Biotechnology Master Program

Joint Biotechnology Master Program

Palestine Polytechnic University
Deanship of Graduate Studies and
Scientific Research

Bethlehem University
Faculty of Science

Microbiological Evaluation of Endophytic Bacteria in Parsley and Mint in the West Bank

By

Sawsan Ibraheem Mahmoud Najajreh

In Partial Fulfillment of the Requirements for the Degree
Master of Science in Biotechnology

January,2021

The undersigned hereby certify that they have read and recommend to the Faculty of Scientific Research and Higher Studies at the Palestine Polytechnic University and the Faculty of Science at Bethlehem University for acceptance a thesis entitled:

"Microbiological Evaluation of Endophytic Bacteria in Parsley and Mint in the West Bank"

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A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science in biotechnology

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ABSTRACT

Mint (*Pepper mint*) and parsley (*Petroselinum crispum*) are two common herbal plants (fresh produce) used in Middle Eastern cuisine. Due to the high market demand, these two herbs are grown year-round in many countries including in Palestine. This study aimed to evaluate the internal (endophytic) microbial content in parsley and mint that are sampled from different markets in Hebron and Bethlehem cities. Samples were surface sterilized to eliminate epiphytic bacteria then an extract was prepared and cultured on two microbiological media, total coliform media and fecal coliform media. Bacterial genera were identified based on colony morphology. For total coliforms and fecal coliforms, CFU/g was calculated and compared between samples. No significant difference in microbial load between the commercial sources was found in both plants. No coliforms were found in the samples taken from home garden or in the negative control. Universal primers for 16S rDNA region were used to identify the bacterial species obtained from the culture step. The PCR products were sequenced and subjected to BLASTn in order to identify the sequenced bacteria. In total, seven different bacterial genera from three families were identified including *Pseudomonas, Pantoea, Enterobacter, Lelliottia, Escherichia, Klebsiella and Salmonella*. Furthermore, twenty-four different strains were identified from the sequenced in the two herbs. The results in this study should be considered to draw more attention regarding the food safety issues in fresh herbs quality and consumption.

Key words

Fresh produce, Fecal coliform, Total coliform, Endophytic bacteria

Arabic Abstract

النقييم الميكروبيولوجي للبكتيريا الداخلية في النباتات الخضراء في البقدونس والنعنع في الضفة الغربية

النعنع(*Pepper mint*) والبقدونس(Petroselinum crispum) من النباتات العشبية الشائعة المستخدمة في مطبخ الشرق الأوسط . نظرًا لارتفاع الطلب في السوق ، تتم زراعة هذين النوعين من الأعشاب على مدار العام في العديد من البلدان بما في ذلك فلسطين. هدفت هذه الدراسة إلى تقييم المحتوى الميكروبي الداخلي (endophytic)في البقدونس والنعنع المأخوذة من أسواق مختلفة في مدينتي الخليل وبيت لحم. تم تعقيم السطح الخارجي للنباتات للتخلص من البكتيريا الخارجية، ثم تم تحضير مستخلص النبات وزراعته على وسطين ميكروبيولوجيين ، (Total coliform and fecal coliform media). تلا ذلك تحديد الأجناس البكتيرية بناءً على مورفولوجيا المستعمرة. بالنسبة لل Total and fecal coliform، تم حساب CFU/g ومقارنتها بين العينات. حيث لم يتم العثور على فرق معنوي في وجود الميكروبات الداخلية بين المصادر التجارية في كلا النباتين. ولم يتم العثور على القولونيات في العينات المأخوذة من حديقة المنزل أو في السيطرة السلبية.

تم استخدام 16S rDNA لتحديد الأنواع البكتيرية التي تم الحصول عليها من خطوة الاستزراع. ثم تسلسل منتجات PCR وتعريضها لـ BLASTn من أجل التعرف على البكتيريا المتسلسلة. في المجموع ، تم تحديد سبعة أجناس بكتيرية من ثلاث عائلات مختلفة كما يلي *Pseudomonas*و *Pantoea* و *Enterobacter* و *Lelliottia*و *Escherichia coli* و *Klebsiella* و *Salmonella.* ،علاوة على ذلك ، تم التعرف على 24 سلالة مختلفة من البكتيريا الناتجة. ينبغي النظر في نتائج هذه الدراسة لجذب المزيد من الاهتمام فيما يتعلق بقضايا سلامة الأغذية في جودة الأعشاب الطازجة واستهلاكها.

DECLARATION

I declare that the Master Thesis entitled “Microbiological Evaluation of Endophytic Bacteria in Parsley and Mint in the West Bank” is my own original work, and hereby certify that unless stated, all work contained within this thesis is my own independent research and has not been submitted for the award of another degree at any institution, except where due acknowledgment is made in the text.

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Dedication

I would like to dedicate this work to my precious mother. She gave me strength and she always gave me inspiration and pushed me to the top.

I would like to sincerely dedicate the completion of this work to my husband Mohammad who is always being supportive and loving.

The last dedication will be to the love of my life; my daughters Sabine and Pinar who have sacrificed a lot to arrive at the completion of this work.

This work is specially dedicated to my father, sisters, brothers and loved ones.

Acknowledgment

Greatest thanks be to Allah for being the main source of strength and motivation throughout this study.

I would like to thank my supervisor Dr. Rami Arafeh for his helpful contribution to this work.

Much appreciation and thanks are due to all the staff at the Biotechnology Research Center. And the lab technicians Mrs. Asma’ Tamimi, Mr. Hasan Taradeh, Mr. Zaid Taradeh, and Mr. Ayman Eideh for their patient and relentless assistance.

Thanks also to the many friends I met while completing this program. Their support and companionship made the experience truly a delight.

Abbreviations

Abbreviation	Word or Sentence
16S rDNA	16S ribosomal RNA subunit gene
DNA	deoxyribonucleic acid
RNA	ribonucleic acid
rDNA	rDNA Ribosomal DNA
rRNA	ribosomal RNA
LB	Liquid Luria Bertani
w/v	weight/volume
rpm	rounds per minute
sec	Second
min	Minute
h	Hour
V	Volts
TBE	tris/borate/EDTA
EDTA	ethylene-diamine-tetra acetic acid
WHO	World Health Organization
EU	European Union
bp	base pair
DdH$_2$O	Deionized water
rpm	Round per minute
PCR	polymerase chain reaction
pH	Potential hydrogen
dNTP	Deoxyribonucleotide triphosphate
UV	Ultraviolet
NCBI	National Center for Biotechnology Information
BLAST	Basic Local Alignment Search Tool
Taq	Thermus aquaticus
CFU	Colony forming unit
µL	Micro liter
µM	Micro Molar
GW	Grey water

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CHAPTER ONE

Introduction

1.1 Consumption of Raw Vegetables and Herbs

Many raw vegetables and herbs are incorporated into fresh dishes, such as ready-to-eat salads and native delicacies. The consumption of these fresh vegetables adds high nutritional value to one’s diet, as they contain vitamins, dietary fibers, and minerals. They are often eaten raw to preserve their natural taste and preserve heat sensitive nutrients. Herbs, Particularly Parsley and mint are widely used in folk medicine in addition to providing nutrients and vitamins. Moreover, the antioxidant content of fresh vegetation is thought to have a protective effect against free radicals, which are implicated in the pathogenesis of most chronic diseases (Carlsen et al., 2010).

Fresh products occupies an increasingly important place in the human food supply because of its health-promoting nutritional properties. However, it must be noted that the consumption of raw vegetation, while nutritionally advantageous, its associated with increased risk of bacterial contamination. Data provided by the World Health Organization (WHO)/Food and Agriculture Organization (FAO) indicate that there was a 4.5% yearly increase in fruit and vegetable consumption between 1990 and 2004, with outbreaks of foodborne illnesses associated with the consumption of fresh produce increasing in frequency simultaneously (World Health Organization, 2008) These salad vegetables and herbs are normally consumed without heating or boiling step to get rid of unwanted contamination, which increases the possibility of food poisoning. The development of advanced diagnostic methods and surveillance systems have also enabled authorities to pinpoint fresh produce as the source of foodborne disease (Naimi et al., 2003).

1.2 Contamination of Vegetables and Herbs

Vegetables and herbs can become contaminated with enteric bacteria, viruses, and parasitic human pathogens throughout their production from planting to consumption. Contamination of products may occur at all stages of production and processing. Possible sources of contamination include soil, feces, water, ice, animals, harvesting and processing equipment, and workers at any stage of production (Harris et al., 2003). Since the early 1990s, awareness of the potential of fresh produce to cause foodborne disease has increased, and the number of reported outbreaks associated with the consumption of fresh vegetables has grown steadily. Most of the reported outbreaks of gastrointestinal disease linked to fresh produce have been associated with bacterial contamination, particularly with members of the *Enterobacteriaceae* family. *Salmonella* spp., *Shigella* spp., pathogenic *Escherichia coli*, *Listeria monocytogenes* and *Campylobacter* spp. (Uneke, 2007).

The quality of irrigation water used in agriculture is a very important factor to avoid contamination of plants for consumption, and is a potential hazard for human health and even plants. The use of untreated wastewater and water supplies contaminated with sewage for irrigation has been implicated as one of the important sources of pathogenic microorganisms contaminating vegetables. Several studies draw the connection between irrigation with contaminated water and the presence of a high microbial load or pathogenic bacteria on the vegetables (Rai & Tripathi, 2007) (Barker-Reid et al., 2009). The World Health Organization has recommended that crops to be eaten should be irrigated only with biologically treated effluent that has been disinfected to achieve a coliform level of not more than 100/100 ml in 80% of the samples.

Studies have also demonstrated that the use of poultry or cow manure as fertilizer during agronomic practices influences the fecal bacterial counts recorded on vegetables (Atidégla et al., 2016). Manure-handling guidelines suggest a composting period before application of manure (Augustin & Rahman, 2010). So it has been found that three days of composting animal manure at 131 F (55°C) is effective at lowering the amount of *E. coli*, *Salmonella* and *Listeria monocytogenes* to undetectable levels (Carlsen et al., 2010).

Post harvesting processes can also prove to be the source of contamination of fresh produce, as the produce pass through several pieces of equipment and are subject to several cooling and/or washing procedures. Studies have found cutting equipment, shredders, and conveyors, as well as other pieces of equipment, as the source of contamination of fresh produce with human pathogens (Buchholz et al., 2012).

Water used to wash produce post-harvesting has also been shown to be the source of contamination that caused large outbreaks of *Salmonella* (Sivapalasingam et al., 2003) (Gagliardi et al., 2003).

1.3 Determination of Microbial Quality

Coliforms are facultative anaerobic, Gram-negative, non-spore forming bacilli that ferment lactose and produce gas. They are commonly found in the environment, such as in soil, and in the intestines of animals, including humans. Total coliform count is commonly used as an indicator of the sanitary quality of food and water. Common genera include *Citrobacter, Enterobacter, Hafnia*, *Klebsiella*, and *Escherichia*.

Fecal coliforms are bacteria that are Gram-negative bacilli, not sporulated, oxidase-negative, facultative aerobic or anaerobic, able to multiply in the presence of bile salts or other surface agents that have equivalent properties, and are able to ferment lactose with acid and gas production in 48 h at the temperature of 44.5°C. Fecal coliforms are the coliform bacteria that generally originate from the intestinal tract of warm-blooded animals. They are cultured by increasing the incubation temperature to 44.5 C and using a somewhat different growth media.

Intestinal bacteria are primarily transmitted to the environment via feces, and therefore it is immensely important to monitor the potential fecal contamination of food and water in order to protect human and environmental health. Because fecal coliforms are considered a more accurate indication of animal or human waste than the total coliforms. However, reference to fecal coliforms by the term "thermotolerant coliforms" is gaining popularity because there exist a few genera of bacteria of non-fecal origin that are detected in testing procedures for fecal coliform. Thermotolerant coliforms include common root and shoot colonizers like *Enterobacter* and *Pantoea*, as well as plant pathogens like *Erwinia*, *Pectobacterium*, pathogenic species of *Pantoea*, and human pathogens such as certain *E. coli* stains, *Salmonella*, and *Shigella*.

E. coli is the most common thermotolerant coliform present in feces (typically >90%) and is regarded as the most specific indication of recent fecal contamination (Paruch & Mæhlum, 2012). The presence of *E. coli* in food is an indicator of direct or indirect fecal contamination, as well as an indicator for the possible presence of enteric pathogens. *E. coli* is the only member of the coliform bacteria and thermotolerant bacteria that is exclusively found in feces, and that does not multiply considerably in the environment (Haller et al., 2009).

Most *E. coli* strains are part of the normal flora of the gut and are harmless. However, there are also pathogenic strains associated with human and animal diseases. The Shiga toxin producing *E.*

coli (STEC) is a group of pathogenic strains of *E. coli* that has over 200 different serotypes. *E. coli* O157:H7 is the most important serotype in this group in regards to public health. This serotype is the main pathogenic bacteria that causes hemorrhagic colitis with bloody diarrhea and Hemolytic Uremic Syndrome. Fresh produce is recognized as an important source of foodborne pathogens; in particular pathogenic *E. coli*. Contaminated fruit and vegetables account for ≈20% of all reported outbreaks of verotoxigenic *E. coli* and notable outbreaks have occurred from spinach, lettuce, and sprouted seed.

1.4 Bacterial Identification

The identification of bacteria has traditionally involved a process of observing phenotypic characteristics, such as colony and cell morphology, by Gram staining or other staining procedures, nutritional and physical requirements for growth, and other factors that have been developed and improved to the point where basic laboratories are able to identify isolates to the species level by fairly simple procedures. The characteristics used in these traditional identification schemes are all phenotypic, meaning that they are the products of gene expression. With the development of new technology, it is now possible to study the microbial genome and identify species by genotypic characteristics. The development of certain technologies, notably PCR and Sanger sequencing, has caused an explosion of published methods for genotyping bacteria.

Some bacterial identification schemes rely on the production of a banding pattern. For example, Pulsed-field gel electrophoresis (PFGE) is a technique that involves the restriction digest of bacterial DNA followed by the electrophoretic separation of the large DNA restriction fragments to generate a highly specific genetic fingerprint. This method is the method of choice in the typing of human bacterial pathogens and the investigation of disease outbreaks; however, it is relatively costly and requires a number of days to obtain a result.

Other techniques for the identification of bacteria to the strain level rely on the sequencing of genetic markers. Multi-locus sequence typing (MLST) involves the sequencing of 400-500 base pair fragments of DNA at seven conserved genes. Multi-locus variable number of tandem repeats analysis (MLVA) is a technique that involves the amplification and sequencing of tandem repeats. MLVA is quicker and simpler to perform than MLST, but the technique suffers from issues with reproducibility.

Many bacterial species can be identified by sequencing specific sections of ribosomal DNA – the 16S rRNA gene is most commonly used - after amplification by PCR, and then comparing the results to sequences stored in a database. Presently, the bacterial ribosomal RNA (rRNA) operon, consisting of the 16S rRNA and 23S rRNA gene as well as an intergenic spacer (IGS) region, is the most frequently used molecular marker in microbial ecology. This is for a number of reasons, namely because of: (i) its universal abundance, (ii) the presence of both variable and highly conserved sequence domains, (iii) its high discriminatory potential, (iv) its multiple-copy nature, and (v) the availability of rDNA sequences in public databases such as GenBank regions. There are enough polymorphisms in the 16S rRNA gene to distinguish between species of bacteria. Because the 16s rRNA gene compromises a conserved region, universal PCR primers can be designed that are complementary to the conserved regions and the sequence of the variable region in between these regions is used for the phylogenetic assessment. The common lengths of sequences to compare are 500 and 1,500 bp, and sequences in databases are of various lengths (Clarridge, 2004).

The 16S rRNA gene sequences for a large number of bacterial strains have been sequenced. GenBank is the largest databank of nucleotide sequences, which includes over 108 million sequences, of which over 90,000 are of 16S rRNA gene. This means that there are many previously deposited sequences against which to compare the sequence of an unknown strain

All of the genotyping methods mentioned above have their limitations. Ideally, the sequence of the entire genome of a microbial isolate would be used to provide reliable typing. Until recently, this would have been very costly and taken years to complete, but with the evolution of next-generation sequencing (NGS) technology, whole genome sequencing (WGS) has become a practical option. Recently WGS has become within the scope of small clinical microbiology and research labs. The costs of NGS machines are falling and an entire bacterial genome can now be sequenced for a price comparable to the cost of MLST typing using conventional PCR/Sanger sequencing.

1.5 Parsley and Mint

Parsley (*Petroselinum crispum*) is a green herbaceous plant that belongs to the Apiaceae or Umbellifera family, which is recognized by aromatic plants and compound flower umbels. The Latin name *Petroselinum crispums* is derived from the Greek word (pétros) which means rock, and selinum which was the Latin name for celery (Parthasarathy et al., 2008)

It is a biennial herb and is widely propagated by seeds, which are sown 1cm below soil in relatively moist and warm conditions, best in a sunny area that receives direct light for 6–8 hours a day, with a pH range of 6–7, forming a plant with spindle-shaped roots and erect stems reaching height of 0.8 meters, with green leaves and yellow green flowers growing in groups. The upper leaves are dark green divided to create feather like-structure. The small greenish yellow flowers have five petals on compound umbels, and the lower leaves are divided into two or three sides. The fresh roots are yellowish, carrot shaped, with a yellowish-white to reddish-yellow clip (Peterson et al., 2006).

Many vegetables such as parsley, carrot and others, have therapeutic health benefits and anticancer activity due to their production of psoralen (5-methoxypsoralen) (Peterson et al., 2006).

Parsley is also known to act as an antioxidant, and have anticancer functionalities to produce phenolic compounds (Zhang et al., 2006).

Parsley extract also has a diuretic and laxative effect by interfering with the function of the Na+/K+ pump in the kidney and the colon through inhibition of the pump, which stimulates Na-K- Cl co-transporter and increases electrolyte and water secretion (Kreydiyyeh et al., 2001).

Mint (*Pepper mint*) is a plant with shallow roots close to the surface of the earth. It is a sterile plant that does not produce seeds. It grows in the spring by planting roots close to the surface, and is grown as a row crop in the first year after planting as it grows to give a solid holder called Meadow mint. The cultivation is preserved for several years by plowing the ground 4 to 6 inches deep in the late fall, which leads to keeping the field longer than 2 or 3 years (Murphy, 1953). Mint is also a plant that contains antioxidants, and has phenolics and polyphenolic compounds in its extract (Kanatt et al., 2007). Also, it has antimicrobial properties against the most prevalent microorganisms in oral infections (Al-Sum & Al-Arfaj, 2013).

1.6 Endophytic Bacteria

Bacteria can associate with plants in a number of ways. They can be pathogens, symbionts, epiphytes, or endophytes. Epiphytic bacteria are typically Gram negative and live on the surface of the plant, where they tend to cluster between epidermal cells, and are found in fewer numbers across the waxy cuticle. Dehydration and UV radiation seem to have a negative effect on the viability of epiphytic bacteria, which explains their relatively low numbers. In any case, visualization of leaves by scanning electron microscopy shows very few bacterial cells on leaves that have been washed, suggesting that epiphytic bacteria can be easily removed (Berg et al., 2005).

Of the four types of interactions between plants and bacteria, endophytic interactions are the least understood. Endophytes are bacteria that enter the interior of plants without causing disease symptoms or forming symbiotic structures like nodules. Endophytic bacteria are of interest because they can improve plant growth and the nutrition of plants through nitrogen fixation. Recent evidence has shown that human-pathogenic bacteria can also colonize plants as alternative hosts. Research has revealed that human enteric pathogenic bacteria can survive as endophytes or epiphytes, but the relationship depends on bacterial species as well as the plant cultivar. The phenomenon is still not well understood, but it may be dependent on the specific microflora of each plant. The phenomenon of pathogenic bacteria colonizing plants as endophytes is of particular interest because it means that human pathogens protected in the internal tissue of the plant cannot effectively be removed by standard post-harvest biocidal treatments or even surface sterilization (Berger et al., 2010).

Attachment of enteric human pathogens to plant tissue is the first step towards colonization of the plant environment. Fimbriae, flagella, and biofilms have a role in this attachment. It has been noted that different strains of *E. coli* differ in their ability to attach to alfalfa sprouts, and sometimes the ability to attach can be gained by the insertion of a plasmid containing the gene for curli (a type of fimbria) production (Jeter & Matthysse, 2005). Continued research in this area is needed to further the understanding of the interactions between different plants and different bacteria and what factors are critical for the establishment of pathogens in the internal plant environment.

As for the routes taken by bacteria to the inside of the plant, it could be by the leaf surface, which has numerous stomata that provide entry into the substomatal cavity. Damage caused by spoilage bacteria or fungi can also enable human pathogens to enter the plant tissue where they are protected. In immature plants, the protective structures such as the casparian strip are not fully formed, which enables the entry of bacteria into the xylem, which forms a continuous tube up to the leaves through which bacteria can travel.

Several studies have been designed to artificially inoculate plants with pathogenic bacteria in order to study the factors that lead to their internalization, such as the bacteria being present in the water or the soil or on the plant surface, and the bacterial load necessary to initiate internalization, as well as the point of entry. Lettuce, because of its commercial importance, has been used as a model to demonstrate the internalization of human pathogens. In one experiment, lettuce seedlings were propagated in soil inoculated with *E. coli* 0157:H7 of different concentrations. At different time intervals samples were taken and washed to remove surface located bacteria. The *E. coli* strain was then recovered from the internal tissues of the seedlings (Solomon et al., 2002).

In a similar study, colonization of plant roots by *E. coli* appeared to follow a process similar to that of some endophytic microflora like *Klebsiella pneumoniae* and *Pectobacterium*, which exploit natural openings, such as emerging lateral roots (Dong et al., 2003).

1.7 Outbreaks Attributed to Fresh Herbs

Fresh herbs, which are grown close to the soil surface are more susceptible to contamination, have been implicated as vehicles for the transmission of microbial foodborne disease worldwide. In the United States, from 1996 to 2015 the FDA reported nine outbreaks linked to basil, parsley, and cilantro, which resulted in 2,699 illnesses and 84 hospitalizations (Control & Prevention, 2014). Of those outbreaks, four were linked to basil, three to cilantro, and two to parsley, prompting microbiological surveillance sampling by the FDA. Other epidemiologic investigations have specifically implicated chopped uncooked parsley as the source of several Shigellosis outbreaks in the United States. The source of contamination was found to be unchlorinated water that was used in hydrocoolers and to make ice in the packing area where the parsley was grown. *Shigella* contamination is of particular concern because of the low infectious dose of about 10 cells, giving these bacteria the potential to cause large outbreaks. Overall, the number of foodborne pathogens that are associated with fresh produce has been increasing, with *E. coli* O157:H7 being the most common pathogen associated with them. In addition to *E. coli* O157:H7, *Salmonella* spp and *Listeria monocytogenes* are the most common pathogens that contaminate leafy green vegetables.

1.8 Fresh herbs (mint and parsley) in Palestine west bank:

The agricultural sector is one of the most important sources of economic growth and employment in Palestine. It is known as economic backbone of the majority of the local population, which, in addition to fulfilling the populations basic nutritional needs, directly benefits 50% percent of the population. For many centuries, the richness of Palestinian soil made it possible to produce of rich crops including fresh-herbs that provided the ingredients for delicious and healthy Palestinian cuisine. This sector carries much promises, but it faces a number of substantial obstacles, as growing herbs requires access to fresh water, technical expertise, and specially trained workers to prevent contamination with foodborne pathogens (Butterfield, 2000).

2. Problem Statement and Objectives

2.1 The main objective of the present study is:

To our knowledge, there is limited information available about the microbiological quality of fresh herbs available in the market in Palestine. Therefore, this study was designed to assess the microbiological quality of fresh parsley and mint in Hebron and Bethlehem and to identify potential risks for the consumers.

2.2 Specific objectives:

1. Explore the content of latent internal microbes

2. Identify the bacteria present in the samples, to determine if bacteria include pathogenic or non-pathogenic species.

CHAPTER TWO

Materials and Methods:

This study was conducted in the microbiology laboratory of Palestine-Korea biotechnology center at Palestine Polytechnic University, Hebron, Palestine.

2.1 Media preparation:

The following media were prepared and used in the experimental parts in this study:

2.1.1 M-Endo Agar LES (Total coliform):

M-Endo agar LES (HI Media Laboratories, 2019), was prepared according to the manufacturer’s instructions, by weighting of 51.05 grams of M-Endo agar LES powder in 980.0 ml deionized water containing 20.0 ml of 95% ethanol, mixed and boiled thoroughly to complete dissolve the powder. the membranes of filtration samples were transferred to the surface of the M-Endo Agar medium in the Petri dishes. the plates were incubated in the inverted position at 37°C for 22 ± 2 hours in the total coliform. Colonies that are red and have a metallic sheen were observed and counted.

2.1.2 M-FC Agar Rosolic acid (Fecal coliform):

M-FC Agar media (HI Media Laboratories, 2019), was prepared according to the manufacturer instructions, by weighting 52.0 g of the media powder in 1.0 L of deionized water mixed them thoroughly and heat it in the microwave with a frequent agitation and boil for 1.0 minute to complete dissolve the powder. Then added 10.0 mL of a 1.0% solution of rosolic acid in 0.2 NaoH with continue heating for 1.0-minute, pH was adjusted to 7.4 the membranes of filtration samples were transferred to the surface of the M-FC Agar medium in the Petri dishes, the plates were incubated in the inverted position at 44.5 ± 0.5°C for 22 ± 2 hours. colonies of fecal coliform that are blue, was observed and counted.

2.1.3 LB Agar, Miller medium

(Luria- Betrani) broth liquid medium, was prepared according to the manufacturer instructions, by weighting 25.0g LB broth, Miller and 15.0g agar in liter of deionized water ,10.0g tryptone, 10.0g sodium chloride (Nacl), and 5.0g yeast extract, mixed them thoroughly to complete dissolve the powder, the pH was adjusted to 7.0, The medium was autoclaved at 121°C for 15 min in regular autoclave. Then Glycerol stock was prepared by using freshly grown overnight culture of bacterial species (50-50% v/v) glycerol stock prepared by taking 500.0 µl of bacteria to 500.0 µl of autoclaved glycerol, mixed thoroughly before being stored at -80°C to be used in the future experiments.

2.2 Sample collection

Fresh parsley and mint were obtained from local groceries in Hebron city from Al-Helman Farms source (7 samples), neighboring markets (Rami-Levy market) (11 samples), and from home garden grown source in Hebron and Bethlehem cities (4 samples). Samples were transferred to the microbiology lab.

2.3 Sample processing

From each sample parsley and mint, (25.0 g) were examined as the following procedures:

a) Plants material was washed with 125.0 mL of 5.0% of sodium hypochlorite which was mixed with 375.0 mL deionized autoclaved water, followed by surface sterilization which was accomplished by using Ethanol 70% for less than 30 sec in order to ensure and eliminate epiphytic bacteria (Warakagoda and Subasinghe, 2011) followed by three times washing with 500.0 mL deionized autoclaved water.

b) The water of the washed samples was run through a membrane with a pore size of 0.45 µm to ensure that there were no external bacteria on the surface of the plant.

c) 5.0 grams of plant parts were grinded with sterilized mortar and pestle, in case of dried plants extract 500.0 µl of deionized autoclaved water were added and mixed well to facilitate grinding.

d) Serial dilution was carried out at 10- fold dilutions of the plant extract.

e) Freshly prepared bacterial cultures were grown overnight incubation, on fecal media Petri dish plates at 44°C, and total media Petri dish plates at 37°C for 24 hours.

f) After 24 hours, some colonies from the grown bacteria were picked with a loop and transferred to LB agar media plates as enrichment step.

2.4 Molecular characterization

2.4.1 Isolation of total genomic DNA

Bacterial total genomic DNA was extracted using a plant DNA purification kit (Norgen Biotek Crop, Ontario, Canada) according to the manufacturer's instructions.

2.4.2 Primer sequences used in this study:

Table 2.1: Sequence names, primer codes, and primer sequences used in this study

Primer code	Primer Sequence	Reference
16S rDNA	Forward 5' agt ttg atc ctg gct cag 3'	Barghouthi, S.A., 2011
16S rDNA	Reverse 5' gga cta cca ggg tat cta at 3'	Barghouthi, S.A., 2011

2.4.3 Polymerase Chain Reaction (PCR) conditions

The PCR protocol used to amplify 16S rDNA region was as follows: PCR mixture (final volume of 25.0µl) which contained 17.4µl molecular grade H_2O, 2.5 µl of 10x PCR buffer, 2.5µl of (20 mM $MgSO_4$)), 0.5µl of (10 µM dNTPs mixture) (Fermantus/DNTp100), 1.0µl of each forward and reverse primer working stock, 1.0 µl DNA template-from colony, and 0.125 µl of Taq-DNA -Polymerase (5units/ µl)(Hy-labs Ltd. Item number HTD0078). The negative control was composed of all the components of the PCR reaction except DNA template. The PCR reactions were carried out in an Applied Biosystem 2720 thermal cycler under the following settings: 95°C for 5.00 min; 34 cycles of 95°C for 1:00 min, 52°C for 1:00 min, 72°C for 1:30 min, and a final elongation at 72°C for 10:00 min.

2.4.4 Agarose Gel Electrophoresis

A 1.4% (w/v) agarose was prepared by dissolving 2.1 g agarose (Ultrapure agarose- Invitrogen REF#16500) in 150 ml 1X TBE buffer and 9.0 µl ethidium bromide (Fluka/46065) was mixed in the gel solution right before casting. Samples (25.0 µl) were then loaded. A100bpDNA ladder (GeneDireX/ DM001-r500) was run with the samples for size approximation. Electrophoreses was performed initially at 80V for 15 min. then changed to final constant power of 120 V for 1:00 hour. The gel was visualized using a Bio-Rad Molecular Imager® Gel Doc™ XR+.

2.4.5 DNA Purification

Purification of DNA was done as the following visualization of PCR bands; strong bands were directly purified from the gel, otherwise weak bands it was purified from the PCR product.

2.4.5.1 Gel Purification

The targeted bands for sequencing were cut from the gel, and then the DNA was purified using Nucleo Spin Gel and PCR Clean-up purification kit. Briefly, the gel containing the DNA was dissolved to get rid of it. Then a mini-column was used to separate the DNA from the degraded gel fragments. DNA was washed and then collected using DNAse- RNAse free water.

2.4.5.2 PCR product purification

Purification of the PCR product was done by Nucleo Spin Gel and PCR Clean-up purification kit. Briefly, buffers were added in proportion to the PCR reaction volume as detailed in the kit. The mixture was transferred to a binding column, which were used to adsorb the target DNA and get rid of other residues such as excess primers. The DNA was washed using the buffers from the kit and then collected.

2.4.6 Sequencing of 16S rDNA

DNA sequencing was performed at Augusta Victoria Labs by sanger sequencing, the samples were sequenced using sequencing PCR program under the following settings:95°C for 1 min, (25 cycles): 95°C for 10 sec, 52°C for 5 sec, 60°C for 4 min, 4°C for ∞.

Purification of the PCR product was done by (Big Dye X-Terminator Purification Kit Protocol P/N 4374403). Briefly, SAM solution and Big Dye X-Terminator Solution were added in proportion to the PCR reaction volume as detailed in the kit. Followed by mixing the contents for 30 minutes and centrifuge at 1000 rpm for 2 min.

2.5 Data analysis and software

The computer programs were used during this study, Microsoft Excel Office 2010 was the main computer program used. The sequences analysis done with BLASTn. and the resulting sequences were edited visually by using Sequencher v.4 software.

CHAPTER THREE

Results and Discussion

The presence of parsley and mint endophytic associated bacteria was revealed by screening various samples of plant material from different sources (Rami Levy, Hebron market, and home garden grown samples) The plant extract from some samples showed heavy contamination in both total coliform and fecal coliform media.

3.1 Isolation of Endophytic Bacteria

After surface sterilization procedure, samples were cultured for 72 h, and no contamination arising from the surface was evident (Figure 3.1). Thus, it was clear that the surface sterilization procedure eliminated all epiphytic bacteria, this was noted by (Warakagoda and Subasinghe, 2011) and all subsequent experiments were done on samples subject to the same procedure, and plant extracts were assumed to contain only endophytic bacteria .

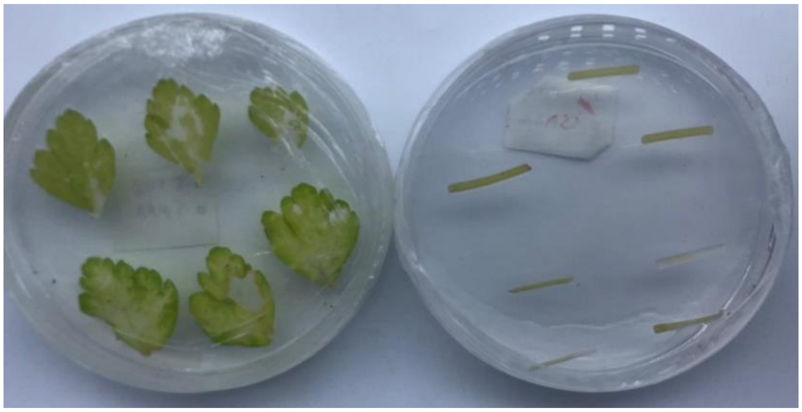

Figure 3.1: Parsley stem and leaves surface sterilized. Plant leaves and stems were cultured on plant growth media after surface sterilization in order to assure that all epiphytic contamination was eliminated.

3.2 Qualitative Analysis

Serial dilutions of samples were plated on total coliform and fecal coliform media. It was observed that total coliform media supported more microbial growth than fecal coliform media (Figure 3.2). Typical coliform genera were identified visually according to the manufacturer's instructions: *E. coli* - Pink to rose-red, green metallic sheen; *Enterobacter/Klebsiella* - Large, mucoid, pink; *Salmonella* - Colorless to pale pink; *Pseudomonas* - Irregular, colorless; *Pantoea* - Yellow pigmented. The number and percentage of positive samples for each genus out of eleven samples from Rami Levy and seven samples from Hebron market are found in Table 3.1. In addition to the above-mentioned genera which were mentioned in the manual, other rod-shaped and beige-pigmented colonies were also observed. These colonies were later identified as a strain of *Lelliottia*. Samples were taken from individual colonies for further molecular identification procedures.

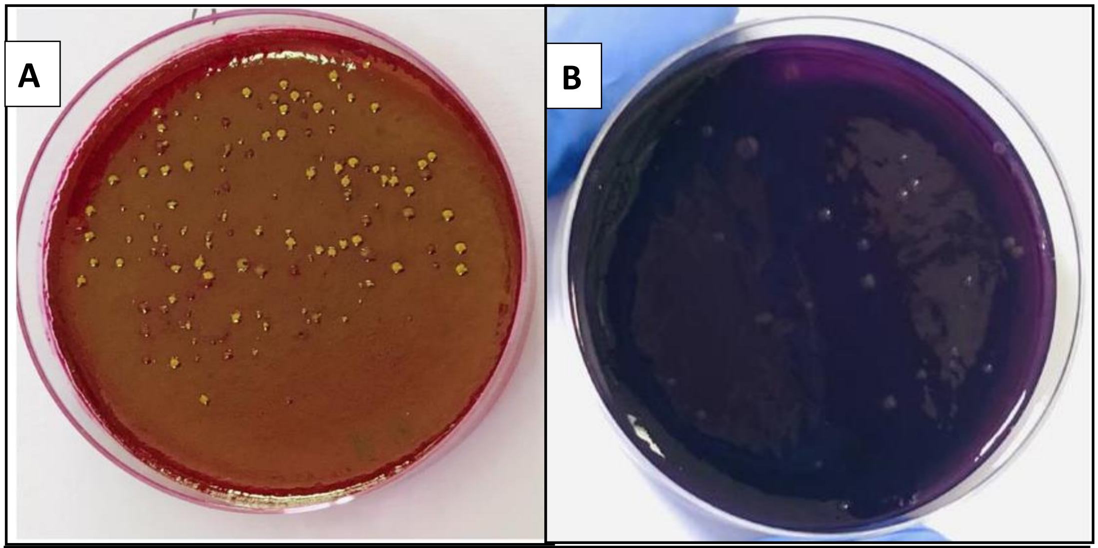

Figure 3.2: Endophytic bacteria on total coliform and fecal coliform media. Plant extracts containing endophytic bacteria were cultured on (A) total coliform and (B) fecal coliform media.

