB	<i>Raoultella terrigena</i>
ID=4435	WP_041146031	Fe-S cluster assembly scaffold SufA	<i>Raoultella ornithinolytica</i>
ID=4437	WP_041146032	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4438	WP_054180807	hypothetical protein	<i>Trabulsiella odontotermis</i>
ID=4439	WP_041146034	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4440	WP_041146035	MULTISPECIES: thioesterase	<i>Raoultella</i>
ID=4441	WP_041146036	FAD-binding oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=4442	WP_045858859	hypothetical protein	<i>Raoultella terrigena</i>
ID=4443	WP_052474623	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4444	WP_041146039	Hcp family T6SS protein CtsH1	<i>Raoultella ornithinolytica</i>
ID=4445	WP_041146040	phosphoenolpyruvate synthase	<i>Raoultella ornithinolytica</i>
ID=4446	WP_041147670	phosphoenolpyruvate synthase regulatory protein	<i>Raoultella ornithinolytica</i>
ID=4447	WP_045858869	3-deoxy-7-phosphoheptulonate synthase	<i>Raoultella terrigena</i>
ID=4448	WP_041146042	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4449	WP_041146043	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4450	WP_041146044	MULTISPECIES: endopeptidase	<i>Raoultella</i>
ID=4451	WP_041146045	vitamin B12 ABC transporter ATP-binding protein BtuD	<i>Raoultella ornithinolytica</i>
ID=4452	WP_045858875	glutathione peroxidase	<i>Raoultella terrigena</i>
ID=4453	WP_045858877	methionine ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=4454	WP_041146048	vitamin B12 ABC transporter permease BtuC	<i>Raoultella ornithinolytica</i>
ID=4455	WP_045858881	hypothetical protein	<i>Raoultella terrigena</i>
ID=4456	WP_041146050	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4457	WP_041146051	amino acid dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=4458	WP_041146052	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4459	WP_004102960	MULTISPECIES: integration host factor subunit alpha	<i>Enterobacteriaceae</i>
ID=4460	WP_041146053	phenylalanine--tRNA ligase subunit beta	<i>Raoultella ornithinolytica</i>
ID=4461	WP_045858896	phenylalanine--tRNA ligase subunit alpha	<i>Raoultella terrigena</i>
ID=4462	WP_032717759	50S ribosomal protein L20	<i>Raoultella ornithinolytica</i>
ID=4463	WP_016941461	50S ribosomal protein L35	<i>Dickeya zeae</i>
ID=4464	WP_004863359	MULTISPECIES: translation initiation factor IF-3, partial	<i>Enterobacteriaceae</i>
ID=4465	WP_045858903	threonine--tRNA ligase	<i>Raoultella terrigena</i>
ID=4466	WP_045858903	threonine--tRNA ligase	<i>Raoultella terrigena</i>
ID=4467	WP_041146056	MULTISPECIES: hypothetical protein	<i>Raoultella</i>

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ID=4468	WP_041146057	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4469	WP_041146058	6-phosphofructokinase II	<i>Raoultella ornithinolytica</i>
ID=4470	WP_041146059	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4471	WP_041146060	fructosamine kinase family protein	<i>Raoultella ornithinolytica</i>
ID=4472	WP_041146061	TonB system transport protein TonB	<i>Raoultella ornithinolytica</i>
ID=4473	WP_041146062	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4474	WP_041146063	cardiolipin synthase A	<i>Raoultella ornithinolytica</i>
ID=4475	WP_041146064	MULTISPECIES: dsDNA-mimic protein	<i>Raoultella</i>
ID=4476	WP_041146065	transporter	<i>Raoultella ornithinolytica</i>
ID=4477	WP_041146066	oligopeptide ABC transporter ATP-binding protein OppF	<i>Raoultella ornithinolytica</i>
ID=4478	WP_041146067	oligopeptide ABC transporter ATP-binding protein OppD	<i>Raoultella ornithinolytica</i>
ID=4479	WP_045858923	peptide ABC transporter permease	<i>Raoultella terrigena</i>
ID=4480	WP_041146069	MULTISPECIES: oligopeptide transporter permease	<i>Raoultella</i>
ID=4481	WP_045858925	oligopeptide ABC transporter substrate-binding protein OppA	<i>Raoultella terrigena</i>
ID=4482	WP_041146071	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4483	WP_041146072	bifunctional acetaldehyde-CoA/alcohol dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=4484	WP_041147671	thymidine kinase	<i>Raoultella ornithinolytica</i>
ID=4485	WP_041146073	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=4486	WP_045858929	UTP--glucose-1-phosphate uridylyltransferase	<i>Raoultella terrigena</i>
ID=4487	WP_041146075	response regulator	<i>Raoultella ornithinolytica</i>
ID=4488	WP_041146076	patatin family protein	<i>Raoultella ornithinolytica</i>
ID=4489	WP_041146077	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4490	WP_041146078	MULTISPECIES: formyltetrahydrofolate deformylase	<i>Raoultella</i>
ID=4491	WP_041146079	AsnC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4492	WP_041146080	multidrug DMT transporter permease	<i>Raoultella ornithinolytica</i>
ID=4493	WP_041146081	MULTISPECIES: respiratory nitrate reductase subunit gamma	<i>Raoultella</i>
ID=4494	WP_045858942	nitrate reductase molybdenum cofactor assembly chaperone	<i>Raoultella terrigena</i>
ID=4495	WP_041146083	nitrate reductase subunit beta	<i>Raoultella ornithinolytica</i>
ID=4496	WP_041146084	nitrate reductase subunit alpha	<i>Raoultella ornithinolytica</i>
ID=4497	WP_041146085	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4498	WP_041146086	nitrate/nitrite two-component system sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=4499	WP_020803248	DNA-binding response regulator	<i>Klebsiella pneumoniae</i>
ID=4500	WP_041146088	YchO family inverse autotransporter domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=4501	WP_041146089	nitrate reductase	<i>Raoultella ornithinolytica</i>
ID=4502	WP_015705091	nitrite reductase	<i>Klebsiella mobilis</i>
ID=4503	WP_041146090	nitrate ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=4504	WP_041146091	MULTISPECIES: nitrate ABC transporter, permease protein	<i>Raoultella</i>
ID=4505	WP_041147673	nitrate ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4506	WP_041146092	nitrate regulatory protein	<i>Raoultella ornithinolytica</i>
ID=4507	WP_041146093	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4508	WP_004103142	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=4509	WP_045858964	transporter	<i>Raoultella terrigena</i>
ID=4510	WP_041146096	MULTISPECIES: cation transport regulator	<i>Raoultella</i>
ID=4511	WP_045858966	sodium-potassium/proton antiporter ChaA	<i>Raoultella terrigena</i>
ID=4512	WP_041146098	3-deoxy-8-phosphooctulonate synthase	<i>Raoultella ornithinolytica</i>
ID=4513	WP_045858970	hypothetical protein	<i>Raoultella terrigena</i>
ID=4514	WP_023317002	transcriptional regulator	<i>Klebsiella pneumoniae</i>
ID=4515	WP_041146101	protein-(glutamine-N5) methyltransferase, release factor-specific	<i>Raoultella ornithinolytica</i>
ID=4516	WP_045858977	peptide chain release factor 1	<i>Raoultella terrigena</i>
ID=4517	WP_041146103	MULTISPECIES: glutamyl-tRNA reductase	<i>Raoultella</i>
ID=4518	WP_041146104	outer membrane lipoprotein LolB	<i>Raoultella ornithinolytica</i>
ID=4519	WP_045858981	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	<i>Raoultella terrigena</i>
ID=4520	WP_004863536	MULTISPECIES: ribose-phosphate pyrophosphokinase	<i>Enterobacteriaceae</i>
ID=4521	WP_041146106	sodium-independent anion transporter	<i>Raoultella ornithinolytica</i>
ID=4522	WP_041146107	MerR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4523	WP_041146108	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4524	WP_041147674	MULTISPECIES: aminoacyl-tRNA hydrolase	<i>Raoultella</i>
ID=4525	WP_041146109	MULTISPECIES: GTP-binding protein YchF	<i>Raoultella</i>
ID=4526	WP_061770089	hypothetical protein	<i>Serratia symbiotica</i>
ID=4527	WP_041146621	malto porin	<i>Raoultella ornithinolytica</i>
ID=4528	WP_041146622	beta-xylosidase	<i>Raoultella ornithinolytica</i>
ID=4529	WP_041146623	Na ⁺ /xyloside symporter related transporter	<i>Raoultella ornithinolytica</i>
ID=4530	WP_041146624	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4531	WP_041147712	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4532	WP_045856147	MFS transporter	<i>Raoultella terrigena</i>
ID=4533	WP_045856150	methyltransferase	<i>Raoultella terrigena</i>
ID=4534	WP_045856152	TetR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=4535	WP_041146628	structural protein MipA	<i>Raoultella ornithinolytica</i>
ID=4536	WP_045856155	transcriptional regulator CynR	<i>Raoultella terrigena</i>