Table 3.1 Bacterial genera isolated from parsley and mint extract

Endophytic Bacteria								
Genus of bacteria	Herb source							
	Rami levy				**Hebron markets**			
	P(F)	P(T)	M(F)	M(T)	P(F)	P(T)	M(F)	M(T)
Pseudomonas no. (%)		1(9%)	3(27%)					
Pantoea no. (%)	4(36%)			2(18%)				
Enterobacter no. (%)	2(18%)	2(18%)		1(9%)	1(14%)	2(28%)		3(42%)
Lelliottia no. (%)								1(14%)
Escherichia coli no. (%)	1(9%)				3(42%)			
Klebsiella no. (%)							4(57%)	
Salmonella no. (%)	1(9%)							

Note

P:(Parsley), M:(Mint) F:(Fecal coliform) T:(Total coliform)

Table (3.1) shows the number of positive samples followed by the percentage of positive samples for each bacterial genus for each herb and source. The most prevalent genus from both commercial sources was *Enterobacter*, which was found in 11 samples, followed by *Pantoea*, which was found in 6 samples, *Klebsiella* in 4 samples, and *E. coli* and *Pseudomonas* in 4 samples. *Salmonella* and *Lolliottia* were each found in only 1 sample.

3.3 Quantitative Analysis

Table 3.2: Microbial load in the samples

Sample	**Source**	**Total coliform media**		**Fecal coliform media**	
		Median	**Range**	**Median**	**Range**
Mint	**Rami Levy**	5.66*	4.81 – 5.88	5.06	4.58 – 5.54
	Hebron market	5.82	5.36 – 6.27	4.65	4.53 – 4.78
	Home garden grown	0.0	0.0	0.0	0.0
Parsley	**Rami Levy**	5.98	5.94 – 6.03	4.96	4.81 – 6.11
	Hebron market	5.60	4.96 – 6.99	4.70	4.58 – 4.82
	Home garden grown	0.0	0.0	0.0	0.0
	Negative control	0.0	0.0	0.0	0.0

Log10 CFU/g*

Note: Samples that were not in the range of enumerated CFU per plate were excluded as they could not be reliably enumerated

3.3.1 Total Coliform Counts

No significant difference in total coliform level was found between the two commercial sources for either herb. The microbial load observed in mint was generally lower in samples taken from Rami Levy, which were found to have a total coliform count ranging from 4.81 – 5.88 Log_{10} CFU/g, compared to 5.36 – 6.27 Log_{10} CFU/g in samples taken from Hebron market. As for parsley samples, the opposite was true, Samples from Rami Levy contained 5.94 – 6.03 Log_{10} CFU/g, and samples from Hebron market contained 4.96 – 6.99 Log_{10} CFU/g. Parsley evidently contained more total coliform endophytic bacteria than mint, but the difference is not significant. No coliforms were found in the samples taken from the home garden source or the negative control.

3.3.2 Fecal Coliform Counts

No significance difference in fecal coliform level was found between the two commercial sources in both herbs. The microbial load observed in mint was generally higher in samples taken from Rami Levy, which were found to have a fecal coliform count ranging from 4.58 – 5.54 Log_{10} CFU/g, compared to 4.53 – 4.78 Log_{10} CFU/g in samples taken from Hebron market. As for parsley samples, the opposite was true, with samples from Rami Levy containing 4.81 – 6.11 Log_{10} CFU/g, and samples from Hebron market containing 4.58 – 4.82 Log_{10} CFU/g. No coliforms were found in the samples taken from the home source or the negative control.

3.4 Molecular Identification of Parsley and Mint Endophytic Bacteria

3.4.1 16s rDNA PCR, Gel electrophoresis and Sequencing

Samples from selected colonies were subjected to PCR using 16S rDNA primers. The amplification of the 16S rDNA region produced band at about 800 bp (Figure 3.3), and the purified bands were sequenced.

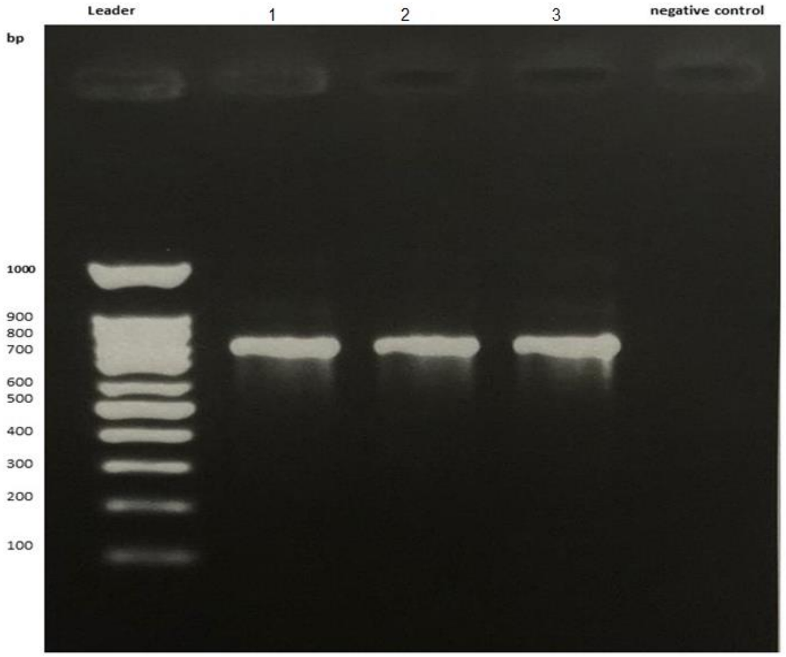

Figure 3.3: Agarose gel electrophoresis of the 16S rDNA region amplified by PCR. Leader - molecular 100 bp ladder; Lane 1,2,3- results of amplification of 16S rDNA region; Last lane - negative control.

Purified samples of the amplified PCR products were sent to Victoria Augusta Hospital in Jerusalem, Palestine for sequencing. DNA sequences were assembled from the forward and reverse sequences and chromatogram data was investigated and showed a single nucleotide signal. The product of the reverse sequence showed clear signals up to a particular point. On the other hand, the product from the forward primer showed double peaks which means there's more than one species in the same colony. Sequences were edited and evaluated visually in sequencher v.4 software. The sequences were subjected to BLAST search on the NCBI (National center of Biotechnology Information) database to explore similarity.

3.4.2 BLASTn Results

The sequences were subjected to BLASTn which identified similar bacterial species that had 100% sequence homology and 100-99% query coverage as shown in the following table (Table 3.5). Twenty-four different strains of bacteria were identified, belonging to seven different bacterial groups.

Table 3.3 Bacteria genera isolated from parsley and mint extract from both commercial sources based on BLASTn analysis of 16s rDNA sequencing data

Sequence number	Reverse sequence Length (after cleaning)	Mint or parsley	First BLASTn result	Query cover	Family	Notes/Pathogenicity
1	492 bp	Mint	*Pseudomonas koreensis* strain SS NBRI 17	100%	Pseudomonadaceae	• Inhibited a certain fungal plant pathogen
2	479 bp	Mint	*Pseudomonas* sp. strain COR10	100%	Pseudomonadaceae	• No information
3	191 bp	Mint	*Pseudomonas* sp A7-2	100%	Pseudomonadaceae	• Causative agents of fish diseases • Reduced nitrate to nitrite
4	213 bp	Parsley	*Pseudomonas putida* strain C1-1	100%	Pseudomonadaceae	• Associated with immunocompromised state • Fish diseases
5	366 bp	Parsley	*Pantoea agglomerans* strain NA131	99%	Erwiniaceae	• Cause of diseases in a range of cultivable plants • Tumorigenic, inducing gall formation on table beet, an ornamental plant gypsophila • Opportunistic human infections • Cause of equine abortion and placentitis and a haemorrhagic disease in dolphin fish
6	439 bp	Mint	*Pantoea agglomerans* strain HTP	100%	Erwiniaceae	
7	400 bp	Parsley	*Pantoea agglomerans* strain +Y43	99%	Erwiniaceae	
8	451 bp	Parsley	*Pantoea agglomerans* strain AA2	100%	Erwiniaceae	
9	350 bp	Mint	*Pantoea ananatis* strain PC2	99%	Erwiniaceae	• Plant pathogen • Capable of infecting humans
10	432 bp	Parsley	*Pantoea* sp strain B26	100%	Erwiniaceae	• Exhibit plant growth promoting abilities

11	424 bp	Parsley	*Pantoea vagans* strain+Y42	100%	Erwiniaceae	- Strain C9-1, is commercially registered as a biological control agent against fire blight
12	426 bp	Parsley	*Enterobacter cloacae* strain BHWSL4.2	100%	Enterobacteriaceae	- Causative agent of Chili pepper seedling
13	551bp	Parsley, mint	*Enterobacter cloacae* strain 3849	100%	Enterobacteriaceae	
14	295 bp	Parsley	*Enterobacter hormaechei* strain SU103	100%	Enterobacteriaceae	- Nosocomial pathogen - Invasive infections
15	357 bp	Mint	*Enterobacter cancerogenus* strain ILQ201	100%	Enterobacteriaceae	- Associated with urinary tract infections in human
16	265 bp	Mint	Uncultured *Enterobacter* sp. clone 65-160B-CB90	99%	Enterobacteriaceae	- No information
17	252 bp	Mint	*Lelliottia* sp. strain S2E38	100%	Enterobacteriaceae	- Play significant roles in environmental and agricultural sustainability
18	213 bp	Parsley	*Escherichia coli* strain 188	100%	Enterobacteriaceae	- No information
19	261 bp	Parsley	*Escherichia coli* strain SCU-397	100%	Enterobacteriaceae	- Carrying antibiotic resistance genes
20	200 bp	Parsley	*Escherichia coli* strain EcPF5	100%	Enterobacteriaceae	- Urinary tract infection
21	444 bp	Mint	*Klebsiella pneumoniae* strain G-A-TGW	100%	Enterobacteriaceae	- Important pathogens in nosocomial infections - Antimicrobial-resistant and multidrug-resistant - Causes foodborne outbreak
22	376 bp	Mint	*klebsiella pneumoniae* subsp. *pneumoniae* strain SU101	100%	Enterobacteriaceae	
23	474 bp	Mint	*Klebsiella quasipneumoniae* subsp. *similipneumoniaestrain* 2437	100%	Enterobacteriaceae	

24	99 bp	Parsley	*Salmonella enterica* strain SA20083039	100%	Enterobacteriaceae	• Associated with foodborne illnesses, causing hospitalizations and deaths

3.4.3 Discussion of BLASTn Results

The various bacterial species identified in this study are widely dispersed throughout the environment and can be found in soil, water, plants, and some in the gastrointestinal tract of animals and humans.

Isolated Bacteria Belonging to Pseudomonadaceae (Sequences 1 – 4)

Four of the sequences attained belong to the family Pseudomonadaceae, and all were of the genus Pseudomonas. BLASTn results revealed high similarity with 100% query cover included: *Pseudomonas koreensis strain SS NBRI*, *Pseudomonas sp. strain COR10, Pseudomonas sp A7-2, and Pseudomonas putida strain C1-1*.

The genus *Pseudomonas* contains more than 140 species, all of which are Gram-negative and aerobic bacilli, and most of which are saprophytic. More than 25 species are associated with humans. Most pseudomonads known to cause disease opportunistic infections in humans, including *Pseudomonas putida* (Baron, 1996). Some *Pseudomonas* species have been reported to be causative agents of disease in fish (SHIOSE et al., 1974).

Following is the available information about the BLASTn results.

Pseudomonas koreensis **strain SS NBRI 17 (Sequence 1)**

This strain is an isolate taken from agricultural soil in Korea, and reported in a study title "Suppression of disease in tomato infected by *Pythium ultimum* with a biosurfactant produced by *Pseudomonas koreensis*", where it was found to produce compounds that inhibit a certain fungal plant pathogen (Hultberg et al., 2010).

Pseudomonas **sp A7-2 (Sequence 3)**

This is a new *Pseudomonas* species, for which the name *Pseudomonas plecoglossicida* is proposed, and was isolated from the cultured fish ayu (*Plecoglossus altivelis*) with bacterial haemorrhagic ascites. The causative agent was similar to *Pseudomonas putida* biovar A in its phenotypic characteristics and on the basis of 16S rRNA gene sequence analysis, but it reduced nitrate to nitrite (Nishimori et al., 2000).

Pseudomonas putida strain C1-1 (Sequence 4)

P. putida is a flagellated member of the fluorescent group of pseudomonads, and is found throughout the natural environment. *P. putida* is an uncommon cause of skin and soft tissue infections, which is often associated with trauma or an immunocompromised state (Thomas et al., 2013).

Isolated Bacteria Belonging to Erwiniaceae (Sequences 5 – 11)

The second bacterial group consisted of 12 bacterial colonies with similar morphotypes, all belong to the *Erwiniaceae* family and genus *Pantoea* based on BLASTn results revealed a high similarity between 99% to 100% query cover which included*: Pantoea agglomerans* strain NA131*, Pantoea agglomerans* strain HTP, *Pantoea agglomerans* strain +Y43, *Pantoea agglomerans* strain AA2*, Pantoea ananatis* strain PC2, *Pantoea* sp. strain B26, and *Pantoea vagans* strain +Y42.

Species of the genus *Pantoea* are usually isolated from fecal matter, plants, and soil, where they exist as either pathogens or commensals.

No information is available about the specific strains obtained by BLASTn belonging to this family. Following is information available about the various bacteria identified at the species level.

Pantoea agglomerans (Sequences 5-8)

Pantoea agglomerans is a bacteria known to be associated with plants. *P. agglomerans* usually occurs in plants as an epi- or endophytic mutualistic symbiont, but nevertheless, this species has also been identified as a cause of diseases in a range of cultivable plants, such as cotton, sweet onion, rice, maize, sorghum, bamboo, walnut, an ornamental plant called Chinese taro (Alocasia cucullata), and a grass called onion couch (Arrhenatherum elatius). Some plant-pathogenic strains of *P. agglomerans* are tumourigenic, inducing gall formation on table beet, an ornamental plant gypsophila (*Gypsophila paniculata*), and wisteria vines (Dutkiewicz et al., 2016)

While it is not an obligate infectious organism in humans, it can be a cause of opportunistic human infections, mostly in infected wounds caused by plant material, or as a hospital-acquired infection, which occurs mostly in immunocompromised individuals. *P. agglomerans* bacteremia has also been documented in association with the contamination of various materials, such as intravenous fluid, total parenteral nutrition, the anesthetic agent propofol, and other blood products (Cruz et al., 2007).

There are few reports of infectious diseases caused by *Pantoea agglomerans* in vertebrate animals other than humans. It has been identified as a possible cause of equine abortion and placentitis and a haemorrhagic disease in dolphin fish (Coryphaena hippurus). *P. agglomerans* strains also occur commonly, usually as symbionts, in insects and other arthropods.

Pantoea ananatis **(Sequence 9)**

Pantoea ananatis is a bacteria that occurs in diverse ecological niches. It is most significantly a plant pathogen, infecting monocotyledonous and dicotyledonous plants, causing disease in a wide range of economically important agricultural crops and forest tree species. It is considered an emerging pathogen based on the increasing number of reports of disease occurring on new hosts in different parts of the world. Unlike the majority of plant pathogenic microbes, *P. ananatis* is capable of infecting humans (Coutinho & Venter, 2009).

Disease symptoms in plants usually include the appearance of leaf blotches and spots, and stalk, fruit, and bulb rot. Center rot of onion was first described in Georgia in 1997. The disease was devastating and accounted for 100% loss in some fields. Since its discovery, *P. ananatis* has been responsible for sporadic losses of onion crops in Georgia, but it has been particularly severe in certain late-maturing cultivars. In addition to onions, the bacteria has been reported to infect cantaloupe, Eucalyptus, honeydew melons, muskmelons, pineapple, and Sudangrass. It has also been associated with a condition known as graywall in the tomato (Gitaitis et al., 2003)

Pantoea sp (Sequence 10)

Pantoea sp. Reported as having the ability to vigorously colonize rice and to exhibit plant growth promoting abilities such as N2 fixation, phytohormone production and phosphate solubilization etc. (Verma et al., 2001) this can be potentially useful for rice plants.

Pantoea vagans (Sequence 11)

Pantoea vagans is closely related to Pantoea agglomerans, and these two species are often isolated from similar environments.

Pantoea vagans is a Gram-negative enterobacterial plant epiphyte of a broad range of plants. One strain Pantoea vagans, strain C9-1, is commercially registered as a biological control agent against fire blight, a disease of pear and apple trees. (Smits et al., 2010)

Isolated Bacteria Belonging to *Enterobacteriaceae* (Sequences 12 – 24)

Sequences from the remaining morphotypes exhibited high homology, and the BLASTn results matched with *Enterobacteriaceae* bacterial family with 99%-100% query cover. The results included the following species: *Enterobacter cloacae* strain BHWSL4.2, *Enterobacter cloacae* strain 3849, *Enterobacter hormaechei* SU103, *Enterobacter cancerogenus* ILQ201, Uncultured *Enterobacter* sp. clone 65-160B-CB90, *Lelliottia* sp. strain S2E38, *Escherichia coli* strain 188, *Escherichia coli* SCU-397, *E. coli* EcPF5, *Klebsiella pneumoniae* G-A-TGW, *Klebsiella pneumoniae* subsp. *pneumoniae* strain SU101, *Klebsiella quasipneumoniae* subsp. *similipneumoniae* strain 2437, *Salmonella enterica* SA20083039.

In cases where the is limited information about the particular strain obtained in the BLASTn result, information is included about the bacteria at the species level.

Enterobacter cloacae (Sequences 12 and 13)

A previously unreported bacterial disease on chili pepper (*Capsicum annuum* L.) seedlings affecting as many as 4% of seedlings was observed in greenhouses in Chihuahua, Mexico. Disease symptoms began as small irregular spots and necrosis on leaf tips, and advanced to defoliation. A Gram negative, rod-shaped bacterium was isolated from diseased chili pepper seedlings. *Enterobacter cloacae* was later identified as the causative agent of this outbreak (García-González et al., 2018).

Enterobacter hormaechei SU103 (Sequence 14)

E. hormaechei is a nosocomial pathogen that can infect vulnerable hospitalized patients, particularly neonates in intensive care units (Wenger et al., 1997)

The Netherlands witnessed a nationwide outbreak with a strain of E. hormaechei. The strain spread through hospitals, despite implementation of internationally accepted infection-prevention guidelines, and caused invasive infections in more than 100 patients (Paauw et al., 2006).

Virulence traits have been tested and all studied strains were shown to have the ability invade gut epithelial, and blood–brain barrier endothelial cells, and to persist in macrophages. Due to misidentification, it has been suggested that E. hormaechei may be an under-reported cause of infection, especially in neonates. Its isolation from various sources, including powdered infant milk formula, also makes it a cause for concern. (Townsend et al., 2008).

Enterobacter cancerogenus **(Sequence 15)**

A study documented four cases of *E. cancerogenus* infection associated with septicemia in two elderly men and two urinary tract infections in patients with underlying medical complications. (Abbott & Janda, 1997).

Lelliottia **(Sequence 17)**

As for *Lelliottia*, it is a genus that has been associated with corn roots inoculated with Canadian woodland soils. It is also known to play significant roles in environmental and agricultural sustainability, and the versatility of this bacterial group allows it to colonize diverse environmental spheres such as the plant rhizosphere, water, and soils. In addition to the ability to adapt in new environments, it also exhibits a wide spectrum of phenotypic traits, including the production of active secondary metabolites (Tchagang et al., 2018).

Escherichia coli strains (Sequences 18 – 20)

Escherichia coli forms part of the normal flora in the gut of humans and other animals. Most *E. coli* are harmless to humans. However, certain pathogenic *E. coli* strains can infect the gut and cause severe illness (Croxen et al., 2013).

E. coli is a commonly used fecal indicator organism. Its presence in food generally indicates direct or indirect fecal contamination. Substantial numbers of E. coli in food suggests a general lack of cleanliness in handling and improper storage. In ready to eat foods it is suggested that a satisfactory level of *E. coli* is <20 CFU/g ((Food & Department, 2014). This study did not enumerate E. coli, but the presence of E. coli warrants further study to quantify the amount, and indicates that there is some form of fecal contamination.

E. coli **strain SCU-397 (Sequence 19)** has been identified as carrying antibiotic resistance genes (Stephens et al., 2020).

***Escherichia coli* strain EcPF5 (Sequence 20)** was identified as uropathogenic in clinical cases of postmenopausal women with recurrent urinary tract infections (Sharon et al., 2020).

Enterohemorrhagic *Escherichia coli* O157:H7 is a major foodborne pathogen that causes severe disease in humans worldwide (Lim et al., 2010).

E coli O157 does not cause disease in cattle and can be found in the feces of healthy cattle, and is transmitted to humans by the fecal-oral route through contaminated food, water, and direct contact with infected people or animals. Human infection, in addition to causing asymptomatic shedding in some individuals, can also be associated with a wide range of clinical illness, including non-bloody diarrhea, haemorrhagic colitis, haemolytic uraemic syndrome, and death (Mead & Griffin, 1998).

Interestingly, for all of the three sequences that were identified as *E. coli* in the BLASTn search, *E. coli* O157:H7 was identified as a secondary result with the same identity and query parameter percentages. The presence of this foodborne pathogen is considered unacceptable, and food safety guidelines suggest that this strain should not be detected in 25 g of ready to eat food (Food & Department, 2014).Without further study it is impossible to know if this foodborne pathogen was present or not.

Klebsiella pneumoniae (Sequences 22 and 23)

Being part of the normal animal and human flora, contamination of food with *K. pneumoniae* may not represent as a public health risk. However, this bacteria can cause destructive changes to human and animal lungs if aspirated, resulting in bloody, brownish or yellow colored jelly like sputum. In the clinical setting, it is the most significant member of the genus *Klebsiella*. In recent years, *Klebsiella* species have become important pathogens in nosocomial infections. This bacteria has also been reported as the cause of a foodborne outbreak (Calbo et al., 2011). This bacterial species is also of concern because of the multiple reports of the presence of antimicrobial-resistant and multidrug-resistant (MDR) *K. pneumoniae* strains in the food chain (Guo et al., 2016)

Some strains have also been reported that have acquired resistance to last-line antibiotics (i.e., carbapenems) (Pitout et al., 2015).

The existence of *K. pneumoniae* isolates that carry antimicrobial resistance genes could potentially be an indirect public health hazard, regardless of their pathogenicity, because they increase the available genetic pool of resistance genes.

Other studies have also found *K. pneumoniae* in fresh produce. A study carried out in Singapore found *K. pneumoniae* in 58% (50 of 86) of raw vegetables (Hartantyo et al., 2020)

Another study reported lower *K. pneumoniae* prevalence rates on raw vegetables from wet markets, compared with those from supermarkets (Puspanadan et al., 2012).

This difference was attributed to quicker turnover of products, suggesting that prolonged storage of vegetables in humid conditions should also be avoided.

Considering the prevalence of this bacteria in food, and the possibility of infection from this bacteria that is known to often have antibiotic resistance, it is not overcautious to suggest additional food safety measures need to be practiced downstream, at retail and in the home.

Klebsiella quasipneumoniae **subsp. similipneumoniaestrain (Sequence 23)**

K. quasipneumoniae was distinguished from *K. pneumoniae* as new species in 2004., whereas they were previously classified *K. pneumoniae* phylogroup KpII, since then isolates have been obtained from clinical samples (Garza-Ramos et al., 2016). and have been reported to have resistance to antibiotics ((Furlan et al., 2020).

Salmonella enterica **(Sequence 24)**

According to the CDC, *Salmonella* accounts for an estimated 1.35 million infections, 26,500 hospitalizations, and 420 deaths in the United States every year (NM, AL, & RI). Most people who get ill from *Salmonella* have diarrhea, fever, and stomach cramps. It is the third most common agent associated with foodborne illnesses, and the No. 1 foodborne pathogen causing most hospitalizations and deaths in the United States.

Salmonella lives in the intestines of most livestock and many wild animals, and is naturally present in the environment. This makes it an important food safety challenge. In the guidelines for foodstuff in some countries, *Salmonella* contamination is not tolerated. For example, in Canada, any ready-to-eat food found to contain *Salmonella* spp. would most likely fall under the classification of a health risk 2 concern and would lead to a food recall. (Ngueng Feze et al., 2018).

CHAPTER FOUR

Conclusions and Future Work

4.1 Conclusions

In this study a considerable amount and diversity of endophytic bacteria was found in the parsley and mint samples studied. Twenty-four different bacterial strains were successfully isolated and identified based on their 16S rDNA sequences. This is in agreement with other studies that also found a rich diversity of endophytic bacteria in fresh produce (Machado-Moreira et al., 2019).

This emphasizes the fact that plant endophytic bacteria are a natural phenomenon and that this association is not restricted to a certain group of plants. As for the source of this endophytic bacteria, these bacterial species could originate from a number of sources, including soil, irrigation water, manure, seeds, workers, insects, bird's feces, and many other factors that affect the bacterial presence in plants.

While most of the bacterial species found in this study are part of the normal flora found in soil and plants, and are only considered opportunistic pathogens, the probable presence of *E. coli O104:H4* and *Salmonella enterica* is concerning, considering the possible implications for human health. Outbreaks of these bacteria over the past decade have been attributed to the consumption of contaminated uncooked foods. Also, the identification of *E. coli* strains in the plant extract means that the samples were exposed to direct or indirect fecal contamination, which could be from the irrigation water, soil, manure, or other sources.

Pathogenic *E. coli* is not only known to cause huge economic losses, but also impacts human health and in some cases even causes death. Infections and intoxication as a result of foodborne outbreaks also cause billions of dollars' worth of damage, public health problems, and agricultural product loss. A considerable portion of these outbreaks is caused by foodborne pathogens on fresh produce. An *E. coli O104:H4* outbreak in Germany in 2011attracted great attention to foodborne outbreaks caused by contaminated fresh produce, and highlighted vulnerability and gaps in the early warning and notification networks in surveillance systems all around the world (Yeni et al., 2016).

It is possible that the source of the bacteria from irrigation water. It has been well-established that raw grey water (GW) is contaminated with pathogens (although less than "full" domestic wastewater) and other chemical contaminants, and thus should be treated before reuse. Potential health risks associated with the spread of pathogenic organisms through the use of treated GW are critical issues. In fact, a number of pathogens are occasionally found in raw GW (RGW), including fecal coliforms, fecal *enterococci*, fecal streptococci, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*, among others. Interestingly, contradicting results regarding increasing levels of fecal coliforms in soils following long term greywater irrigation were reported. Studies concluded that disinfection of treated greywater may reduce the risks not only from the potential presence of pathogens but also from the presence of ARB and antibiotic resistance genes (Troiano et al., 2018).

The striking difference in results between commercial sources of parsley and mint and home garden grown parsley and mint also need an explanation. The absence of endophytic bacteria in home garden grown parsley and mint could be due to the soil quality and irrigation water used. People usually water plants in and around their home garden using municipality water. Chlorine is widely used by municipal water systems to disinfect water from bacteria, viruses and other microorganisms that cause diseases. The use of this treated water to irrigate home garden grown plants may inadvertently kill coliform bacteria that would otherwise be left to colonize the plant. This effect has been demonstrated in experiments on spinach irrigated with water containing chlorine dioxide (Truchado et al., 2018).

Interestingly, the bacteria that were found to be particularly susceptible to the disinfected water belonged to the *Pseudomonaceae* and *Enterobacteriaceae* bacterial families, to which most of the bacteria identified in this study belong.

On the other hand, the assessment of the natural microbiome of consumable plants is important, as natural microbial communities may reduce the likelihood of pathogen colonization or survival. For example, reduced levels of *Salmonella enterica* colonization have been observed in lettuce that had a more diverse endophyte community. The mechanism for the reduction in pathogen numbers with increased endophyte diversity is not conclusively known, but may be due to an increased likelihood of the presence of antagonists to *S. enterica* being present with an increase in overall diversity.

Additional support for this concept comes from a study examining the viability of *E. coli* O157:H7 in romaine lettuce, where the phyllo-sphere bacterial diversity in plants that had culturable *E. coli* O157:H7 cells differed from that on plants where the *E. coli* was no longer viable. Native plant-associated microorganisms can act as competitors to potential human pathogens such as *Salmonella* species and *E. coli* O157:H7, suggesting that even in the absence of specific antagonistic interactions, natural phyllo-sphere and endophytic communities may limit the presence and abundance of pathogenic bacteria by simply outcompeting them in the living plant. Determining the structure of these communities might therefore provide insights into produce-borne outbreaks of disease, and even lead to the development of tools to assess the likelihood of these outbreaks occurring. Intentional inoculation of competitive native microbiota has even been proposed as a potential method to reduce pathogenic contamination of fresh produce (Jackson et al., 2015).

4.2 Future Work

Consumers have the right to be informed and must be warned about any health hazard in their food and household products. Greater attention should be paid to the prevention and control of foodborne pathogens, as well as the identification of outbreaks. Thus, it is very important to develop a rapid and reliable method for foodborne pathogenic bacteria detection.

Being that this preliminary study produced concerning results, such as the presence of *E. coli* and *Salmonella,* it is suggested that further inclusive and intensive screening of the soil, irrigation water, manure, and plants is carried out to pinpoint the source of the fecal coliform bacteria. Surveys should be expanded to include more samples, taken from other markets and sources.

It is also suggested to do more intensive screening of epiphytic as well as endophytic bacteria associated with raw plants, especially those that have close contact to the soil surface. Researchers can use selective media for known pathogenic bacteria, and can use *E. coli* as an indicator for fecal contamination. Whole genome sequencing should also be carried out on samples to characterize the bacteria more precisely.

Further studies should also be carried out to elucidate if the endophytic microflora may benefit the plants. Identifying the interactions between environment and bacterial organisms should be investigated to know what is behind these interactions and any benefits for human or animal health.

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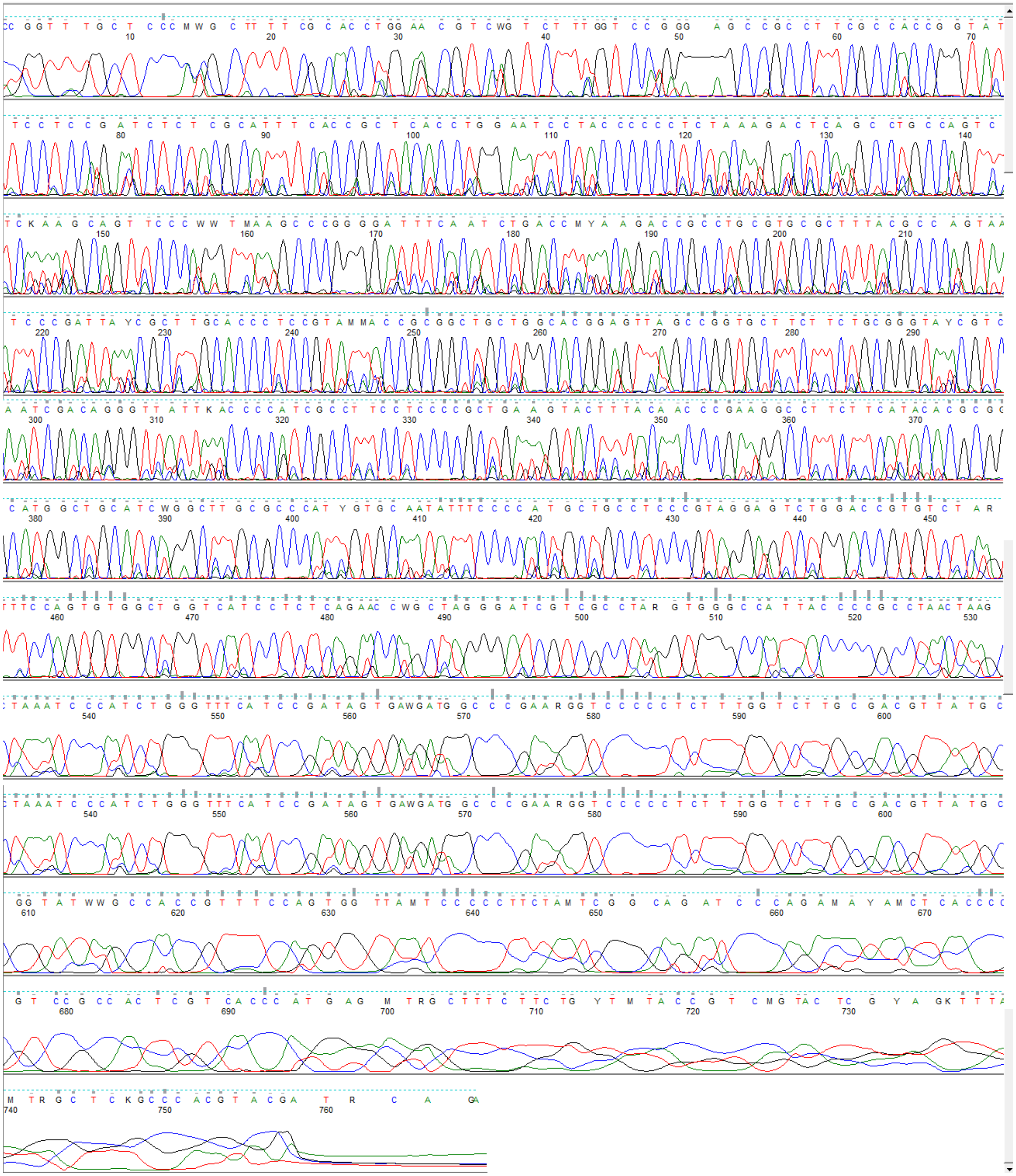
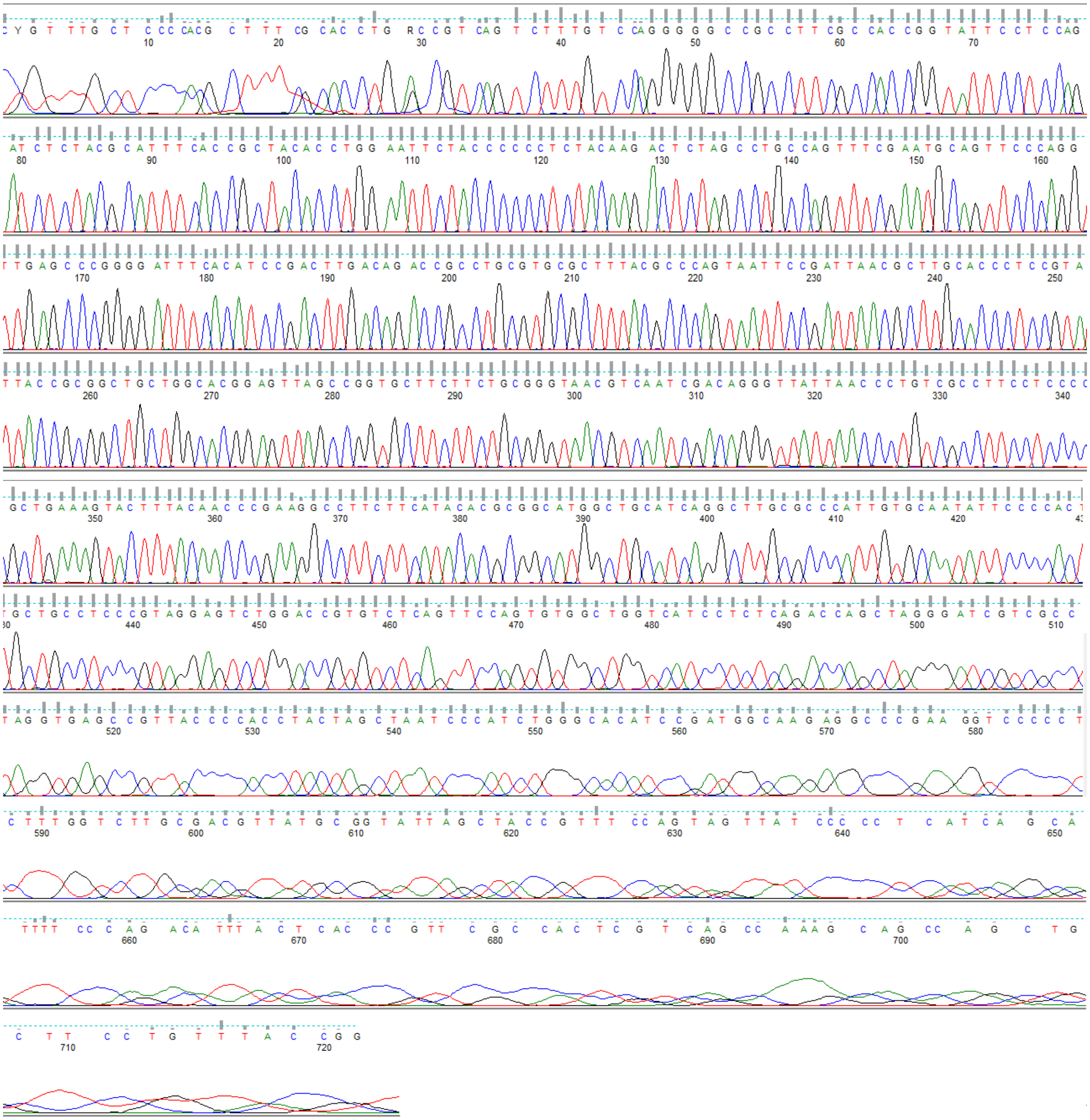
APPENDICES