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ID=4537	WP_041146630	cyanate transporter	<i>Raoultella ornithinolytica</i>
ID=4538	WP_045856159	alanine transaminase	<i>Raoultella terrigena</i>
ID=4539	WP_041146632	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4540	WP_041147713	DNA-binding response regulator	<i>Raoultella ornithinolytica</i>
ID=4541	WP_041146633	MULTISPECIES: glucokinase	<i>Raoultella</i>
ID=4542	WP_041146634	ion channel protein	<i>Raoultella ornithinolytica</i>
ID=4543	WP_041146635	indolepyruvate decarboxylase	<i>Raoultella ornithinolytica</i>
ID=4544	WP_045856168	glyceraldehyde 3-phosphate reductase	<i>Raoultella terrigena</i>
ID=4545	WP_045856170	hypothetical protein	<i>Raoultella terrigena</i>
ID=4546	WP_045856173	manganese transporter MntH	<i>Raoultella terrigena</i>
ID=4547	WP_041146639	MULTISPECIES: nucleoside permease	<i>Raoultella</i>
ID=4548	WP_041146640	sensor domain-containing phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=4549	WP_041146641	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4550	WP_041147714	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4551	WP_041146642	glutamate--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=4552	WP_041146643	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4553	WP_041146644	bile acid:sodium symporter	<i>Raoultella ornithinolytica</i>
ID=4554	WP_041147715	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=4555	WP_041146645	DNA ligase (NAD(+)) LigA	<i>Raoultella ornithinolytica</i>
ID=4556	WP_045856187	cell division protein ZipA	<i>Raoultella terrigena</i>
ID=4557	WP_041146646	cell division protein ZipA	<i>Raoultella ornithinolytica</i>
ID=4558	WP_045856451	sulfate transporter CysZ	<i>Raoultella terrigena</i>
ID=4559	WP_041146648	MULTISPECIES: cysteine synthase A	<i>Raoultella</i>
ID=4560	WP_000487600	MULTISPECIES: phosphocarrier protein HPr	<i>Proteobacteria</i>
ID=4561	WP_041146649	phosphoenolpyruvate--protein phosphotransferase	<i>Raoultella ornithinolytica</i>
ID=4562	WP_041146650	MULTISPECIES: glucose-specific phosphotransferase enzyme IIA component	<i>Raoultella</i>
ID=4563	WP_041146651	bifunctional pyridoxal kinase/hydroxymethylpyrimidine kinase	<i>Raoultella ornithinolytica</i>
ID=4564	WP_041146652	transcriptional regulator PtsJ	<i>Raoultella ornithinolytica</i>
ID=4565	WP_045856198	hypothetical protein	<i>Raoultella terrigena</i>
ID=4566	WP_045856199	cysteine synthase B	<i>Raoultella terrigena</i>
ID=4567	WP_045856201	sulfate/thiosulfate transporter subunit	<i>Raoultella terrigena</i>
ID=4568	WP_045856202	sulfate/thiosulfate transporter permease subunit	<i>Raoultella terrigena</i>
ID=4569	WP_041146657	sulfate/thiosulfate transporter subunit	<i>Raoultella ornithinolytica</i>
ID=4570	WP_041146658	thiosulfate transporter subunit	<i>Raoultella ornithinolytica</i>
ID=4571	WP_041146659	peroxidase	<i>Raoultella ornithinolytica</i>
ID=4572	WP_041146660	DUF1131 domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=4573	WP_041146661	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4574	WP_041146662	MULTISPECIES: GNAT family acetyltransferase	<i>Raoultella</i>
ID=4575	WP_064170362	N-acetylmuramoyl-L-alanine amidase	<i>Klebsiella pneumoniae</i>
ID=4576	WP_041146664	coproporphyrinogen III oxidase	<i>Raoultella ornithinolytica</i>
ID=4577	WP_041146665	malic enzyme	<i>Raoultella ornithinolytica</i>
ID=4578	WP_045856220	transketolase	<i>Raoultella terrigena</i>
ID=4579	WP_041146667	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4580	WP_041146668	GDP-mannose pyrophosphatase NudK	<i>Raoultella ornithinolytica</i>
ID=4581	WP_041146669	oxidoreductase FeS-binding subunit	<i>Raoultella ornithinolytica</i>
ID=4582	WP_041146670	multidrug efflux RND transporter permease subunit	<i>Raoultella ornithinolytica</i>
ID=4583	WP_041146671	arsenate reductase	<i>Raoultella ornithinolytica</i>
ID=4584	WP_041146672	succinyl-diaminopimelate desuccinylase	<i>Raoultella ornithinolytica</i>
ID=4585	WP_041146673	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4586	WP_041146674	esterase	<i>Raoultella ornithinolytica</i>
ID=4587	WP_041146675	tRNA(Met) cytidine acetyltransferase TmcA	<i>Raoultella ornithinolytica</i>
ID=4588	WP_041146676	neutral zinc metalloproteinase	<i>Raoultella ornithinolytica</i>
ID=4589	WP_041146677	MULTISPECIES: phosphoribosylaminoimidazolesuccinocarboxamide synthase	<i>Raoultella</i>
ID=4590	WP_041146678	outer membrane protein assembly factor BamC	<i>Raoultella ornithinolytica</i>
ID=4591	WP_041146679	4-hydroxy-tetrahydrodipicolinate synthase	<i>Raoultella ornithinolytica</i>
ID=4592	WP_041146680	glycine cleavage system transcriptional repressor	<i>Raoultella ornithinolytica</i>
ID=4593	WP_041146681	MULTISPECIES: peroxiredoxin	<i>Raoultella</i>
ID=4594	WP_045856257	AI-2E family transporter	<i>Raoultella terrigena</i>
ID=4595	WP_041146683	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4596	WP_041146684	MULTISPECIES: arsenate reductase (glutaredoxin)	<i>Raoultella</i>
ID=4597	WP_041146685	MULTISPECIES: DnaA regulatory inactivator Hda	<i>Raoultella</i>
ID=4598	WP_045856263	uracil/xanthine transporter	<i>Raoultella terrigena</i>
ID=4599	WP_041146687	uracil phosphoribosyltransferase	<i>Raoultella ornithinolytica</i>
ID=4600	WP_045856267	6-phospho-beta-glucosidase	<i>Raoultella terrigena</i>
ID=4601	WP_045856269	beta-glucoside kinase	<i>Raoultella terrigena</i>
ID=4602	WP_041146690	phosphoribosylformylglycinamide cyclo-ligase	<i>Raoultella ornithinolytica</i>
ID=4603	WP_041146691	MULTISPECIES: phosphoribosylglycinamide formyltransferase	<i>Raoultella</i>
ID=4604	WP_045856273	RNA degradosome polyphosphate kinase	<i>Raoultella terrigena</i>
ID=4605	WP_041146693	exopolyphosphatase	<i>Raoultella ornithinolytica</i>

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ID=4606	WP_041146694	sensor domain-containing phosphodiesterase	<i>Raoultella ornithinolytica</i>
ID=4607	WP_041146696	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4608	WP_041146697	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4609	WP_041146698	SAM-dependent methyltransferase	<i>Raoultella ornithinolytica</i>
ID=4610	WP_041146699	short-chain dehydrogenase/reductase	<i>Raoultella ornithinolytica</i>
ID=4611	WP_041146700	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4612	WP_020801502	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4613	WP_004853132	MULTISPECIES: prevent-host-death protein	<i>Enterobacterales</i>
ID=4614	WP_018435960	short-chain dehydrogenase/reductase	<i>Burkholderia sp.</i>
ID=4615	WP_018435958	oxidoreductase	<i>Burkholderia sp.</i>
ID=4616	WP_018435957	AraC family transcriptional regulator	<i>Burkholderia sp.</i>
ID=4617	WP_041146701	GMP synthetase	<i>Raoultella ornithinolytica</i>
ID=4618	WP_041146702	MULTISPECIES: IMP dehydrogenase	<i>Raoultella</i>
ID=4619	WP_041146703	exodeoxyribonuclease VII large subunit	<i>Raoultella ornithinolytica</i>
ID=4620	WP_045856297	hypothetical protein	<i>Raoultella terrigena</i>
ID=4621	WP_041146705	oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=4622	WP_023279819	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=4623	WP_049085553	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=4624	WP_049014216	hypothetical protein	<i>Klebsiella quasipneumoniae</i>
ID=4625	WP_049085551	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=4626	WP_041146775	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4627	WP_045856415	lipoprotein	<i>Raoultella terrigena</i>
ID=4628	WP_041146773	phosphatidylserine synthase	<i>Raoultella ornithinolytica</i>
ID=4629	WP_041146772	protein acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=4630	WP_045856409	DTW domain-containing protein YfiP	<i>Raoultella terrigena</i>
ID=4631	WP_041146770	MULTISPECIES: thiol disulfide reductase thioredoxin	<i>Raoultella</i>
ID=4632	WP_045856407	tRNA/rRNA methyltransferase	<i>Raoultella terrigena</i>
ID=4633	WP_041146769	tRNA/rRNA methyltransferase	<i>Raoultella ornithinolytica</i>
ID=4634	WP_041146768	uracil-DNA glycosylase	<i>Raoultella ornithinolytica</i>
ID=4635	WP_041146767	autonomous glycyl radical cofactor GrcA	<i>Raoultella ornithinolytica</i>
ID=4636	WP_045856403	PTS sugar transporter	<i>Raoultella terrigena</i>
ID=4637	WP_041146765	2-dehydro-3-deoxy-6-phosphogalactonate aldolase	<i>Raoultella ornithinolytica</i>
ID=4638	WP_041146764	GntR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4639	WP_041146763	ATP-dependent RNA helicase SrmB	<i>Raoultella ornithinolytica</i>
ID=4640	WP_041146762	tRNA (adenine-N(6)-)-methyltransferase	<i>Raoultella ornithinolytica</i>
ID=4641	WP_045856391	L-aspartate oxidase	<i>Raoultella terrigena</i>
ID=4642	WP_016532642	L-aspartate oxidase, partial	<i>Klebsiella pneumoniae</i>
ID=4643	WP_041146761	L-aspartate oxidase	<i>Raoultella ornithinolytica</i>
ID=4644	WP_045856391	L-aspartate oxidase	<i>Raoultella terrigena</i>
ID=4645	WP_041146760	MULTISPECIES: RNA polymerase sigma factor RpoE	<i>Raoultella</i>
ID=4646	WP_041146759	MULTISPECIES: anti-RNA polymerase sigma factor SigE	<i>Raoultella</i>
ID=4647	WP_041146758	sigma-E factor regulatory protein RseB	<i>Raoultella ornithinolytica</i>
ID=4648	WP_041146757	SoxR reducing system protein RseC	<i>Raoultella ornithinolytica</i>
ID=4649	WP_041146756	elongation factor 4	<i>Raoultella ornithinolytica</i>
ID=4650	WP_041146755	S26 family signal peptidase	<i>Raoultella ornithinolytica</i>
ID=4651	WP_041146753	MULTISPECIES: ribonuclease III	<i>Raoultella</i>
ID=4652	WP_041146752	MULTISPECIES: GTPase Era	<i>Raoultella</i>
ID=4653	WP_041147718	DNA repair protein RecO	<i>Raoultella ornithinolytica</i>
ID=4654	WP_045856382	pyridoxine 5'-phosphate synthase	<i>Raoultella terrigena</i>
ID=4655	WP_041146750	holo-ACP synthase	<i>Raoultella ornithinolytica</i>
ID=4656	WP_041146749	ferredoxin	<i>Raoultella ornithinolytica</i>
ID=4657	WP_041146748	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4658	WP_041146747	HAD family hydrolase	<i>Raoultella ornithinolytica</i>
ID=4659	WP_045856373	tRNA-specific adenosine deaminase	<i>Raoultella terrigena</i>
ID=4660	WP_045856371	lytic transglycosylase F	<i>Raoultella terrigena</i>
ID=4661	WP_041146744	phosphoribosylformylglycinamide synthase	<i>Raoultella ornithinolytica</i>
ID=4662	WP_041146743	two-component sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=4663	WP_041146742	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4664	WP_041146741	two-component system response regulator GltR	<i>Raoultella ornithinolytica</i>
ID=4665	WP_041146740	MULTISPECIES: nitrogen regulatory protein P-II 1	<i>Raoultella</i>
ID=4666	WP_045856362	flavohemoprotein	<i>Raoultella terrigena</i>
ID=4667	WP_045856360	serine hydroxymethyltransferase	<i>Raoultella terrigena</i>
ID=4668	WP_041147717	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4669	WP_041146737	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4670	WP_041146736	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4671	WP_041146735	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4672	WP_045856352	aldose epimerase	<i>Raoultella terrigena</i>
ID=4673	WP_041146733	3-phenylpropionic acid transporter	<i>Raoultella ornithinolytica</i>
ID=4674	WP_045856349	stationary phase inducible protein CsiE	<i>Raoultella terrigena</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=4675	WP_041146731	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4676	WP_041146730	nickel transporter	<i>Raoultella ornithinolytica</i>
ID=4677	WP_041146729	inositol monophosphatase	<i>Raoultella ornithinolytica</i>
ID=4678	WP_041146728	tRNA (cytosine(32)/uridine(32)-2'-O)-methyltransferase TrmJ	<i>Raoultella ornithinolytica</i>
ID=4679	WP_041146727	Fe-S cluster assembly transcriptional regulator IscR	<i>Raoultella ornithinolytica</i>
ID=4680	WP_041146726	cysteine desulfurase	<i>Raoultella ornithinolytica</i>
ID=4681	WP_004866383	MULTISPECIES: iron-sulfur cluster scaffold-like protein	<i>Enterobacteriaceae</i>
ID=4682	WP_041146725	MULTISPECIES: iron-binding protein	<i>Raoultella</i>
ID=4683	WP_041146724	co-chaperone HscB	<i>Raoultella ornithinolytica</i>
ID=4684	WP_041146723	molecular chaperone HscA	<i>Raoultella ornithinolytica</i>
ID=4685	WP_041146722	MULTISPECIES: ferredoxin, 2Fe-2S type, ISC system	<i>Raoultella</i>
ID=4686	WP_041146721	MULTISPECIES: Fe-S assembly protein IscX	<i>Raoultella</i>
ID=4687	WP_045856330	aminopeptidase PepB	<i>Raoultella terrigena</i>
ID=4688	WP_041146719	enhanced serine sensitivity protein SseB	<i>Raoultella ornithinolytica</i>
ID=4689	WP_045856327	3-mercaptopyruvate sulfurtransferase	<i>Raoultella terrigena</i>
ID=4690	WP_041146715	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4691	WP_041146714	penicillin-binding protein 1C	<i>Raoultella ornithinolytica</i>
ID=4692	WP_041146713	MULTISPECIES: nucleoside-diphosphate kinase	<i>Raoultella</i>
ID=4693	WP_041146712	23S rRNA (adenine(2503)-C(2))-methyltransferase RlmN	<i>Raoultella ornithinolytica</i>
ID=4694	WP_041146711	cytoskeletal protein RodZ	<i>Raoultella ornithinolytica</i>
ID=4695	WP_041146710	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	<i>Raoultella ornithinolytica</i>
ID=4696	WP_041146709	histidine--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=4697	WP_045856302	membrane protein	<i>Raoultella terrigena</i>
ID=4698	WP_041146707	MULTISPECIES: outer membrane protein assembly factor BamB	<i>Raoultella</i>
ID=4699	WP_045856301	ribosome biogenesis GTPase Der	<i>Raoultella terrigena</i>
ID=4700	WP_049162890	integrase	<i>Klebsiella variicola</i>
ID=4701	WP_049164344	hypothetical protein	<i>Klebsiella variicola</i>
ID=4702	WP_049014567	hypothetical protein	<i>Citrobacter freundii</i>
ID=4703	WP_042866809	antirepressor	<i>Enterobacter cloacae</i>
ID=4704	WP_039184609	Rha family transcriptional regulator	<i>Hafnia paralvei</i>
ID=4705	WP_064144322	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4706	WP_064144323	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4707	WP_048295757	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4708	WP_064359262	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4709	WP_065903931	hypothetical protein	<i>Klebsiella quasipneumoniae</i>
ID=4710	WP_064157979	DNA primase	<i>Klebsiella pneumoniae</i>
ID=4711	WP_015701153	PerC family transcriptional regulator	<i>Pantoea ananatis</i>
ID=4712	WP_048265897	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4713	WP_048294174	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=4714	WP_070544235	single-stranded DNA-binding protein	<i>Klebsiella sp.</i>
ID=4715	WP_040180231	phage portal protein, partial	<i>Klebsiella pneumoniae</i>
ID=4716	WP_063528759	hypothetical protein	<i>Pseudoalteromonas shioyasakiensis</i>
ID=4717	WP_014232319	TIGR04255 family protein	<i>Vibrio sp.</i>
ID=4718	WP_032689153	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=4719	WP_064374574	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=4720	WP_020323942	MULTISPECIES: thioredoxin	<i>Klebsiella</i>
ID=4721	WP_060619515	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4722	WP_069476178	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4723	WP_064177550	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4724	WP_046878700	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4725	WP_049866874	hypothetical protein	<i>Enterobacter cloacae</i>
ID=4726	WP_025203305	hypothetical protein	<i>Enterobacter cloacae</i>
ID=4727	WP_048293386	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=4728	WP_043875996	hypothetical protein	<i>Klebsiella variicola</i>
ID=4730	WP_045853421	glutamate/aspartate:proton symporter GltP	<i>Raoultella terrigena</i>
ID=4731	WP_041143640	acetyl-coenzyme A synthetase	<i>Raoultella ornithinolytica</i>
ID=4732	WP_045853423	membrane protein	<i>Raoultella terrigena</i>
ID=4733	WP_041143638	cation acetate symporter	<i>Raoultella ornithinolytica</i>
ID=4734	WP_041143637	murein hydrolase effector protein	<i>Raoultella ornithinolytica</i>
ID=4735	WP_041143636	CidA/LrgA family protein	<i>Raoultella ornithinolytica</i>
ID=4736	WP_041143635	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4737	WP_041143634	Na ⁺ /H ⁺ antiporter	<i>Raoultella ornithinolytica</i>
ID=4738	WP_045853429	permease	<i>Raoultella terrigena</i>
ID=4739	WP_045853430	glutathione S-transferase	<i>Raoultella terrigena</i>
ID=4740	WP_041143631	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=4741	WP_041143630	MULTISPECIES: AraC family transcriptional regulator	<i>Raoultella</i>
ID=4742	WP_045853431	cyclic diguanylate phosphodiesterase	<i>Raoultella terrigena</i>
ID=4744	WP_041143628	MULTISPECIES: membrane protein	<i>Raoultella</i>
ID=4745	WP_041143627	spermidine/putrescine ABC transporter permease	<i>Raoultella ornithinolytica</i>

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ID=4746	WP_041143626	ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=4747	WP_041143625	ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4748	WP_041143624	putrescine/spermidine ABC transporter ATPase	<i>Raoultella ornithinolytica</i>
ID=4749	WP_045853436	ribonuclease Z	<i>Raoultella terrigena</i>
ID=4750	WP_045853437	LacI family transcriptional regulator	<i>Raoultella terrigena</i>
ID=4751	WP_041143621	inositol monophosphatase	<i>Raoultella ornithinolytica</i>
ID=4752	WP_052474449	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4753	WP_052474605	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4754	WP_045853439	hypothetical protein	<i>Raoultella terrigena</i>
ID=4755	WP_041143617	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=4756	WP_041143616	fimbrial protein	<i>Raoultella ornithinolytica</i>
ID=4757	WP_045853510	hypothetical protein	<i>Raoultella terrigena</i>
ID=4758	WP_041143615	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4759	WP_041147504	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4760	WP_045853444	outer membrane protein assembly factor BamA	<i>Raoultella terrigena</i>
ID=4761	WP_041143612	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4762	WP_041143611	lytic transglycosylase F	<i>Raoultella ornithinolytica</i>
ID=4763	WP_045853446	porin	<i>Raoultella terrigena</i>
ID=4764	WP_045853447	sodium:galactoside symporter	<i>Raoultella terrigena</i>
ID=4765	WP_041143608	1,4-beta-xylanase	<i>Raoultella ornithinolytica</i>
ID=4766	WP_045853449	ssDNA-binding protein	<i>Raoultella terrigena</i>
ID=4767	WP_041143606	ABC-ATPase UvrA	<i>Raoultella ornithinolytica</i>
ID=4768	WP_045853451	hypothetical protein	<i>Raoultella terrigena</i>
ID=4769	WP_041143604	acid phosphatase/phosphotransferase	<i>Raoultella ornithinolytica</i>
ID=4770	WP_041143603	aromatic amino acid aminotransferase	<i>Raoultella ornithinolytica</i>
ID=4771	WP_041143602	alanine racemase	<i>Raoultella ornithinolytica</i>
ID=4772	WP_041143601	replicative DNA helicase	<i>Raoultella ornithinolytica</i>
ID=4773	WP_045853455	quinone oxidoreductase	<i>Raoultella terrigena</i>
ID=4774	WP_032689944	MULTISPECIES: phage-shock protein	<i>Enterobacteriaceae</i>
ID=4775	WP_045853512	tRNA-dihydrouridine synthase A	<i>Raoultella terrigena</i>
ID=4776	WP_041143598	cupin	<i>Raoultella ornithinolytica</i>
ID=4777	WP_041143597	transcriptional repressor	<i>Raoultella ornithinolytica</i>
ID=4778	WP_041143596	MULTISPECIES: CsbD family protein	<i>Raoultella</i>
ID=4779	WP_041143595	MATE family efflux transporter	<i>Raoultella ornithinolytica</i>
ID=4780	WP_041143594	repressor LexA	<i>Raoultella ornithinolytica</i>
ID=4781	WP_023336598	MULTISPECIES: diacylglycerol kinase	<i>Enterobacter cloacae</i>
ID=4782	WP_045853461	glycerol-3-phosphate 1-O-acyltransferase	<i>Raoultella terrigena</i>
ID=4783	WP_041143591	4-hydroxybenzoate octaprenyltransferase	<i>Raoultella ornithinolytica</i>
ID=4784	WP_041143590	chorismate lyase	<i>Raoultella ornithinolytica</i>
ID=4785	WP_045853464	maltose operon protein MalM	<i>Raoultella terrigena</i>
ID=4786	WP_041143588	maltoporin	<i>Raoultella ornithinolytica</i>
ID=4787	WP_041143587	MULTISPECIES: maltose/maltodextrin transporter ATP-binding protein	<i>Raoultella</i>
ID=4788	WP_041143586	maltose ABC transporter substrate-binding protein MalE	<i>Raoultella ornithinolytica</i>
ID=4789	WP_041143585	maltose ABC transporter permease MalF	<i>Raoultella ornithinolytica</i>
ID=4790	WP_041143584	maltose transporter permease	<i>Raoultella ornithinolytica</i>
ID=4791	WP_041143583	phosphate-starvation-inducible protein PsiE	<i>Raoultella ornithinolytica</i>
ID=4792	WP_041143582	alanine acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=4793	WP_041143581	UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase	<i>Raoultella ornithinolytica</i>
ID=4794	WP_041147502	glucose-6-phosphate isomerase	<i>Raoultella ornithinolytica</i>
ID=4795	WP_041143580	lysine-sensitive aspartokinase 3	<i>Raoultella ornithinolytica</i>
ID=4796	WP_045853472	bile acid:sodium symporter	<i>Raoultella terrigena</i>
ID=4797	WP_041143578	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4798	WP_041143577	MULTISPECIES: 23S rRNA pseudouridine synthase F	<i>Raoultella</i>
ID=4799	WP_045853474	Cro/C1 family transcriptional regulator	<i>Raoultella terrigena</i>
ID=4800	WP_041143575	sorbitol-6-phosphate 2-dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=4801	WP_045853476	PTS sorbose transporter subunit IIA	<i>Raoultella terrigena</i>
ID=4802	WP_041143573	PTS fructose transporter subunit IIB	<i>Raoultella ornithinolytica</i>
ID=4803	WP_041143572	MULTISPECIES: PTS mannose/fructose/sorbose transporter subunit IIC	<i>Raoultella</i>
ID=4804	WP_041143571	MULTISPECIES: PTS mannose transporter subunit IID	<i>Raoultella</i>
ID=4805	WP_041143570	L-sorbose 1-phosphate reductase	<i>Raoultella ornithinolytica</i>
ID=4806	WP_041143569	shikimate 5-dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=4807	WP_041143568	dipeptidase E	<i>Raoultella ornithinolytica</i>
ID=4808	WP_041143567	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4809	WP_041143566	methionine synthase	<i>Raoultella ornithinolytica</i>
ID=4810	WP_041143565	transcriptional regulator IclR	<i>Raoultella ornithinolytica</i>
ID=4811	WP_041143564	ASCH domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=4812	WP_041143563	bifunctional isocitrate dehydrogenase kinase/phosphatase	<i>Raoultella ornithinolytica</i>
ID=4813	WP_041143562	isocitrate lyase	<i>Raoultella ornithinolytica</i>
ID=4814	WP_041143561	malate synthase A	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=4815	WP_041143560	homoserine O-succinyltransferase	<i>Raoultella ornithinolytica</i>
ID=4816	WP_041146621	malto porin	<i>Raoultella ornithinolytica</i>
ID=4817	WP_041143298	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4818	WP_041143299	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4819	WP_069323424	hypothetical protein	<i>Citrobacter</i> sp.
ID=4820	WP_045853774	hexose phosphate transporter	<i>Raoultella terrigena</i>
ID=4821	WP_041143301	regulatory protein UhpC	<i>Raoultella ornithinolytica</i>
ID=4822	WP_041143302	two-component system sensor histidine kinase UhpB	<i>Raoultella ornithinolytica</i>
ID=4823	WP_041143303	DNA-binding response regulator	<i>Raoultella ornithinolytica</i>
ID=4824	WP_041143304	DUF4432 domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=4825	WP_041143305	L-fucose:H ⁺ symporter permease	<i>Raoultella ornithinolytica</i>
ID=4826	WP_041143306	MULTISPECIES: ribokinase	<i>Raoultella</i>
ID=4827	WP_041143307	DeoR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4828	WP_041143308	MULTISPECIES: acetolactate synthase isozyme 1 small subunit	<i>Raoultella</i>
ID=4829	WP_041143309	acetolactate synthase catalytic subunit	<i>Raoultella ornithinolytica</i>
ID=4830	WP_004145059	type I toxin-antitoxin system toxin TisB	<i>Klebsiella pneumoniae</i>
ID=4831	WP_041143310	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=4832	WP_041143311	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4833	WP_041143312	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4834	WP_052474439	DNA-binding transcriptional regulator DsdC	<i>Raoultella ornithinolytica</i>
ID=4835	WP_041143313	D-serine transporter DsdX	<i>Raoultella ornithinolytica</i>
ID=4836	WP_041143314	D-serine dehydratase	<i>Raoultella ornithinolytica</i>
ID=4837	WP_041147490	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4838	WP_041143315	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4839	WP_032690177	MULTISPECIES: membrane protein	<i>Enterobacteriaceae</i>
ID=4840	WP_041143317	6-phospho-alpha-glucosidase	<i>Raoultella ornithinolytica</i>
ID=4841	WP_045853757	PTS alpha-glucoside transporter subunit IICB	<i>Raoultella terrigena</i>
ID=4842	WP_041143319	MULTISPECIES: GntR family transcriptional regulator	<i>Raoultella</i>
ID=4843	WP_045853756	transporter	<i>Raoultella terrigena</i>
ID=4844	WP_041143321	heat-shock protein IbpB	<i>Raoultella ornithinolytica</i>
ID=4845	WP_041143322	MULTISPECIES: heat-shock protein IbpA	<i>Raoultella</i>
ID=4846	WP_045853754	hypothetical protein	<i>Raoultella terrigena</i>
ID=4847	WP_041143324	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4848	WP_041143324	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4849	WP_041143325	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4850	WP_045853751	galactonate dehydratase	<i>Raoultella terrigena</i>
ID=4851	WP_041143327	2-dehydro-3-deoxy-6-phosphogalactonate aldolase	<i>Raoultella ornithinolytica</i>
ID=4852	WP_041143328	2-oxo-3-deoxygalactonate kinase	<i>Raoultella ornithinolytica</i>
ID=4853	WP_041143329	MULTISPECIES: transcriptional regulator	<i>Raoultella</i>
ID=4854	WP_041143330	membrane protein	<i>Raoultella ornithinolytica</i>
ID=4855	WP_041143331	sugar-phosphatase	<i>Raoultella ornithinolytica</i>
ID=4856	WP_045853747	DNA gyrase subunit B	<i>Raoultella terrigena</i>
ID=4857	WP_041143333	DNA replication/repair protein RecF	<i>Raoultella ornithinolytica</i>
ID=4858	WP_041143334	DNA polymerase III subunit beta	<i>Raoultella ornithinolytica</i>
ID=4859	WP_041143335	chromosomal replication initiation protein DnaA	<i>Raoultella ornithinolytica</i>
ID=4860	WP_006817857	ribonuclease P protein component	<i>Yokenella regensburgei</i>
ID=4861	WP_041143337	membrane protein insertase YidC	<i>Raoultella ornithinolytica</i>
ID=4862	WP_041143338	tRNA modification GTPase	<i>Raoultella ornithinolytica</i>
ID=4863	WP_041143339	multidrug transporter subunit MdtL	<i>Raoultella ornithinolytica</i>
ID=4864	WP_04585384	DNA-binding transcriptional regulator	<i>Raoultella terrigena</i>
ID=4865	WP_045853740	hypothetical protein	<i>Raoultella terrigena</i>
ID=4866	WP_041143341	MULTISPECIES: NAD(P)H-dependent oxidoreductase	<i>Raoultella</i>
ID=4867	WP_041143342	adenine permease PurP	<i>Raoultella ornithinolytica</i>
ID=4868	WP_041143343	6-phosphogluconate phosphatase	<i>Raoultella ornithinolytica</i>
ID=4869	WP_064344049	transcriptional regulator PhoU	<i>Klebsiella oxytoca</i>
ID=4870	WP_041143344	MULTISPECIES: phosphate ABC transporter ATP-binding protein	<i>Raoultella</i>
ID=4871	WP_045853737	phosphate transporter permease subunit PtsA	<i>Raoultella terrigena</i>
ID=4872	WP_041143346	phosphate transporter permease subunit PstC	<i>Raoultella ornithinolytica</i>
ID=4873	WP_045853735	phosphate ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=4874	WP_041143348	amidohydrolase	<i>Raoultella ornithinolytica</i>
ID=4875	WP_041143349	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4876	WP_041143350	glutamine--fructose-6-phosphate aminotransferase	<i>Raoultella ornithinolytica</i>
ID=4877	WP_041143351	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/..glucosamine-1-phosphate acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=4878	WP_041143352	pectate lyase	<i>Raoultella ornithinolytica</i>
ID=4879	WP_044348371	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4880	WP_041143353	MULTISPECIES: FO1 ATP synthase subunit epsilon	<i>Raoultella</i>
ID=4881	WP_041143354	MULTISPECIES: ATP synthase subunit beta	<i>Raoultella</i>
ID=4882	WP_041143355	MULTISPECIES: FO1 ATP synthase subunit gamma	<i>Raoultella</i>