Appendix A: Chromatograms

Appendix Figure 1: 16S rDNA forward chromatogram



Appendix Figure 2: 16S rDNA Reverse chromatogram



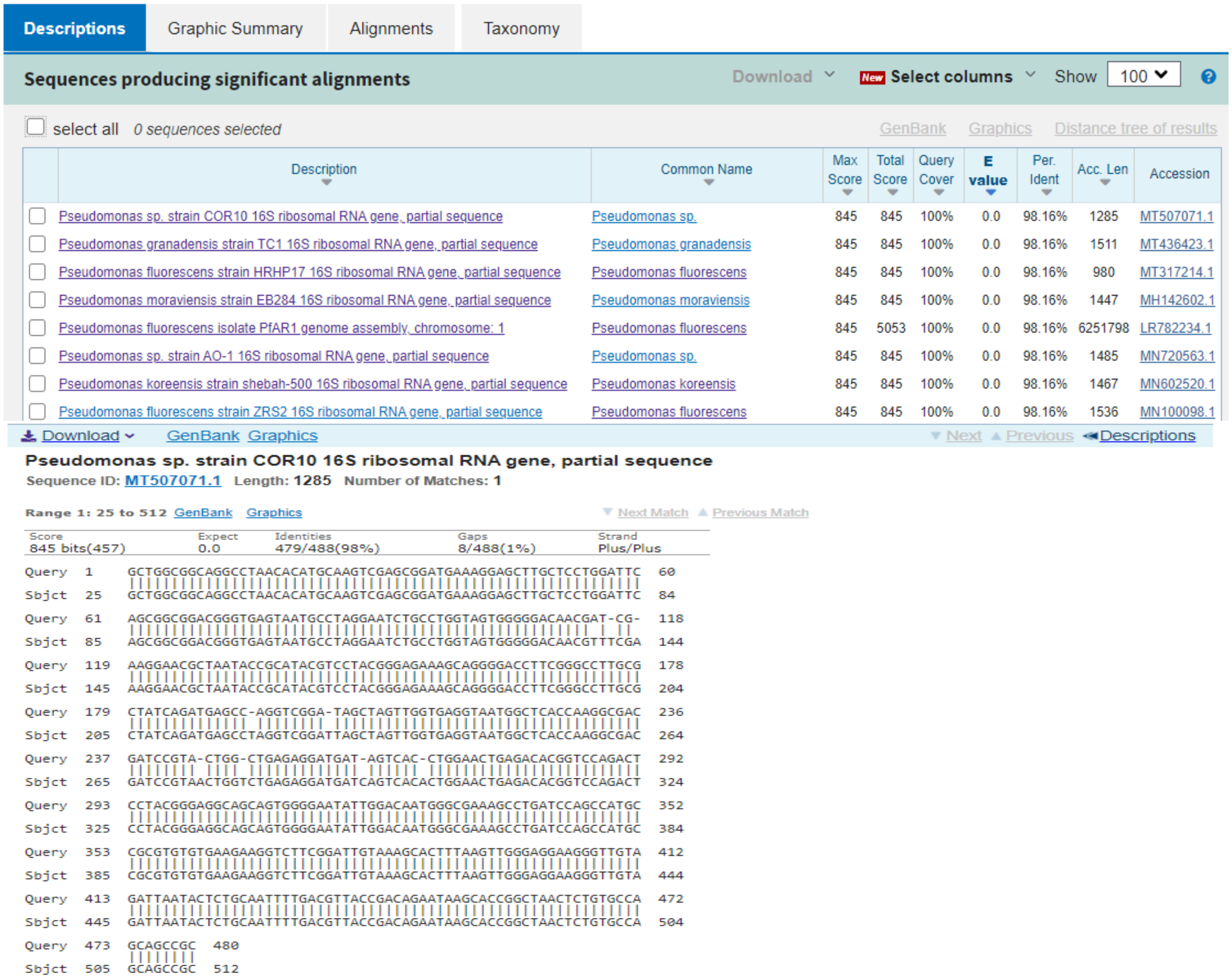
Appendix C: BLASTn Results and DNA sequences

Appendix Figures: BLASTn results with the obtained 16S rDNA sequence as the query

The morphotypes were sequenced for a fragment of the 16S rDNA region and compared with published sequences using BLAST

(Rami levy mint): *Pseudomonas* sp strain COR10

GCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGAAAGGAGCTTGCTCCTGG
ATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAA
CGATCGAAGGAACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTC
GGGCCTTGCGCTATCAGATGAGCCAGGTCGGATAGCTAGTTGGTGAGGTAATGGCTC
ACCAAGGCGACGATCCGTACTGGCTGAGAGGATGATAGTCAcCTGGAACTGAGACA
CGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGC
CTGATCCAGCCATGCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAG
TTGGGAGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACAGAATAA
GCACCGGCTAACTCTGTGCCAGCAGCCGC



Sequences producing significant alignments

☐ select all *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Pseudomonas sp. strain COR10 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	845	845	100%	0.0	98.16%	1285	MT507071.1
☐	Pseudomonas granadensis strain TC1 16S ribosomal RNA gene, partial sequence	Pseudomonas granadensis	845	845	100%	0.0	98.16%	1511	MT436423.1
☐	Pseudomonas fluorescens strain HRHP17 16S ribosomal RNA gene, partial sequence	Pseudomonas fluorescens	845	845	100%	0.0	98.16%	980	MT317214.1
☐	Pseudomonas moraviensis strain EB284 16S ribosomal RNA gene, partial sequence	Pseudomonas moraviensis	845	845	100%	0.0	98.16%	1447	MH142602.1
☐	Pseudomonas fluorescens isolate PfAR1 genome assembly, chromosome: 1	Pseudomonas fluorescens	845	5053	100%	0.0	98.16%	6251798	LR782234.1
☐	Pseudomonas sp. strain AO-1 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	845	845	100%	0.0	98.16%	1485	MN720563.1
☐	Pseudomonas koreensis strain shebah-500 16S ribosomal RNA gene, partial sequence	Pseudomonas koreensis	845	845	100%	0.0	98.16%	1467	MN602520.1
☐	Pseudomonas fluorescens strain ZRS2 16S ribosomal RNA gene, partial sequence	Pseudomonas fluorescens	845	845	100%	0.0	98.16%	1536	MN100098.1

Pseudomonas sp. strain COR10 16S ribosomal RNA gene, partial sequence
Sequence ID: MT507071.1 Length: 1285 Number of Matches: 1