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ID=4883	WP_041143356	MULTISPECIES: ATP synthase subunit alpha	<i>Raoultella</i>
ID=4884	WP_041143357	F0F1 ATP synthase subunit delta	<i>Raoultella ornithinolytica</i>
ID=4885	WP_041143358	MULTISPECIES: ATP synthase subunit B	<i>Raoultella</i>
ID=4886	WP_006890850	ATP synthase subunit C	<i>Salmonella enterica</i>
ID=4887	WP_041143359	MULTISPECIES: F0F1 ATP synthase subunit A	<i>Raoultella</i>
ID=4888	WP_041143360	ATP F0F1 synthase subunit I	<i>Raoultella ornithinolytica</i>
ID=4889	WP_041147492	16S rRNA methyltransferase G	<i>Raoultella ornithinolytica</i>
ID=4890	WP_045853729	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	<i>Raoultella terrigena</i>
ID=4891	WP_041143362	FMN-binding protein MioC	<i>Raoultella ornithinolytica</i>
ID=4892	WP_045853727	transcriptional regulator AsnC	<i>Raoultella terrigena</i>
ID=4893	WP_041143364	aspartate--ammonia ligase	<i>Raoultella ornithinolytica</i>
ID=4894	WP_045853725	hypothetical protein	<i>Raoultella terrigena</i>
ID=4895	WP_045853724	ATPase RavA	<i>Raoultella terrigena</i>
ID=4896	WP_041143367	potassium transporter Kup	<i>Raoultella ornithinolytica</i>
ID=4897	WP_041143368	D-ribose pyranase	<i>Raoultella ornithinolytica</i>
ID=4898	WP_045853721	ribose ABC transporter ATP-binding protein RbsA	<i>Raoultella terrigena</i>
ID=4899	WP_041143370	MULTISPECIES: ribose ABC transporter permease	<i>Raoultella</i>
ID=4900	WP_041143371	D-ribose ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4901	WP_041147493	ribokinase	<i>Raoultella ornithinolytica</i>
ID=4902	WP_041143372	transcriptional regulator RbsR	<i>Raoultella ornithinolytica</i>
ID=4903	WP_045853718	MFS transporter	<i>Raoultella terrigena</i>
ID=4904	WP_045853717	GntR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=4905	WP_041143375	molybdopterin-guanine dinucleotide biosynthesis protein MobB	<i>Raoultella ornithinolytica</i>
ID=4906	WP_041143376	molybdenum cofactor guanylyltransferase	<i>Raoultella ornithinolytica</i>
ID=4907	WP_041143377	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4908	WP_041143378	stress response kinase A	<i>Raoultella ornithinolytica</i>
ID=4909	WP_041143379	MULTISPECIES: protein disulfide oxidoreductase DsbA	<i>Raoultella</i>
ID=4910	WP_041143380	acyltransferase	<i>Raoultella ornithinolytica</i>
ID=4911	WP_041143381	DNA polymerase I	<i>Raoultella ornithinolytica</i>
ID=4912	WP_041143382	MULTISPECIES: YihA family ribosome biogenesis GTP-binding protein	<i>Raoultella</i>
ID=4913	WP_041143383	GTPase-activating protein	<i>Raoultella ornithinolytica</i>
ID=4914	WP_041143384	oxygen-independent coproporphyrinogen III oxidase	<i>Raoultella ornithinolytica</i>
ID=4915	WP_041143385	MULTISPECIES: nitrogen regulation protein NR(I)	<i>Raoultella</i>
ID=4916	WP_041143386	PAS domain-containing sensor histidine kinase	<i>Raoultella ornithinolytica</i>
ID=4917	WP_041143387	glutamine synthetase	<i>Raoultella ornithinolytica</i>
ID=4918	WP_041143388	GTP-binding protein	<i>Raoultella ornithinolytica</i>
ID=4919	WP_041143389	glucose-1-phosphatase	<i>Raoultella ornithinolytica</i>
ID=4920	WP_041147494	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4921	WP_045853698	D-tyrosyl-tRNA(Tyr) deacylase	<i>Raoultella terrigena</i>
ID=4922	WP_041143391	GNAT family N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=4923	WP_041143392	lipase	<i>Raoultella ornithinolytica</i>
ID=4924	WP_045853695	formate dehydrogenase accessory protein FdhE	<i>Raoultella terrigena</i>
ID=4925	WP_041143394	formate dehydrogenase cytochrome b556 subunit	<i>Raoultella ornithinolytica</i>
ID=4926	WP_041143395	formate dehydrogenase subunit beta	<i>Raoultella ornithinolytica</i>
ID=4927	WP_041143396	formate dehydrogenase-N subunit alpha	<i>Raoultella ornithinolytica</i>
ID=4928	WP_041143397	sulfate ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4929	WP_041143398	formate dehydrogenase accessory protein FdhD	<i>Raoultella ornithinolytica</i>
ID=4930	WP_045853688	cyclic nucleotide-binding protein	<i>Raoultella terrigena</i>
ID=4931	WP_041143399	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4932	WP_045853686	branched-chain amino acid transport	<i>Raoultella terrigena</i>
ID=4933	WP_041143408	branched-chain amino acid ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=4934	WP_045853684	DNA-binding protein	<i>Raoultella terrigena</i>
ID=4935	WP_045853683	transcriptional regulator	<i>Raoultella terrigena</i>
ID=4936	WP_041143411	alpha-galactosidase	<i>Raoultella ornithinolytica</i>
ID=4937	WP_041147495	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=4938	WP_041143412	galactoside O-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=4939	WP_041143413	porin	<i>Raoultella ornithinolytica</i>
ID=4940	WP_045853679	L-rhamnose mutarotase	<i>Raoultella terrigena</i>
ID=4941	WP_041143415	lactaldehyde reductase	<i>Raoultella ornithinolytica</i>
ID=4942	WP_045853677	branched-chain amino acid ABC transporter permease	<i>Raoultella terrigena</i>
ID=4943	WP_041143417	branched-chain amino acid ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=4944	WP_041143418	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=4945	WP_041143419	rhamnose ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=4946	WP_041143420	rhamnulose-1-phosphate aldolase	<i>Raoultella ornithinolytica</i>
ID=4947	WP_045853672	L-rhamnose isomerase	<i>Raoultella terrigena</i>
ID=4948	WP_041143422	rhamnulokinase	<i>Raoultella ornithinolytica</i>
ID=4949	WP_041143423	transcriptional activator RhaS	<i>Raoultella ornithinolytica</i>
ID=4950	WP_045853669	transcriptional regulator	<i>Raoultella terrigena</i>
ID=4951	WP_041143425	rhamnose/proton symporter RhaT	<i>Raoultella ornithinolytica</i>