Range 1: 25 to 512 GenBank Graphics

```
Score            Expect   Identities        Gaps          Strand
845 bits(457)    0.0      479/488(98%)      8/488(1%)     Plus/Plus

Query  1    GCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGAAAGGAGCTTGCTCCTGGATTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  25   GCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGAAAGGAGCTTGCTCCTGGATTC  84

Query  61   AGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGAT-CG-  118
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| | || 
Sbjct  85   AGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGA  144

Query  119  AAGGAACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTGCG  178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  145  AAGGAACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTGCG  204

Query  179  CTATCAGATGAGCC-AGGTCGGA-TAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGAC  236
            |||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  205  CTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGAC  264

Query  237  GATCCGTA-CTGG-CTGAGAGGATGAT-AGTCAC-CTGGAACTGAGACACGGTCCAGACT  292
            |||||||| |||| ||||||||||||| |||||| |||||||||||||||||||||||||
Sbjct  265  GATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACT  324

Query  293  CCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGC  352
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  325  CCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGC  384

Query  353  CGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGTTGTA  412
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  385  CGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGTTGTA  444

Query  413  GATTAATACTCTGCAATTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCA  472
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  445  GATTAATACTCTGCAATTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCA  504

Query  473  GCAGCCGC  480
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Sbjct  505  GCAGCCGC  512
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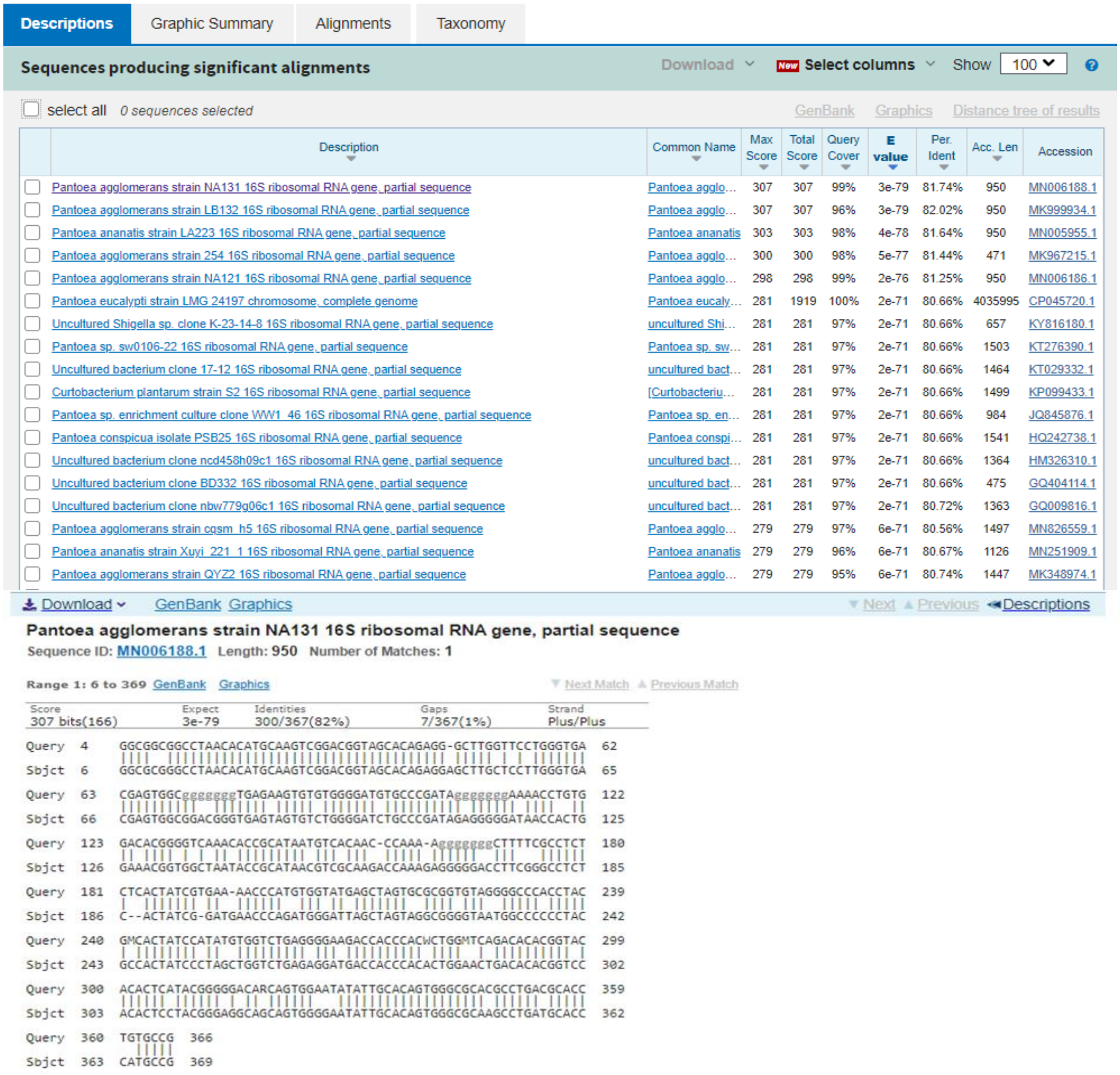
(Rami levy parsley): *Pantoea agglomerans* strain NA131

GCTGGCGGCGGCCTAACACATGCAAGTCGGACGGTAGCACAGAGGGCTTGGtTcCTG
GGTGACGAGTGGCGGGGGGTGAGAAGTGTGTGGGGaTGTGCCCGATAGGGGGGGA
AAACCTGTGGACACGGGGTCAAACACCGCATAATGTCaCAACCCAAAAGGGGGGGC
TTTTCGCCTCTCTCACTATCGTGAAAACCCATGTGGTATGAGCTAGTGcGCGGtGTAG
GGGCCCAcCTACGMCACTATCCATATGTGGTCTGAGGGGAAGACCACCCACWCTGG
MTCAGACACACGGTACACACTCATACGGGGGACARCAGTGGAATATATTGCACAGT
GGGCGCACGCCTGACGCACCTGTGCCG



Sequences producing significant alignments

☐ select all *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Pantoea agglomerans strain NA131 16S ribosomal RNA gene, partial sequence	Pantoea agglo...	307	307	99%	3e-79	81.74%	950	MN006188.1
☐	Pantoea agglomerans strain LB132 16S ribosomal RNA gene, partial sequence	Pantoea agglo...	307	307	96%	3e-79	82.02%	950	MK999934.1
☐	Pantoea ananatis strain LA223 16S ribosomal RNA gene, partial sequence	Pantoea ananatis	303	303	98%	4e-78	81.64%	950	MN005955.1
☐	Pantoea agglomerans strain 254 16S ribosomal RNA gene, partial sequence	Pantoea agglo...	300	300	98%	5e-77	81.44%	471	MK967215.1
☐	Pantoea agglomerans strain NA121 16S ribosomal RNA gene, partial sequence	Pantoea agglo...	298	298	99%	2e-76	81.25%	950	MN006186.1
☐	Pantoea eucalypti strain LMG 24197 chromosome, complete genome	Pantoea eucaly...	281	1919	100%	2e-71	80.66%	4035995	CP045720.1
☐	Uncultured Shigella sp. clone K-23-14-8 16S ribosomal RNA gene, partial sequence	uncultured Shi...	281	281	97%	2e-71	80.66%	657	KY816180.1
☐	Pantoea sp. sw0106-22 16S ribosomal RNA gene, partial sequence	Pantoea sp. sw...	281	281	97%	2e-71	80.66%	1503	KT276390.1
☐	Uncultured bacterium clone 17-12 16S ribosomal RNA gene, partial sequence	uncultured bact...	281	281	97%	2e-71	80.66%	1464	KT029332.1
☐	Curtobacterium plantarum strain S2 16S ribosomal RNA gene, partial sequence	[Curtobacteriu...	281	281	97%	2e-71	80.66%	1499	KP099433.1
☐	Pantoea sp. enrichment culture clone WW1_46 16S ribosomal RNA gene, partial sequence	Pantoea sp. en...	281	281	97%	2e-71	80.66%	984	JQ845876.1
☐	Pantoea conspicua isolate PSB25 16S ribosomal RNA gene, partial sequence	Pantoea conspi...	281	281	97%	2e-71	80.66%	1541	HQ242738.1
☐	Uncultured bacterium clone ncd458h09c1 16S ribosomal RNA gene, partial sequence	uncultured bact...	281	281	97%	2e-71	80.66%	1364	HM326310.1
☐	Uncultured bacterium clone BD332 16S ribosomal RNA gene, partial sequence	uncultured bact...	281	281	97%	2e-71	80.66%	475	GQ404114.1
☐	Uncultured bacterium clone nbw779g06c1 16S ribosomal RNA gene, partial sequence	uncultured bact...	281	281	97%	2e-71	80.72%	1363	GQ009816.1
☐	Pantoea agglomerans strain cqsm_h5 16S ribosomal RNA gene, partial sequence	Pantoea agglo...	279	279	97%	6e-71	80.56%	1497	MN826559.1
☐	Pantoea ananatis strain Xuyi_221_1 16S ribosomal RNA gene, partial sequence	Pantoea ananatis	279	279	96%	6e-71	80.67%	1126	MN251909.1
☐	Pantoea agglomerans strain QYZ2 16S ribosomal RNA gene, partial sequence	Pantoea agglo...	279	279	95%	6e-71	80.74%	1447	MK348974.1

Pantoea agglomerans strain NA131 16S ribosomal RNA gene, partial sequence

Sequence ID: MN006188.1 Length: 950 Number of Matches: 1

Range 1: 6 to 369 GenBank Graphics

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Score            Expect   Identities       Gaps        Strand
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Query  4    GGCGGCGGCCTAACACATGCAAGTCGGACGGTAGCACAGAGG-GCTTGGTTCCTGGGTGA  62
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Sbjct  6    GGCGCGGGCCTAACACATGCAAGTCGGACGGTAGCACAGAGGAGCTTGCTCCTTGGGTGA  65

Query  63   CGAGTGGCgggggggTGAGAAGTGTGTGGGGATGTGCCCGATAgggggggAAAACCTGTG  122
            ||||||||||  ||||||| ||||| ||||||| |||||||||| |||||| ||||  ||
Sbjct  66   CGAGTGGCGGACGGGTGAGTAGTGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTG  125

Query  123  GACACGGGGTCAAACACCGCATAATGTCACAAC-CCAAA-AgggggggCTTTTCGCCTCT  180
            || |||| | | || ||||||||| ||| |||  ||||| ||||||  |||   ||||||
Sbjct  126  GAAACGGTGGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCT  185

Query  181  CTCACTATCGTGAA-AACCCATGTGGTATGAGCTAGTGCGCGGTGTAGGGGCCCACCTAC  239
            |  ||||||| ||  ||||||  ||| || |||||||  |||| |||  ||||| |||||
Sbjct  186  C--ACTATCG-GATGAACCCAGATGGGATTAGCTAGTAGGCGGGGTAATGGCCCCCCTAC  242

Query  240  GMCACTATCCATATGTGGTCTGAGGGGAAGACCACCCACWCTGGMTCAGACACACGGTAC  299
            | |||||||| ||  ||||||||| ||| |||||||||| ||||  | |||||||||| |
Sbjct  243  GCCACTATCCCTAGCTGGTCTGAGAGGATGACCACCCACACTGGAACTGACACACGGTCC  302

Query  300  ACACTCATACGGGGGACARCAGTGGAATATATTGCACAGTGGGCGCACGCCTGACGCACC  359
            |||||| |||||| | || ||||||   ||||||||||||||||||| |||||| |||||
Sbjct  303  ACACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAGTGGGCGCAAGCCTGATGCACC  362

Query  360  TGTGCCG  366
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Sbjct  363  CATGCCG  369
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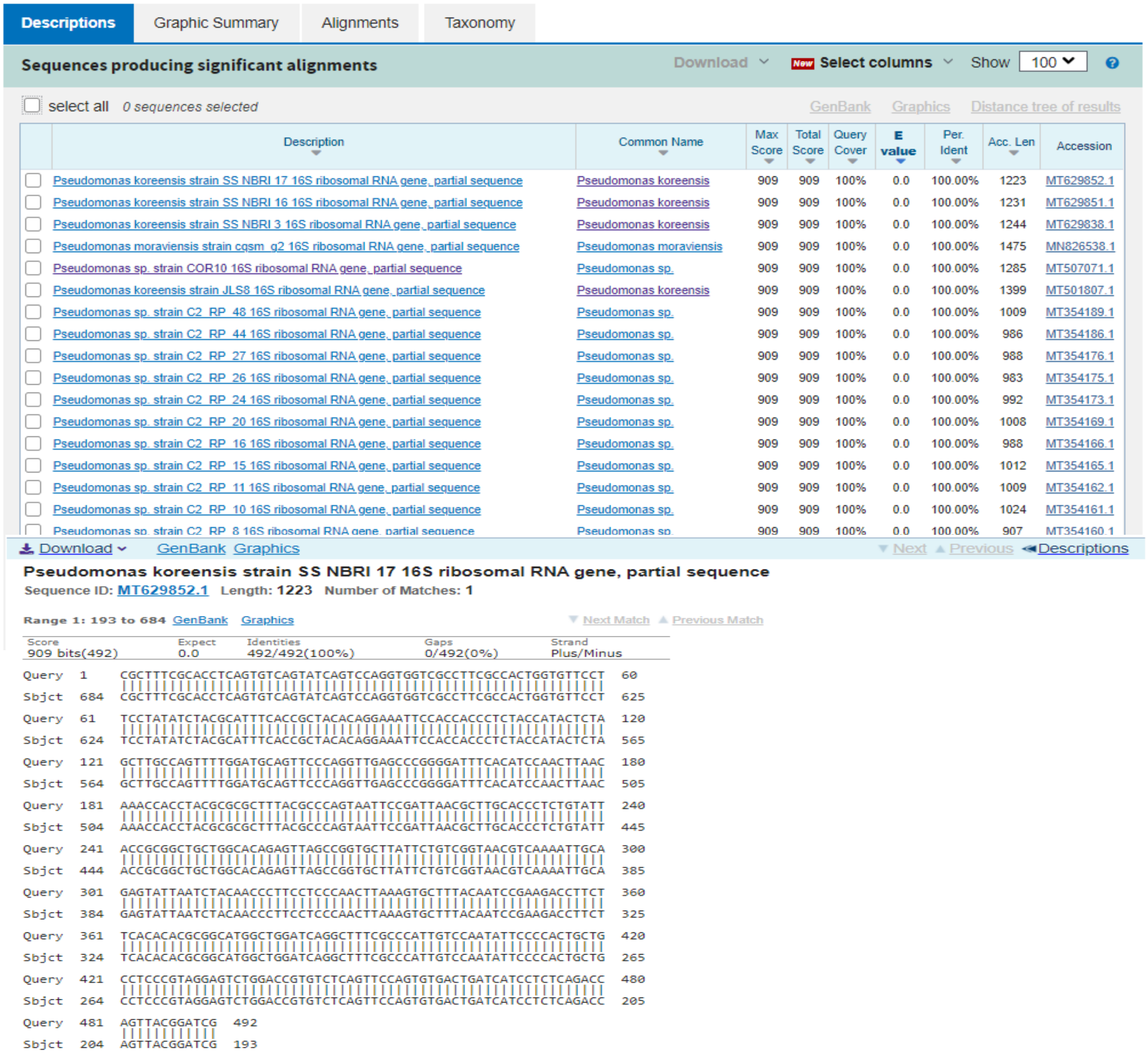
(Rami levy mint): *Pseudomonas koreensis* strain SS NBRI 17

CGCTTTCGCACCTCAGTGTCAGTATCAGTCCAGGTGGTCGCCTTCGCCACTGGTGTTCCTTCCTATATCTACGCATTTCACCGCTACACAGGAAATTCCACCACCCTCTACCATACTCTAGCTTGCCAGTTTTGGATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCAACTTAACAAACCACCTACGCGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCTGTATTACCGCGGCTGCTGGCACAGAGTTAGCCGGTGCTTATTCTGTCGGTAACGTCAAAATTGCAGAGTATTAATCTACAACCCTTCCTCCCAACTTAAAGTGCTTTACAATCCGAAGACCTTCTTCACACACGCGGCATGGCTGGATCAGGCTTTCGCCCATTGTCCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGACTGATCATCCTCTCAGACCAGTTACGGATCG



Sequences producing significant alignments

☐ select all *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Pseudomonas koreensis strain SS NBRI 17 16S ribosomal RNA gene, partial sequence	Pseudomonas koreensis	909	909	100%	0.0	100.00%	1223	MT629852.1
☐	Pseudomonas koreensis strain SS NBRI 16 16S ribosomal RNA gene, partial sequence	Pseudomonas koreensis	909	909	100%	0.0	100.00%	1231	MT629851.1
☐	Pseudomonas koreensis strain SS NBRI 3 16S ribosomal RNA gene, partial sequence	Pseudomonas koreensis	909	909	100%	0.0	100.00%	1244	MT629838.1
☐	Pseudomonas moraviensis strain cqsm_g2 16S ribosomal RNA gene, partial sequence	Pseudomonas moraviensis	909	909	100%	0.0	100.00%	1475	MN826538.1
☐	Pseudomonas sp. strain COR10 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	909	909	100%	0.0	100.00%	1285	MT507071.1
☐	Pseudomonas koreensis strain JLS8 16S ribosomal RNA gene, partial sequence	Pseudomonas koreensis	909	909	100%	0.0	100.00%	1399	MT501807.1
☐	Pseudomonas sp. strain C2_RP_48 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	909	909	100%	0.0	100.00%	1009	MT354189.1
☐	Pseudomonas sp. strain C2_RP_44 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	909	909	100%	0.0	100.00%	986	MT354186.1
☐	Pseudomonas sp. strain C2_RP_27 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	909	909	100%	0.0	100.00%	988	MT354176.1
☐	Pseudomonas sp. strain C2_RP_26 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	909	909	100%	0.0	100.00%	983	MT354175.1
☐	Pseudomonas sp. strain C2_RP_24 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	909	909	100%	0.0	100.00%	992	MT354173.1
☐	Pseudomonas sp. strain C2_RP_20 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	909	909	100%	0.0	100.00%	1008	MT354169.1
☐	Pseudomonas sp. strain C2_RP_16 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	909	909	100%	0.0	100.00%	988	MT354166.1
☐	Pseudomonas sp. strain C2_RP_15 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	909	909	100%	0.0	100.00%	1012	MT354165.1
☐	Pseudomonas sp. strain C2_RP_11 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	909	909	100%	0.0	100.00%	1009	MT354162.1
☐	Pseudomonas sp. strain C2_RP_10 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	909	909	100%	0.0	100.00%	1024	MT354161.1
☐	Pseudomonas sp. strain C2_RP_8 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	909	909	100%	0.0	100.00%	907	MT354160.1

Pseudomonas koreensis strain SS NBRI 17 16S ribosomal RNA gene, partial sequence

Sequence ID: MT629852.1 Length: 1223 Number of Matches: 1

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Score           Expect    Identities        Gaps         Strand
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Sbjct  684  CGCTTTCGCACCTCAGTGTCAGTATCAGTCCAGGTGGTCGCCTTCGCCACTGGTGTTCCT  625

Query  61   TCCTATATCTACGCATTTCACCGCTACACAGGAAATTCCACCACCCTCTACCATACTCTA  120
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Sbjct  624  TCCTATATCTACGCATTTCACCGCTACACAGGAAATTCCACCACCCTCTACCATACTCTA  565

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Sbjct  564  GCTTGCCAGTTTTGGATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCAACTTAAC  505

Query  181  AAACCACCTACGCGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCTGTATT  240
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Query  301  GAGTATTAATCTACAACCCTTCCTCCCAACTTAAAGTGCTTTACAATCCGAAGACCTTCT  360
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Sbjct  384  GAGTATTAATCTACAACCCTTCCTCCCAACTTAAAGTGCTTTACAATCCGAAGACCTTCT  325

Query  361  TCACACACGCGGCATGGCTGGATCAGGCTTTCGCCCATTGTCCAATATTCCCCACTGCTG  420
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Sbjct  324  TCACACACGCGGCATGGCTGGATCAGGCTTTCGCCCATTGTCCAATATTCCCCACTGCTG  265

Query  421  CCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGACTGATCATCCTCTCAGACC  480
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Sbjct  264  CCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGACTGATCATCCTCTCAGACC  205

Query  481  AGTTACGGATCG  492
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Sbjct  204  AGTTACGGATCG  193
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(Rami levy parsley): *Pseudomonas putida* strain C1-1

ACATGCAGTCGAGCGGATGACTGGTTAGCTTGCTCCTTGATTCAGCGGCGGA
CGGGTGAGTAATGCCTAGGAATCTGCCCTGGTAGTGGGGGACAACGTTTCGA
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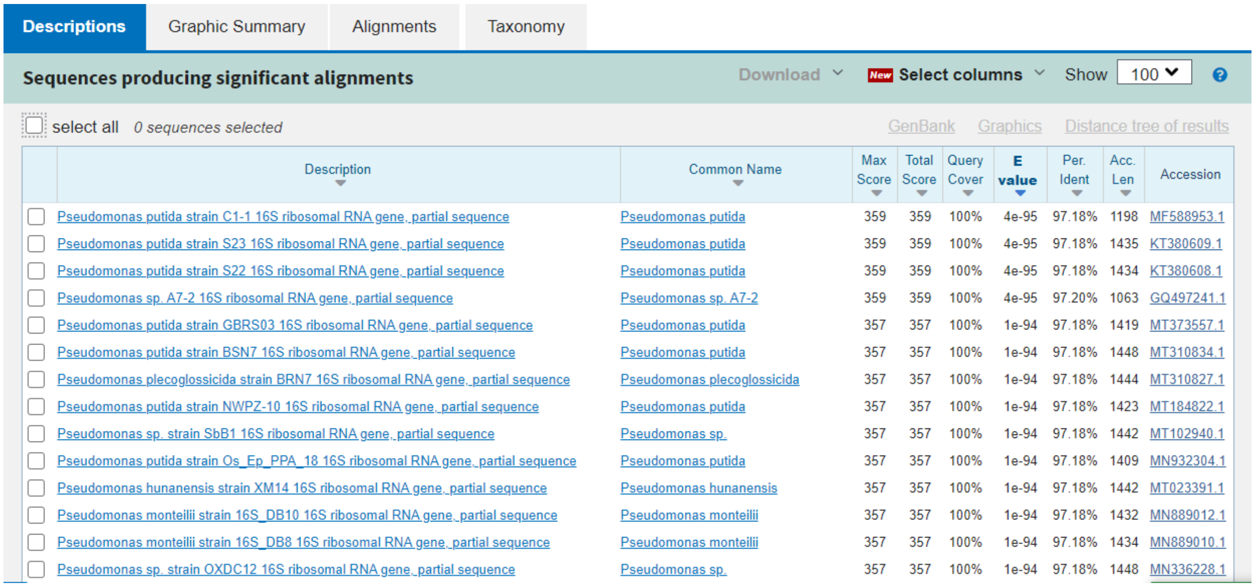
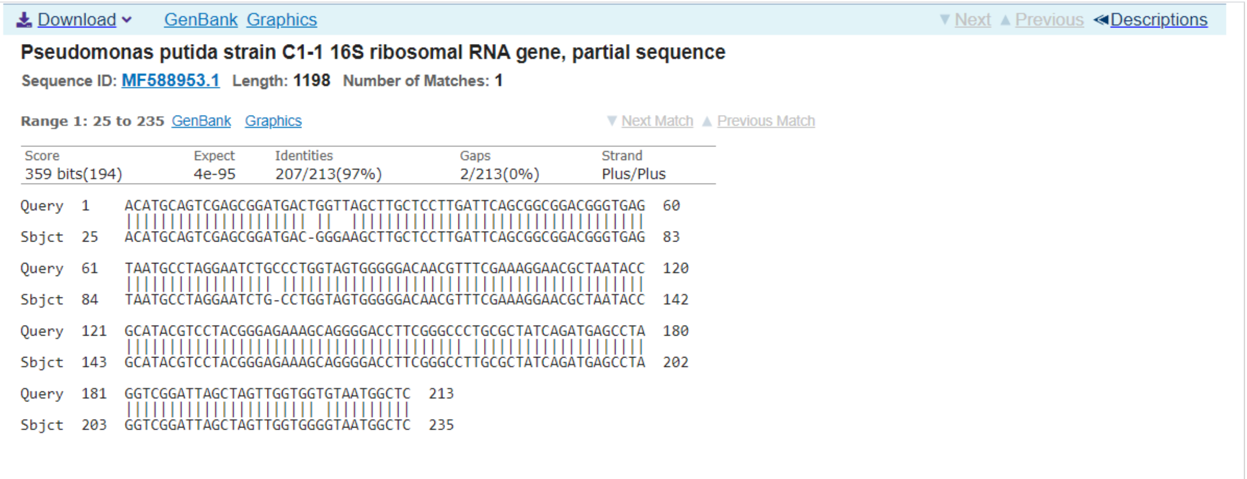
TGGCTC



Sequences producing significant alignments

☐ select all *0 sequences selected*

☐	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Pseudomonas putida strain C1-1 16S ribosomal RNA gene, partial sequence	Pseudomonas putida	359	359	100%	4e-95	97.18%	1198	MF588953.1
☐	Pseudomonas putida strain S23 16S ribosomal RNA gene, partial sequence	Pseudomonas putida	359	359	100%	4e-95	97.18%	1435	KT380609.1
☐	Pseudomonas putida strain S22 16S ribosomal RNA gene, partial sequence	Pseudomonas putida	359	359	100%	4e-95	97.18%	1434	KT380608.1
☐	Pseudomonas sp. A7-2 16S ribosomal RNA gene, partial sequence	Pseudomonas sp. A7-2	359	359	100%	4e-95	97.20%	1063	GQ497241.1
☐	Pseudomonas putida strain GBRS03 16S ribosomal RNA gene, partial sequence	Pseudomonas putida	357	357	100%	1e-94	97.18%	1419	MT373557.1
☐	Pseudomonas putida strain BSN7 16S ribosomal RNA gene, partial sequence	Pseudomonas putida	357	357	100%	1e-94	97.18%	1448	MT310834.1
☐	Pseudomonas plecoglossicida strain BRN7 16S ribosomal RNA gene, partial sequence	Pseudomonas plecoglossicida	357	357	100%	1e-94	97.18%	1444	MT310827.1
☐	Pseudomonas putida strain NWPZ-10 16S ribosomal RNA gene, partial sequence	Pseudomonas putida	357	357	100%	1e-94	97.18%	1423	MT184822.1
☐	Pseudomonas sp. strain SbB1 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	357	357	100%	1e-94	97.18%	1442	MT102940.1
☐	Pseudomonas putida strain Os_Ep_PPA_18 16S ribosomal RNA gene, partial sequence	Pseudomonas putida	357	357	100%	1e-94	97.18%	1409	MN932304.1
☐	Pseudomonas hunanensis strain XM14 16S ribosomal RNA gene, partial sequence	Pseudomonas hunanensis	357	357	100%	1e-94	97.18%	1442	MT023391.1
☐	Pseudomonas monteilii strain 16S_DB10 16S ribosomal RNA gene, partial sequence	Pseudomonas monteilii	357	357	100%	1e-94	97.18%	1432	MN889012.1
☐	Pseudomonas monteilii strain 16S_DB8 16S ribosomal RNA gene, partial sequence	Pseudomonas monteilii	357	357	100%	1e-94	97.18%	1434	MN889010.1
☐	Pseudomonas sp. strain OXDC12 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	357	357	100%	1e-94	97.18%	1448	MN336228.1



Pseudomonas putida strain C1-1 16S ribosomal RNA gene, partial sequence

Sequence ID: MF588953.1 Length: **1198** Number of Matches: **1**

Range 1: 25 to 235 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
359 bits(194)	4e-95	207/213(97%)	2/213(0%)	Plus/Plus

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Sbjct  25   ACATGCAGTCGAGCGGATGAC-GGGAAGCTTGCTCCTTGATTCAGCGGCGGACGGGTGAG  83

Query  61   TAATGCCTAGGAATCTGCCCTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTAATACC  120
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  84   TAATGCCTAGGAATCTG-CCTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTAATACC  142

Query  121  GCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCCTGCGCTATCAGATGAGCCTA  180
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  143  GCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTGCGCTATCAGATGAGCCTA  202

Query  181  GGTCGGATTAGCTAGTTGGTGGTGTAATGGCTC  213
            |||||||||||||||||||||| ||||||||||
Sbjct  203  GGTCGGATTAGCTAGTTGGTGGGGTAATGGCTC  235
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(Rami levy mint): *Pantoea agglomerans* strain HTP

TTTCGCCACCTGACGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTAT
TCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCT
ACAAGACTCAAGCCTGCCAGTTTCAAATGCAGTTTCCCAGGTTAAGCCSGGG
GATTTCACATCTGACTTAACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATT
CCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGC
CGGTGCTTCTTCTGCGGGTAACGTCAATCGACAGGGTTATTAACCCCGTCGCC
TTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACGCGG
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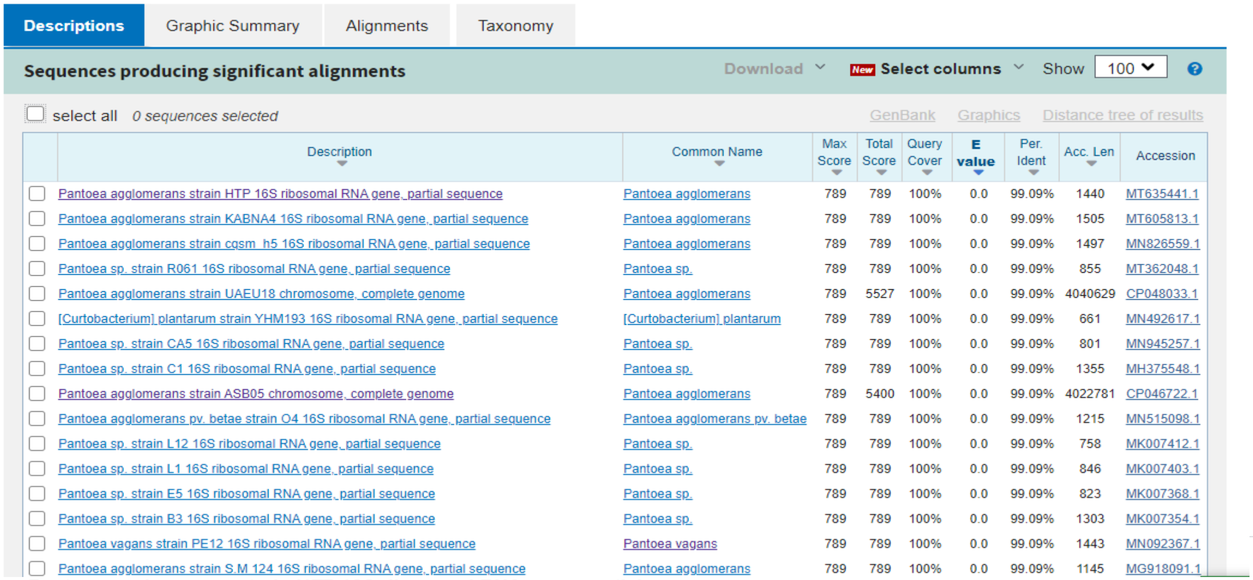
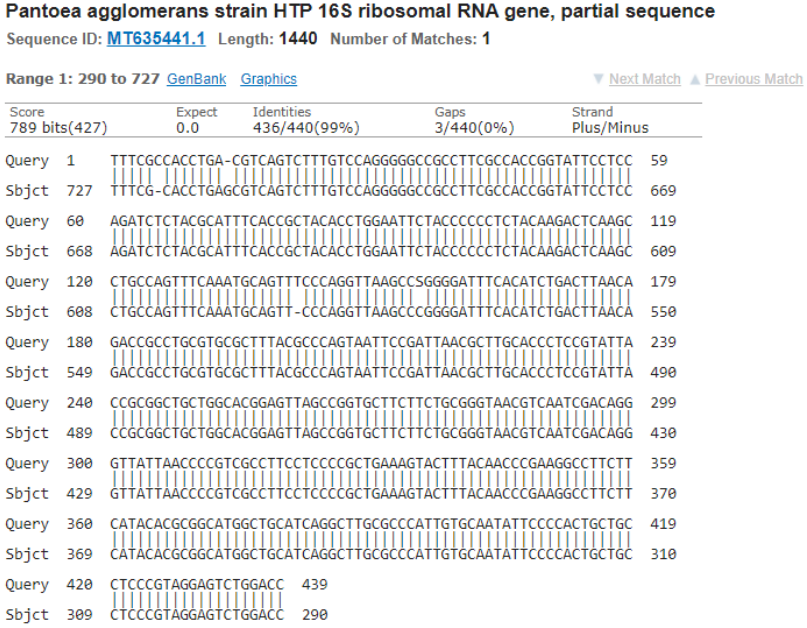


Sequences producing significant alignments

☐ select all *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Pantoea agglomerans strain HTP 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	789	789	100%	0.0	99.09%	1440	MT635441.1
☐	Pantoea agglomerans strain KABNA4 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	789	789	100%	0.0	99.09%	1505	MT605813.1
☐	Pantoea agglomerans strain cgsm_h5 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	789	789	100%	0.0	99.09%	1497	MN826559.1
☐	Pantoea sp. strain R061 16S ribosomal RNA gene, partial sequence	Pantoea sp.	789	789	100%	0.0	99.09%	855	MT362048.1
☐	Pantoea agglomerans strain UAEU18 chromosome, complete genome	Pantoea agglomerans	789	5527	100%	0.0	99.09%	4040629	CP048033.1
☐	[Curtobacterium] plantarum strain YHM193 16S ribosomal RNA gene, partial sequence	[Curtobacterium] plantarum	789	789	100%	0.0	99.09%	661	MN492617.1
☐	Pantoea sp. strain CA5 16S ribosomal RNA gene, partial sequence	Pantoea sp.	789	789	100%	0.0	99.09%	801	MN945257.1
☐	Pantoea sp. strain C1 16S ribosomal RNA gene, partial sequence	Pantoea sp.	789	789	100%	0.0	99.09%	1355	MH375548.1
☐	Pantoea agglomerans strain ASB05 chromosome, complete genome	Pantoea agglomerans	789	5400	100%	0.0	99.09%	4022781	CP046722.1
☐	Pantoea agglomerans pv. betae strain O4 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans pv. betae	789	789	100%	0.0	99.09%	1215	MN515098.1
☐	Pantoea sp. strain L12 16S ribosomal RNA gene, partial sequence	Pantoea sp.	789	789	100%	0.0	99.09%	758	MK007412.1
☐	Pantoea sp. strain L1 16S ribosomal RNA gene, partial sequence	Pantoea sp.	789	789	100%	0.0	99.09%	846	MK007403.1
☐	Pantoea sp. strain E5 16S ribosomal RNA gene, partial sequence	Pantoea sp.	789	789	100%	0.0	99.09%	823	MK007368.1
☐	Pantoea sp. strain B3 16S ribosomal RNA gene, partial sequence	Pantoea sp.	789	789	100%	0.0	99.09%	1303	MK007354.1
☐	Pantoea vagans strain PE12 16S ribosomal RNA gene, partial sequence	Pantoea vagans	789	789	100%	0.0	99.09%	1443	MN092367.1
☐	Pantoea agglomerans strain S.M 124 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	789	789	100%	0.0	99.09%	1145	MG918091.1



Pantoea agglomerans strain HTP 16S ribosomal RNA gene, partial sequence

Sequence ID: MT635441.1 **Length:** 1440 **Number of Matches:** 1

Range 1: 290 to 727 GenBank Graphics

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Query  60   AGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCAAGC  119
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Sbjct  668  AGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCAAGC  609

Query  120  CTGCCAGTTTCAAATGCAGTTTCCCAGGTTAAGCCSGGGGATTTCACATCTGACTTAACA  179
            ||||||||||||||||||||| ||||||||||||| ||||||||||||||||||||||||
Sbjct  608  CTGCCAGTTTCAAATGCAGTT-CCCAGGTTAAGCCCGGGGATTTCACATCTGACTTAACA  550

Query  180  GACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTA  239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  549  GACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTA  490

Query  240  CCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAGG  299
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Sbjct  489  CCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAGG  430

Query  300  GTTATTAACCCCGTCGCCTTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTT  359
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Sbjct  429  GTTATTAACCCCGTCGCCTTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTT  370

Query  360  CATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGC  419
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Sbjct  369  CATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGC  310

Query  420  CTCCCGTAGGAGTCTGGACC  439
            ||||||||||||||||||||
Sbjct  309  CTCCCGTAGGAGTCTGGACC  290
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(Rami levy parsley): *Pantoea sp* strain B26
TGCAGTCGGAGGTAGCACAGAGARCTTGCTCYCGKGTGACRAGTGGCGGACGGGTG
AGTAATGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTA
ATACCGCATAACGTCGCAAGACCCAAGAGGGGGACCTTCAGGCCTCTCACTATCGG
ATGAACCCAGATGGGATTAGCTAGTAGGCGGGGTAATGGCCCACCTATGCGACAAT
CCCTATCTGGTCTGAGAGGATGACCACCCACACTGGAACTGAGACACGGTCCACAC
TCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCACGCCTGATGCACC
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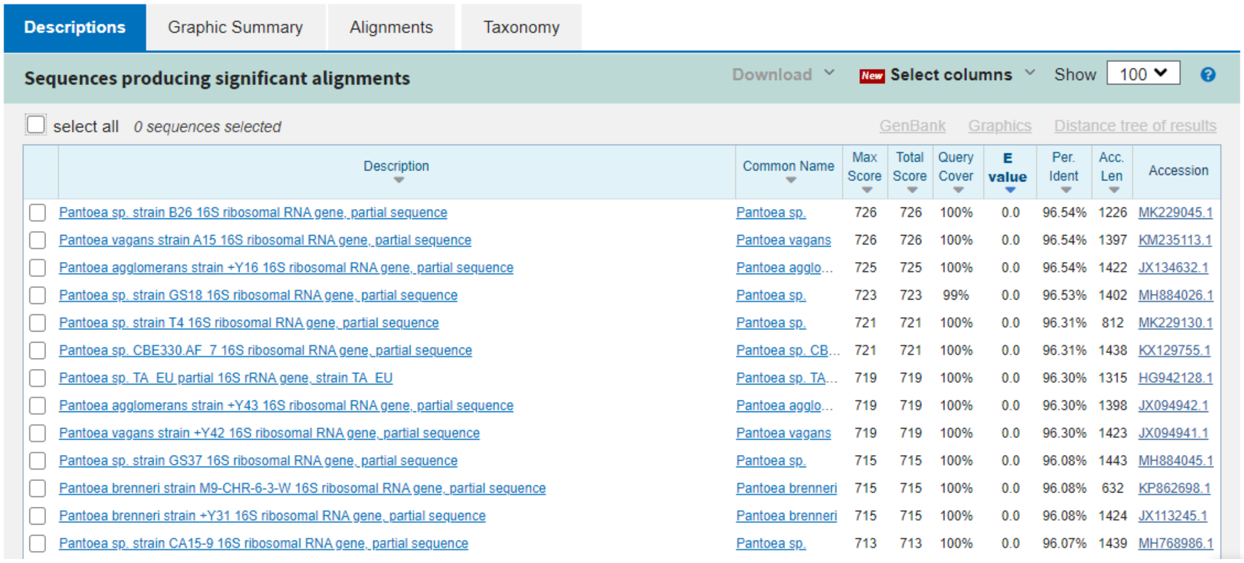
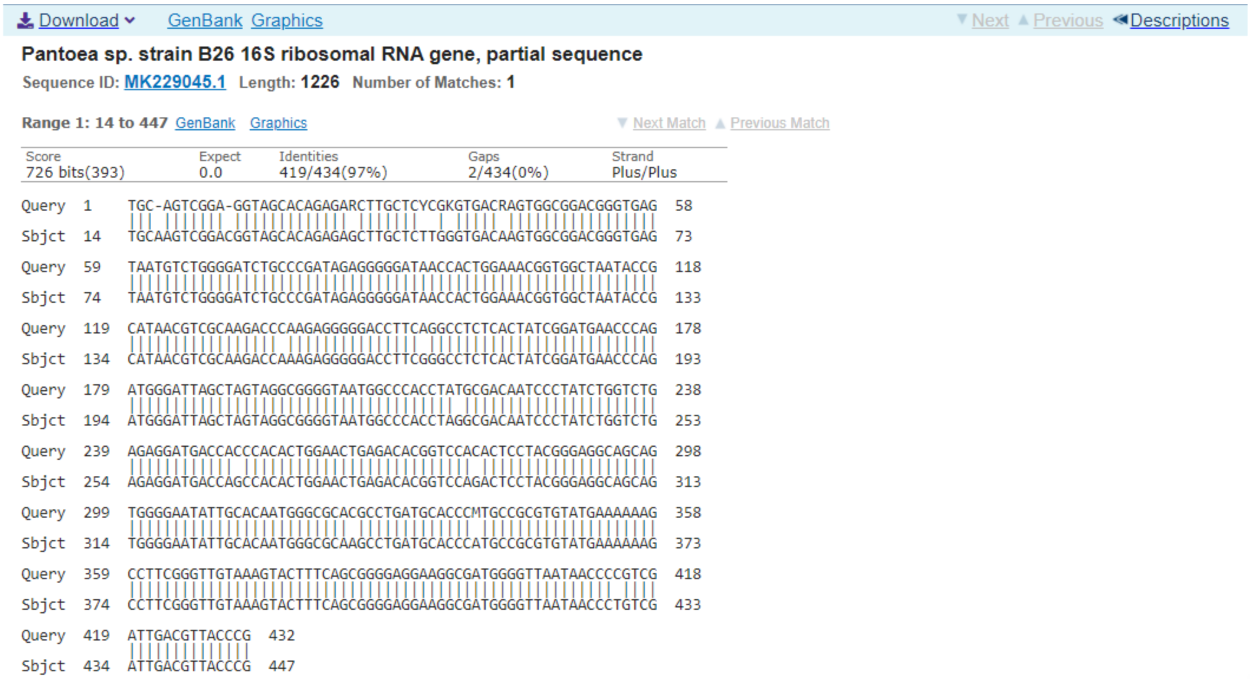


Sequences producing significant alignments

☐ select all *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Pantoea sp. strain B26 16S ribosomal RNA gene, partial sequence	Pantoea sp.	726	726	100%	0.0	96.54%	1226	MK229045.1
☐	Pantoea vagans strain A15 16S ribosomal RNA gene, partial sequence	Pantoea vagans	726	726	100%	0.0	96.54%	1397	KM235113.1
☐	Pantoea agglomerans strain +Y16 16S ribosomal RNA gene, partial sequence	Pantoea agglo...	725	725	100%	0.0	96.54%	1422	JX134632.1
☐	Pantoea sp. strain GS18 16S ribosomal RNA gene, partial sequence	Pantoea sp.	723	723	99%	0.0	96.53%	1402	MH884026.1
☐	Pantoea sp. strain T4 16S ribosomal RNA gene, partial sequence	Pantoea sp.	721	721	100%	0.0	96.31%	812	MK229130.1
☐	Pantoea sp. CBE330.AF_7 16S ribosomal RNA gene, partial sequence	Pantoea sp. CB...	721	721	100%	0.0	96.31%	1438	KX129755.1
☐	Pantoea sp. TA_EU partial 16S rRNA gene, strain TA_EU	Pantoea sp. TA...	719	719	100%	0.0	96.30%	1315	HG942128.1
☐	Pantoea agglomerans strain +Y43 16S ribosomal RNA gene, partial sequence	Pantoea agglo...	719	719	100%	0.0	96.30%	1398	JX094942.1
☐	Pantoea vagans strain +Y42 16S ribosomal RNA gene, partial sequence	Pantoea vagans	719	719	100%	0.0	96.30%	1423	JX094941.1
☐	Pantoea sp. strain GS37 16S ribosomal RNA gene, partial sequence	Pantoea sp.	715	715	100%	0.0	96.08%	1443	MH884045.1
☐	Pantoea brenneri strain M9-CHR-6-3-W 16S ribosomal RNA gene, partial sequence	Pantoea brenneri	715	715	100%	0.0	96.08%	632	KP862698.1
☐	Pantoea brenneri strain +Y31 16S ribosomal RNA gene, partial sequence	Pantoea brenneri	715	715	100%	0.0	96.08%	1424	JX113245.1
☐	Pantoea sp. strain CA15-9 16S ribosomal RNA gene, partial sequence	Pantoea sp.	713	713	100%	0.0	96.07%	1439	MH768986.1



Pantoea sp. strain B26 16S ribosomal RNA gene, partial sequence

Sequence ID: MK229045.1 Length: **1226** Number of Matches: **1**

Range 1: 14 to 447 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
726 bits(393)	0.0	419/434(97%)	2/434(0%)	Plus/Plus

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Query  1    TGC-AGTCGGA-GGTAGCACAGAGARCTTGCTCYCGKGTGACRAGTGGCGGACGGGTGAG  58
            ||| ||||||| ||||||||||||| |||||||  | ||||| |||||||||||||||||
Sbjct  14   TGCAAGTCGGACGGTAGCACAGAGAGCTTGCTCTTGGGTGACAAGTGGCGGACGGGTGAG  73

Query  59   TAATGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCG  118
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  74   TAATGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCG  133

Query  119  CATAACGTCGCAAGACCCAAGAGGGGGACCTTCAGGCCTCTCACTATCGGATGAACCCAG  178
            ||||||||||||||||| ||||||||||||||| ||||||||||||||||||||||||||
Sbjct  134  CATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTCACTATCGGATGAACCCAG  193

Query  179  ATGGGATTAGCTAGTAGGCGGGGTAATGGCCCACCTATGCGACAATCCCTATCTGGTCTG  238
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  194  ATGGGATTAGCTAGTAGGCGGGGTAATGGCCCACCTAGGCGACAATCCCTATCTGGTCTG  253

Query  239  AGAGGATGACCACCCACACTGGAACTGAGACACGGTCCACACTCCTACGGGAGGCAGCAG  298
            |||||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  254  AGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAG  313

Query  299  TGGGGAATATTGCACAATGGGCGCACGCCTGATGCACCCMTGCCGCGTGTATGAAAAAAG  358
            ||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||||
Sbjct  314  TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCACCCATGCCGCGTGTATGAAAAAAG  373

Query  359  CCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCGATGGGGTTAATAACCCCGTCG  418
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  374  CCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCGATGGGGTTAATAACCCTGTCG  433

Query  419  ATTGACGTTACCCG  432
            ||||||||||||||
Sbjct  434  ATTGACGTTACCCG  447
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(Rami levy parsley): *Pantoea vagans* strain +Y42

CCTAAACATGCAGTCGGAGGTAGCACAGAGAGCTTGCTTTCGGGTGACGAGTGGcG
GACGGGTGAGTAATGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTGtGAAC
GGtGGCTAATACCGCATAACGTCGCAAGACCCCAGAGGGGGACCTTCGGGCCTCTCA
CTATCGGATGAACCCAGATGGGATTAGCTATTAGGCGGGGTAATGGGCCACCTAGG
CGACAATCCCTATCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGt
CCAcACTCtTACGGGAGGCASCAGTGGGGAATATTGCACAATGGGCGCACGCCTGAT
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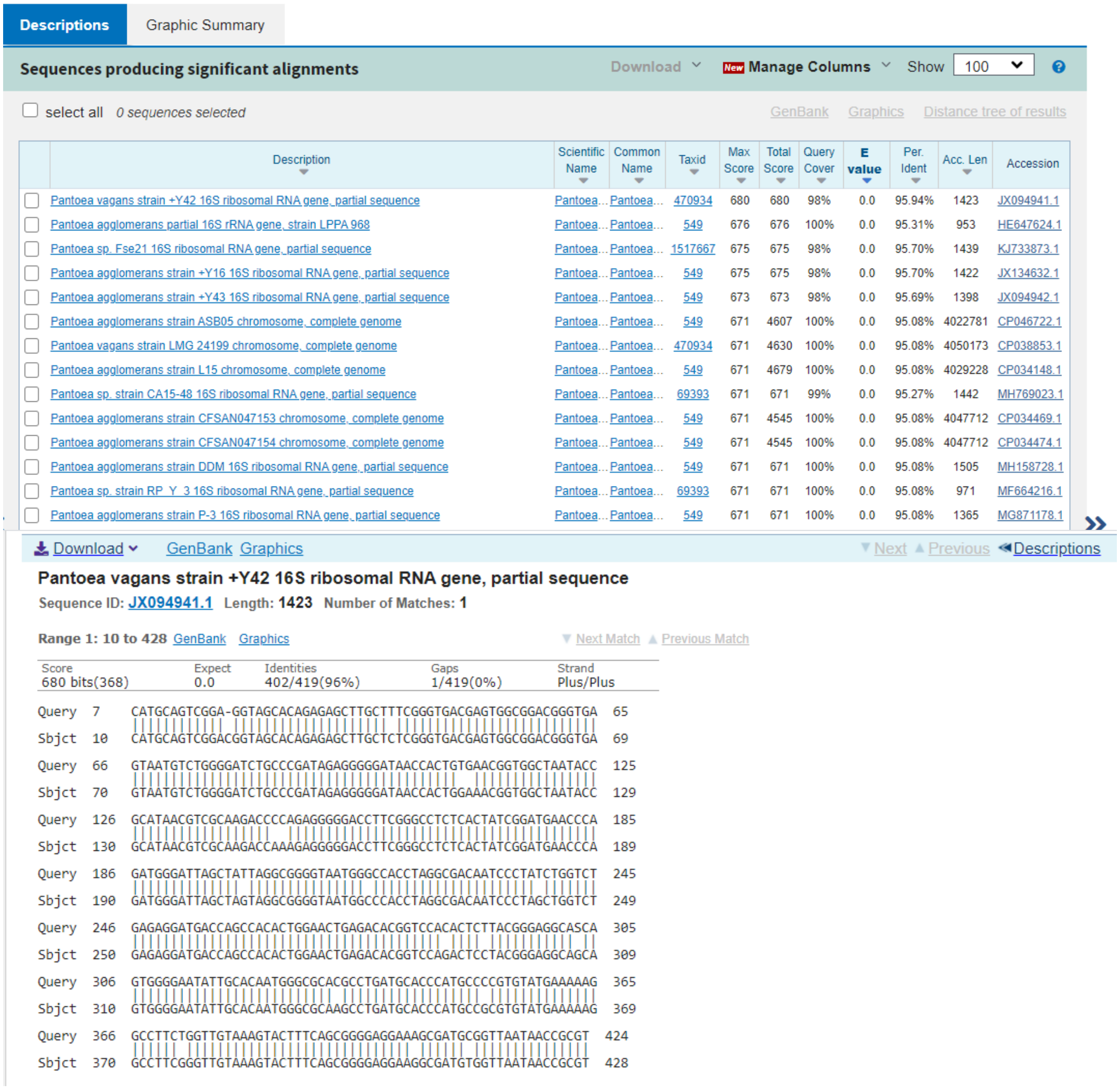

Sequences producing significant alignments

	Description	Scientific Name	Common Name	Taxid	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Pantoea vagans strain +Y42 16S ribosomal RNA gene, partial sequence	Pantoea...	Pantoea...	470934	680	680	98%	0.0	95.94%	1423	JX094941.1
☐	Pantoea agglomerans partial 16S rRNA gene, strain LPPA 968	Pantoea...	Pantoea...	549	676	676	100%	0.0	95.31%	953	HE647624.1
☐	Pantoea sp. Fse21 16S ribosomal RNA gene, partial sequence	Pantoea...	Pantoea...	1517667	675	675	98%	0.0	95.70%	1439	KJ733873.1
☐	Pantoea agglomerans strain +Y16 16S ribosomal RNA gene, partial sequence	Pantoea...	Pantoea...	549	675	675	98%	0.0	95.70%	1422	JX134632.1
☐	Pantoea agglomerans strain +Y43 16S ribosomal RNA gene, partial sequence	Pantoea...	Pantoea...	549	673	673	98%	0.0	95.69%	1398	JX094942.1
☐	Pantoea agglomerans strain ASB05 chromosome, complete genome	Pantoea...	Pantoea...	549	671	4607	100%	0.0	95.08%	4022781	CP046722.1
☐	Pantoea vagans strain LMG 24199 chromosome, complete genome	Pantoea...	Pantoea...	470934	671	4630	100%	0.0	95.08%	4050173	CP038853.1
☐	Pantoea agglomerans strain L15 chromosome, complete genome	Pantoea...	Pantoea...	549	671	4679	100%	0.0	95.08%	4029228	CP034148.1
☐	Pantoea sp. strain CA15-48 16S ribosomal RNA gene, partial sequence	Pantoea...	Pantoea...	69393	671	671	99%	0.0	95.27%	1442	MH769023.1
☐	Pantoea agglomerans strain CFSAN047153 chromosome, complete genome	Pantoea...	Pantoea...	549	671	4545	100%	0.0	95.08%	4047712	CP034469.1
☐	Pantoea agglomerans strain CFSAN047154 chromosome, complete genome	Pantoea...	Pantoea...	549	671	4545	100%	0.0	95.08%	4047712	CP034474.1
☐	Pantoea agglomerans strain DDM 16S ribosomal RNA gene, partial sequence	Pantoea...	Pantoea...	549	671	671	100%	0.0	95.08%	1505	MH158728.1
☐	Pantoea sp. strain RP_Y_3 16S ribosomal RNA gene, partial sequence	Pantoea...	Pantoea...	69393	671	671	100%	0.0	95.08%	971	MF664216.1
☐	Pantoea agglomerans strain P-3 16S ribosomal RNA gene, partial sequence	Pantoea...	Pantoea...	549	671	671	100%	0.0	95.08%	1365	MG871178.1

Pantoea vagans strain +Y42 16S ribosomal RNA gene, partial sequence

Sequence ID: JX094941.1 Length: **1423** Number of Matches: **1**

Range 1: 10 to 428 GenBank Graphics

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Score           Expect  Identities       Gaps         Strand
680 bits(368)   0.0     402/419(96%)     1/419(0%)    Plus/Plus

Query  7    CATGCAGTCGGA-GGTAGCACAGAGAGCTTGCTTTCGGGTGACGAGTGGCGGACGGTGA  65
            |||||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  10   CATGCAGTCGGACGGTAGCACAGAGAGCTTGCTCTCGGGTGACGAGTGGCGGACGGTGA  69

Query  66   GTAATGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTGTGAACGGTGGCTAATACC  125
            ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Sbjct  70   GTAATGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACC  129

Query  126  GCATAACGTCGCAAGACCCCAGAGGGGGACCTTCGGGCCTCTCACTATCGGATGAACCCA  185
            ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Sbjct  130  GCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTCACTATCGGATGAACCCA  189

Query  186  GATGGGATTAGCTATTAGGCGGGGTAATGGGCCACCTAGGCGACAATCCCTATCTGGTCT  245
            |||||||||||||| ||||||||||||||| ||||||||||||||||||||| |||||||
Sbjct  190  GATGGGATTAGCTAGTAGGCGGGGTAATGGCCCACCTAGGCGACAATCCCTAGCTGGTCT  249

Query  246  GAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCACACTCTTACGGGAGGCASCA  305
            |||||||||||||||||||||||||||||||||||||||| |||| ||||||||||| ||
Sbjct  250  GAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCA  309

Query  306  GTGGGGAATATTGCACAATGGGCGCACGCCTGATGCACCCATGCCCCGTGTATGAAAAAG  365
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Sbjct  310  GTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCACCCATGCCGCGTGTATGAAAAAG  369

Query  366  GCCTTCTGGTTGTAAAGTACTTTCAGCGGGGAGGAAAGCGATGCGGTTAATAACCGCGT  424
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Sbjct  370  GCCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCGATGTGGTTAATAACCGCGT  428
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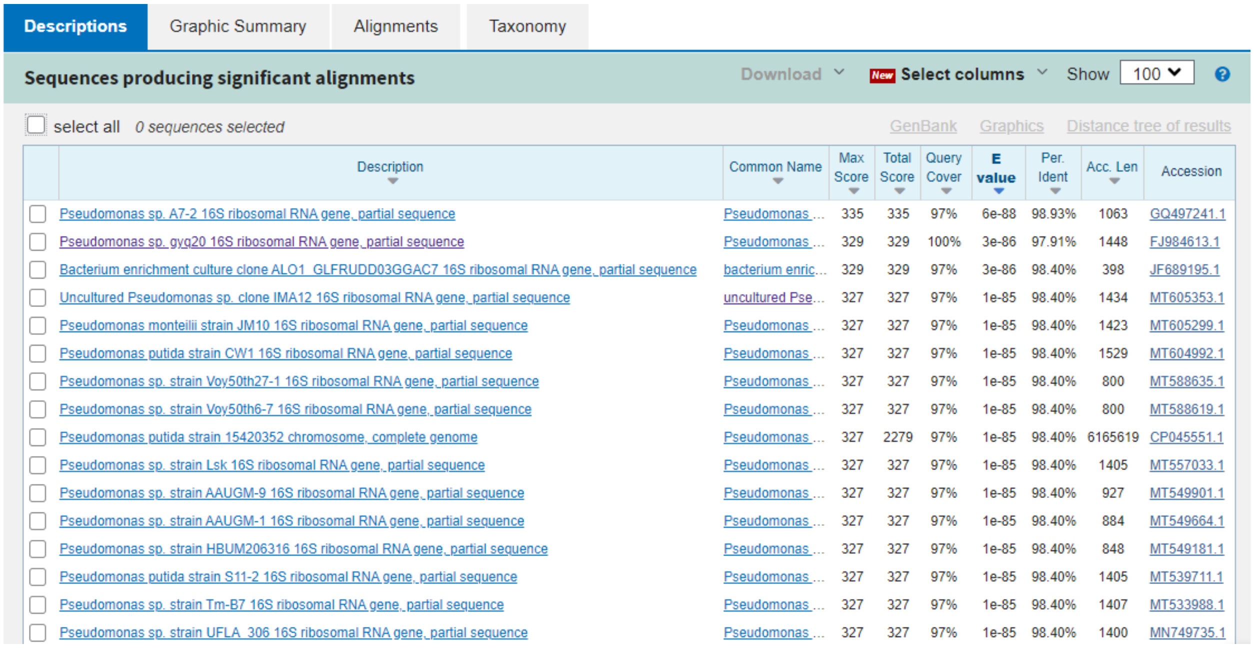
(Rami levy mint): *Pseudomonas* sp A7-2

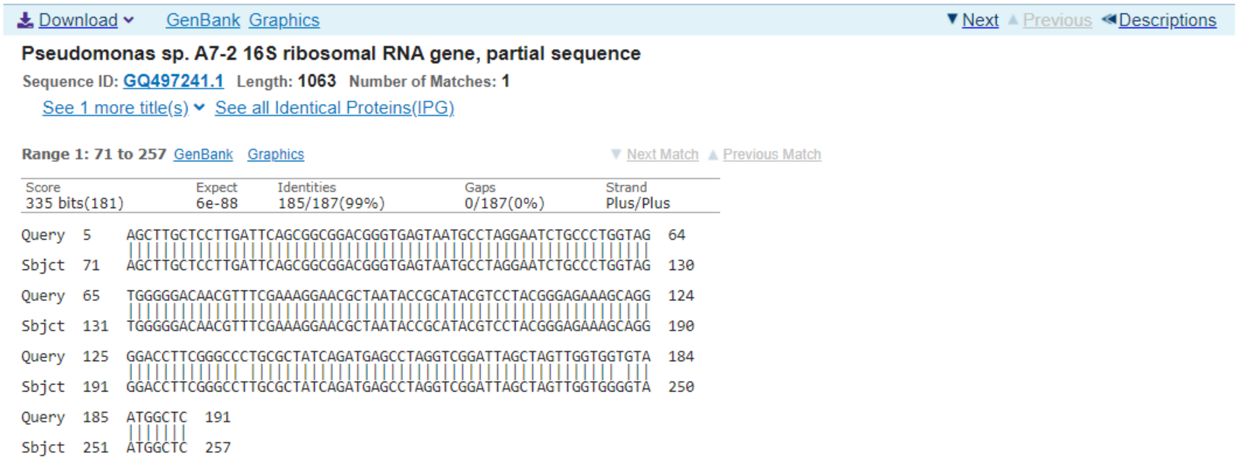
GGTTAGCTTGCTCCTTGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCC
CTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTAATACCGCATACGTCCTACGG
GAGAAAGCAGGGGACCTTCGGGCCCTGCGCTATCAGATGAGCCTAGGTCGGATTAG
CTAGTTGGTGGTGTAATGGCTC



Sequences producing significant alignments

☐ select all *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Pseudomonas sp. A7-2 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	335	335	97%	6e-88	98.93%	1063	GQ497241.1
☐	Pseudomonas sp. gyq20 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	329	329	100%	3e-86	97.91%	1448	FJ984613.1
☐	Bacterium enrichment culture clone ALO1_GLFRUDD03GGAC7 16S ribosomal RNA gene, partial sequence	bacterium enric...	329	329	97%	3e-86	98.40%	398	JF689195.1
☐	Uncultured Pseudomonas sp. clone IMA12 16S ribosomal RNA gene, partial sequence	uncultured Pse...	327	327	97%	1e-85	98.40%	1434	MT605353.1
☐	Pseudomonas monteilii strain JM10 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	327	327	97%	1e-85	98.40%	1423	MT605299.1
☐	Pseudomonas putida strain CW1 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	327	327	97%	1e-85	98.40%	1529	MT604992.1
☐	Pseudomonas sp. strain Voy50th27-1 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	327	327	97%	1e-85	98.40%	800	MT588635.1
☐	Pseudomonas sp. strain Voy50th6-7 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	327	327	97%	1e-85	98.40%	800	MT588619.1
☐	Pseudomonas putida strain 15420352 chromosome, complete genome	Pseudomonas ...	327	2279	97%	1e-85	98.40%	6165619	CP045551.1
☐	Pseudomonas sp. strain Lsk 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	327	327	97%	1e-85	98.40%	1405	MT557033.1
☐	Pseudomonas sp. strain AAUGM-9 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	327	327	97%	1e-85	98.40%	927	MT549901.1
☐	Pseudomonas sp. strain AAUGM-1 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	327	327	97%	1e-85	98.40%	884	MT549664.1
☐	Pseudomonas sp. strain HBUM206316 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	327	327	97%	1e-85	98.40%	848	MT549181.1
☐	Pseudomonas putida strain S11-2 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	327	327	97%	1e-85	98.40%	1405	MT539711.1
☐	Pseudomonas sp. strain Tm-B7 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	327	327	97%	1e-85	98.40%	1407	MT533988.1
☐	Pseudomonas sp. strain UFLA_306 16S ribosomal RNA gene, partial sequence	Pseudomonas ...	327	327	97%	1e-85	98.40%	1400	MN749735.1



Pseudomonas sp. A7-2 16S ribosomal RNA gene, partial sequence

Sequence ID: GQ497241.1 Length: 1063 Number of Matches: 1

See 1 more title(s) See all Identical Proteins(IPG)

Range 1: 71 to 257 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
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Query  5    AGCTTGCTCCTTGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCCTGGTAG  64
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Sbjct  71   AGCTTGCTCCTTGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCCTGGTAG  130

Query  65   TGGGGGACAACGTTTCGAAAGGAACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGG  124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  131  TGGGGGACAACGTTTCGAAAGGAACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGG  190

Query  125  GGACCTTCGGGCCCTGCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGTGTA  184
            ||||||||||||| |||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  191  GGACCTTCGGGCCTTGCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTA  250

Query  185  ATGGCTC  191
            |||||||
Sbjct  251  ATGGCTC  257
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(Hebron market parsley): *Enterobacter cloacae* strain 3849

GCTTTCGCACCTGACGTCGTCTTTGTCCGGGGGCCGCCTTCGCCCCGGTATTCCTCCA
GATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTA
GCCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTT
GACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTC
CGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTC
AATCGACAGGGTTATTAACCCTGTCGCCTTCCTCCCCGCTGAAAGTACTTTACAACC
CGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAA
TATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCT
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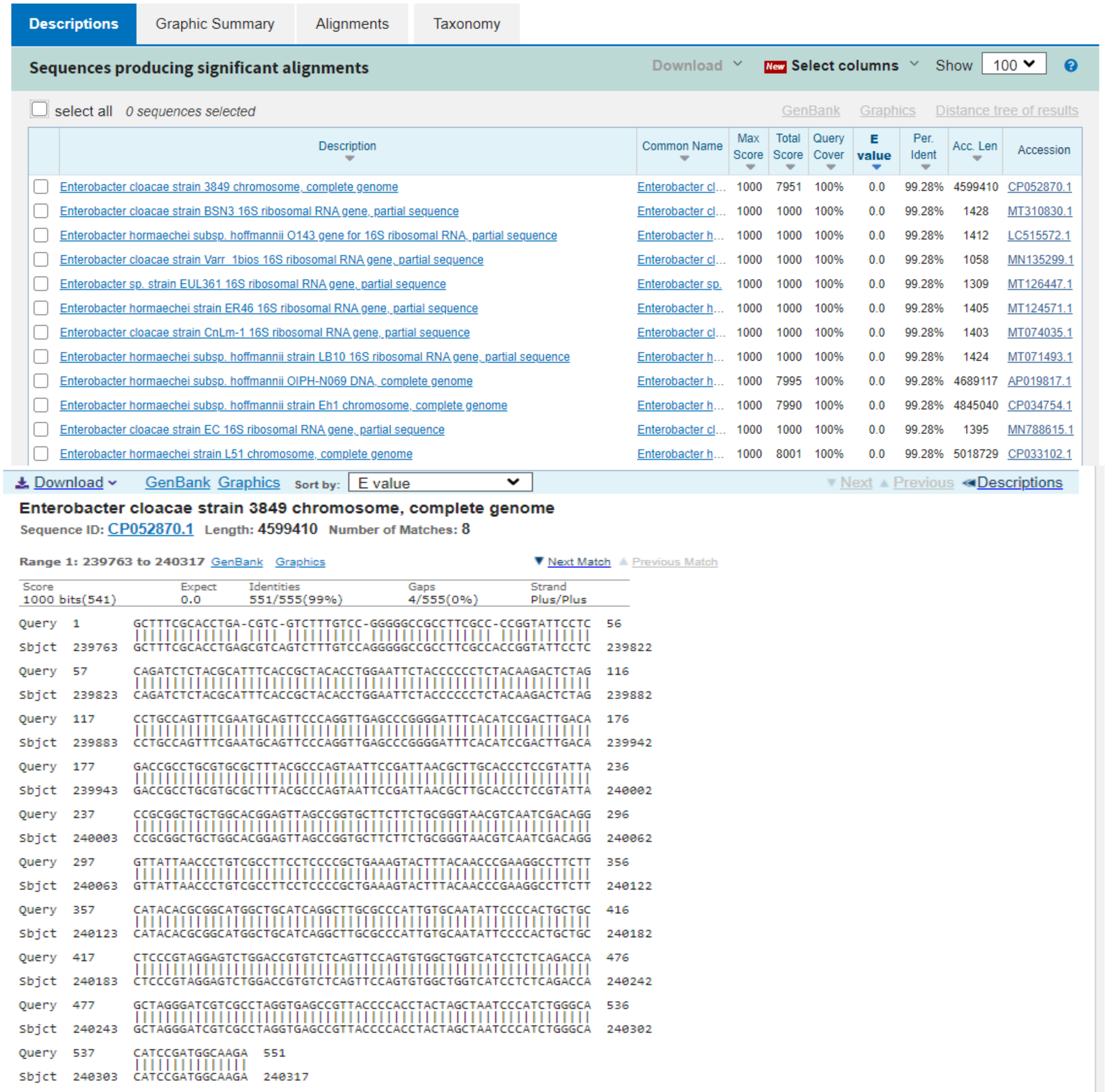

Sequences producing significant alignments

☐ select all *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Enterobacter cloacae strain 3849 chromosome, complete genome	Enterobacter cl...	1000	7951	100%	0.0	99.28%	4599410	CP052870.1
☐	Enterobacter cloacae strain BSN3 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	1000	1000	100%	0.0	99.28%	1428	MT310830.1
☐	Enterobacter hormaechei subsp. hoffmannii O143 gene for 16S ribosomal RNA, partial sequence	Enterobacter h...	1000	1000	100%	0.0	99.28%	1412	LC515572.1
☐	Enterobacter cloacae strain Varr_1bios 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	1000	1000	100%	0.0	99.28%	1058	MN135299.1
☐	Enterobacter sp. strain EUL361 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	1000	1000	100%	0.0	99.28%	1309	MT126447.1
☐	Enterobacter hormaechei strain ER46 16S ribosomal RNA gene, partial sequence	Enterobacter h...	1000	1000	100%	0.0	99.28%	1405	MT124571.1
☐	Enterobacter cloacae strain CnLm-1 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	1000	1000	100%	0.0	99.28%	1403	MT074035.1
☐	Enterobacter hormaechei subsp. hoffmannii strain LB10 16S ribosomal RNA gene, partial sequence	Enterobacter h...	1000	1000	100%	0.0	99.28%	1424	MT071493.1
☐	Enterobacter hormaechei subsp. hoffmannii OIPH-N069 DNA, complete genome	Enterobacter h...	1000	7995	100%	0.0	99.28%	4689117	AP019817.1
☐	Enterobacter hormaechei subsp. hoffmannii strain Eh1 chromosome, complete genome	Enterobacter h...	1000	7990	100%	0.0	99.28%	4845040	CP034754.1
☐	Enterobacter cloacae strain EC 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	1000	1000	100%	0.0	99.28%	1395	MN788615.1
☐	Enterobacter hormaechei strain L51 chromosome, complete genome	Enterobacter h...	1000	8001	100%	0.0	99.28%	5018729	CP033102.1

Sort by: E value

Enterobacter cloacae strain 3849 chromosome, complete genome

Sequence ID: CP052870.1 Length: 4599410 Number of Matches: 8

Range 1: 239763 to 240317 GenBank Graphics

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Score            Expect   Identities       Gaps          Strand
1000 bits(541)   0.0      551/555(99%)     4/555(0%)     Plus/Plus

Query  1       GCTTTCGCACCTGA-CGTC-GTCTTTGTCC-GGGGGCCGCCTTCGCC-CCGGTATTCCTC  56
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Sbjct  239763  GCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTC  239822

Query  57      CAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAG  116
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239823  CAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAG  239882

Query  117     CCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACA  176
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239883  CCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACA  239942

Query  177     GACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTA  236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239943  GACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTA  240002

Query  237     CCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAGG  296
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240003  CCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAGG  240062

Query  297     GTTATTAACCCTGTCGCCTTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTT  356
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240063  GTTATTAACCCTGTCGCCTTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTT  240122

Query  357     CATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGC  416
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240123  CATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGC  240182

Query  417     CTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCTGGTCATCCTCTCAGACCA  476
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240183  CTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCTGGTCATCCTCTCAGACCA  240242

Query  477     GCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTACTAGCTAATCCCATCTGGGCA  536
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240243  GCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTACTAGCTAATCCCATCTGGGCA  240302

Query  537     CATCCGATGGCAAGA  551
               |||||||||||||||
Sbjct  240303  CATCCGATGGCAAGA  240317
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(Hebron market mint): *Klebsiella pneumoniae* strain G-A-TGW

GCTTTTCGCACCTGRCGTCGTCTTTGTCCGGGGGCCGCCTTCGCCACCGGTATTCCTC
CAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCT
AGCCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACT
TGACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCT
CCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGT
CAATCGACAAGGTTATTAACCTTRTCGCCTTCCTCCCCGCTGAAAGTGCTTTACAAC
CCGAAGGCCTTCTTCACACACACGGCATGGCTGCWTCAGGCTTGCGCCCATTGTGCA
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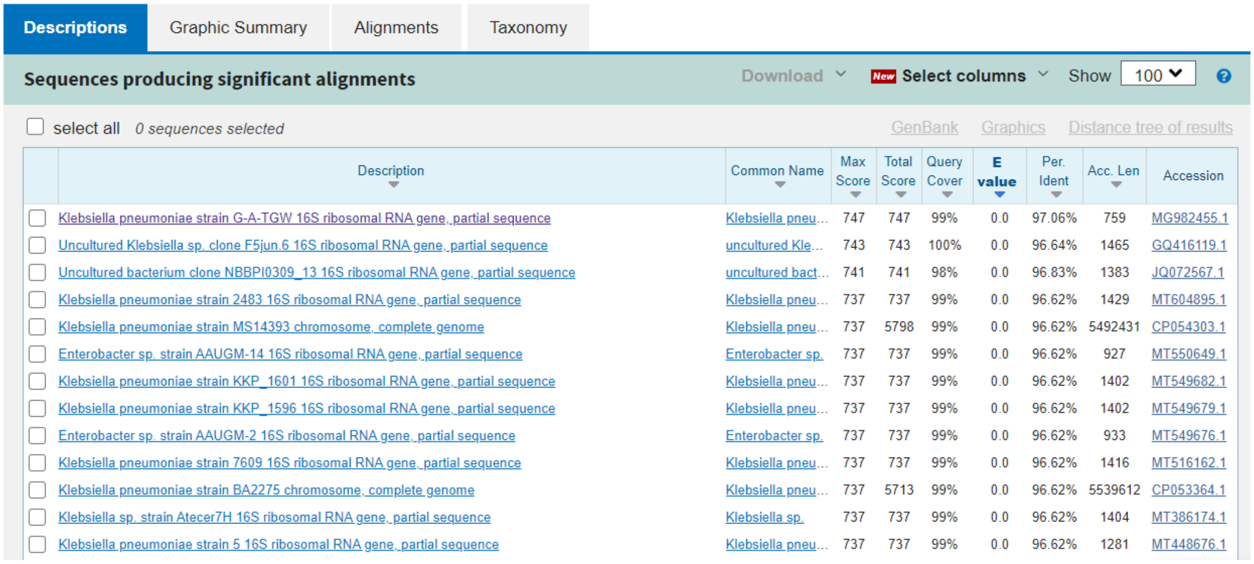
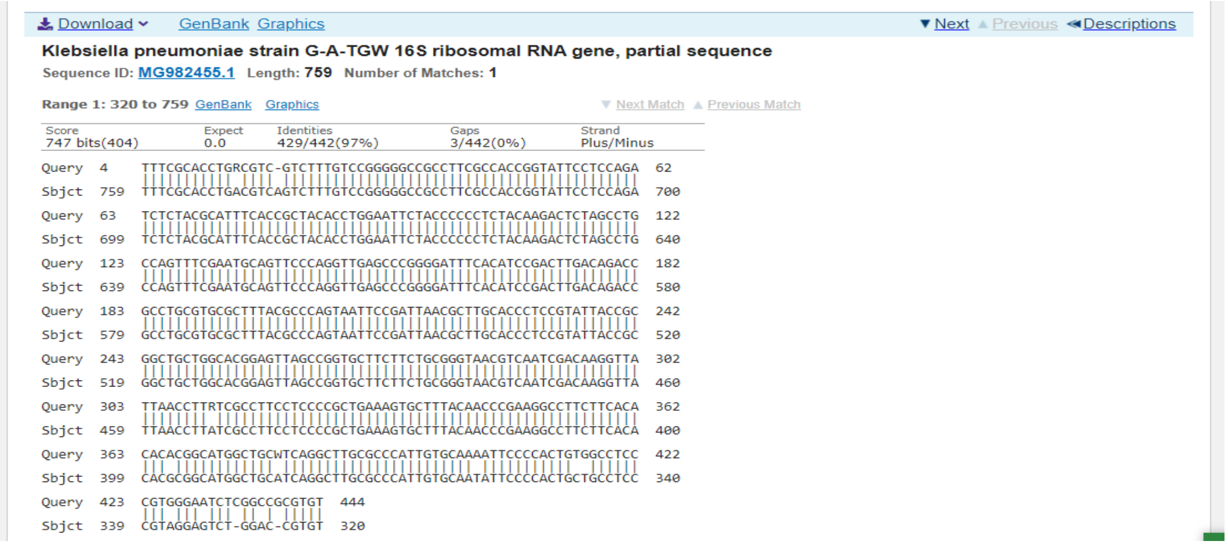


Sequences producing significant alignments

☐ select all   *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Klebsiella pneumoniae strain G-A-TGW 16S ribosomal RNA gene, partial sequence	Klebsiella pneu...	747	747	99%	0.0	97.06%	759	MG982455.1
☐	Uncultured Klebsiella sp. clone F5jun.6 16S ribosomal RNA gene, partial sequence	uncultured Kle...	743	743	100%	0.0	96.64%	1465	GQ416119.1
☐	Uncultured bacterium clone NBBPI0309_13 16S ribosomal RNA gene, partial sequence	uncultured bact...	741	741	98%	0.0	96.83%	1383	JQ072567.1
☐	Klebsiella pneumoniae strain 2483 16S ribosomal RNA gene, partial sequence	Klebsiella pneu...	737	737	99%	0.0	96.62%	1429	MT604895.1
☐	Klebsiella pneumoniae strain MS14393 chromosome, complete genome	Klebsiella pneu...	737	5798	99%	0.0	96.62%	5492431	CP054303.1
☐	Enterobacter sp. strain AAUGM-14 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	737	737	99%	0.0	96.62%	927	MT550649.1
☐	Klebsiella pneumoniae strain KKP_1601 16S ribosomal RNA gene, partial sequence	Klebsiella pneu...	737	737	99%	0.0	96.62%	1402	MT549682.1
☐	Klebsiella pneumoniae strain KKP_1596 16S ribosomal RNA gene, partial sequence	Klebsiella pneu...	737	737	99%	0.0	96.62%	1402	MT549679.1
☐	Enterobacter sp. strain AAUGM-2 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	737	737	99%	0.0	96.62%	933	MT549676.1
☐	Klebsiella pneumoniae strain 7609 16S ribosomal RNA gene, partial sequence	Klebsiella pneu...	737	737	99%	0.0	96.62%	1416	MT516162.1
☐	Klebsiella pneumoniae strain BA2275 chromosome, complete genome	Klebsiella pneu...	737	5713	99%	0.0	96.62%	5539612	CP053364.1
☐	Klebsiella sp. strain Atecer7H 16S ribosomal RNA gene, partial sequence	Klebsiella sp.	737	737	99%	0.0	96.62%	1404	MT386174.1
☐	Klebsiella pneumoniae strain 5 16S ribosomal RNA gene, partial sequence	Klebsiella pneu...	737	737	99%	0.0	96.62%	1281	MT448676.1



Klebsiella pneumoniae strain G-A-TGW 16S ribosomal RNA gene, partial sequence

Sequence ID: MG982455.1 Length: 759 Number of Matches: 1

Range 1: 320 to 759 GenBank Graphics

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Score            Expect   Identities      Gaps          Strand
747 bits(404)    0.0      429/442(97%)    3/442(0%)     Plus/Minus

Query  4    TTTCGCACCTGRCGTC-GTCTTTGTCCGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGA  62
            ||||||||||| |||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  759  TTTCGCACCTGACGTCAGTCTTTGTCCGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGA  700

Query  63   TCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTG  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  699  TCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTG  640

Query  123  CCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACC  182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  639  CCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACC  580

Query  183  GCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGC  242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  579  GCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGC  520

Query  243  GGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAAGGTTA  302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  519  GGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAAGGTTA  460

Query  303  TTAACCTTRTCGCCTTCCTCCCCGCTGAAAGTGCTTTACAACCCGAAGGCCTTCTTCACA  362
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  459  TTAACCTTATCGCCTTCCTCCCCGCTGAAAGTGCTTTACAACCCGAAGGCCTTCTTCACA  400

Query  363  CACACGGCATGGCTGCWTCAGGCTTGCGCCCATTGTGCAAAATTCCCCACTGTGGCCTCC  422
            ||| |||||||||||| ||||||||||||||||||||||| |||||||||||  ||||||
Sbjct  399  CACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGCCTCC  340

Query  423  CGTGGGAATCTCGGCCGCGTGT  444
            ||| ||| ||| || | |||||
Sbjct  339  CGTAGGAGTCT-GGAC-CGTGT  320
```
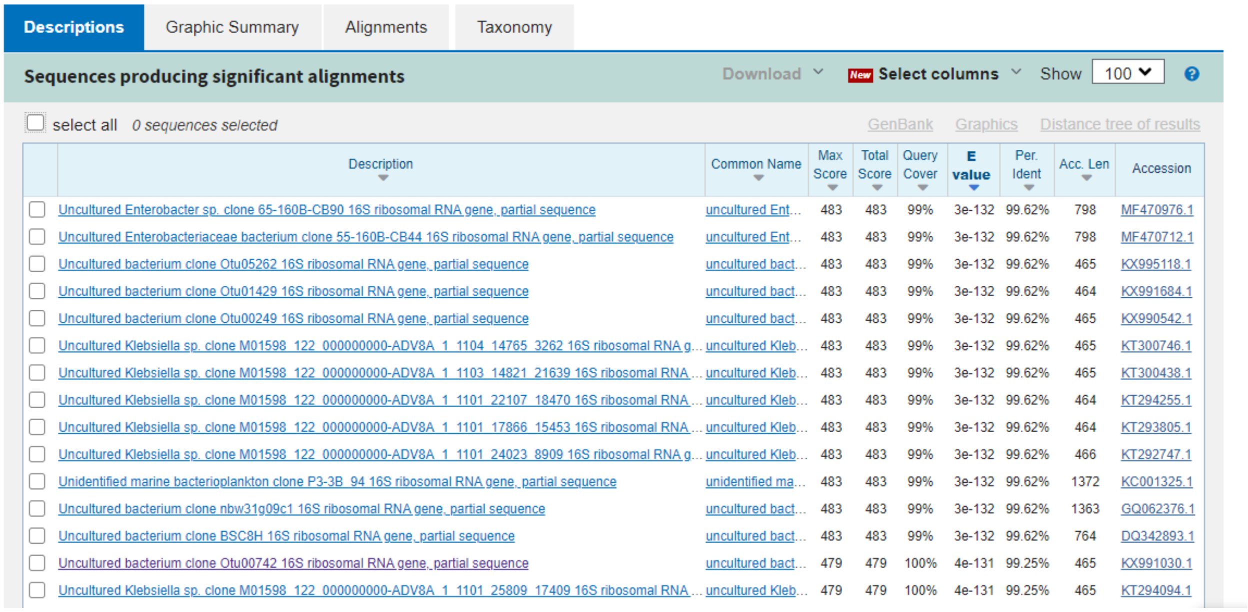