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ID=4952	WP_041143426	MULTISPECIES: superoxide dismutase	<i>Raoultella</i>
ID=4953	WP_041143427	6-N-hydroxylaminopurine resistance protein	<i>Raoultella ornithinolytica</i>
ID=4954	WP_064378056	two-component system sensor histidine kinase CpxA	<i>Klebsiella oxytoca</i>
ID=4955	WP_064166968	DNA-binding response regulator	<i>Klebsiella pneumoniae</i>
ID=4956	WP_041143429	periplasmic repressor CpxP	<i>Raoultella ornithinolytica</i>
ID=4957	WP_041143430	cation-efflux pump FieF	<i>Raoultella ornithinolytica</i>
ID=4959	WP_041143431	ATP-dependent 6-phosphofructokinase	<i>Raoultella ornithinolytica</i>
ID=4960	WP_041143432	MULTISPECIES: ribonuclease E activity regulator RraA	<i>Raoultella</i>
ID=4961	WP_041143433	1,4-dihydroxy-2-naphthoate polyprenyltransferase	<i>Raoultella ornithinolytica</i>
ID=4962	WP_041143434	ATP-dependent protease ATP-binding subunit HslU	<i>Raoultella ornithinolytica</i>
ID=4963	WP_041143435	ATP-dependent protease subunit HslV	<i>Raoultella ornithinolytica</i>
ID=4964	WP_041143436	cell division protein FtsN	<i>Raoultella ornithinolytica</i>
ID=4965	WP_041143437	MULTISPECIES: DNA-binding transcriptional regulator CytR	<i>Raoultella</i>
ID=4966	WP_041143438	primosomal protein N'	<i>Raoultella ornithinolytica</i>
ID=4967	WP_004869405	MULTISPECIES: transcriptional regulator	<i>Enterobacteriaceae</i>
ID=4968	WP_045853657	cystathionine gamma-synthase	<i>Raoultella terrigena</i>
ID=4969	WP_041143441	bifunctional aspartokinase II/homoserine dehydrogenase II	<i>Raoultella ornithinolytica</i>
ID=4970	WP_041143442	4-carboxymuconolactone decarboxylase	<i>Raoultella ornithinolytica</i>
ID=4971	WP_041143443	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4972	WP_041143444	MULTISPECIES: 5,10-methylenetetrahydrofolate reductase	<i>Raoultella</i>
ID=4973	WP_041143445	glycerol dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=4974	WP_041143446	fructose-6-phosphate aldolase	<i>Raoultella ornithinolytica</i>
ID=4975	WP_041143447	AraC family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=4976	WP_041143448	MULTISPECIES: metal-binding protein ZinT	<i>Raoultella</i>
ID=4977	WP_041143449	phosphoenolpyruvate carboxylase	<i>Raoultella ornithinolytica</i>
ID=4978	WP_045853649	acetylornithine deacetylase	<i>Raoultella terrigena</i>
ID=4979	WP_041143451	N-acetyl-gamma-glutamyl-phosphate reductase	<i>Raoultella ornithinolytica</i>
ID=4980	WP_045853647	acetylglutamate kinase	<i>Raoultella terrigena</i>
ID=4981	WP_045853646	argininosuccinate lyase	<i>Raoultella terrigena</i>
ID=4982	XP_011566851	PREDICTED: probable RuBisCO transcriptional regulator	<i>Plutella xylostella</i>
ID=4983	WP_041143454	MULTISPECIES: DNA-binding transcriptional regulator OxyR	<i>Raoultella</i>
ID=4984	WP_041143455	NAD(P)(+) transhydrogenase	<i>Raoultella ornithinolytica</i>
ID=4985	WP_041143455	NAD(P)(+) transhydrogenase	<i>Raoultella ornithinolytica</i>
ID=4986	WP_045853644	DNA-binding transcriptional regulator FabR	<i>Raoultella terrigena</i>
ID=4987	WP_045853643	hypothetical protein	<i>Raoultella terrigena</i>
ID=4988	WP_041143458	tRNA (uridine(54)-C5)-methyltransferase TrmA	<i>Raoultella ornithinolytica</i>
ID=4989	WP_045853641	vitamin B12/cobalamin outer membrane transporter	<i>Raoultella terrigena</i>
ID=4990	WP_045853640	glutamate racemase	<i>Raoultella terrigena</i>
ID=4991	WP_041143461	transcriptional regulator HdfR	<i>Raoultella ornithinolytica</i>
ID=4992	WP_041143462	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=4993	WP_041143463	ATP-dependent protease	<i>Raoultella ornithinolytica</i>
ID=4994	WP_041143464	acetolactate synthase 2 catalytic subunit	<i>Raoultella ornithinolytica</i>
ID=4995	WP_041143465	MULTISPECIES: acetolactate synthase 2 small subunit	<i>Raoultella</i>
ID=4996	WP_041143466	branched chain amino acid aminotransferase	<i>Raoultella ornithinolytica</i>
ID=4997	WP_041143467	dihydroxy-acid dehydratase	<i>Raoultella ornithinolytica</i>
ID=4998	WP_041143468	PLP-dependent threonine dehydratase	<i>Raoultella ornithinolytica</i>
ID=4999	WP_041143469	transcriptional regulator IlvY	<i>Raoultella ornithinolytica</i>
ID=5000	WP_041143470	ketol-acid reductoisomerase	<i>Raoultella ornithinolytica</i>
ID=5001	WP_045853631	SAM-dependent methyltransferase	<i>Raoultella terrigena</i>
ID=5002	WP_045853630	Rrf2 family transcriptional regulator	<i>Raoultella terrigena</i>
ID=5003	WP_045853629	hypothetical protein	<i>Raoultella terrigena</i>
ID=5004	WP_024555327	MULTISPECIES: peptidylprolyl isomerase	<i>Enterobacteriaceae</i>
ID=5005	WP_041143471	peptidylprolyl isomerase	<i>Raoultella ornithinolytica</i>
ID=5006	WP_045853626	ATP-dependent DNA helicase Rep	<i>Raoultella terrigena</i>
ID=5007	WP_041143473	guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase	<i>Raoultella ornithinolytica</i>
ID=5008	WP_041143474	ATP-dependent RNA helicase RhlB	<i>Raoultella ornithinolytica</i>
ID=5009	WP_041143475	thiol reductase thioredoxin	<i>Raoultella ornithinolytica</i>
ID=5010	WP_002883293	MULTISPECIES: transcription termination factor Rho	<i>Enterobacterales</i>
ID=5011	WP_019725500	undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase	<i>Klebsiella pneumoniae</i>
ID=5012	WP_041143477	polysaccharide chain length modulation protein	<i>Raoultella ornithinolytica</i>
ID=5013	WP_052474441	UDP-N-acetyl glucosamine 2-epimerase	<i>Raoultella ornithinolytica</i>
ID=5014	WP_041143479	UDP-N-acetyl-D-mannosamine dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=5015	WP_041147496	TDP-fucosamine acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=5016	WP_045853713	dTDP-4-amino-4,6-dideoxy-D-glucose transaminase	<i>Raoultella terrigena</i>
ID=5017	WP_041143480	O-antigen translocase	<i>Raoultella ornithinolytica</i>
ID=5018	WP_041143481	4-alpha-L-fucosyltransferase	<i>Raoultella ornithinolytica</i>
ID=5019	WP_045853614	enterobacterial common antigen polymerase	<i>Raoultella terrigena</i>
ID=5020	WP_045853613	lipopolysaccharide N-acetylmannosaminouronosyltransferase	<i>Raoultella terrigena</i>
ID=5021	WP_041143484	amino acid permease	<i>Raoultella ornithinolytica</i>

Gene ID	NCBI Accession #	Predicted gene product	Origin of gene
ID=5022	WP_041143485	protoheme IX biogenesis protein HemY	<i>Raoultella ornithinolytica</i>
ID=5023	WP_045853610	uroporphyrinogen-III C-methyltransferase	<i>Raoultella terrigena</i>
ID=5024	WP_045853609	uroporphyrinogen-III synthase	<i>Raoultella terrigena</i>
ID=5025	WP_045853608	hydroxymethylbilane synthase	<i>Raoultella terrigena</i>
ID=5026	WP_045853607	adenylate cyclase	<i>Raoultella terrigena</i>
ID=5027	WP_041143490	MULTISPECIES: iron donor protein CyaY	<i>Raoultella</i>
ID=5028	WP_041143491	membrane protein	<i>Raoultella ornithinolytica</i>
ID=5029	WP_041147498	diaminopimelate epimerase	<i>Raoultella ornithinolytica</i>
ID=5030	WP_041143492	MULTISPECIES: DUF484 family protein	<i>Raoultella</i>
ID=5031	WP_041143493	tyrosine recombinase XerC	<i>Raoultella ornithinolytica</i>
ID=5032	WP_041143494	flavin mononucleotide phosphatase	<i>Raoultella ornithinolytica</i>
ID=5033	WP_045853603	DNA-dependent helicase II	<i>Raoultella terrigena</i>
ID=5034	WP_041143496	magnesium transporter CorA	<i>Raoultella ornithinolytica</i>
ID=5035	WP_041143497	endonuclease	<i>Raoultella ornithinolytica</i>
ID=5036	WP_041143498	chloramphenicol resistance permease RarD	<i>Raoultella ornithinolytica</i>
ID=5037	WP_041143499	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=5038	WP_045853600	phospholipase A	<i>Raoultella terrigena</i>
ID=5039	WP_045853599	ATP-dependent DNA helicase RecQ	<i>Raoultella terrigena</i>
ID=5040	WP_045853598	threonine export protein RhtC	<i>Raoultella terrigena</i>
ID=5041	WP_041143503	homoserine/homoserine lactone efflux protein	<i>Raoultella ornithinolytica</i>
ID=5042	WP_041143504	lysophospholipase L2	<i>Raoultella ornithinolytica</i>
ID=5043	WP_041143505	sugar/pyridoxal phosphate phosphatase YigL	<i>Raoultella ornithinolytica</i>
ID=5044	WP_045853594	membrane protein	<i>Raoultella terrigena</i>
ID=5045	WP_041143507	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=5046	WP_045853592	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	<i>Raoultella terrigena</i>
ID=5047	WP_045853591	carboxymethylenebutenolidase	<i>Raoultella terrigena</i>
ID=5048	WP_041143515	MULTISPECIES: uridine phosphorylase	<i>Raoultella</i>
ID=5049	WP_041143516	DNA recombination protein RmuC	<i>Raoultella ornithinolytica</i>
ID=5050	WP_041143517	MULTISPECIES: bifunctional demethylmenaquinone methyltransferase/..2-methoxy-6-polyprenyl-1,4-benzoquinol methylase	<i>Raoultella</i>
ID=5051	WP_041143518	SCP2 domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=5052	WP_041143519	ubiquinone biosynthesis regulatory protein kinase UbiB	<i>Raoultella ornithinolytica</i>
ID=5053	WP_041143520	MULTISPECIES: Sec-independent protein translocase TatA	<i>Raoultella</i>
ID=5054	WP_041143521	sec-independent translocase	<i>Raoultella ornithinolytica</i>
ID=5055	WP_041143522	preprotein translocase subunit TatC	<i>Raoultella ornithinolytica</i>
ID=5056	WP_045853585	DNase TatD	<i>Raoultella terrigena</i>
ID=5057	WP_041143524	MULTISPECIES: transcriptional activator RfaH	<i>Raoultella</i>
ID=5058	WP_041143525	MULTISPECIES: 3-octaprenyl-4-hydroxybenzoate decarboxylase	<i>Raoultella</i>
ID=5059	WP_041143526	NAD(P)H-flavin reductase	<i>Raoultella ornithinolytica</i>
ID=5060	WP_045853583	3-ketoacyl-CoA thiolase	<i>Raoultella terrigena</i>
ID=5061	WP_041143528	multifunctional fatty acid oxidation complex subunit alpha	<i>Raoultella ornithinolytica</i>
ID=5062	WP_041143529	Xaa-Pro dipeptidase	<i>Raoultella ornithinolytica</i>
ID=5063	WP_041143530	YigZ family protein	<i>Raoultella ornithinolytica</i>
ID=5064	WP_041143531	potassium transporter	<i>Raoultella ornithinolytica</i>
ID=5065	WP_041143532	protoporphyrinogen oxidase	<i>Raoultella ornithinolytica</i>
ID=5067	WP_041145280	methyltransferase	<i>Raoultella ornithinolytica</i>
ID=5068	WP_041145281	transporter	<i>Raoultella ornithinolytica</i>
ID=5069	WP_045855149	DSBA oxidoreductase	<i>Raoultella terrigena</i>
ID=5070	WP_041145283	MFS transporter	<i>Raoultella ornithinolytica</i>
ID=5071	WP_041145284	MarR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=5072	WP_041145285	MULTISPECIES: glutamate dehydrogenase	<i>Raoultella</i>
ID=5073	WP_041145286	acetylornithine aminotransferase	<i>Raoultella ornithinolytica</i>
ID=5074	WP_041145287	arginine N-succinyltransferase	<i>Raoultella ornithinolytica</i>
ID=5075	WP_041145288	N-succinylglutamate 5-semialdehyde dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=5076	WP_041145289	succinylarginine dihydrolase	<i>Raoultella ornithinolytica</i>
ID=5077	WP_041145290	succinylglutamate desuccinylase	<i>Raoultella ornithinolytica</i>
ID=5078	WP_041145291	amino acid transporter	<i>Raoultella ornithinolytica</i>
ID=5079	WP_045855158	hypothetical protein	<i>Raoultella terrigena</i>
ID=5080	WP_041145293	aldehyde dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=5081	WP_045855160	type I glyceraldehyde-3-phosphate dehydrogenase	<i>Raoultella terrigena</i>
ID=5083	WP_052698712	hypothetical protein	<i>Raoultella terrigena</i>
ID=5084	WP_041145295	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5085	WP_041145296	GGDEF domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=5086	WP_052698713	hypothetical protein	<i>Raoultella terrigena</i>
ID=5087	WP_041145302	isochorismatase	<i>Raoultella ornithinolytica</i>
ID=5088	WP_052474616	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=5089	WP_041145303	esterase	<i>Raoultella ornithinolytica</i>
ID=5090	WP_045855172	alpha/beta hydrolase	<i>Raoultella terrigena</i>
ID=5091	WP_045855173	AP endonuclease	<i>Raoultella terrigena</i>

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ID=5092	WP_041145306	TetR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=5094	WP_060415576	DNA-invertase	<i>Klebsiella pneumoniae</i>
ID=5095	WP_063202340	colicin-D	<i>Serratia plymuthica</i>
ID=5096	WP_063202407	pyocin	<i>Serratia plymuthica</i>
ID=5097	WP_045855179	cytochrome b561	<i>Raoultella terrigena</i>
ID=5098	WP_041145320	N-acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=5099	WP_041147608	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=5100	WP_041145321	S-(hydroxymethyl)glutathione dehydrogenase/class III alcohol dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=5101	WP_041145322	glucose dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=5102	WP_041145323	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5103	WP_041145324	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=5104	WP_045855185	protocatechuate 3,4-dioxygenase subunit alpha	<i>Raoultella terrigena</i>
ID=5105	WP_045855186	protocatechuate 3,4-dioxygenase subunit beta	<i>Raoultella terrigena</i>
ID=5106	WP_041145327	DUF1338 domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=5107	WP_041145328	carboxylesterase	<i>Raoultella ornithinolytica</i>
ID=5108	WP_041145329	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=5109	WP_041145329	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=5110	WP_041145330	MULTISPECIES: hydrolase	<i>Raoultella</i>
ID=5111	WP_041145331	methionine aminotransferase	<i>Raoultella ornithinolytica</i>
ID=5112	WP_045855191	ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=5113	WP_041145333	glucan biosynthesis protein D	<i>Raoultella ornithinolytica</i>
ID=5114	WP_041145334	ribosomal protein L7/L12-serine acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=5115	WP_045855194	LpxA-like enzyme	<i>Raoultella terrigena</i>
ID=5116	WP_041145336	dicarboxylate transporter/tellurite-resistance protein TehA	<i>Raoultella ornithinolytica</i>
ID=5117	WP_041145337	tellurite resistance methyltransferase TehB	<i>Raoultella ornithinolytica</i>
ID=5118	WP_041145338	peptidase T	<i>Raoultella ornithinolytica</i>
ID=5119	WP_016530209	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=5120	WP_047934983	hypothetical protein	<i>Klebsiella michiganensis</i>
ID=5121	WP_049100498	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=5122	WP_064579035	hypothetical protein	<i>Klebsiella mobilis</i>
ID=5123	WP_032652477	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=5124	WP_032723231	hypothetical protein	<i>Klebsiella mobilis</i>
ID=5125	WP_032428838	DNA-binding protein	<i>Klebsiella pneumoniae</i>
ID=5126	WP_064343388	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=5127	WP_032419900	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5128	WP_064187486	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5129	WP_064381545	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=5130	WP_064381542	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=5132	WP_038157749	hypothetical protein	<i>Trabulsiella guamensis</i>
ID=5133	WP_025714644	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=5134	WP_032716398	MULTISPECIES: peptidase S24	<i>Enterobacteriaceae</i>
ID=5135	WP_064381540	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=5136	WP_032409417	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5137	WP_031592539	DNA-binding protein	<i>Klebsiella pneumoniae</i>
ID=5138	WP_064385960	AAA family ATPase	<i>Klebsiella oxytoca</i>
ID=5139	WP_047934967	helicase	<i>Klebsiella michiganensis</i>
ID=5140	WP_047934966	endodeoxyribonuclease RusA	<i>Klebsiella michiganensis</i>
ID=5141	WP_040251442	molecular chaperone	<i>Klebsiella pneumoniae</i>
ID=5142	WP_032419909	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=5143	WP_032419910	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=5144	WP_040225058	lysis protein	<i>Klebsiella pneumoniae</i>
ID=5145	WP_023302589	lysozyme	<i>Klebsiella pneumoniae</i>
ID=5146	WP_025999114	DUF2570 domain-containing protein	<i>Klebsiella pneumoniae</i>
ID=5147	WP_048325000	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5148	WP_040164886	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5149	WP_047719216	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5150	WP_064388686	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=5151	WP_053090477	terminase	<i>Raoultella planticola</i>
ID=5152	WP_032735077	MULTISPECIES: phage head-tail adapter protein	<i>Klebsiella</i>
ID=5153	WP_048263915	MULTISPECIES: phage portal protein	<i>Klebsiella</i>
ID=5154	WP_065812904	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5155	WP_043875822	toxin Bro	<i>Klebsiella variicola</i>
ID=5156	WP_070544225	hypothetical protein	<i>Klebsiella sp.</i>
ID=5157	WP_064169504	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5158	WP_064169505	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5159	WP_064169506	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5160	WP_001250274	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=5161	WP_021538179	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=5162	WP_045854075	2,5-didehydrogluconate reductase B	<i>Raoultella terrigena</i>

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ID=5163	WP_041144158	LysR family transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=5164	WP_041144159	MULTISPECIES: MFS transporter	<i>Raoultella</i>
ID=5165	WP_045854077	EEP domain-containing protein	<i>Raoultella terrigena</i>
ID=5166	WP_041144161	SAM-dependent methyltransferase	<i>Raoultella ornithinolytica</i>
ID=5167	WP_041144162	lytic transglycosylase	<i>Raoultella ornithinolytica</i>
ID=5168	WP_041144163	hydroxyacylglutathione hydrolase	<i>Raoultella ornithinolytica</i>
ID=5169	WP_041144164	SAM-dependent methyltransferase	<i>Raoultella ornithinolytica</i>
ID=5170	WP_041144165	ribonuclease HI	<i>Raoultella ornithinolytica</i>
ID=5171	WP_041144166	DNA polymerase III subunit epsilon	<i>Raoultella ornithinolytica</i>
ID=5172	WP_041144167	transporter	<i>Raoultella ornithinolytica</i>
ID=5173	WP_041144168	AI-2E family transporter	<i>Raoultella ornithinolytica</i>
ID=5174	WP_041147524	amidohydrolase	<i>Raoultella ornithinolytica</i>
ID=5175	WP_041144169	acyl-CoA dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=5176	WP_004133848	MULTISPECIES: phosphoheptose isomerase	<i>Enterobacteriaceae</i>
ID=5177	WP_041144171	transpeptidase	<i>Raoultella ornithinolytica</i>
ID=5178	WP_041144172	NADH:ubiquinone reductase (Na(+)-transporting) subunit A	<i>Raoultella ornithinolytica</i>
ID=5179	WP_041144173	NADH:ubiquinone reductase (Na(+)-transporting) subunit B	<i>Raoultella ornithinolytica</i>
ID=5180	WP_041144174	NADH:ubiquinone reductase (Na(+)-transporting) subunit C	<i>Raoultella ornithinolytica</i>
ID=5181	WP_041144175	MULTISPECIES: NADH:ubiquinone reductase (Na(+)-transporting) subunit D	<i>Raoultella</i>
ID=5182	WP_041144176	NADH:ubiquinone reductase (Na(+)-transporting) subunit E	<i>Raoultella ornithinolytica</i>
ID=5183	WP_045854103	NADH:ubiquinone reductase (Na(+)-transporting) subunit F	<i>Raoultella terrigena</i>
ID=5184	WP_041147525	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=5185	WP_041144178	DNA polymerase IV	<i>Raoultella ornithinolytica</i>
ID=5186	WP_041147526	acyltransferase	<i>Raoultella ornithinolytica</i>
ID=5187	WP_041144179	cytosol nonspecific dipeptidase	<i>Raoultella ornithinolytica</i>
ID=5188	WP_041144180	MULTISPECIES: xanthine phosphoribosyltransferase	<i>Raoultella</i>
ID=5189	WP_041144181	fermentation/respiration switch protein	<i>Raoultella ornithinolytica</i>
ID=5190	WP_041144182	MULTISPECIES: sigma factor-binding protein Crl	<i>Raoultella</i>
ID=5191	WP_048228395	CbbBc protein	<i>Klebsiella mobilis</i>
ID=5193	WP_041144183	type I-F CRISPR-associated endoribonuclease Cas6/Csy4	<i>Raoultella ornithinolytica</i>
ID=5194	WP_059305012	hypothetical protein	<i>Klebsiella mobilis</i>
ID=5195	WP_041144185	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=5196	WP_041144186	NAD-dependent succinate-semialdehyde dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=5197	WP_041144187	hydroxyglutarate oxidase	<i>Raoultella ornithinolytica</i>
ID=5198	WP_041144188	carbon starvation induced protein	<i>Raoultella ornithinolytica</i>
ID=5199	WP_041144189	steroid Delta-isomerase	<i>Raoultella ornithinolytica</i>
ID=5200	WP_041144190	C4-dicarboxylate ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=5201	WP_041144191	C4-dicarboxylate ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=5202	WP_040190608	MULTISPECIES: transposase	<i>Enterobacteriaceae</i>
ID=5203	WP_041147137	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5204	WP_045857168	isopentenyl-diphosphate Delta-isomerase	<i>Raoultella terrigena</i>
ID=5205	WP_041147139	lysine--tRNA ligase	<i>Raoultella ornithinolytica</i>
ID=5206	WP_059287904	MULTISPECIES: peptide chain release factor 2	<i>Enterobacter</i>
ID=5207	WP_041147140	ssDNA exonuclease RecJ	<i>Raoultella ornithinolytica</i>
ID=5208	WP_045857161	bifunctional protein-disulfide isomerase/oxidoreductase DsbC	<i>Raoultella terrigena</i>
ID=5209	WP_041147142	site-specific tyrosine recombinase XerD	<i>Raoultella ornithinolytica</i>
ID=5210	WP_041147143	flavodoxin FldB	<i>Raoultella ornithinolytica</i>
ID=5211	WP_041147144	membrane protein	<i>Raoultella ornithinolytica</i>
ID=5212	WP_041147145	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5213	WP_041147146	folate-binding protein	<i>Raoultella ornithinolytica</i>
ID=5214	WP_041147747	hemolysin III family protein	<i>Raoultella ornithinolytica</i>
ID=5215	WP_045857151	ASCH domain-containing protein	<i>Raoultella terrigena</i>
ID=5216	WP_045857150	transcriptional regulator	<i>Raoultella terrigena</i>
ID=5217	WP_041147149	6-phospho-beta-glucosidase	<i>Raoultella ornithinolytica</i>
ID=5218	WP_041147150	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5219	WP_045857147	protein-disulfide reductase	<i>Raoultella terrigena</i>
ID=5220	WP_041147152	DSBA oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=5221	WP_041147153	protein disulfide oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=5222	WP_041147154	NAD(P)-dependent oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=5223	WP_045857143	glycine dehydrogenase (aminomethyl-transferring)	<i>Raoultella terrigena</i>
ID=5224	WP_041147156	MULTISPECIES: glycine cleavage system protein H	<i>Raoultella</i>
ID=5225	WP_041147157	glycine cleavage system protein T	<i>Raoultella ornithinolytica</i>
ID=5226	WP_041147158	MULTISPECIES: 2-octaprenylphenol hydroxylase	<i>Raoultella</i>
ID=5227	WP_041147159	2-octaprenyl-6-methoxyphenyl hydroxylase	<i>Raoultella ornithinolytica</i>
ID=5228	WP_041147160	Xaa-Pro aminopeptidase	<i>Raoultella ornithinolytica</i>
ID=5229	WP_041147161	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5230	WP_041147162	MULTISPECIES: Z-ring-associated protein	<i>Raoultella</i>
ID=5231	WP_041147163	5-formyltetrahydrofolate cyclo-ligase	<i>Raoultella ornithinolytica</i>
ID=5232	WP_041147164	hypothetical protein	<i>Raoultella ornithinolytica</i>