(Hebron market mint): *uncultured Enterobacter* sp. clone 65-160B-CB90

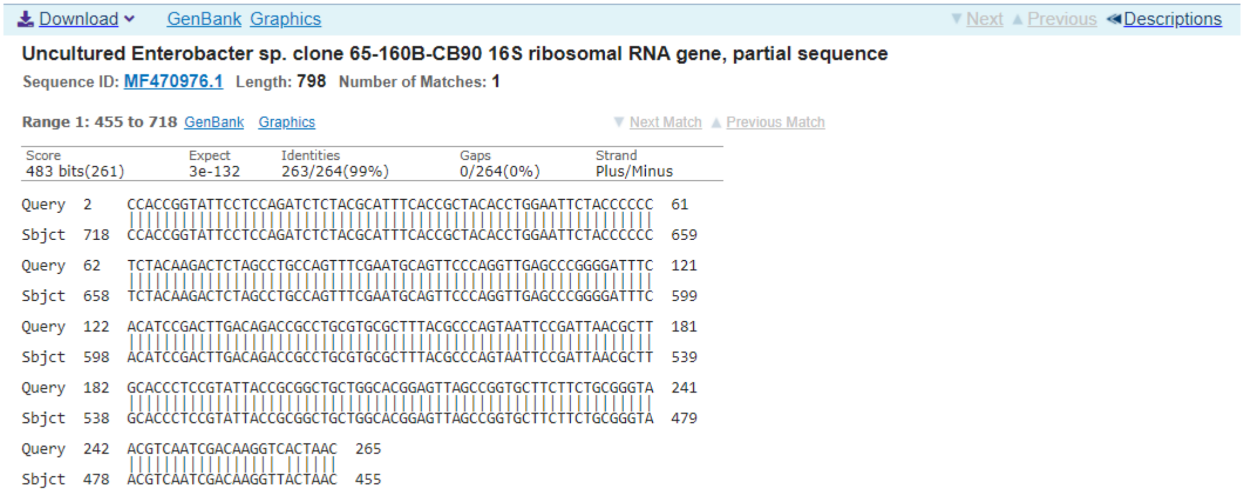
CCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCC
CCCTCTACAAGACTCTAGCCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGG
GATTTCACATCCGACTTGACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGA
TTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTT
CTTCTGCGGGTAACGTCAATCGACAAGGTCACTAAC



Sequences producing significant alignments

0 sequences selected

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Uncultured Enterobacter sp. clone 65-160B-CB90 16S ribosomal RNA gene, partial sequence	uncultured Ent...	483	483	99%	3e-132	99.62%	798	MF470976.1
☐	Uncultured Enterobacteriaceae bacterium clone 55-160B-CB44 16S ribosomal RNA gene, partial sequence	uncultured Ent...	483	483	99%	3e-132	99.62%	798	MF470712.1
☐	Uncultured bacterium clone Otu05262 16S ribosomal RNA gene, partial sequence	uncultured bact...	483	483	99%	3e-132	99.62%	465	KX995118.1
☐	Uncultured bacterium clone Otu01429 16S ribosomal RNA gene, partial sequence	uncultured bact...	483	483	99%	3e-132	99.62%	464	KX991684.1
☐	Uncultured bacterium clone Otu00249 16S ribosomal RNA gene, partial sequence	uncultured bact...	483	483	99%	3e-132	99.62%	465	KX990542.1
☐	Uncultured Klebsiella sp. clone M01598_122_000000000-ADV8A_1_1104_14765_3262 16S ribosomal RNA g...	uncultured Kleb...	483	483	99%	3e-132	99.62%	465	KT300746.1
☐	Uncultured Klebsiella sp. clone M01598_122_000000000-ADV8A_1_1103_14821_21639 16S ribosomal RNA ...	uncultured Kleb...	483	483	99%	3e-132	99.62%	465	KT300438.1
☐	Uncultured Klebsiella sp. clone M01598_122_000000000-ADV8A_1_1101_22107_18470 16S ribosomal RNA ...	uncultured Kleb...	483	483	99%	3e-132	99.62%	464	KT294255.1
☐	Uncultured Klebsiella sp. clone M01598_122_000000000-ADV8A_1_1101_17866_15453 16S ribosomal RNA ...	uncultured Kleb...	483	483	99%	3e-132	99.62%	464	KT293805.1
☐	Uncultured Klebsiella sp. clone M01598_122_000000000-ADV8A_1_1101_24023_8909 16S ribosomal RNA g...	uncultured Kleb...	483	483	99%	3e-132	99.62%	466	KT292747.1
☐	Unidentified marine bacterioplankton clone P3-3B_94 16S ribosomal RNA gene, partial sequence	unidentified ma...	483	483	99%	3e-132	99.62%	1372	KC001325.1
☐	Uncultured bacterium clone nbw31g09c1 16S ribosomal RNA gene, partial sequence	uncultured bact...	483	483	99%	3e-132	99.62%	1363	GQ062376.1
☐	Uncultured bacterium clone BSC8H 16S ribosomal RNA gene, partial sequence	uncultured bact...	483	483	99%	3e-132	99.62%	764	DQ342893.1
☐	Uncultured bacterium clone Otu00742 16S ribosomal RNA gene, partial sequence	uncultured bact...	479	479	100%	4e-131	99.25%	465	KX991030.1
☐	Uncultured Klebsiella sp. clone M01598_122_000000000-ADV8A_1_1101_25809_17409 16S ribosomal RNA ...	uncultured Kleb...	479	479	100%	4e-131	99.25%	465	KT294094.1



Uncultured Enterobacter sp. clone 65-160B-CB90 16S ribosomal RNA gene, partial sequence

Sequence ID: MF470976.1 Length: 798 Number of Matches: 1

Range 1: 455 to 718 GenBank Graphics

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Score            Expect     Identities          Gaps           Strand
483 bits(261)    3e-132     263/264(99%)        0/264(0%)      Plus/Minus

Query  2    CCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCC  61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  718  CCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCC  659

Query  62   TCTACAAGACTCTAGCCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTC  121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  658  TCTACAAGACTCTAGCCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTC  599

Query  122  ACATCCGACTTGACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTT  181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  598  ACATCCGACTTGACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTT  539

Query  182  GCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTA  241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  538  GCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTA  479

Query  242  ACGTCAATCGACAAGGTCACTAAC  265
            ||||||||||||||||| ||||||
Sbjct  478  ACGTCAATCGACAAGGTTACTAAC  455
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(Hebron market parsley): *Enterobacter cloacae* strain BHWSL4.2

GCTTTCGCACCTGACGTCGTCTTTGTCCGGGGGCCGCCTTCGCCACCGGTATTCCTCC
AGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCT
AGCCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACT
TGACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCT
CCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGT
CAATCGACAGGGTTATTAACCCTGTCGCCTTCCTCCCCGCTGAAAGTACTTTACAAC
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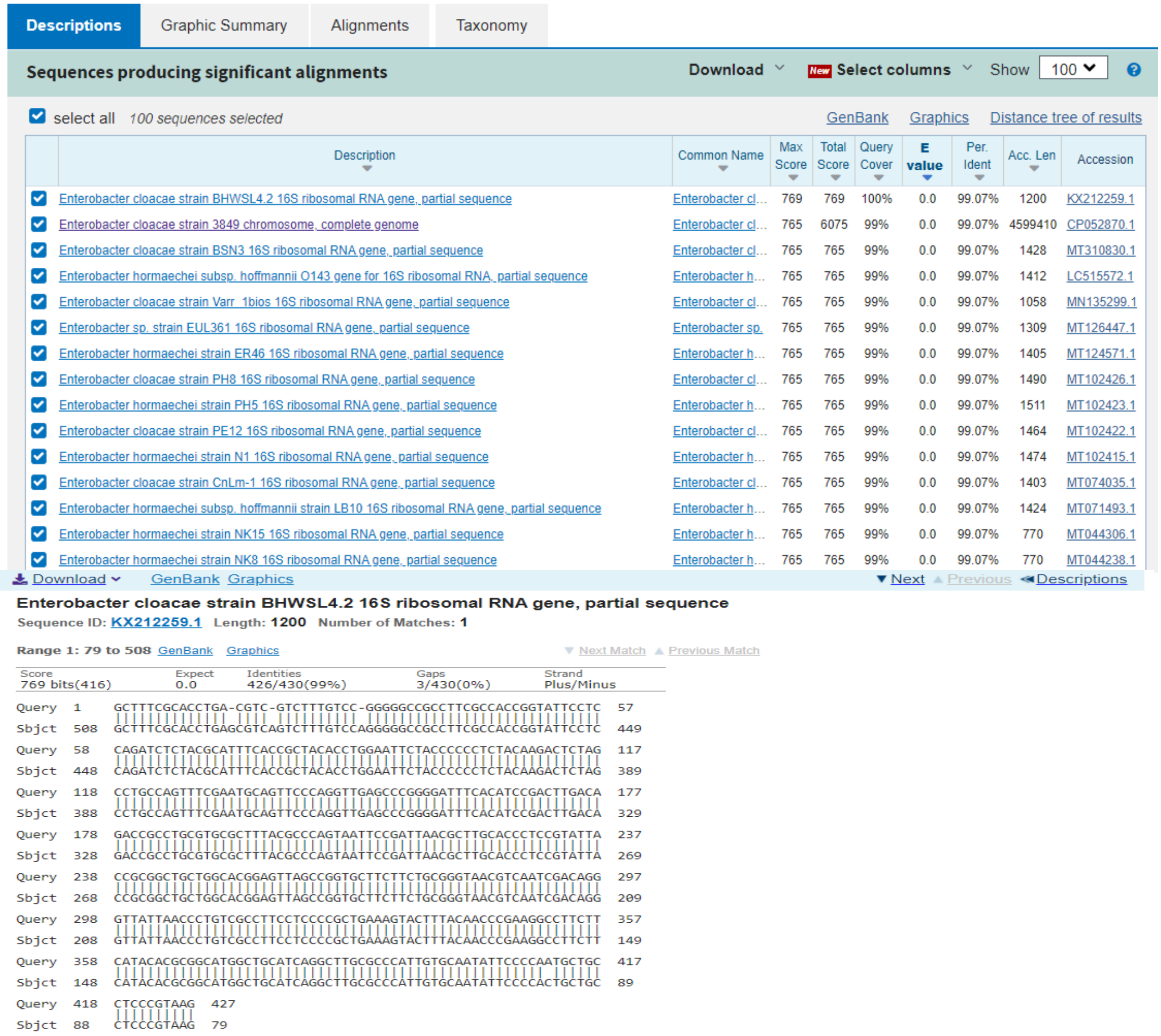
ATATTCCCCAATGCTGCCTCCCGTAAG



☑	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	Enterobacter cloacae strain BHWSL4.2 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	769	769	100%	0.0	99.07%	1200	KX212259.1
☑	Enterobacter cloacae strain 3849 chromosome, complete genome	Enterobacter cl...	765	6075	99%	0.0	99.07%	4599410	CP052870.1
☑	Enterobacter cloacae strain BSN3 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	765	765	99%	0.0	99.07%	1428	MT310830.1
☑	Enterobacter hormaechei subsp. hoffmannii O143 gene for 16S ribosomal RNA, partial sequence	Enterobacter h...	765	765	99%	0.0	99.07%	1412	LC515572.1
☑	Enterobacter cloacae strain Varr_1bios 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	765	765	99%	0.0	99.07%	1058	MN135299.1
☑	Enterobacter sp. strain EUL361 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	765	765	99%	0.0	99.07%	1309	MT126447.1
☑	Enterobacter hormaechei strain ER46 16S ribosomal RNA gene, partial sequence	Enterobacter h...	765	765	99%	0.0	99.07%	1405	MT124571.1
☑	Enterobacter cloacae strain PH8 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	765	765	99%	0.0	99.07%	1490	MT102426.1
☑	Enterobacter hormaechei strain PH5 16S ribosomal RNA gene, partial sequence	Enterobacter h...	765	765	99%	0.0	99.07%	1511	MT102423.1
☑	Enterobacter cloacae strain PE12 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	765	765	99%	0.0	99.07%	1464	MT102422.1
☑	Enterobacter hormaechei strain N1 16S ribosomal RNA gene, partial sequence	Enterobacter h...	765	765	99%	0.0	99.07%	1474	MT102415.1
☑	Enterobacter cloacae strain CnLm-1 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	765	765	99%	0.0	99.07%	1403	MT074035.1
☑	Enterobacter hormaechei subsp. hoffmannii strain LB10 16S ribosomal RNA gene, partial sequence	Enterobacter h...	765	765	99%	0.0	99.07%	1424	MT071493.1
☑	Enterobacter hormaechei strain NK15 16S ribosomal RNA gene, partial sequence	Enterobacter h...	765	765	99%	0.0	99.07%	770	MT044306.1
☑	Enterobacter hormaechei strain NK8 16S ribosomal RNA gene, partial sequence	Enterobacter h...	765	765	99%	0.0	99.07%	770	MT044238.1

Enterobacter cloacae strain BHWSL4.2 16S ribosomal RNA gene, partial sequence

Sequence ID: KX212259.1 Length: 1200 Number of Matches: 1

Range 1: 79 to 508 GenBank Graphics

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Score           Expect   Identities       Gaps          Strand
769 bits(416)   0.0      426/430(99%)     3/430(0%)     Plus/Minus

Query  1    GCTTTCGCACCTGA-CGTC-GTCTTTGTCC-GGGGGCCGCCTTCGCCACCGGTATTCCTC  57
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Sbjct  508  GCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTC  449

Query  58   CAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAG  117
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  448  CAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAG  389

Query  118  CCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACA  177
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  388  CCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACA  329

Query  178  GACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTA  237
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  328  GACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTA  269

Query  238  CCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAGG  297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  268  CCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAGG  209

Query  298  GTTATTAACCCTGTCGCCTTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTT  357
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  208  GTTATTAACCCTGTCGCCTTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTT  149

Query  358  CATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCAATGCTGC  417
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  148  CATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGC  89

Query  418  CTCCCGTAAG  427
            ||||||||||
Sbjct  88   CTCCCGTAAG  79
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(Hebron market parsley): *E. coli* strain 188

TACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTT
CGGGCCTCTTGCCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACG
GCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAA
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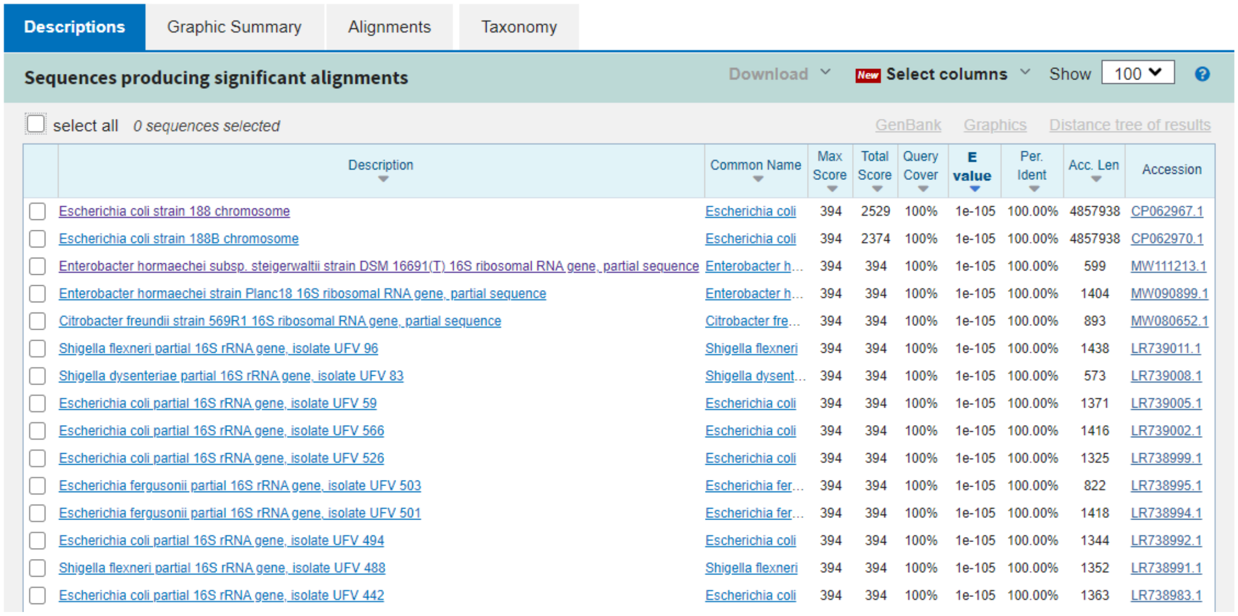
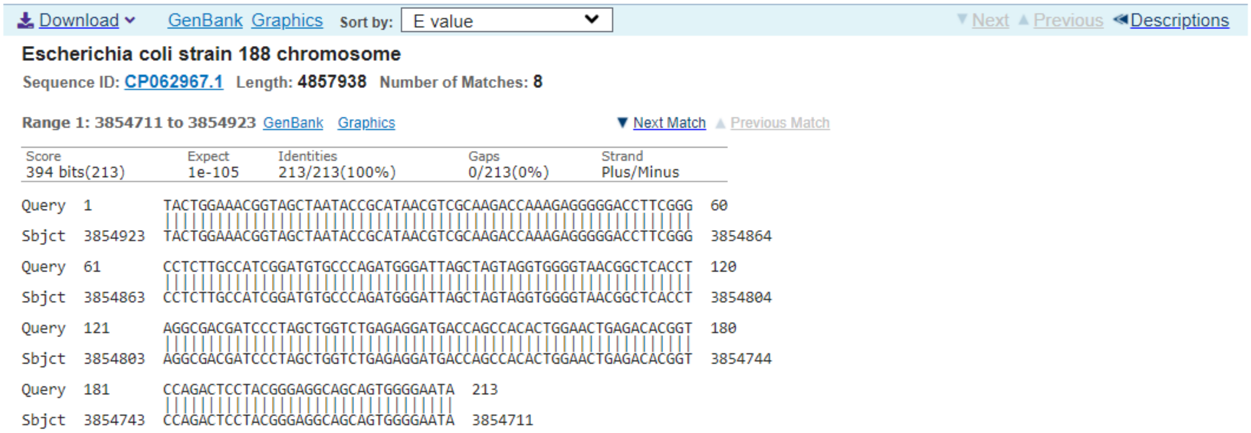