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ID=5233	WP_041147165	D-3-phosphoglycerate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=5234	WP_041147166	ribose 5-phosphate isomerase A	<i>Raoultella ornithinolytica</i>
ID=5235	WP_041147167	MULTISPECIES: transcriptional regulator ArgP	<i>Raoultella</i>
ID=5236	WP_041147168	MULTISPECIES: oxidative stress defense protein	<i>Raoultella</i>
ID=5237	WP_041147169	arginine exporter protein	<i>Raoultella ornithinolytica</i>
ID=5238	WP_041147170	MULTISPECIES: mechanosensitive ion channel protein MscS	<i>Raoultella</i>
ID=5239	WP_041147171	class II fructose-bisphosphate aldolase	<i>Raoultella ornithinolytica</i>
ID=5240	WP_015960329	phosphoglycerate kinase	<i>Enterobacter</i> sp.
ID=5241	WP_041147173	MULTISPECIES: erythrose-4-phosphate dehydrogenase	<i>Raoultella</i>
ID=5242	WP_045721975	hypothetical protein	<i>Salmonella enterica</i>
ID=5243	WP_041146776	protein disaggregation chaperone	<i>Raoultella ornithinolytica</i>
ID=5244	WP_045855678	hypothetical protein	<i>Raoultella terrigena</i>
ID=5245	WP_041146778	23S rRNA pseudouridine(1911/1915/1917) synthase	<i>Raoultella ornithinolytica</i>
ID=5246	WP_041146779	MULTISPECIES: outer membrane protein assembly factor BamD	<i>Raoultella</i>
ID=5247	WP_041146780	translation inhibitor protein RaiA	<i>Raoultella ornithinolytica</i>
ID=5248	WP_041146781	bifunctional chorismate mutase/prephenate dehydratase	<i>Raoultella ornithinolytica</i>
ID=5249	WP_041147719	gluconolactonase	<i>Raoultella ornithinolytica</i>
ID=5250	WP_041146782	MULTISPECIES: bifunctional chorismate mutase/prephenate dehydrogenase	<i>Raoultella</i>
ID=5251	WP_041146783	phospho-2-dehydro-3-deoxyheptonate aldolase	<i>Raoultella ornithinolytica</i>
ID=5252	WP_032718208	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=5253	WP_041146784	GGDEF domain-containing protein	<i>Raoultella ornithinolytica</i>
ID=5254	WP_041146785	membrane protein	<i>Raoultella ornithinolytica</i>
ID=5255	WP_041146786	membrane protein	<i>Raoultella ornithinolytica</i>
ID=5256	WP_041146787	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5257	WP_041146788	MULTISPECIES: 50S ribosomal protein L19	<i>Enterobacteriaceae</i>
ID=5258	WP_000264785	MULTISPECIES: tRNA (guanosine(37)-N1)-methyltransferase TrmD	<i>Escherichia</i>
ID=5259	WP_041146790	ribosome maturation factor RimM	<i>Raoultella ornithinolytica</i>
ID=5260	WP_041146791	MULTISPECIES: 30S ribosomal protein S16	<i>Raoultella</i>
ID=5261	WP_041146792	MULTISPECIES: signal recognition particle protein	<i>Raoultella</i>
ID=5262	WP_041146793	inner membrane protein YpjD	<i>Raoultella ornithinolytica</i>
ID=5263	WP_041146794	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5264	WP_041146795	nucleotide exchange factor GrpE	<i>Raoultella ornithinolytica</i>
ID=5265	WP_041146796	MULTISPECIES: NAD(+) kinase	<i>Raoultella</i>
ID=5266	WP_041146797	DNA repair protein RecN	<i>Raoultella ornithinolytica</i>
ID=5267	WP_041146798	MULTISPECIES: outer membrane protein assembly factor BamE	<i>Raoultella</i>
ID=5268	WP_045855709	RnfH family protein	<i>Raoultella terrigena</i>
ID=5269	WP_041146800	MULTISPECIES: ubiquinone-binding protein	<i>Raoultella</i>
ID=5270	WP_041146801	SsrA-binding protein	<i>Raoultella ornithinolytica</i>
ID=5271	WP_041146807	transcriptional regulator	<i>Raoultella ornithinolytica</i>
ID=5272	WP_041146808	multidrug efflux RND transporter permease subunit OqxB	<i>Raoultella ornithinolytica</i>
ID=5273	WP_045857840	MexE family multidrug efflux RND transporter periplasmic adaptor subunit	<i>Raoultella terrigena</i>
ID=5274	WP_045857838	kinase	<i>Raoultella terrigena</i>
ID=5275	WP_045857836	hypothetical protein	<i>Raoultella terrigena</i>
ID=5276	WP_045857834	hydroxyacid dehydrogenase	<i>Raoultella terrigena</i>
ID=5277	WP_045857833	MFS transporter	<i>Raoultella terrigena</i>
ID=5278	WP_045857831	hypothetical protein	<i>Raoultella terrigena</i>
ID=5279	WP_045721975	hypothetical protein	<i>Salmonella enterica</i>
ID=5280	WP_064171024	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5281	WP_041145974	acetoin reductase	<i>Raoultella ornithinolytica</i>
ID=5282	WP_041145973	acetolactate synthase	<i>Raoultella ornithinolytica</i>
ID=5283	WP_045858713	alpha-acetolactate decarboxylase	<i>Raoultella terrigena</i>
ID=5284	WP_045858711	transcriptional regulator	<i>Raoultella terrigena</i>
ID=5285	WP_041145969	3-hydroxybutyrate dehydrogenase	<i>Raoultella ornithinolytica</i>
ID=5286	WP_041145968	MULTISPECIES: transporter	<i>Raoultella</i>
ID=5287	WP_045858704	3-hydroxybutyryl-CoA dehydrogenase	<i>Raoultella terrigena</i>
ID=5288	WP_041145966	acetyl-CoA acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=5289	WP_041145965	succinyl-CoA--3-ketoacid-CoA transferase	<i>Raoultella ornithinolytica</i>
ID=5290	WP_041145964	succinyl-CoA--3-ketoacid-CoA transferase	<i>Raoultella ornithinolytica</i>
ID=5291	WP_045858695	LysR family transcriptional regulator	<i>Raoultella terrigena</i>
ID=5292	WP_057173434	cystathionine beta-lyase	<i>Klebsiella michiganensis</i>
ID=5293	WP_004136708	MULTISPECIES: Na ⁺ /H ⁺ antiporter NhaC-like protein	<i>Klebsiella</i>
ID=5294	WP_048025259	endoribonuclease L-PSP	<i>Raoultella ornithinolytica</i>
ID=5295	WP_015585338	D-cysteine desulfhydrase	<i>Raoultella ornithinolytica</i>
ID=5296	WP_032728705	membrane protein	<i>Klebsiella oxytoca</i>
ID=5297	WP_032639964	MULTISPECIES: hypothetical protein	<i>Enterobacter cloacae</i>
ID=5298	WP_045858693	hypothetical protein	<i>Raoultella terrigena</i>
ID=5299	WP_045858690	glucose dehydrogenase	<i>Raoultella terrigena</i>
ID=5300	WP_041145960	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>
ID=5301	WP_041145959	ABC transporter ATP-binding protein	<i>Raoultella ornithinolytica</i>

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ID=5302	WP_041145958	peptide ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=5303	WP_041145957	diguanylate cyclase	<i>Raoultella ornithinolytica</i>
ID=5304	WP_045858680	ABC transporter substrate-binding protein	<i>Raoultella terrigena</i>
ID=5305	WP_041145955	ABC transporter	<i>Raoultella ornithinolytica</i>
ID=5306	WP_041145954	methionine ABC transporter substrate-binding protein	<i>Raoultella ornithinolytica</i>
ID=5307	WP_041145953	metal ABC transporter permease	<i>Raoultella ornithinolytica</i>
ID=5308	WP_041145952	SfnB family sulfur acquisition oxidoreductase	<i>Raoultella ornithinolytica</i>
ID=5309	WP_041145951	chloramphenicol acetyltransferase	<i>Raoultella ornithinolytica</i>
ID=5310	WP_041145950	bleomycin resistance protein	<i>Raoultella ornithinolytica</i>
ID=5311	WP_041145949	decarboxylase	<i>Raoultella ornithinolytica</i>
ID=5312	WP_044643839	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=5313	WP_045858039	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/..	<i>Raoultella terrigena</i>
		..inosine monophosphate cyclohydrolase	
ID=5314	WP_041143558	phosphoribosylamine--glycine ligase	<i>Raoultella ornithinolytica</i>
ID=5315	WP_045858041	membrane protein	<i>Raoultella terrigena</i>
ID=5316	WP_004097675	MULTISPECIES: transcriptional regulator	<i>Enterobacterales</i>
ID=5317	WP_041143557	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5318	WP_041143556	endonuclease V	<i>Raoultella ornithinolytica</i>
ID=5319	WP_041143555	MULTISPECIES: uroporphyrinogen decarboxylase	<i>Raoultella</i>
ID=5320	WP_041143554	NADH pyrophosphatase	<i>Raoultella ornithinolytica</i>
ID=5321	WP_041143553	sigma D regulator	<i>Raoultella ornithinolytica</i>
ID=5322	WP_041143552	phosphomethylpyrimidine synthase ThiC	<i>Raoultella ornithinolytica</i>
ID=5323	WP_041143551	thiamine phosphate synthase	<i>Raoultella ornithinolytica</i>
ID=5324	WP_041143550	molybdopterin biosynthesis protein MoeB	<i>Raoultella ornithinolytica</i>
ID=5325	WP_041143548	MULTISPECIES: thiazole synthase	<i>Raoultella</i>
ID=5326	WP_041143547	thiamine biosynthesis protein ThiH	<i>Raoultella ornithinolytica</i>
ID=5327	WP_041143546	sensor domain-containing diguanylate cyclase	<i>Raoultella ornithinolytica</i>
ID=5328	WP_041143545	MULTISPECIES: PTS sugar transporter subunit IIB	<i>Raoultella</i>
ID=5329	WP_041143544	MULTISPECIES: PTS lactose transporter subunit IIA	<i>Raoultella</i>
ID=5330	WP_041143543	anaerobic C4-dicarboxylate transporter	<i>Raoultella ornithinolytica</i>
ID=5331	WP_041143542	DNA-directed RNA polymerase subunit beta'	<i>Raoultella ornithinolytica</i>
ID=5332	WP_041143541	DNA-directed RNA polymerase subunit beta	<i>Raoultella ornithinolytica</i>
ID=5333	WP_004118416	MULTISPECIES: 50S ribosomal protein L7/L12	<i>Enterobacteriaceae</i>
ID=5334	WP_041143540	50S ribosomal protein L10	<i>Raoultella ornithinolytica</i>
ID=5335	WP_041143539	50S ribosomal protein L1	<i>Raoultella ornithinolytica</i>
ID=5336	WP_041143538	MULTISPECIES: 50S ribosomal protein L11	<i>Raoultella</i>
ID=5337	WP_041143537	MULTISPECIES: transcription termination/antitermination protein NusG	<i>Raoultella</i>
ID=5338	WP_041143536	MULTISPECIES: preprotein translocase subunit SecE	<i>Raoultella</i>
ID=5339	WP_044328210	hypothetical protein	<i>Citrobacter amalonaticus</i>
ID=5340	WP_064175190	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5341	WP_062164643	hypothetical protein	<i>Asaia bogorensis</i>
ID=5342	WP_062790432	hypothetical protein	<i>Serratia sp.</i>
ID=5343	WP_064359386	phage tail protein	<i>Raoultella ornithinolytica</i>
ID=5344	WP_064359387	phage baseplate protein	<i>Raoultella ornithinolytica</i>
ID=5345	WP_025713556	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=5346	WP_032717767	MULTISPECIES: baseplate assembly protein	<i>Enterobacteriaceae</i>
ID=5347	WP_025713558	MULTISPECIES: tail protein	<i>Enterobacteriaceae</i>
ID=5348	WP_064359389	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5349	WP_025713560	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=5350	WP_032717770	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5351	WP_025713562	MULTISPECIES: phage tail protein	<i>Enterobacteriaceae</i>
ID=5352	WP_025713563	MULTISPECIES: tail protein	<i>Enterobacteriaceae</i>
ID=5353	WP_064359393	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=5354	WP_064359394	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=5355	WP_048263921	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=5356	WP_048263920	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=5357	WP_064388697	capsid protein	<i>Klebsiella oxytoca</i>
ID=5358	WP_064388694	head decoration protein	<i>Klebsiella oxytoca</i>
ID=5359	WP_048263917	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=5360	WP_064388691	serine peptidase	<i>Klebsiella oxytoca</i>
ID=5361	WP_042944979	MULTISPECIES: phage portal protein	<i>Klebsiella</i>
ID=5362	WP_012540188	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5363	WP_064377765	hypothetical protein	<i>Klebsiella oxytoca</i>
ID=5364	WP_053289904	MULTISPECIES: tail assembly chaperone	<i>Enterobacteriaceae</i>
ID=5365	WP_048294177	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5366	WP_039184609	Rha family transcriptional regulator	<i>Hafnia paralvei</i>
ID=5367	WP_064180732	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5368	WP_064180723	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5370	WP_058836934	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>