Sequences producing significant alignments

0 sequences selected

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Escherichia coli strain 188 chromosome	Escherichia coli	394	2529	100%	1e-105	100.00%	4857938	CP062967.1
☐	Escherichia coli strain 188B chromosome	Escherichia coli	394	2374	100%	1e-105	100.00%	4857938	CP062970.1
☐	Enterobacter hormaechei subsp. steigerwaltii strain DSM 16691(T) 16S ribosomal RNA gene, partial sequence	Enterobacter h...	394	394	100%	1e-105	100.00%	599	MW111213.1
☐	Enterobacter hormaechei strain Planc18 16S ribosomal RNA gene, partial sequence	Enterobacter h...	394	394	100%	1e-105	100.00%	1404	MW090899.1
☐	Citrobacter freundii strain 569R1 16S ribosomal RNA gene, partial sequence	Citrobacter fre...	394	394	100%	1e-105	100.00%	893	MW080652.1
☐	Shigella flexneri partial 16S rRNA gene, isolate UFV 96	Shigella flexneri	394	394	100%	1e-105	100.00%	1438	LR739011.1
☐	Shigella dysenteriae partial 16S rRNA gene, isolate UFV 83	Shigella dysent...	394	394	100%	1e-105	100.00%	573	LR739008.1
☐	Escherichia coli partial 16S rRNA gene, isolate UFV 59	Escherichia coli	394	394	100%	1e-105	100.00%	1371	LR739005.1
☐	Escherichia coli partial 16S rRNA gene, isolate UFV 566	Escherichia coli	394	394	100%	1e-105	100.00%	1416	LR739002.1
☐	Escherichia coli partial 16S rRNA gene, isolate UFV 526	Escherichia coli	394	394	100%	1e-105	100.00%	1325	LR738999.1
☐	Escherichia fergusonii partial 16S rRNA gene, isolate UFV 503	Escherichia fer...	394	394	100%	1e-105	100.00%	822	LR738995.1
☐	Escherichia fergusonii partial 16S rRNA gene, isolate UFV 501	Escherichia fer...	394	394	100%	1e-105	100.00%	1418	LR738994.1
☐	Escherichia coli partial 16S rRNA gene, isolate UFV 494	Escherichia coli	394	394	100%	1e-105	100.00%	1344	LR738992.1
☐	Shigella flexneri partial 16S rRNA gene, isolate UFV 488	Shigella flexneri	394	394	100%	1e-105	100.00%	1352	LR738991.1
☐	Escherichia coli partial 16S rRNA gene, isolate UFV 442	Escherichia coli	394	394	100%	1e-105	100.00%	1363	LR738983.1



Sort by: E value

Escherichia coli strain 188 chromosome

Sequence ID: CP062967.1 Length: 4857938 Number of Matches: 8

Range 1: 3854711 to 3854923 GenBank Graphics

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Score            Expect    Identities       Gaps        Strand
394 bits(213)    1e-105    213/213(100%)    0/213(0%)   Plus/Minus

Query  1        TACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGG  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3854923  TACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGG  3854864

Query  61       CCTCTTGCCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3854863  CCTCTTGCCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCT  3854804

Query  121      AGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGT  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3854803  AGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGT  3854744

Query  181      CCAGACTCCTACGGGAGGCAGCAGTGGGGAATA  213
                |||||||||||||||||||||||||||||||||
Sbjct  3854743  CCAGACTCCTACGGGAGGCAGCAGTGGGGAATA  3854711
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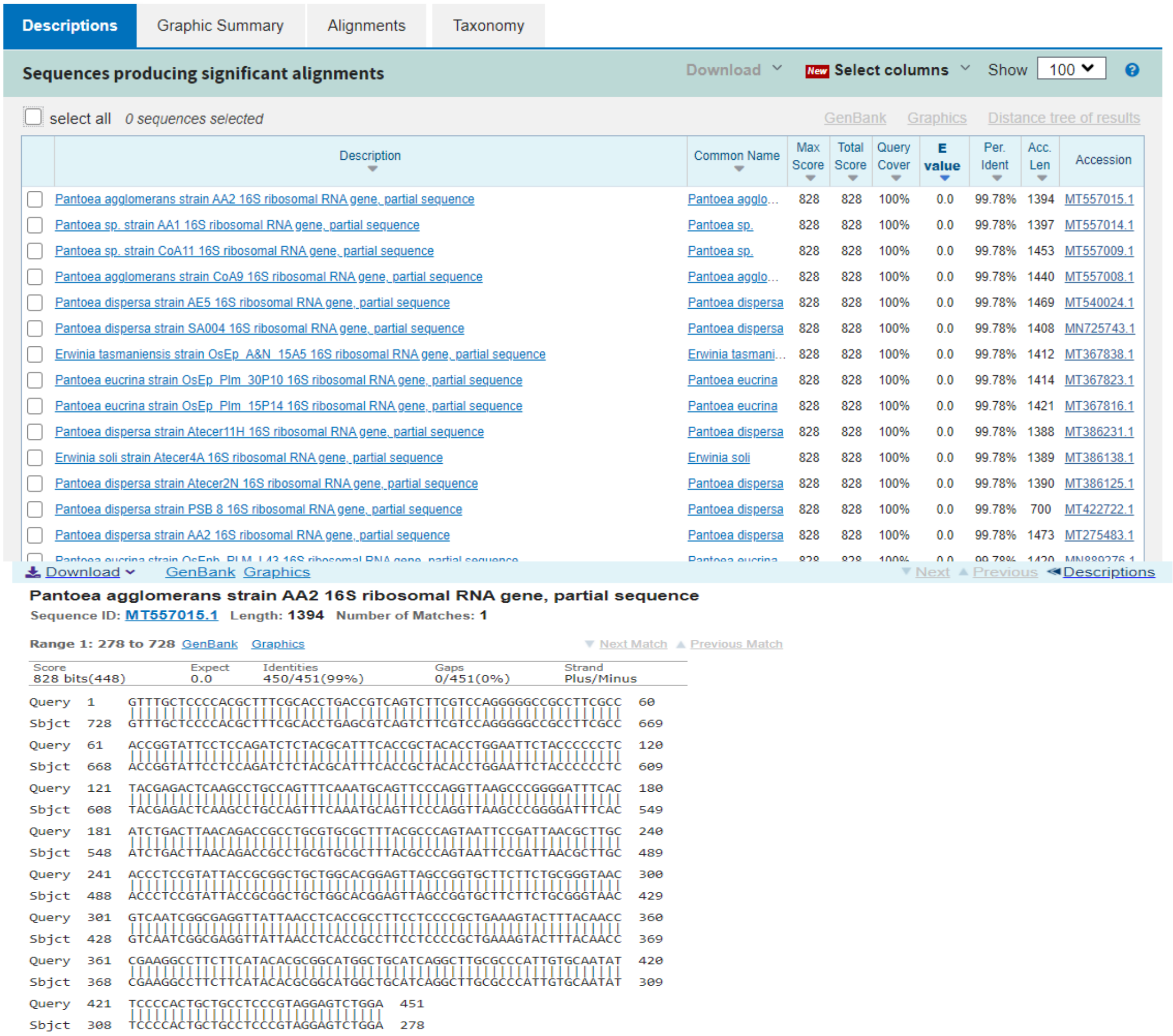
(Rami levy parsley): *Pantoea agglomerans* strain AA2

GTTTGCTCCCCACGCTTTCGCACCTGACCGTCAGTCTTCGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACGAGACTCAAGCCTGCCAGTTTCAAATGCAGTTCCCAGGTTAAGCCCGGGGATTTCACATCTGACTTAACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGGCGAGGTTATTAACCTCACCGCCTTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGA



Sequences producing significant alignments

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Pantoea agglomerans strain AA2 16S ribosomal RNA gene, partial sequence	Pantoea agglo...	828	828	100%	0.0	99.78%	1394	MT557015.1
☐	Pantoea sp. strain AA1 16S ribosomal RNA gene, partial sequence	Pantoea sp.	828	828	100%	0.0	99.78%	1397	MT557014.1
☐	Pantoea sp. strain CoA11 16S ribosomal RNA gene, partial sequence	Pantoea sp.	828	828	100%	0.0	99.78%	1453	MT557009.1
☐	Pantoea agglomerans strain CoA9 16S ribosomal RNA gene, partial sequence	Pantoea agglo...	828	828	100%	0.0	99.78%	1440	MT557008.1
☐	Pantoea dispersa strain AE5 16S ribosomal RNA gene, partial sequence	Pantoea dispersa	828	828	100%	0.0	99.78%	1469	MT540024.1
☐	Pantoea dispersa strain SA004 16S ribosomal RNA gene, partial sequence	Pantoea dispersa	828	828	100%	0.0	99.78%	1408	MN725743.1
☐	Erwinia tasmaniensis strain OsEp_A&N_15A5 16S ribosomal RNA gene, partial sequence	Erwinia tasmani...	828	828	100%	0.0	99.78%	1412	MT367838.1
☐	Pantoea eucrina strain OsEp_Plm_30P10 16S ribosomal RNA gene, partial sequence	Pantoea eucrina	828	828	100%	0.0	99.78%	1414	MT367823.1
☐	Pantoea eucrina strain OsEp_Plm_15P14 16S ribosomal RNA gene, partial sequence	Pantoea eucrina	828	828	100%	0.0	99.78%	1421	MT367816.1
☐	Pantoea dispersa strain Atecer11H 16S ribosomal RNA gene, partial sequence	Pantoea dispersa	828	828	100%	0.0	99.78%	1388	MT386231.1
☐	Erwinia soli strain Atecer4A 16S ribosomal RNA gene, partial sequence	Erwinia soli	828	828	100%	0.0	99.78%	1389	MT386138.1
☐	Pantoea dispersa strain Atecer2N 16S ribosomal RNA gene, partial sequence	Pantoea dispersa	828	828	100%	0.0	99.78%	1390	MT386125.1
☐	Pantoea dispersa strain PSB 8 16S ribosomal RNA gene, partial sequence	Pantoea dispersa	828	828	100%	0.0	99.78%	700	MT422722.1
☐	Pantoea dispersa strain AA2 16S ribosomal RNA gene, partial sequence	Pantoea dispersa	828	828	100%	0.0	99.78%	1473	MT275483.1

Pantoea agglomerans strain AA2 16S ribosomal RNA gene, partial sequence

Sequence ID: MT557015.1 Length: 1394 Number of Matches: 1

Range 1: 278 to 728 GenBank Graphics

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Score          Expect   Identities      Gaps         Strand
828 bits(448)  0.0      450/451(99%)    0/451(0%)    Plus/Minus

Query  1     GTTTGCTCCCCACGCTTTCGCACCTGACCGTCAGTCTTCGTCCAGGGGGCCGCCTTCGCC  60
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Sbjct  728   GTTTGCTCCCCACGCTTTCGCACCTGAGCGTCAGTCTTCGTCCAGGGGGCCGCCTTCGCC  669

Query  61    ACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  668   ACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTC  609

Query  121   TACGAGACTCAAGCCTGCCAGTTTCAAATGCAGTTCCCAGGTTAAGCCCGGGGATTTCAC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  608   TACGAGACTCAAGCCTGCCAGTTTCAAATGCAGTTCCCAGGTTAAGCCCGGGGATTTCAC  549

Query  181   ATCTGACTTAACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  548   ATCTGACTTAACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGC  489

Query  241   ACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAAC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  488   ACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAAC  429

Query  301   GTCAATCGGCGAGGTTATTAACCTCACCGCCTTCCTCCCCGCTGAAAGTACTTTACAACC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  428   GTCAATCGGCGAGGTTATTAACCTCACCGCCTTCCTCCCCGCTGAAAGTACTTTACAACC  369

Query  361   CGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATAT  420
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Sbjct  368   CGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATAT  309

Query  421   TCCCCACTGCTGCCTCCCGTAGGAGTCTGGA  451
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Sbjct  308   TCCCCACTGCTGCCTCCCGTAGGAGTCTGGA  278
```

(Rami levy parsley): *E. coli* strain SCU-397

GTGTCACTTTCGCTTTGGCAGCAGTGTCTTGCCCGATTGCAGGATGAGTTACCAGCCACAGA
ATTCAGTATGTGGATACGCCCATTGCAGGCGGAACTGAGCGATAACACGCTGGCCCTGTACG
CGCCAAATCGTTTTGTCCTCGATTGGGTACGGGACAAGTACCTTAATAATATCAATGGACTG
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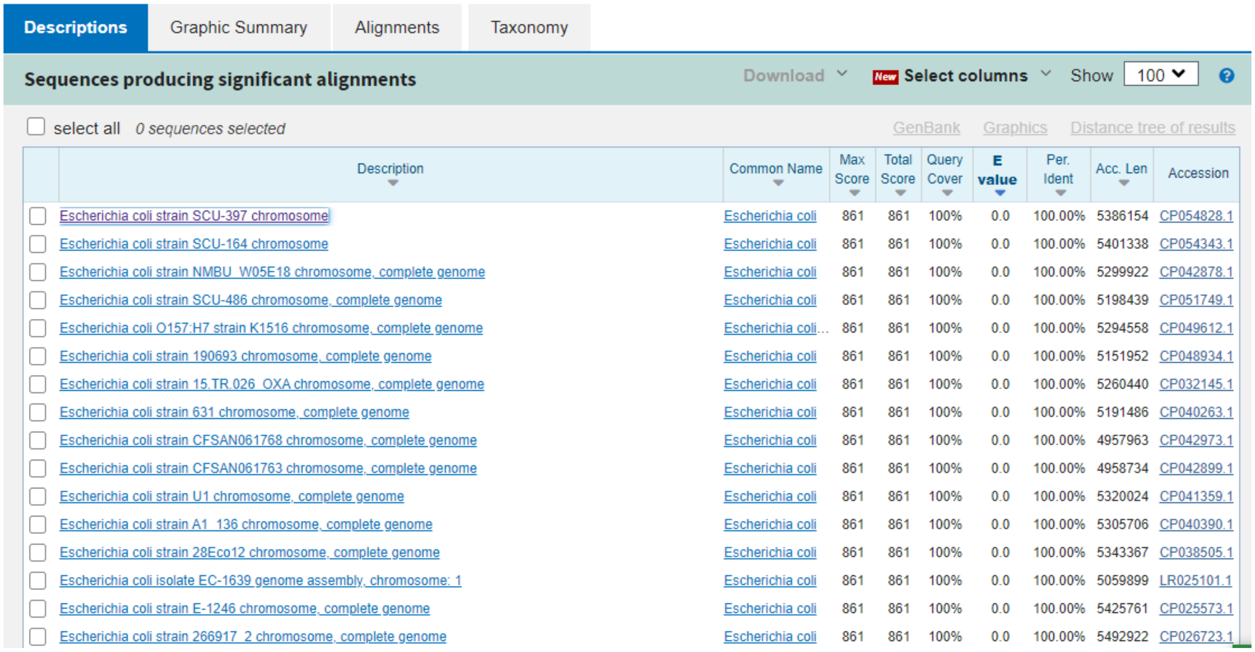
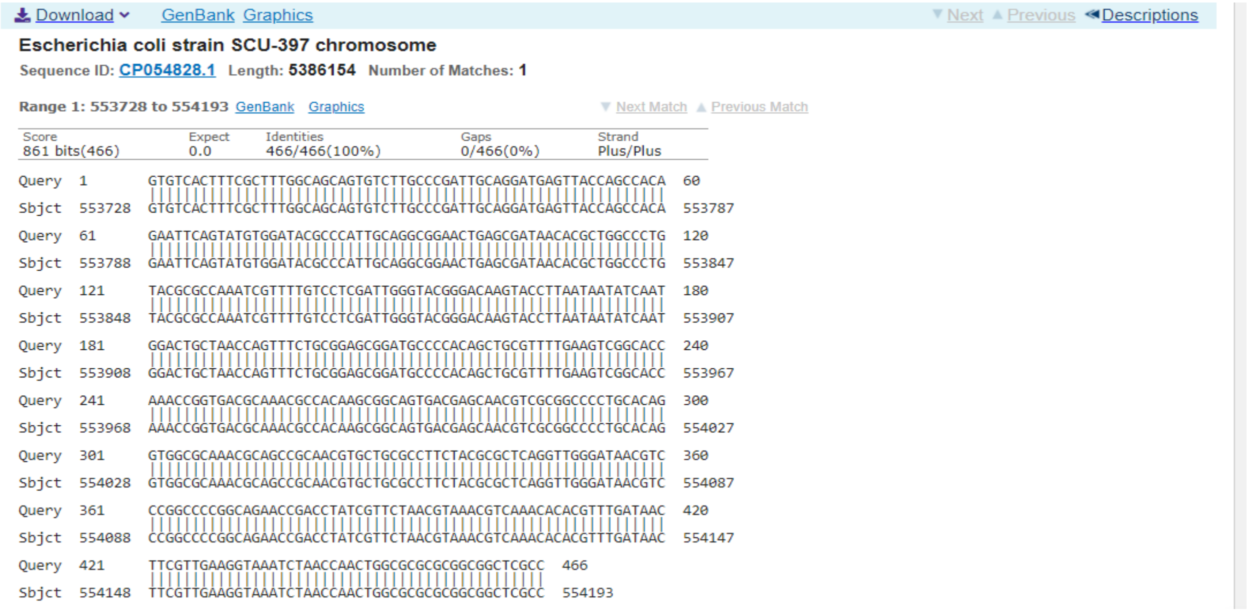
GACGCAAACGCCA



Sequences producing significant alignments

☐ select all *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Escherichia coli strain SCU-397 chromosome	Escherichia coli	861	861	100%	0.0	100.00%	5386154	CP054828.1
☐	Escherichia coli strain SCU-164 chromosome	Escherichia coli	861	861	100%	0.0	100.00%	5401338	CP054343.1
☐	Escherichia coli strain NMBU_W05E18 chromosome, complete genome	Escherichia coli	861	861	100%	0.0	100.00%	5299922	CP042878.1
☐	Escherichia coli strain SCU-486 chromosome, complete genome	Escherichia coli	861	861	100%	0.0	100.00%	5198439	CP051749.1
☐	Escherichia coli O157:H7 strain K1516 chromosome, complete genome	Escherichia coli...	861	861	100%	0.0	100.00%	5294558	CP049612.1
☐	Escherichia coli strain 190693 chromosome, complete genome	Escherichia coli	861	861	100%	0.0	100.00%	5151952	CP048934.1
☐	Escherichia coli strain 15.TR.026_OXA chromosome, complete genome	Escherichia coli	861	861	100%	0.0	100.00%	5260440	CP032145.1
☐	Escherichia coli strain 631 chromosome, complete genome	Escherichia coli	861	861	100%	0.0	100.00%	5191486	CP040263.1
☐	Escherichia coli strain CFSAN061768 chromosome, complete genome	Escherichia coli	861	861	100%	0.0	100.00%	4957963	CP042973.1
☐	Escherichia coli strain CFSAN061763 chromosome, complete genome	Escherichia coli	861	861	100%	0.0	100.00%	4958734	CP042899.1
☐	Escherichia coli strain U1 chromosome, complete genome	Escherichia coli	861	861	100%	0.0	100.00%	5320024	CP041359.1
☐	Escherichia coli strain A1_136 chromosome, complete genome	Escherichia coli	861	861	100%	0.0	100.00%	5305706	CP040390.1
☐	Escherichia coli strain 28Eco12 chromosome, complete genome	Escherichia coli	861	861	100%	0.0	100.00%	5343367	CP038505.1
☐	Escherichia coli isolate EC-1639 genome assembly, chromosome: 1	Escherichia coli	861	861	100%	0.0	100.00%	5059899	LR025101.1
☐	Escherichia coli strain E-1246 chromosome, complete genome	Escherichia coli	861	861	100%	0.0	100.00%	5425761	CP025573.1
☐	Escherichia coli strain 266917_2 chromosome, complete genome	Escherichia coli	861	861	100%	0.0	100.00%	5492922	CP026723.1



Escherichia coli strain SCU-397 chromosome

Sequence ID: CP054828.1 Length: 5386154 Number of Matches: 1

Range 1: 553728 to 554193 GenBank Graphics

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Sbjct  553728  GTGTCACTTTCGCTTTGGCAGCAGTGTCTTGCCCGATTGCAGGATGAGTTACCAGCCACA  553787

Query  61      GAATTCAGTATGTGGATACGCCCATTGCAGGCGGAACTGAGCGATAACACGCTGGCCCTG  120
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Sbjct  553788  GAATTCAGTATGTGGATACGCCCATTGCAGGCGGAACTGAGCGATAACACGCTGGCCCTG  553847

Query  121     TACGCGCCAAATCGTTTTGTCCTCGATTGGGTACGGGACAAGTACCTTAATAATATCAAT  180
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Sbjct  553848  TACGCGCCAAATCGTTTTGTCCTCGATTGGGTACGGGACAAGTACCTTAATAATATCAAT  553907

Query  181     GGACTGCTAACCAGTTTCTGCGGAGCGGATGCCCCACAGCTGCGTTTTGAAGTCGGCACC  240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  553908  GGACTGCTAACCAGTTTCTGCGGAGCGGATGCCCCACAGCTGCGTTTTGAAGTCGGCACC  553967

Query  241     AAACCGGTGACGCAAACGCCACAAGCGGCAGTGACGAGCAACGTCGCGGCCCCTGCACAG  300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  553968  AAACCGGTGACGCAAACGCCACAAGCGGCAGTGACGAGCAACGTCGCGGCCCCTGCACAG  554027

Query  301     GTGGCGCAAACGCAGCCGCAACGTGCTGCGCCTTCTACGCGCTCAGGTTGGGATAACGTC  360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  554028  GTGGCGCAAACGCAGCCGCAACGTGCTGCGCCTTCTACGCGCTCAGGTTGGGATAACGTC  554087

Query  361     CCGGCCCCGGCAGAACCGACCTATCGTTCTAACGTAAACGTCAAACACACGTTTGATAAC  420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  554088  CCGGCCCCGGCAGAACCGACCTATCGTTCTAACGTAAACGTCAAACACACGTTTGATAAC  554147

Query  421     TTCGTTGAAGGTAAATCTAACCAACTGGCGCGCGCGGCGGCTCGCC  466
               ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  554148  TTCGTTGAAGGTAAATCTAACCAACTGGCGCGCGCGGCGGCTCGCC  554193
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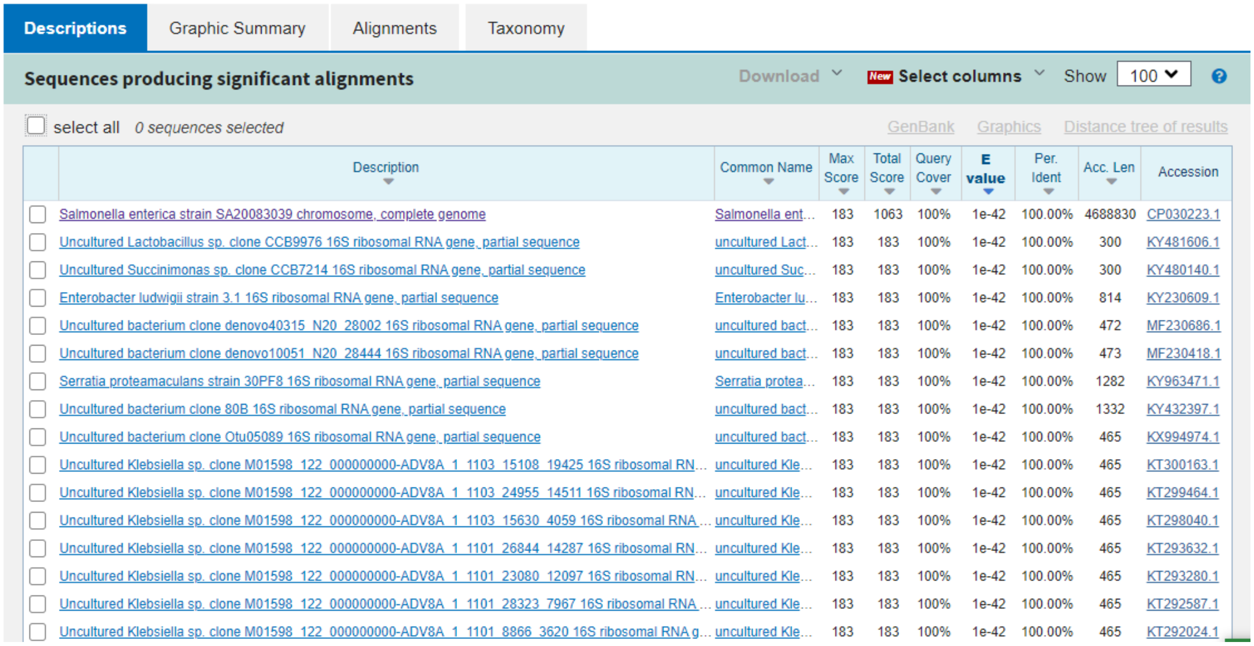
(Rami levy parsley): *salmonella* enterica

GTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTCTACGC ATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAAC



Sequences producing significant alignments

☐ select all *0 sequences selected*

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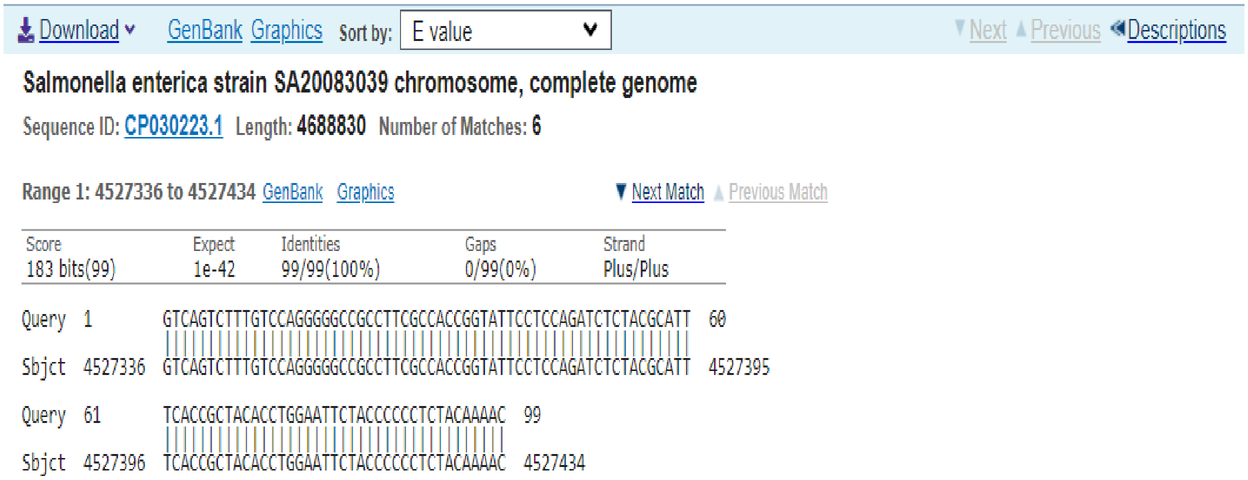
☐	Salmonella enterica strain SA20083039 chromosome, complete genome	Salmonella ent...	183	1063	100%	1e-42	100.00%	4688830	CP030223.1
☐	Uncultured Lactobacillus sp. clone CCB9976 16S ribosomal RNA gene, partial sequence	uncultured Lact...	183	183	100%	1e-42	100.00%	300	KY481606.1
☐	Uncultured Succinimonas sp. clone CCB7214 16S ribosomal RNA gene, partial sequence	uncultured Suc...	183	183	100%	1e-42	100.00%	300	KY480140.1
☐	Enterobacter ludwigii strain 3.1 16S ribosomal RNA gene, partial sequence	Enterobacter lu...	183	183	100%	1e-42	100.00%	814	KY230609.1
☐	Uncultured bacterium clone denovo40315 N20 28002 16S ribosomal RNA gene, partial sequence	uncultured bact...	183	183	100%	1e-42	100.00%	472	MF230686.1
☐	Uncultured bacterium clone denovo10051 N20 28444 16S ribosomal RNA gene, partial sequence	uncultured bact...	183	183	100%	1e-42	100.00%	473	MF230418.1
☐	Serratia proteamaculans strain 30PF8 16S ribosomal RNA gene, partial sequence	Serratia protea...	183	183	100%	1e-42	100.00%	1282	KY963471.1
☐	Uncultured bacterium clone 80B 16S ribosomal RNA gene, partial sequence	uncultured bact...	183	183	100%	1e-42	100.00%	1332	KY432397.1
☐	Uncultured bacterium clone Otu05089 16S ribosomal RNA gene, partial sequence	uncultured bact...	183	183	100%	1e-42	100.00%	465	KX994974.1
☐	Uncultured Klebsiella sp. clone M01598 122 000000000-ADV8A 1 1103 15108 19425 16S ribosomal RN...	uncultured Kle...	183	183	100%	1e-42	100.00%	465	KT300163.1
☐	Uncultured Klebsiella sp. clone M01598 122 000000000-ADV8A 1 1103 24955 14511 16S ribosomal RN...	uncultured Kle...	183	183	100%	1e-42	100.00%	465	KT299464.1
☐	Uncultured Klebsiella sp. clone M01598 122 000000000-ADV8A 1 1103 15630 4059 16S ribosomal RNA ...	uncultured Kle...	183	183	100%	1e-42	100.00%	465	KT298040.1
☐	Uncultured Klebsiella sp. clone M01598 122 000000000-ADV8A 1 1101 26844 14287 16S ribosomal RN...	uncultured Kle...	183	183	100%	1e-42	100.00%	465	KT293632.1
☐	Uncultured Klebsiella sp. clone M01598 122 000000000-ADV8A 1 1101 23080 12097 16S ribosomal RN...	uncultured Kle...	183	183	100%	1e-42	100.00%	465	KT293280.1
☐	Uncultured Klebsiella sp. clone M01598 122 000000000-ADV8A 1 1101 28323 7967 16S ribosomal RNA ...	uncultured Kle...	183	183	100%	1e-42	100.00%	465	KT292587.1
☐	Uncultured Klebsiella sp. clone M01598 122 000000000-ADV8A 1 1101 8866 3620 16S ribosomal RNA g...	uncultured Kle...	183	183	100%	1e-42	100.00%	465	KT292024.1



Sort by: E value

Salmonella enterica strain SA20083039 chromosome, complete genome

Sequence ID: CP030223.1 Length: 4688830 Number of Matches: 6

Range 1: 4527336 to 4527434 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
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Query  61       TCACCGCTACACCTGGAATTCTACCCCCCTCTACAAAAC  99
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Sbjct  4527396  TCACCGCTACACCTGGAATTCTACCCCCCTCTACAAAAC  4527434
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(Hebron market parsley): *Enterobacter hormaechei*

GCACCTGACGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGA
TCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCC
TGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGAC
AGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGT
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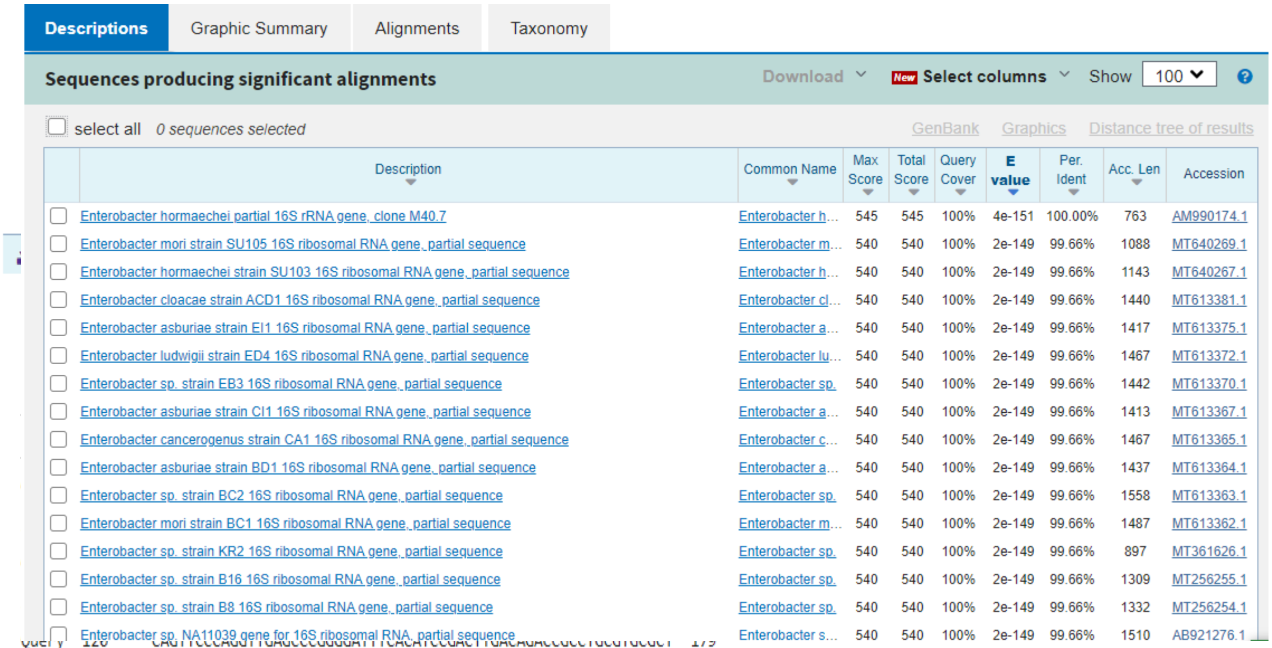
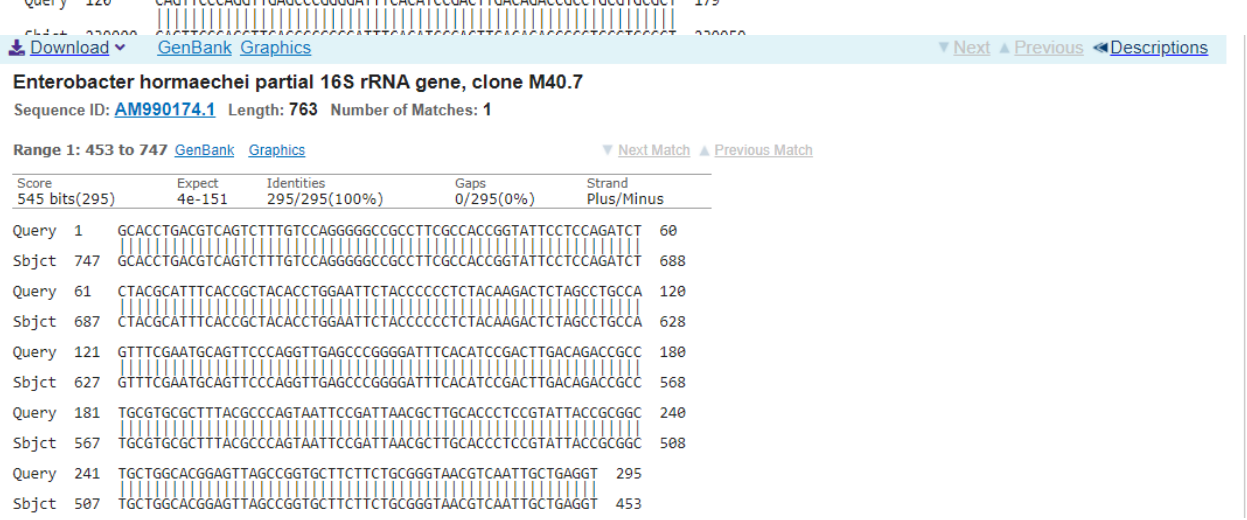
TGCTGAGGT



Sequences producing significant alignments

☐ select all *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Enterobacter hormaechei partial 16S rRNA gene, clone M40.7	Enterobacter h...	545	545	100%	4e-151	100.00%	763	AM990174.1
☐	Enterobacter mori strain SU105 16S ribosomal RNA gene, partial sequence	Enterobacter m...	540	540	100%	2e-149	99.66%	1088	MT640269.1
☐	Enterobacter hormaechei strain SU103 16S ribosomal RNA gene, partial sequence	Enterobacter h...	540	540	100%	2e-149	99.66%	1143	MT640267.1
☐	Enterobacter cloacae strain ACD1 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	540	540	100%	2e-149	99.66%	1440	MT613381.1
☐	Enterobacter asburiae strain EI1 16S ribosomal RNA gene, partial sequence	Enterobacter a...	540	540	100%	2e-149	99.66%	1417	MT613375.1
☐	Enterobacter ludwigii strain ED4 16S ribosomal RNA gene, partial sequence	Enterobacter lu...	540	540	100%	2e-149	99.66%	1467	MT613372.1
☐	Enterobacter sp. strain EB3 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	540	540	100%	2e-149	99.66%	1442	MT613370.1
☐	Enterobacter asburiae strain CI1 16S ribosomal RNA gene, partial sequence	Enterobacter a...	540	540	100%	2e-149	99.66%	1413	MT613367.1
☐	Enterobacter cancerogenus strain CA1 16S ribosomal RNA gene, partial sequence	Enterobacter c...	540	540	100%	2e-149	99.66%	1467	MT613365.1
☐	Enterobacter asburiae strain BD1 16S ribosomal RNA gene, partial sequence	Enterobacter a...	540	540	100%	2e-149	99.66%	1437	MT613364.1
☐	Enterobacter sp. strain BC2 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	540	540	100%	2e-149	99.66%	1558	MT613363.1
☐	Enterobacter mori strain BC1 16S ribosomal RNA gene, partial sequence	Enterobacter m...	540	540	100%	2e-149	99.66%	1487	MT613362.1
☐	Enterobacter sp. strain KR2 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	540	540	100%	2e-149	99.66%	897	MT361626.1
☐	Enterobacter sp. strain B16 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	540	540	100%	2e-149	99.66%	1309	MT256255.1
☐	Enterobacter sp. strain B8 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	540	540	100%	2e-149	99.66%	1332	MT256254.1
☐	Enterobacter sp. NA11039 gene for 16S ribosomal RNA, partial sequence	Enterobacter s...	540	540	100%	2e-149	99.66%	1510	AB921276.1



Enterobacter hormaechei partial 16S rRNA gene, clone M40.7

Sequence ID: AM990174.1 **Length:** 763 **Number of Matches:** 1

Range 1: 453 to 747 GenBank Graphics

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Score            Expect     Identities          Gaps         Strand
545 bits(295)    4e-151     295/295(100%)       0/295(0%)    Plus/Minus

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Sbjct  747  GCACCTGACGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCT  688

Query  61   CTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCA  120
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Sbjct  687  CTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCA  628

Query  121  GTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCC  180
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Sbjct  627  GTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCC  568

Query  181  TGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  567  TGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGC  508

Query  241  TGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATTGCTGAGGT  295
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507  TGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATTGCTGAGGT  453
```
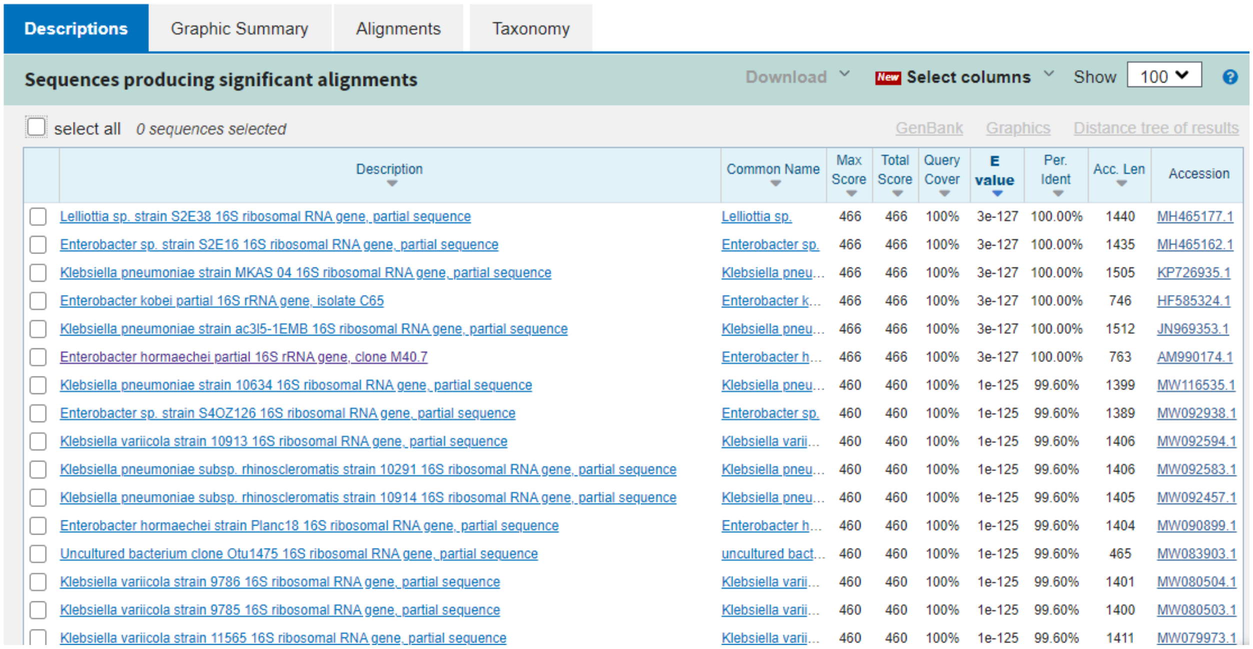

(Hebron market mint): *lelliottia* sp strain S2E38

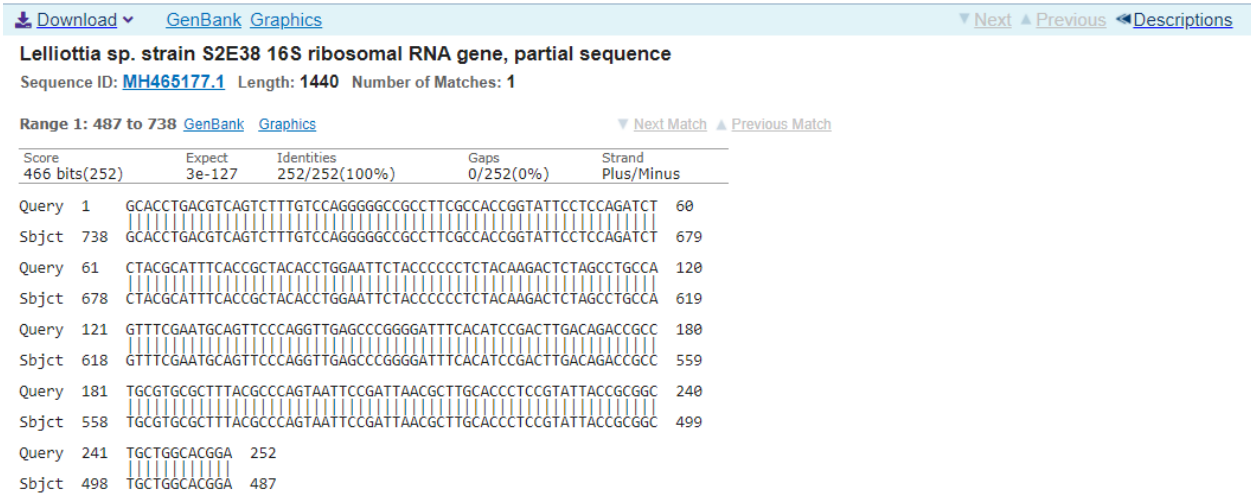
GCACCTGACGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGA
TCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCC
TGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGAC
AGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGT
ATTACCGCGGCTGCTGGCACGGA



Sequences producing significant alignments

☐ select all *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Lelliottia sp. strain S2E38 16S ribosomal RNA gene, partial sequence	Lelliottia sp.	466	466	100%	3e-127	100.00%	1440	MH465177.1
☐	Enterobacter sp. strain S2E16 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	466	466	100%	3e-127	100.00%	1435	MH465162.1
☐	Klebsiella pneumoniae strain MKAS 04 16S ribosomal RNA gene, partial sequence	Klebsiella pneu...	466	466	100%	3e-127	100.00%	1505	KP726935.1
☐	Enterobacter kobei partial 16S rRNA gene, isolate C65	Enterobacter k...	466	466	100%	3e-127	100.00%	746	HF585324.1
☐	Klebsiella pneumoniae strain ac3l5-1EMB 16S ribosomal RNA gene, partial sequence	Klebsiella pneu...	466	466	100%	3e-127	100.00%	1512	JN969353.1
☐	Enterobacter hormaechei partial 16S rRNA gene, clone M40.7	Enterobacter h...	466	466	100%	3e-127	100.00%	763	AM990174.1
☐	Klebsiella pneumoniae strain 10634 16S ribosomal RNA gene, partial sequence	Klebsiella pneu...	460	460	100%	1e-125	99.60%	1399	MW116535.1
☐	Enterobacter sp. strain S4OZ126 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	460	460	100%	1e-125	99.60%	1389	MW092938.1
☐	Klebsiella variicola strain 10913 16S ribosomal RNA gene, partial sequence	Klebsiella varii...	460	460	100%	1e-125	99.60%	1406	MW092594.1
☐	Klebsiella pneumoniae subsp. rhinoscleromatis strain 10291 16S ribosomal RNA gene, partial sequence	Klebsiella pneu...	460	460	100%	1e-125	99.60%	1406	MW092583.1
☐	Klebsiella pneumoniae subsp. rhinoscleromatis strain 10914 16S ribosomal RNA gene, partial sequence	Klebsiella pneu...	460	460	100%	1e-125	99.60%	1405	MW092457.1
☐	Enterobacter hormaechei strain Planc18 16S ribosomal RNA gene, partial sequence	Enterobacter h...	460	460	100%	1e-125	99.60%	1404	MW090899.1
☐	Uncultured bacterium clone Otu1475 16S ribosomal RNA gene, partial sequence	uncultured bact...	460	460	100%	1e-125	99.60%	465	MW083903.1
☐	Klebsiella variicola strain 9786 16S ribosomal RNA gene, partial sequence	Klebsiella varii...	460	460	100%	1e-125	99.60%	1401	MW080504.1
☐	Klebsiella variicola strain 9785 16S ribosomal RNA gene, partial sequence	Klebsiella varii...	460	460	100%	1e-125	99.60%	1400	MW080503.1
☐	Klebsiella variicola strain 11565 16S ribosomal RNA gene, partial sequence	Klebsiella varii...	460	460	100%	1e-125	99.60%	1411	MW079973.1



Lelliottia sp. strain S2E38 16S ribosomal RNA gene, partial sequence

Sequence ID: MH465177.1 Length: 1440 Number of Matches: 1

Range 1: 487 to 738 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
466 bits(252)	3e-127	252/252(100%)	0/252(0%)	Plus/Minus

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Sbjct  738  GCACCTGACGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCT  679

Query  61   CTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  678  CTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCA  619

Query  121  GTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCC  180
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Sbjct  618  GTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCC  559

Query  181  TGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  558  TGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGC  499

Query  241  TGCTGGCACGGA  252
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Sbjct  498  TGCTGGCACGGA  487
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(Hebron market mint): *Klebsiella quasipneumoniae* subsp. *similipneumoniae* strain 2437

ACCTGACGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATC
TCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTG
CCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAG
ACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATT
ACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGA
YRAGGTTATTAACCTTATCGCCTTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGG
CCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCC
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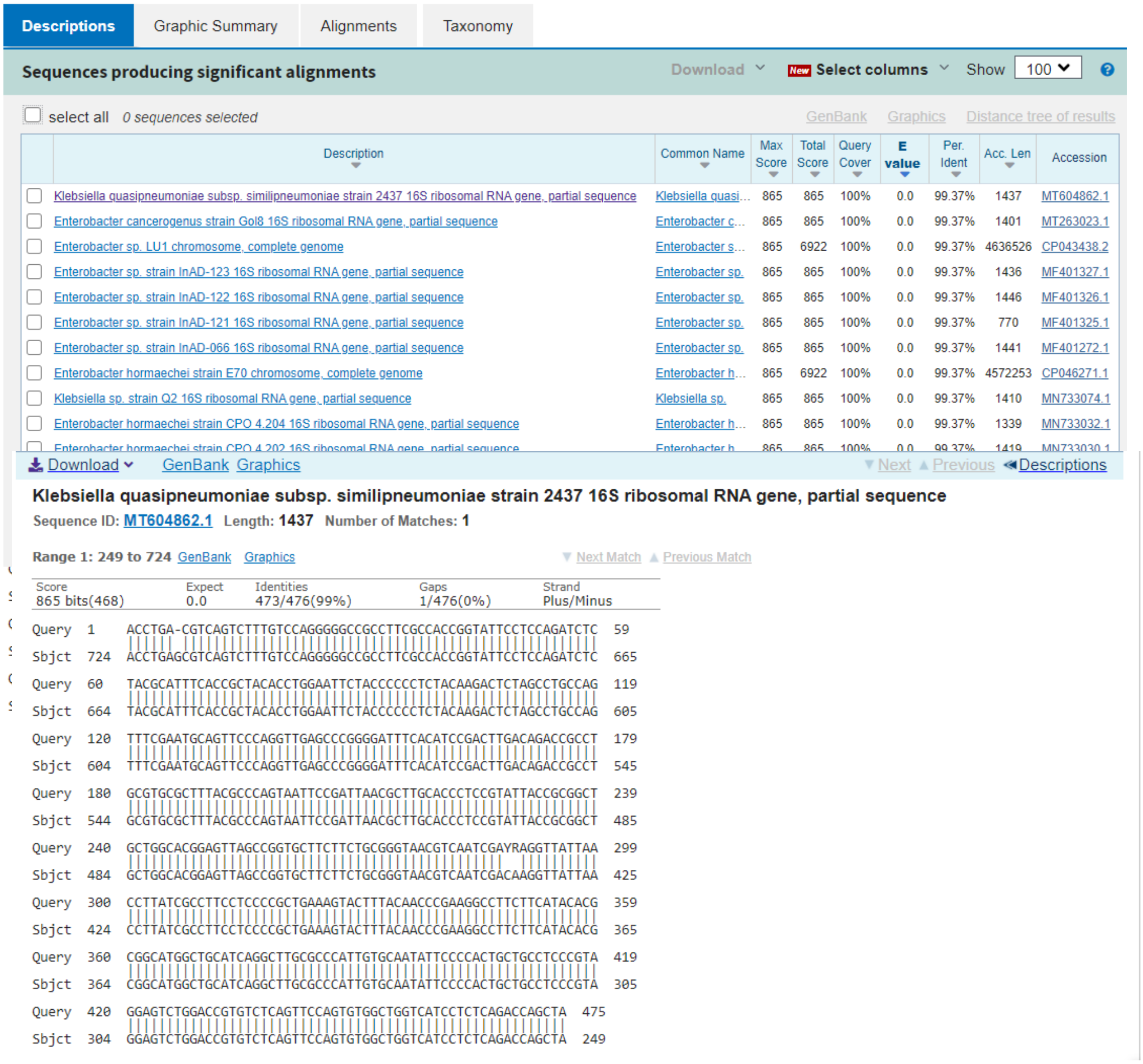
TCCTCTCAGACCAGCTA



Sequences producing significant alignments

0 sequences selected

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Klebsiella quasipneumoniae subsp. similipneumoniae strain 2437 16S ribosomal RNA gene, partial sequence	Klebsiella quasi...	865	865	100%	0.0	99.37%	1437	MT604862.1
☐	Enterobacter cancerogenus strain Gol8 16S ribosomal RNA gene, partial sequence	Enterobacter c...	865	865	100%	0.0	99.37%	1401	MT263023.1
☐	Enterobacter sp. LU1 chromosome, complete genome	Enterobacter s...	865	6922	100%	0.0	99.37%	4636526	CP043438.2
☐	Enterobacter sp. strain InAD-123 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	865	865	100%	0.0	99.37%	1436	MF401327.1
☐	Enterobacter sp. strain InAD-122 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	865	865	100%	0.0	99.37%	1446	MF401326.1
☐	Enterobacter sp. strain InAD-121 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	865	865	100%	0.0	99.37%	770	MF401325.1
☐	Enterobacter sp. strain InAD-066 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	865	865	100%	0.0	99.37%	1441	MF401272.1
☐	Enterobacter hormaechei strain E70 chromosome, complete genome	Enterobacter h...	865	6922	100%	0.0	99.37%	4572253	CP046271.1
☐	Klebsiella sp. strain Q2 16S ribosomal RNA gene, partial sequence	Klebsiella sp.	865	865	100%	0.0	99.37%	1410	MN733074.1
☐	Enterobacter hormaechei strain CPO 4.204 16S ribosomal RNA gene, partial sequence	Enterobacter h...	865	865	100%	0.0	99.37%	1339	MN733032.1
☐	Enterobacter hormaechei strain CPO 4.202 16S ribosomal RNA gene, partial sequence	Enterobacter h...	865	865	100%	0.0	99.37%	1419	MN733030.1

Klebsiella quasipneumoniae subsp. similipneumoniae strain 2437 16S ribosomal RNA gene, partial sequence

Sequence ID: MT604862.1 Length: 1437 Number of Matches: 1

Range 1: 249 to 724

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865 bits(468)  0.0     473/476(99%)   1/476(0%)  Plus/Minus

Query  1    ACCTGA-CGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTC  59
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Sbjct  724  ACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTC  665

Query  60   TACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAG  119
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  664  TACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAG  605

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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  604  TTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCT  545

Query  180  GCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCT  239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  544  GCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCT  485

Query  240  GCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGAYRAGGTTATTAA  299
            ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Sbjct  484  GCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAAGGTTATTAA  425

Query  300  CCTTATCGCCTTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACG  359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  424  CCTTATCGCCTTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACG  365

Query  360  CGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTA  419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  364  CGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTA  305

Query  420  GGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCTGGTCATCCTCTCAGACCAGCTA  475
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Sbjct  304  GGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCTGGTCATCCTCTCAGACCAGCTA  249
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(Hebron market mint): *klebsiella pneumoniae* strain G-A-TGW

GCTTTTCGCACCTGACGTCGTCTTTGTCCGGGGGCCGCCTTCGCCACCGGTATTCCTC
CAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCT
AGCCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACT
TGACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCT
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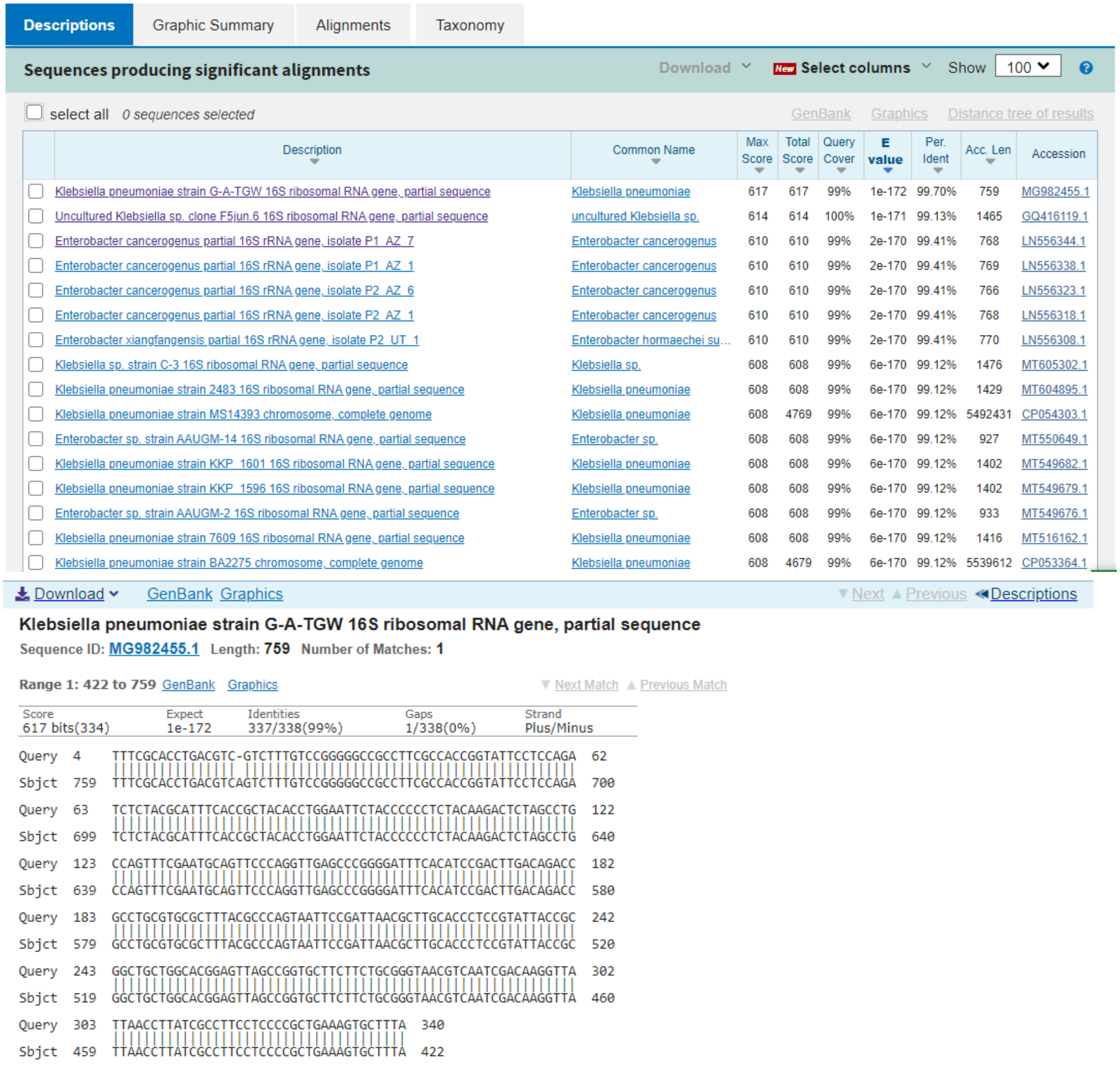

Sequences producing significant alignments

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Klebsiella pneumoniae strain G-A-TGW 16S ribosomal RNA gene, partial sequence	Klebsiella pneumoniae	617	617	99%	1e-172	99.70%	759	MG982455.1
☐	Uncultured Klebsiella sp. clone F5jun.6 16S ribosomal RNA gene, partial sequence	uncultured Klebsiella sp.	614	614	100%	1e-171	99.13%	1465	GQ416119.1
☐	Enterobacter cancerogenus partial 16S rRNA gene, isolate P1_AZ_7	Enterobacter cancerogenus	610	610	99%	2e-170	99.41%	768	LN556344.1
☐	Enterobacter cancerogenus partial 16S rRNA gene, isolate P1_AZ_1	Enterobacter cancerogenus	610	610	99%	2e-170	99.41%	769	LN556338.1
☐	Enterobacter cancerogenus partial 16S rRNA gene, isolate P2_AZ_6	Enterobacter cancerogenus	610	610	99%	2e-170	99.41%	766	LN556323.1
☐	Enterobacter cancerogenus partial 16S rRNA gene, isolate P2_AZ_1	Enterobacter cancerogenus	610	610	99%	2e-170	99.41%	768	LN556318.1
☐	Enterobacter xiangfangensis partial 16S rRNA gene, isolate P2_UT_1	Enterobacter hormaechei su...	610	610	99%	2e-170	99.41%	770	LN556308.1
☐	Klebsiella sp. strain C-3 16S ribosomal RNA gene, partial sequence	Klebsiella sp.	608	608	99%	6e-170	99.12%	1476	MT605302.1
☐	Klebsiella pneumoniae strain 2483 16S ribosomal RNA gene, partial sequence	Klebsiella pneumoniae	608	608	99%	6e-170	99.12%	1429	MT604895.1
☐	Klebsiella pneumoniae strain MS14393 chromosome, complete genome	Klebsiella pneumoniae	608	4769	99%	6e-170	99.12%	5492431	CP054303.1
☐	Enterobacter sp. strain AAUGM-14 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	608	608	99%	6e-170	99.12%	927	MT550649.1
☐	Klebsiella pneumoniae strain KKP_1601 16S ribosomal RNA gene, partial sequence	Klebsiella pneumoniae	608	608	99%	6e-170	99.12%	1402	MT549682.1
☐	Klebsiella pneumoniae strain KKP_1596 16S ribosomal RNA gene, partial sequence	Klebsiella pneumoniae	608	608	99%	6e-170	99.12%	1402	MT549679.1
☐	Enterobacter sp. strain AAUGM-2 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	608	608	99%	6e-170	99.12%	933	MT549676.1
☐	Klebsiella pneumoniae strain 7609 16S ribosomal RNA gene, partial sequence	Klebsiella pneumoniae	608	608	99%	6e-170	99.12%	1416	MT516162.1
☐	Klebsiella pneumoniae strain BA2275 chromosome, complete genome	Klebsiella pneumoniae	608	4679	99%	6e-170	99.12%	5539612	CP053364.1

Klebsiella pneumoniae strain G-A-TGW 16S ribosomal RNA gene, partial sequence

Sequence ID: MG982455.1 Length: 759 Number of Matches: 1

Range 1: 422 to 759 GenBank Graphics

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Score          Expect    Identities      Gaps          Strand
617 bits(334)  1e-172    337/338(99%)    1/338(0%)     Plus/Minus

Query  4    TTTCGCACCTGACGTC-GTCTTTGTCCGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGA  62
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Sbjct  759  TTTCGCACCTGACGTCAGTCTTTGTCCGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGA  700

Query  63   TCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTG  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  699  TCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTG  640

Query  123  CCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACC  182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  639  CCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACC  580

Query  183  GCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGC  242
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Sbjct  579  GCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGC  520

Query  243  GGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAAGGTTA  302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  519  GGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAAGGTTA  460

Query  303  TTAACCTTATCGCCTTCCTCCCCGCTGAAAGTGCTTTA  340
            ||||||||||||||||||||||||||||||||||||||
Sbjct  459  TTAACCTTATCGCCTTCCTCCCCGCTGAAAGTGCTTTA  422
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(Rami levy mint): *Pantoea ananatis* strain PC2

CATGCAGTCGGAGGTAGCACAGAGAGCTTGCTCTCGGGTGACGAGTGGCGGACGGG
TGAGTAATGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTGKAAACGGTGGC
TAATACCGCATAACGTCGCAAGACCCAAGAGGGGGACCTTCGGGCCTCTCACTATC
GGATGAACCCASATGGGATTAGCTAGTAGGCGGGGTAATGGCCCACCTATGCGACA
ATCCCTATCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAC
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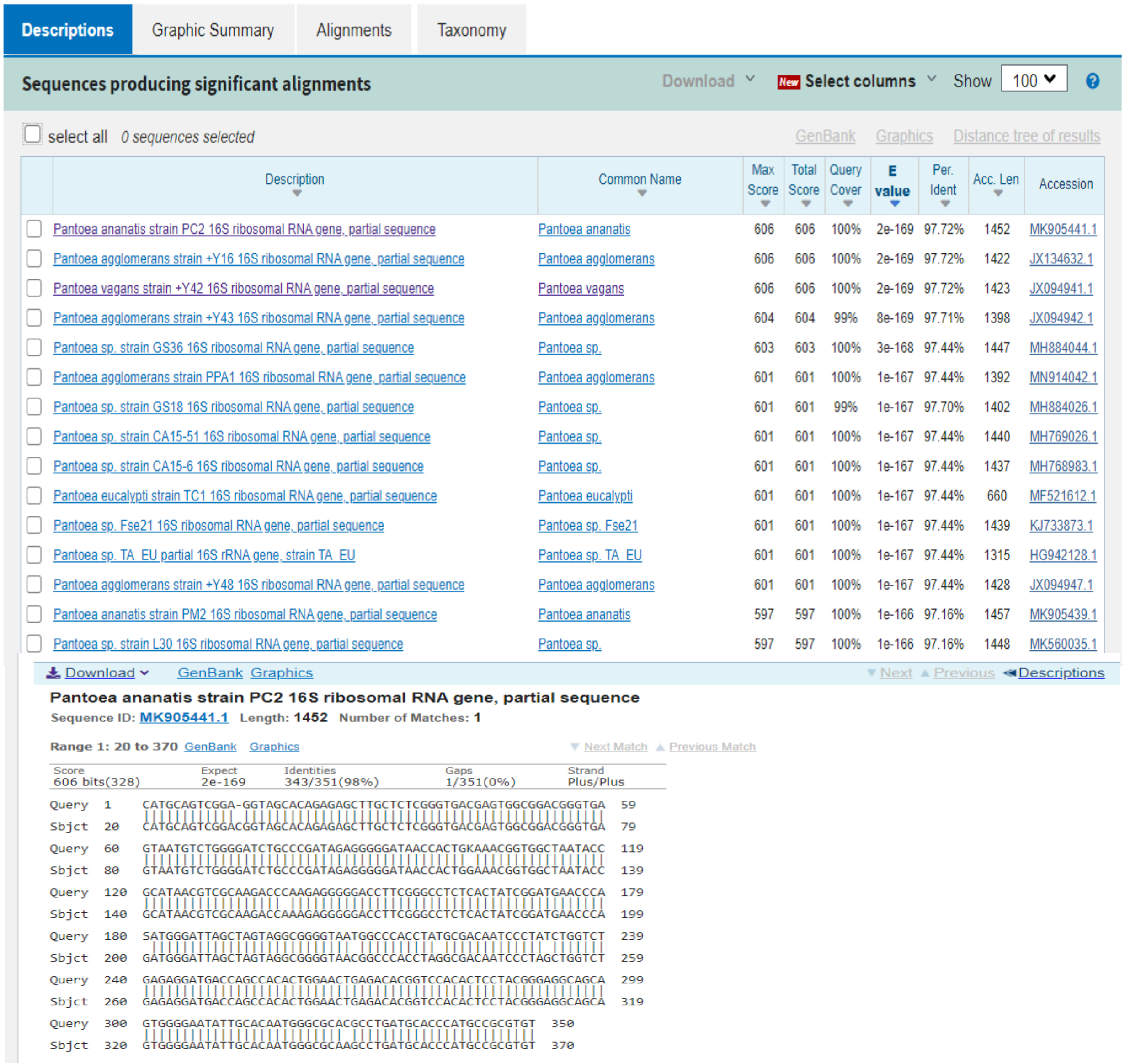

Sequences producing significant alignments

☐ select all *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Pantoea ananatis strain PC2 16S ribosomal RNA gene, partial sequence	Pantoea ananatis	606	606	100%	2e-169	97.72%	1452	MK905441.1
☐	Pantoea agglomerans strain +Y16 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	606	606	100%	2e-169	97.72%	1422	JX134632.1
☐	Pantoea vagans strain +Y42 16S ribosomal RNA gene, partial sequence	Pantoea vagans	606	606	100%	2e-169	97.72%	1423	JX094941.1
☐	Pantoea agglomerans strain +Y43 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	604	604	99%	8e-169	97.71%	1398	JX094942.1
☐	Pantoea sp. strain GS36 16S ribosomal RNA gene, partial sequence	Pantoea sp.	603	603	100%	3e-168	97.44%	1447	MH884044.1
☐	Pantoea agglomerans strain PPA1 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	601	601	100%	1e-167	97.44%	1392	MN914042.1
☐	Pantoea sp. strain GS18 16S ribosomal RNA gene, partial sequence	Pantoea sp.	601	601	99%	1e-167	97.70%	1402	MH884026.1
☐	Pantoea sp. strain CA15-51 16S ribosomal RNA gene, partial sequence	Pantoea sp.	601	601	100%	1e-167	97.44%	1440	MH769026.1
☐	Pantoea sp. strain CA15-6 16S ribosomal RNA gene, partial sequence	Pantoea sp.	601	601	100%	1e-167	97.44%	1437	MH768983.1
☐	Pantoea eucalypti strain TC1 16S ribosomal RNA gene, partial sequence	Pantoea eucalypti	601	601	100%	1e-167	97.44%	660	MF521612.1
☐	Pantoea sp. Fse21 16S ribosomal RNA gene, partial sequence	Pantoea sp. Fse21	601	601	100%	1e-167	97.44%	1439	KJ733873.1
☐	Pantoea sp. TA_EU partial 16S rRNA gene, strain TA_EU	Pantoea sp. TA_EU	601	601	100%	1e-167	97.44%	1315	HG942128.1
☐	Pantoea agglomerans strain +Y48 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	601	601	100%	1e-167	97.44%	1428	JX094947.1
☐	Pantoea ananatis strain PM2 16S ribosomal RNA gene, partial sequence	Pantoea ananatis	597	597	100%	1e-166	97.16%	1457	MK905439.1
☐	Pantoea sp. strain L30 16S ribosomal RNA gene, partial sequence	Pantoea sp.	597	597	100%	1e-166	97.16%	1448	MK560035.1

Pantoea ananatis strain PC2 16S ribosomal RNA gene, partial sequence

Sequence ID: MK905441.1 Length: 1452 Number of Matches: 1

Range 1: 20 to 370 GenBank Graphics

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Score            Expect    Identities       Gaps         Strand
606 bits(328)    2e-169    343/351(98%)     1/351(0%)    Plus/Plus

Query  1    CATGCAGTCGGA-GGTAGCACAGAGAGCTTGCTCTCGGGTGACGAGTGGCGGACGGGTGA  59
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Query  60   GTAATGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTGKAAACGGTGGCTAATACC  119
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Sbjct  80   GTAATGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACC  139

Query  120  GCATAACGTCGCAAGACCCAAGAGGGGGACCTTCGGGCCTCTCACTATCGGATGAACCCA  179
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Sbjct  140  GCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTCACTATCGGATGAACCCA  199

Query  180  SATGGGATTAGCTAGTAGGCGGGGTAATGGCCCACCTATGCGACAATCCCTATCTGGTCT  239
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Sbjct  200  GATGGGATTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACAATCCCTAGCTGGTCT  259

Query  240  GAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCACACTCCTACGGGAGGCAGCA  299
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Sbjct  260  GAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCACACTCCTACGGGAGGCAGCA  319

Query  300  GTGGGGAATATTGCACAATGGGCGCACGCCTGATGCACCCATGCCGCGTGT  350
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Sbjct  320  GTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCACCCATGCCGCGTGT  370
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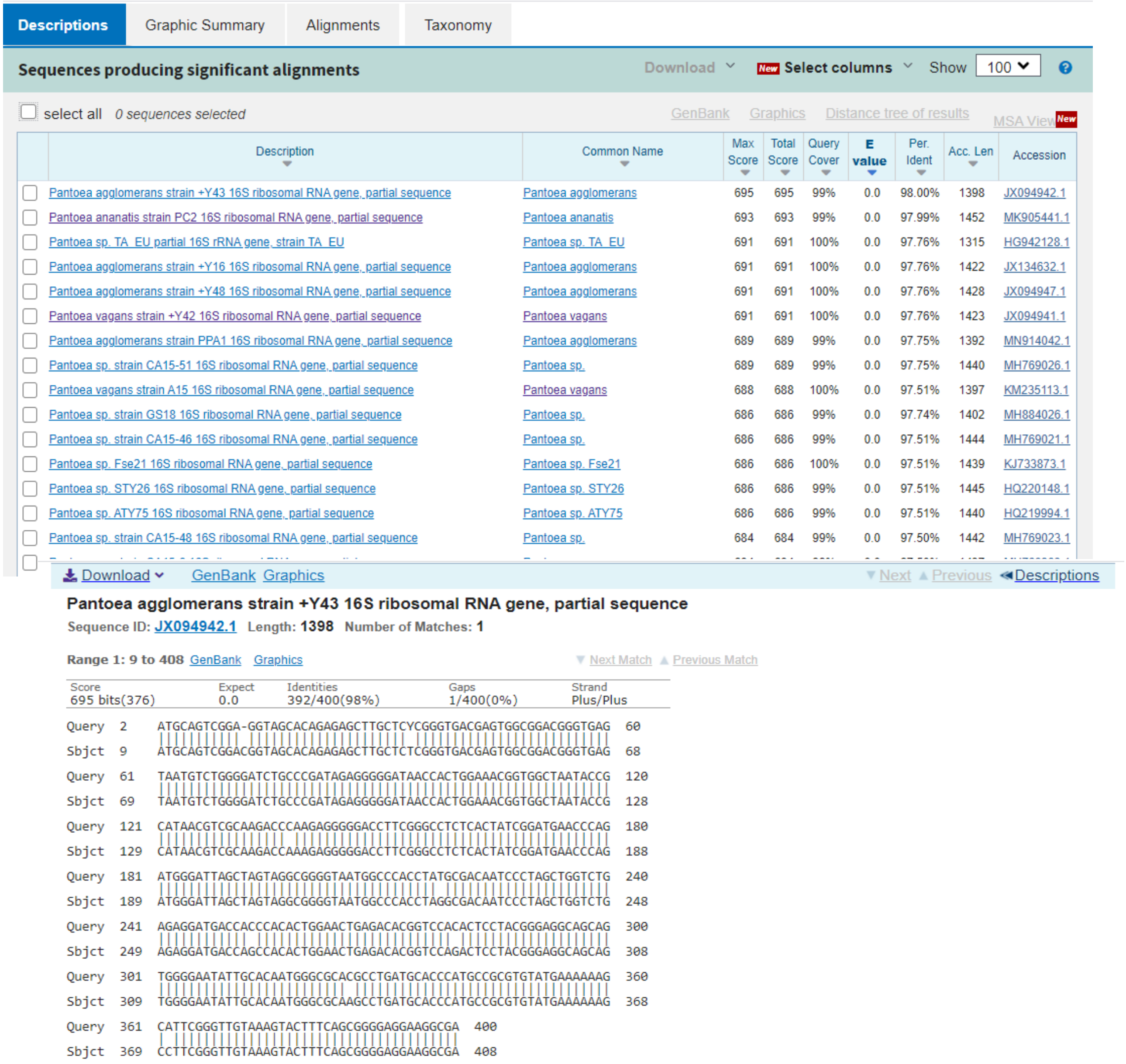
(Rami levy parsley): *Pantoea agglomerans* strain +Y43