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ID=5371	WP_058836933	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=5372	WP_064169508	DNA primase	<i>Klebsiella pneumoniae</i>
ID=5373	WP_045854074	gamma carbonic anhydrase family protein	<i>Raoultella terrigena</i>
ID=5374	WP_045854072	shikimate dehydrogenase	<i>Raoultella terrigena</i>
ID=5375	WP_041142951	L-threonylcarbamoyladenylate synthase TsaC	<i>Raoultella ornithinolytica</i>
ID=5376	WP_015369441	MULTISPECIES: hypothetical protein	<i>Enterobacteriaceae</i>
ID=5377	WP_041142952	MULTISPECIES: hypothetical protein	<i>Raoultella</i>
ID=5378	WP_041142953	DNA processing protein DprA	<i>Raoultella ornithinolytica</i>
ID=5379	WP_041142954	MULTISPECIES: peptide deformylase	<i>Raoultella</i>
ID=5380	WP_045854069	methionyl-tRNA formyltransferase	<i>Raoultella terrigena</i>
ID=5381	WP_041142955	methionyl-tRNA formyltransferase	<i>Raoultella ornithinolytica</i>
ID=5382	WP_041142956	16S rRNA m5C967 methyltransferase	<i>Raoultella ornithinolytica</i>
ID=5383	WP_041142957	MULTISPECIES: Trk system potassium transport protein TrkA	<i>Raoultella</i>
ID=5384	WP_041142958	MULTISPECIES: large-conductance mechanosensitive channel	<i>Raoultella</i>
ID=5385	WP_041142959	MULTISPECIES: ribosome rescue factor A	<i>Raoultella</i>
ID=5386	WP_041142960	MULTISPECIES: heavy metal-responsive transcriptional regulator	<i>Raoultella</i>
ID=5387	WP_041142961	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5388	WP_042873079	50S ribosomal protein L17	<i>Dickeya sp.</i>
ID=5389	WP_002919219	MULTISPECIES: DNA-directed RNA polymerase subunit alpha	<i>Proteobacteria</i>
ID=5390	WP_004868345	MULTISPECIES: 30S ribosomal protein S4	<i>Enterobacteriaceae</i>
ID=5391	WP_041142962	30S ribosomal protein S13	<i>Raoultella ornithinolytica</i>
ID=5392	WP_008807050	MULTISPECIES: preprotein translocase subunit SecY	<i>Klebsiella</i>
ID=5393	WP_041142964	MULTISPECIES: 50S ribosomal protein L15	<i>Raoultella</i>
ID=5394	WP_001140434	MULTISPECIES: 50S ribosomal protein L30	<i>GammaProteobacteria</i>
ID=5395	WP_004106339	MULTISPECIES: 30S ribosomal protein S5	<i>Enterobacteriales</i>
ID=5396	WP_062863346	50S ribosomal protein L18	<i>Escherichia coli</i>
ID=5397	WP_004868354	MULTISPECIES: 50S ribosomal protein L6	<i>Enterobacteriaceae</i>
ID=5398	WP_004106343	MULTISPECIES: 30S ribosomal protein S8	<i>Enterobacteriales</i>
ID=5399	WP_002919667	MULTISPECIES: 30S ribosomal protein S14	<i>Enterobacteriales</i>
ID=5400	WP_041142966	MULTISPECIES: 50S ribosomal protein L5	<i>Raoultella</i>
ID=5401	WP_041142967	MULTISPECIES: 50S ribosomal protein L24	<i>Raoultella</i>
ID=5402	WP_002919748	MULTISPECIES: 50S ribosomal protein L14	<i>Proteobacteria</i>
ID=5403	WP_041142968	MULTISPECIES: 30S ribosomal protein S17	<i>Raoultella</i>
ID=5404	WP_015962740	50S ribosomal protein L29	<i>Enterobacteriaceae bacterium</i>
ID=5405	WP_002919759	MULTISPECIES: 50S ribosomal protein L16	<i>Proteobacteria</i>
ID=5406	WP_002919766	MULTISPECIES: 30S ribosomal protein S3	<i>Enterobacteriales</i>
ID=5407	WP_000448832	MULTISPECIES: 50S ribosomal protein L22	<i>Enterobacteriaceae</i>
ID=5408	WP_001138115	MULTISPECIES: 30S ribosomal protein S19	<i>Enterobacteriales</i>
ID=5409	WP_041142969	50S ribosomal protein L2	<i>Raoultella ornithinolytica</i>
ID=5410	WP_052902730	50S ribosomal protein L23	<i>Erwinia iniecta</i>
ID=5411	WP_015960716	MULTISPECIES: 50S ribosomal protein L4	<i>Enterobacteriaceae</i>
ID=5412	WP_004868374	MULTISPECIES: 50S ribosomal protein L3	<i>Enterobacteriaceae</i>
ID=5413	WP_001181005	MULTISPECIES: 30S ribosomal protein S10	<i>Proteobacteria</i>
ID=5414	WP_041142971	MULTISPECIES: bacterioferritin	<i>Raoultella</i>
ID=5415	WP_044328210	hypothetical protein	<i>Citrobacter amalonaticus</i>
ID=5416	WP_032710320	hypothetical protein	<i>Klebsiella mobilis</i>
ID=5418	WP_038020864	transcriptional regulator	<i>Tatumella morbirosei</i>
ID=5419	WP_038020467	hypothetical protein	<i>Tatumella morbirosei</i>
ID=5420	WP_038020469	hypothetical protein	<i>Tatumella morbirosei</i>
ID=5421	WP_069785694	hypothetical protein	<i>Aeromonas caviae</i>
ID=5422	WP_038020471	hypothetical protein	<i>Tatumella morbirosei</i>
ID=5423	WP_058316550	capsid protein, partial	<i>Thalassobius sp.</i>
ID=5424	WP_000084700	MULTISPECIES: scaffolding protein D	<i>Bacteria</i>
ID=5425	WP_001224515	MULTISPECIES: hypothetical protein	<i>Bacteria</i>
ID=5426	WP_040977597	protein A*, partial	<i>Necropsobacter massiliensis</i>
ID=5427	WP_001450027	MULTISPECIES: minor spike protein H	<i>Proteobacteria</i>
ID=5428	WP_002417289	hypothetical protein, partial	<i>Enterococcus faecalis</i>
ID=5429	WP_032543344	phage capsid protein, partial	<i>Clostridioides difficile</i>
ID=5430	WP_032543344	phage capsid protein, partial	<i>Clostridioides difficile</i>
ID=5431	WP_058316550	capsid protein, partial	<i>Thalassobius sp.</i>
ID=5432	WP_041147500	UDP-N-acetylenolpyruvoylglucosamine reductase	<i>Raoultella ornithinolytica</i>
ID=5433	WP_041143533	bifunctional biotin-[acetyl-CoA-carboxylase] synthetase/biotin operon repressor	<i>Raoultella ornithinolytica</i>
ID=5434	WP_041143534	type I pantothenate kinase	<i>Raoultella ornithinolytica</i>
ID=5435	WP_058198466	hypothetical protein, partial	<i>Pseudomonas aeruginosa</i>
ID=5436	WP_066929792	endonuclease	<i>Mycobacterium sp.</i>
ID=5437	WP_061680676	hypothetical protein	<i>Bacillus cereus</i>
ID=5438	WP_061680676	hypothetical protein	<i>Bacillus cereus</i>
ID=5439	XP_017411387	PREDICTED: LINE-1 retrotransposable element ORF2 protein, partial	<i>Vigna angularis</i>
ID=5440	WP_041147174	transketolase	<i>Raoultella ornithinolytica</i>

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ID=5441	WP_032717684	spermidine/putrescine ABC transporter substrate-binding protein, partial	<i>Raoultella ornithinolytica</i>
ID=5442	WP_045853419	formate dehydrogenase subunit alpha	<i>Raoultella terrigena</i>
ID=5443	WP_032717259	hypothetical protein	<i>Raoultella ornithinolytica</i>
ID=5444	WP_025711640	IS110 family transposase	<i>Klebsiella</i> sp.
ID=5445	WP_041143642	Sell repeat	<i>Raoultella ornithinolytica</i>
ID=5446	WP_044643839	MULTISPECIES: hypothetical protein	<i>Klebsiella</i>
ID=5447	WP_039291612	transposase	<i>Cedecea neteri</i>
ID=5448	WP_017494427	hypothetical protein	<i>Gamma Proteobacterium</i>
ID=5449	WP_034888138	transposase	<i>Erwinia typographi</i>
ID=5450	WP_045856141	maltoporin	<i>Raoultella terrigena</i>
ID=5451	WP_041142972	MULTISPECIES: elongation factor Tu	<i>Raoultella</i>
ID=5452	WP_064175190	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5453	WP_064323901	hypothetical protein	<i>Klebsiella pneumoniae</i>
ID=5455	WP_021666093	MULTISPECIES: hypothetical protein	<i>Bacteria</i>
ID=5456	WP_021739601	MULTISPECIES: hypothetical protein	<i>Firmicutes</i>
ID=5457	WP_006687654	transposase	<i>Escherichia coli</i>
ID=5458	WP_040190608	MULTISPECIES: transposase	<i>Enterobacteriaceae</i>
ID=5459	XP_003403541	PREDICTED: uncharacterized protein LOC100652901	<i>Homo sapiens</i>
ID=5460	WP_012737454	MULTISPECIES: transposase	<i>Enterobacterales</i>
ID=5461	XP_007109663	PREDICTED: tigger transposable element-derived protein 1-like	<i>Physeter catodon</i>
ID=5462	WP_044781239	hypothetical protein	<i>Campylobacter jejuni</i>

Appendix VI: Gene – Node position

The following Appendix contains information relating to the node each gene ID (Appendix V) belongs to. The 21 largest nodes contain 5,619,566 bps and 5245 predicted genes, while the 21 smallest nodes contain 195,347 bps and 217 predicted genes.

NODE	NODE Length	Gene ID's	NODE	NODE Length	Gene ID's
1	1,452,774	1 – 1357	22	39,519	5246 – 5283
2	564,661	1358 – 1823	23	34,969	5284 – 5312
3	384,967	1824 – 2178	24	31,686	5313 – 5340
4	373,185	2179 – 2519	25	30,622	5341 – 5372
5	362,189	2520 – 2857	26	26,663	5373 – 5415
6	333,809	2858 – 3184	27	7,227	5416 – 5422
7	290,685	3185 – 3484	28	5,513	5423 – 5431
8	263,208	3485 – 3723	29	4,634	5432 – 5436
9	259,250	3724 – 3966	32	2,010	5437 – 5439
10	216,584	3967 – 4171	33	1,892	5440
11	184,501	4172 – 4379	34	1,882	5441 – 5443
12	178,364	4380 – 4530	35	1,742	5444 – 5446
13	112,654	4531 – 4625	37	1,237	5447 – 5450
14	103,965	4626 – 4728	40	1,013	4551
15	100,776	4729 – 4815	41	970	5452 – 5453
16	97,070	4816 – 4906	44	696	5454 – 5456
17	92,984	4907 – 4993	47	661	5457 – 5458
18	84,653	4994 – 5065	48	657	5459
19	79,058	5066 – 5161	50	626	5460
20	43,033	5162 – 5201	51	609	5461
21	41,196	5202 – 5245	55	519	5462
	Total	Total		Total	Total
	5,619,566	5245		195,347	217

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