CATGCAGTCGGAGGTAGCACAGAGAGCTTGCTCYCGGGTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAACGTCGCAAGACCCAAGAGGGGGACCTTCGGGCCTCTCACTATCGGATGAACCCAGATGGGATTAGCTAGTAGGCGGGGTAATGGCCCACCTATGCGACAATCCCTAGCTGGTCTGAGAGGATGACCACCCACACTGGAACTGAGACACGGTCCACACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCACGCCTGATGCACCCATGCCGCGTGTATGAAAAAAGCATTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCGA



Sequences producing significant alignments

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Pantoea agglomerans strain +Y43 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	695	695	99%	0.0	98.00%	1398	JX094942.1
☐	Pantoea ananatis strain PC2 16S ribosomal RNA gene, partial sequence	Pantoea ananatis	693	693	99%	0.0	97.99%	1452	MK905441.1
☐	Pantoea sp. TA_EU partial 16S rRNA gene, strain TA_EU	Pantoea sp. TA_EU	691	691	100%	0.0	97.76%	1315	HG942128.1
☐	Pantoea agglomerans strain +Y16 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	691	691	100%	0.0	97.76%	1422	JX134632.1
☐	Pantoea agglomerans strain +Y48 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	691	691	100%	0.0	97.76%	1428	JX094947.1
☐	Pantoea vagans strain +Y42 16S ribosomal RNA gene, partial sequence	Pantoea vagans	691	691	100%	0.0	97.76%	1423	JX094941.1
☐	Pantoea agglomerans strain PPA1 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	689	689	99%	0.0	97.75%	1392	MN914042.1
☐	Pantoea sp. strain CA15-51 16S ribosomal RNA gene, partial sequence	Pantoea sp.	689	689	99%	0.0	97.75%	1440	MH769026.1
☐	Pantoea vagans strain A15 16S ribosomal RNA gene, partial sequence	Pantoea vagans	688	688	100%	0.0	97.51%	1397	KM235113.1
☐	Pantoea sp. strain GS18 16S ribosomal RNA gene, partial sequence	Pantoea sp.	686	686	99%	0.0	97.74%	1402	MH884026.1
☐	Pantoea sp. strain CA15-46 16S ribosomal RNA gene, partial sequence	Pantoea sp.	686	686	99%	0.0	97.51%	1444	MH769021.1
☐	Pantoea sp. Fse21 16S ribosomal RNA gene, partial sequence	Pantoea sp. Fse21	686	686	100%	0.0	97.51%	1439	KJ733873.1
☐	Pantoea sp. STY26 16S ribosomal RNA gene, partial sequence	Pantoea sp. STY26	686	686	99%	0.0	97.51%	1445	HQ220148.1
☐	Pantoea sp. ATY75 16S ribosomal RNA gene, partial sequence	Pantoea sp. ATY75	686	686	99%	0.0	97.51%	1440	HQ219994.1
☐	Pantoea sp. strain CA15-48 16S ribosomal RNA gene, partial sequence	Pantoea sp.	684	684	99%	0.0	97.50%	1442	MH769023.1

Pantoea agglomerans strain +Y43 16S ribosomal RNA gene, partial sequence

Sequence ID: JX094942.1 Length: 1398 Number of Matches: 1

Range 1: 9 to 408 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
695 bits(376)	0.0	392/400(98%)	1/400(0%)	Plus/Plus

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Query  2    ATGCAGTCGGA-GGTAGCACAGAGAGCTTGCTCYCGGGTGACGAGTGGCGGACGGGTGAG  60
            ||||||||||| ||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  9    ATGCAGTCGGACGGTAGCACAGAGAGCTTGCTCTCGGGTGACGAGTGGCGGACGGGTGAG  68

Query  61   TAATGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  69   TAATGTCTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCG  128

Query  121  CATAACGTCGCAAGACCCAAGAGGGGGACCTTCGGGCCTCTCACTATCGGATGAACCCAG  180
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Sbjct  129  CATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTCACTATCGGATGAACCCAG  188

Query  181  ATGGGATTAGCTAGTAGGCGGGGTAATGGCCCACCTATGCGACAATCCCTAGCTGGTCTG  240
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  189  ATGGGATTAGCTAGTAGGCGGGGTAATGGCCCACCTAGGCGACAATCCCTAGCTGGTCTG  248

Query  241  AGAGGATGACCACCCACACTGGAACTGAGACACGGTCCACACTCCTACGGGAGGCAGCAG  300
            |||||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  249  AGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAG  308

Query  301  TGGGGAATATTGCACAATGGGCGCACGCCTGATGCACCCATGCCGCGTGTATGAAAAAAG  360
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  309  TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCACCCATGCCGCGTGTATGAAAAAAG  368

Query  361  CATTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCGA  400
            | ||||||||||||||||||||||||||||||||||||||
Sbjct  369  CCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCGA  408
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(Hebron market mint): *Enterobacter cancerogenus* Strain ILQ201

CATGCAAGTCGAGCGGTAGCACAGGGAGCTTGCTCCTGGGTGACGAGCGGCGGACG
GGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTA
GCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCA
TCAGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGA
CGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCC
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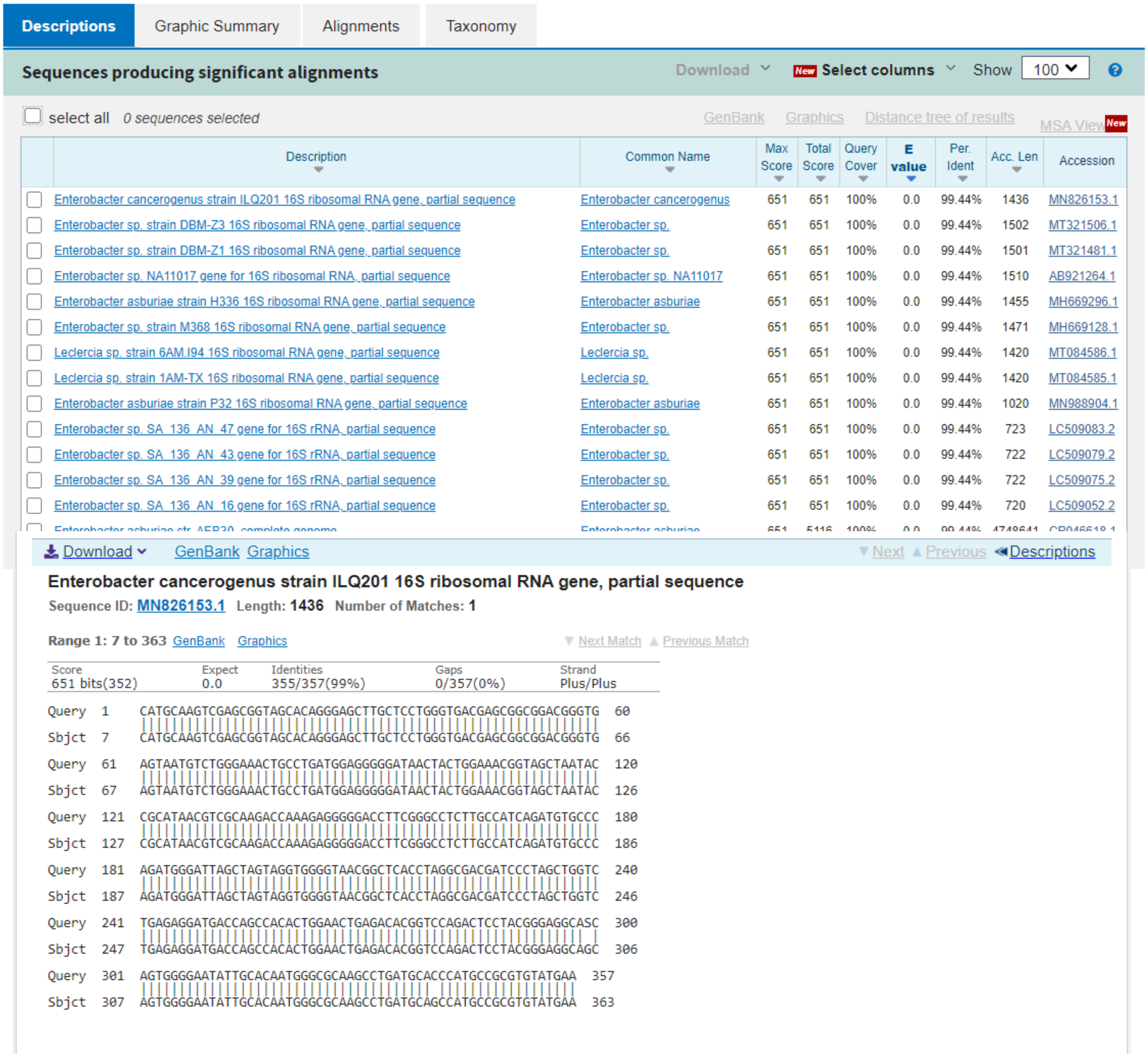
CACCCATGCCGCGTGTATGAA



Sequences producing significant alignments

☐	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Enterobacter cancerogenus strain ILQ201 16S ribosomal RNA gene, partial sequence	Enterobacter cancerogenus	651	651	100%	0.0	99.44%	1436	MN826153.1
☐	Enterobacter sp. strain DBM-Z3 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	651	651	100%	0.0	99.44%	1502	MT321506.1
☐	Enterobacter sp. strain DBM-Z1 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	651	651	100%	0.0	99.44%	1501	MT321481.1
☐	Enterobacter sp. NA11017 gene for 16S ribosomal RNA, partial sequence	Enterobacter sp. NA11017	651	651	100%	0.0	99.44%	1510	AB921264.1
☐	Enterobacter asburiae strain H336 16S ribosomal RNA gene, partial sequence	Enterobacter asburiae	651	651	100%	0.0	99.44%	1455	MH669296.1
☐	Enterobacter sp. strain M368 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	651	651	100%	0.0	99.44%	1471	MH669128.1
☐	Leclercia sp. strain 6AM.I94 16S ribosomal RNA gene, partial sequence	Leclercia sp.	651	651	100%	0.0	99.44%	1420	MT084586.1
☐	Leclercia sp. strain 1AM-TX 16S ribosomal RNA gene, partial sequence	Leclercia sp.	651	651	100%	0.0	99.44%	1420	MT084585.1
☐	Enterobacter asburiae strain P32 16S ribosomal RNA gene, partial sequence	Enterobacter asburiae	651	651	100%	0.0	99.44%	1020	MN988904.1
☐	Enterobacter sp. SA_136_AN_47 gene for 16S rRNA, partial sequence	Enterobacter sp.	651	651	100%	0.0	99.44%	723	LC509083.2
☐	Enterobacter sp. SA_136_AN_43 gene for 16S rRNA, partial sequence	Enterobacter sp.	651	651	100%	0.0	99.44%	722	LC509079.2
☐	Enterobacter sp. SA_136_AN_39 gene for 16S rRNA, partial sequence	Enterobacter sp.	651	651	100%	0.0	99.44%	722	LC509075.2
☐	Enterobacter sp. SA_136_AN_16 gene for 16S rRNA, partial sequence	Enterobacter sp.	651	651	100%	0.0	99.44%	720	LC509052.2
☐	Enterobacter asburiae str. AEB30, complete genome	Enterobacter asburiae	651	5116	100%	0.0	99.44%	4748641	CP046618.1

Enterobacter cancerogenus strain ILQ201 16S ribosomal RNA gene, partial sequence

Sequence ID: MN826153.1 Length: 1436 Number of Matches: 1

Range 1: 7 to 363 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
651 bits(352)	0.0	355/357(99%)	0/357(0%)	Plus/Plus

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Query  1    CATGCAAGTCGAGCGGTAGCACAGGGAGCTTGCTCCTGGGTGACGAGCGGCGGACGGGTG  60
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Sbjct  7    CATGCAAGTCGAGCGGTAGCACAGGGAGCTTGCTCCTGGGTGACGAGCGGCGGACGGGTG  66

Query  61   AGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  67   AGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATAC  126

Query  121  CGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCAGATGTGCCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  127  CGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCAGATGTGCCC  186

Query  181  AGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  187  AGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTC  246

Query  241  TGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCASC  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  247  TGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC  306

Query  301  AGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCACCCATGCCGCGTGTATGAA  357
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  307  AGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAA  363
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(Hebron market mint): *klebsiella pneumoniae* subsp. pneumoniae strain SU101

CATGCAAGTCGAGCGGTAGCACAGTAGAGCTTGCTCTCGGGTGACGAGCGGCGGAC
GGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGT
AGCTAATACCGCATAACGTCGCAAGACCAAAGTGGGGGACCTTCGGGCCTCATGCC
ATCAGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCG
ACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTC
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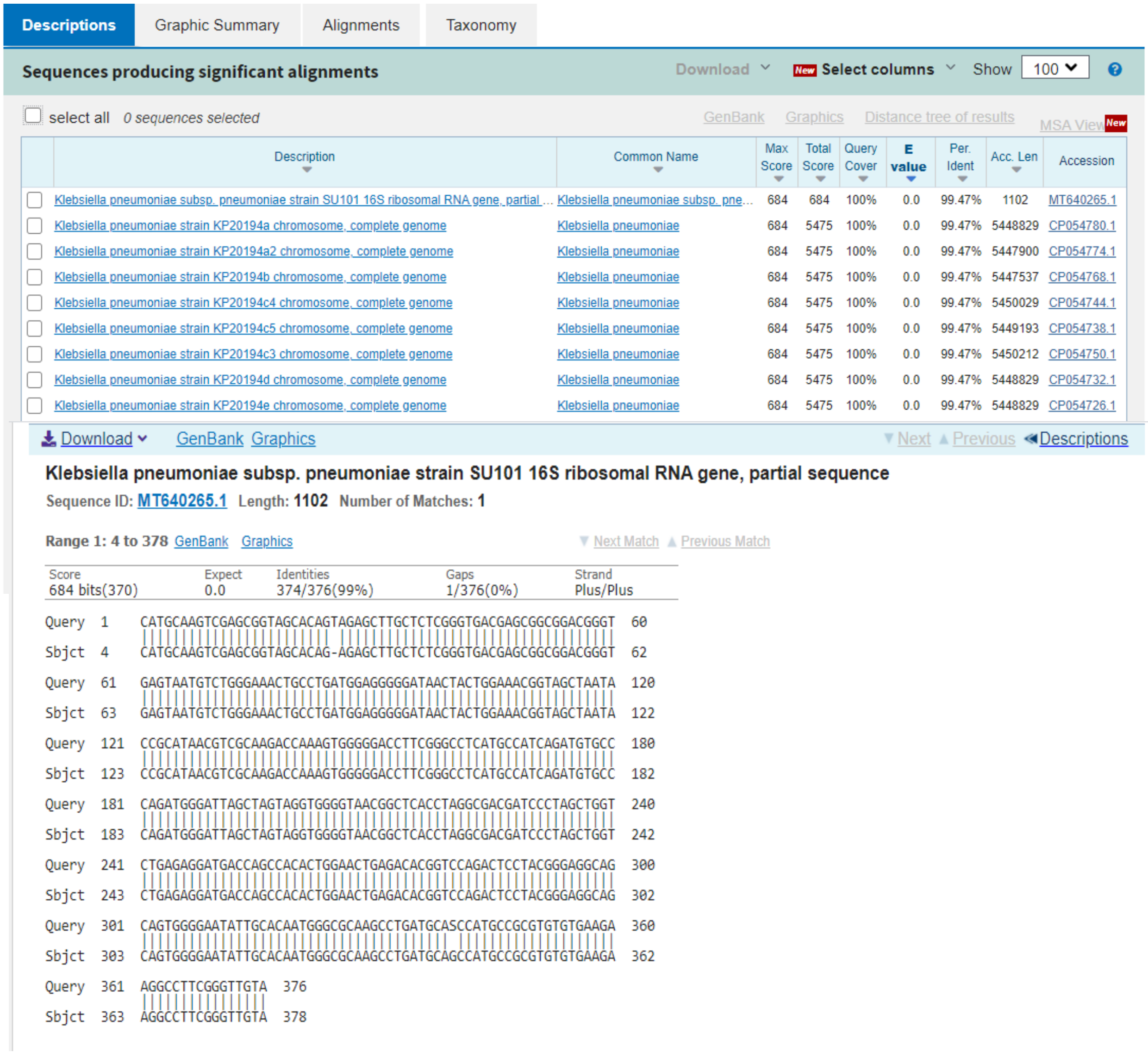
GCASCCATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTA



Sequences producing significant alignments

☐ select all 0 sequences selected

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Klebsiella pneumoniae subsp. pneumoniae strain SU101 16S ribosomal RNA gene, partial ...	Klebsiella pneumoniae subsp. pne...	684	684	100%	0.0	99.47%	1102	MT640265.1
☐	Klebsiella pneumoniae strain KP20194a chromosome, complete genome	Klebsiella pneumoniae	684	5475	100%	0.0	99.47%	5448829	CP054780.1
☐	Klebsiella pneumoniae strain KP20194a2 chromosome, complete genome	Klebsiella pneumoniae	684	5475	100%	0.0	99.47%	5447900	CP054774.1
☐	Klebsiella pneumoniae strain KP20194b chromosome, complete genome	Klebsiella pneumoniae	684	5475	100%	0.0	99.47%	5447537	CP054768.1
☐	Klebsiella pneumoniae strain KP20194c4 chromosome, complete genome	Klebsiella pneumoniae	684	5475	100%	0.0	99.47%	5450029	CP054744.1
☐	Klebsiella pneumoniae strain KP20194c5 chromosome, complete genome	Klebsiella pneumoniae	684	5475	100%	0.0	99.47%	5449193	CP054738.1
☐	Klebsiella pneumoniae strain KP20194c3 chromosome, complete genome	Klebsiella pneumoniae	684	5475	100%	0.0	99.47%	5450212	CP054750.1
☐	Klebsiella pneumoniae strain KP20194d chromosome, complete genome	Klebsiella pneumoniae	684	5475	100%	0.0	99.47%	5448829	CP054732.1
☐	Klebsiella pneumoniae strain KP20194e chromosome, complete genome	Klebsiella pneumoniae	684	5475	100%	0.0	99.47%	5448829	CP054726.1

Klebsiella pneumoniae subsp. pneumoniae strain SU101 16S ribosomal RNA gene, partial sequence

Sequence ID: MT640265.1 Length: **1102** Number of Matches: **1**

Range 1: 4 to 378 GenBank Graphics

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Score           Expect  Identities       Gaps          Strand
684 bits(370)   0.0     374/376(99%)     1/376(0%)     Plus/Plus

Query  1    CATGCAAGTCGAGCGGTAGCACAGTAGAGCTTGCTCTCGGGTGACGAGCGGCGGACGGGT  60
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Sbjct  4    CATGCAAGTCGAGCGGTAGCACAG-AGAGCTTGCTCTCGGGTGACGAGCGGCGGACGGGT  62

Query  61   GAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  63   GAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATA  122

Query  121  CCGCATAACGTCGCAAGACCAAAGTGGGGGACCTTCGGGCCTCATGCCATCAGATGTGCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123  CCGCATAACGTCGCAAGACCAAAGTGGGGGACCTTCGGGCCTCATGCCATCAGATGTGCC  182

Query  181  CAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  183  CAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGT  242

Query  241  CTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAG  300
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Sbjct  243  CTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAG  302

Query  301  CAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCASCCATGCCGCGTGTGTGAAGA  360
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Sbjct  303  CAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTGTGAAGA  362

Query  361  AGGCCTTCGGGTTGTA  376
            ||||||||||||||||
Sbjct  363  AGGCCTTCGGGTTGTA  378
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(Hebron market parsley): *E. coli* strain EcPF5
CATGCAAGTCGAACGGTAACAGGAAGCAGCTTGCTGCTTTGCTGACGAGTGGCGGA
CGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGG
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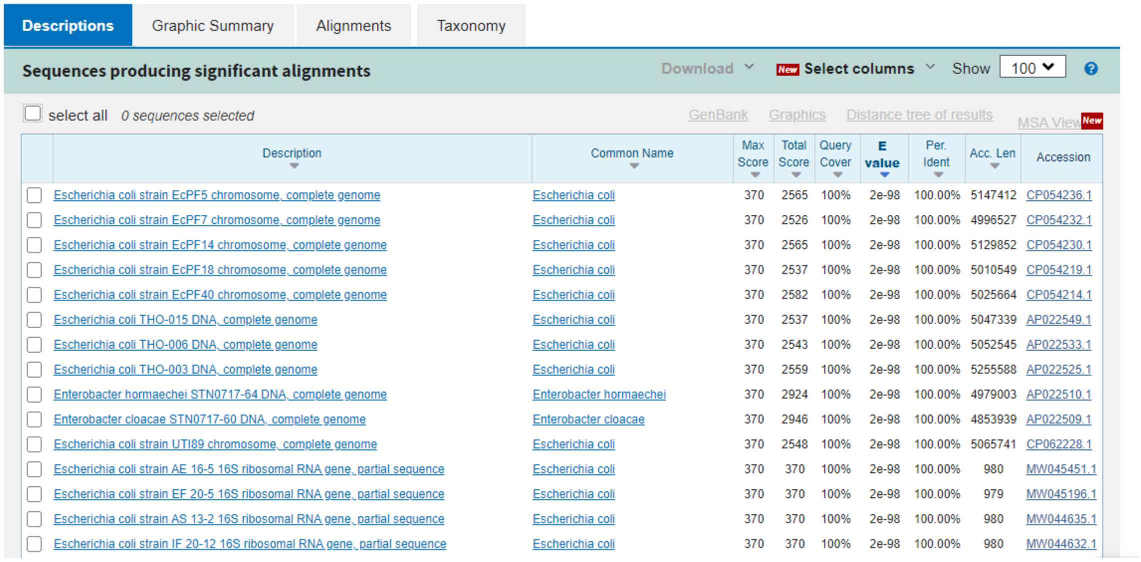

Sequences producing significant alignments

☐ select all *0 sequences selected*

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Escherichia coli strain EcPF5 chromosome, complete genome	Escherichia coli	370	2565	100%	2e-98	100.00%	5147412	CP054236.1
☐	Escherichia coli strain EcPF7 chromosome, complete genome	Escherichia coli	370	2526	100%	2e-98	100.00%	4996527	CP054232.1
☐	Escherichia coli strain EcPF14 chromosome, complete genome	Escherichia coli	370	2565	100%	2e-98	100.00%	5129852	CP054230.1
☐	Escherichia coli strain EcPF18 chromosome, complete genome	Escherichia coli	370	2537	100%	2e-98	100.00%	5010549	CP054219.1
☐	Escherichia coli strain EcPF40 chromosome, complete genome	Escherichia coli	370	2582	100%	2e-98	100.00%	5025664	CP054214.1
☐	Escherichia coli THO-015 DNA, complete genome	Escherichia coli	370	2537	100%	2e-98	100.00%	5047339	AP022549.1
☐	Escherichia coli THO-006 DNA, complete genome	Escherichia coli	370	2543	100%	2e-98	100.00%	5052545	AP022533.1
☐	Escherichia coli THO-003 DNA, complete genome	Escherichia coli	370	2559	100%	2e-98	100.00%	5255588	AP022525.1
☐	Enterobacter hormaechei STN0717-64 DNA, complete genome	Enterobacter hormaechei	370	2924	100%	2e-98	100.00%	4979003	AP022510.1
☐	Enterobacter cloacae STN0717-60 DNA, complete genome	Enterobacter cloacae	370	2946	100%	2e-98	100.00%	4853939	AP022509.1
☐	Escherichia coli strain UTI89 chromosome, complete genome	Escherichia coli	370	2548	100%	2e-98	100.00%	5065741	CP062228.1
☐	Escherichia coli strain AE 16-5 16S ribosomal RNA gene, partial sequence	Escherichia coli	370	370	100%	2e-98	100.00%	980	MW045451.1
☐	Escherichia coli strain EF 20-5 16S ribosomal RNA gene, partial sequence	Escherichia coli	370	370	100%	2e-98	100.00%	979	MW045196.1
☐	Escherichia coli strain AS 13-2 16S ribosomal RNA gene, partial sequence	Escherichia coli	370	370	100%	2e-98	100.00%	980	MW044635.1
☐	Escherichia coli strain IF 20-12 16S ribosomal RNA gene, partial sequence	Escherichia coli	370	370	100%	2e-98	100.00%	980	MW044632.1

Escherichia coli strain EcPF5 chromosome, complete genome

Sequence ID: CP054236.1 Length: 5147412 Number of Matches: 7

Range 1: 1568831 to 1569030 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
370 bits(200)	2e-98	200/200(100%)	0/200(0%)	Plus/Plus

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Query  61       TGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAAT  120
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Sbjct  1568891  TGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAAT  1568950

Query  121      ACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGC  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1568951  ACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGC  1569010

Query  181      CCAGATGGGATTAGCTAGTA  200
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Sbjct  1569011  CCAGATGGGATTAGCTAGTA  1569030
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(Rami levy parsley): *Enterobacter cloacae* strain 3849

GCTTTCGCACCTGACGTCGTCTTTGTCCGGGGGCCGCCTTCGCCACCGGTATTCCTCC
AGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCT
AGCCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACT
TGACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCT
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CAATCGACAGGGTTATTAACCCTGTCGCCTTCCTCCCCGCTGAAAGTACTTTACAAC
CCGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCA
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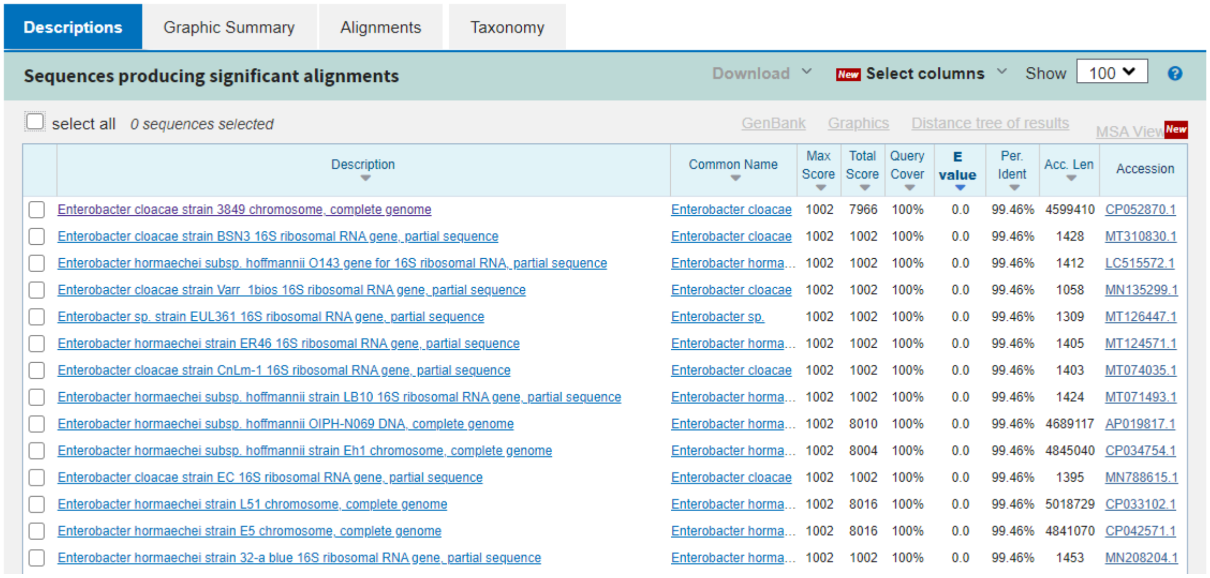
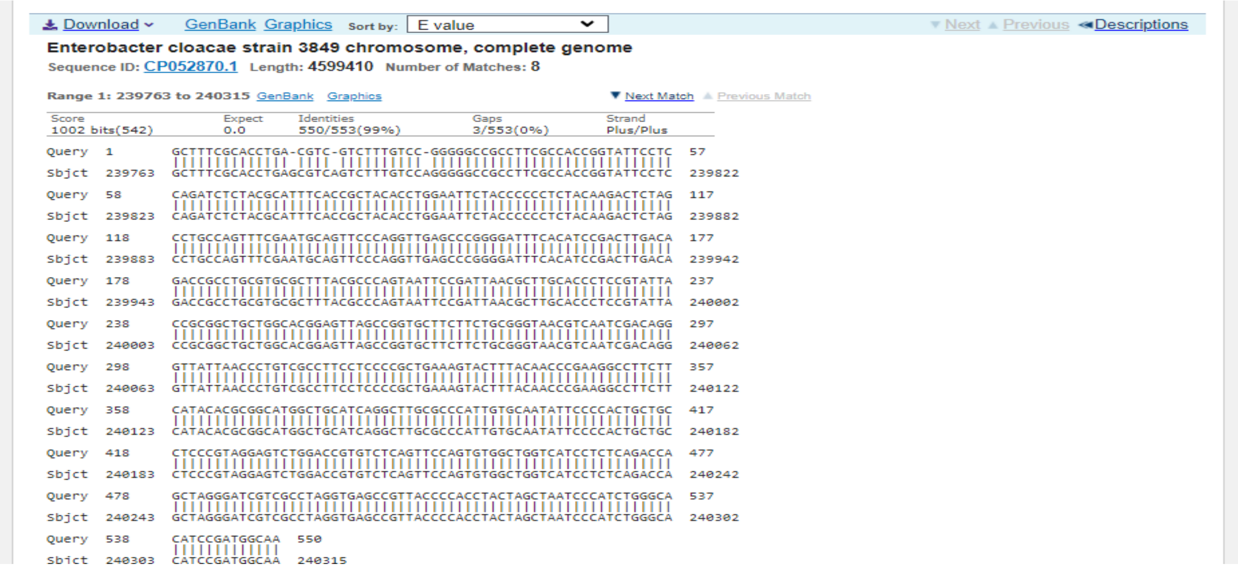


Sequences producing significant alignments

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Enterobacter cloacae strain 3849 chromosome, complete genome	Enterobacter cloacae	1002	7966	100%	0.0	99.46%	4599410	CP052870.1
☐	Enterobacter cloacae strain BSN3 16S ribosomal RNA gene, partial sequence	Enterobacter cloacae	1002	1002	100%	0.0	99.46%	1428	MT310830.1
☐	Enterobacter hormaechei subsp. hoffmannii O143 gene for 16S ribosomal RNA, partial sequence	Enterobacter horma...	1002	1002	100%	0.0	99.46%	1412	LC515572.1
☐	Enterobacter cloacae strain Varr_1bios 16S ribosomal RNA gene, partial sequence	Enterobacter cloacae	1002	1002	100%	0.0	99.46%	1058	MN135299.1
☐	Enterobacter sp. strain EUL361 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	1002	1002	100%	0.0	99.46%	1309	MT126447.1
☐	Enterobacter hormaechei strain ER46 16S ribosomal RNA gene, partial sequence	Enterobacter horma...	1002	1002	100%	0.0	99.46%	1405	MT124571.1
☐	Enterobacter cloacae strain CnLm-1 16S ribosomal RNA gene, partial sequence	Enterobacter cloacae	1002	1002	100%	0.0	99.46%	1403	MT074035.1
☐	Enterobacter hormaechei subsp. hoffmannii strain LB10 16S ribosomal RNA gene, partial sequence	Enterobacter horma...	1002	1002	100%	0.0	99.46%	1424	MT071493.1
☐	Enterobacter hormaechei subsp. hoffmannii OIPH-N069 DNA, complete genome	Enterobacter horma...	1002	8010	100%	0.0	99.46%	4689117	AP019817.1
☐	Enterobacter hormaechei subsp. hoffmannii strain Eh1 chromosome, complete genome	Enterobacter horma...	1002	8004	100%	0.0	99.46%	4845040	CP034754.1
☐	Enterobacter cloacae strain EC 16S ribosomal RNA gene, partial sequence	Enterobacter cloacae	1002	1002	100%	0.0	99.46%	1395	MN788615.1
☐	Enterobacter hormaechei strain L51 chromosome, complete genome	Enterobacter horma...	1002	8016	100%	0.0	99.46%	5018729	CP033102.1
☐	Enterobacter hormaechei strain E5 chromosome, complete genome	Enterobacter horma...	1002	8016	100%	0.0	99.46%	4841070	CP042571.1
☐	Enterobacter hormaechei strain 32-a blue 16S ribosomal RNA gene, partial sequence	Enterobacter horma...	1002	1002	100%	0.0	99.46%	1453	MN208204.1



Enterobacter cloacae strain 3849 chromosome, complete genome

Sequence ID: CP052870.1 Length: 4599410 Number of Matches: 8

Range 1: 239763 to 240315 GenBank Graphics

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Score             Expect   Identities        Gaps          Strand
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Query  1       GCTTTCGCACCTGA-CGTC-GTCTTTGTCC-GGGGGCCGCCTTCGCCACCGGTATTCCTC  57
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(Hebron market mint) *Enterobacter cloacae* strain 3849

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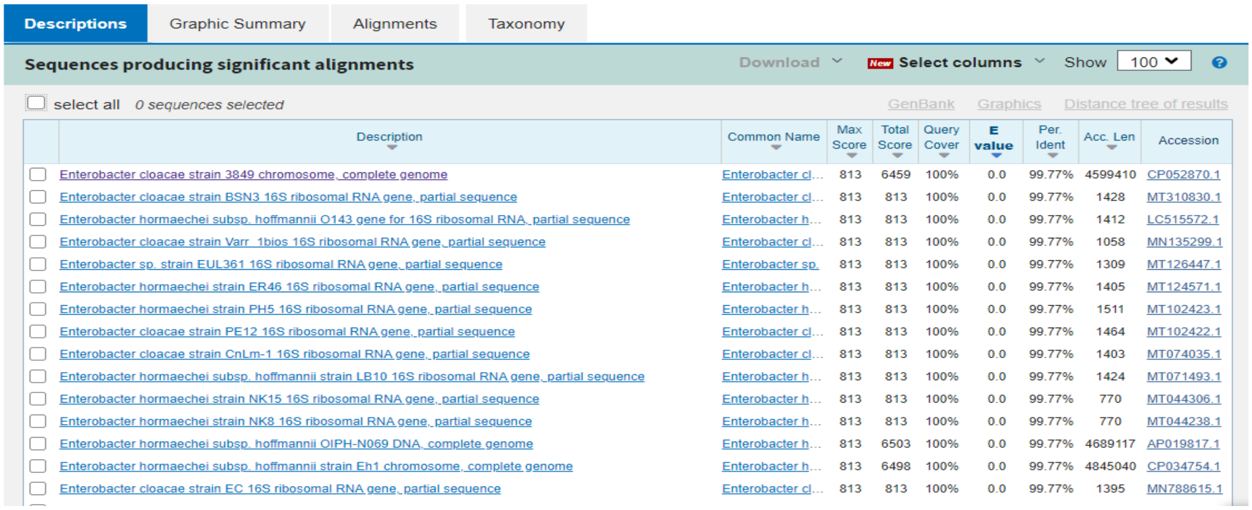
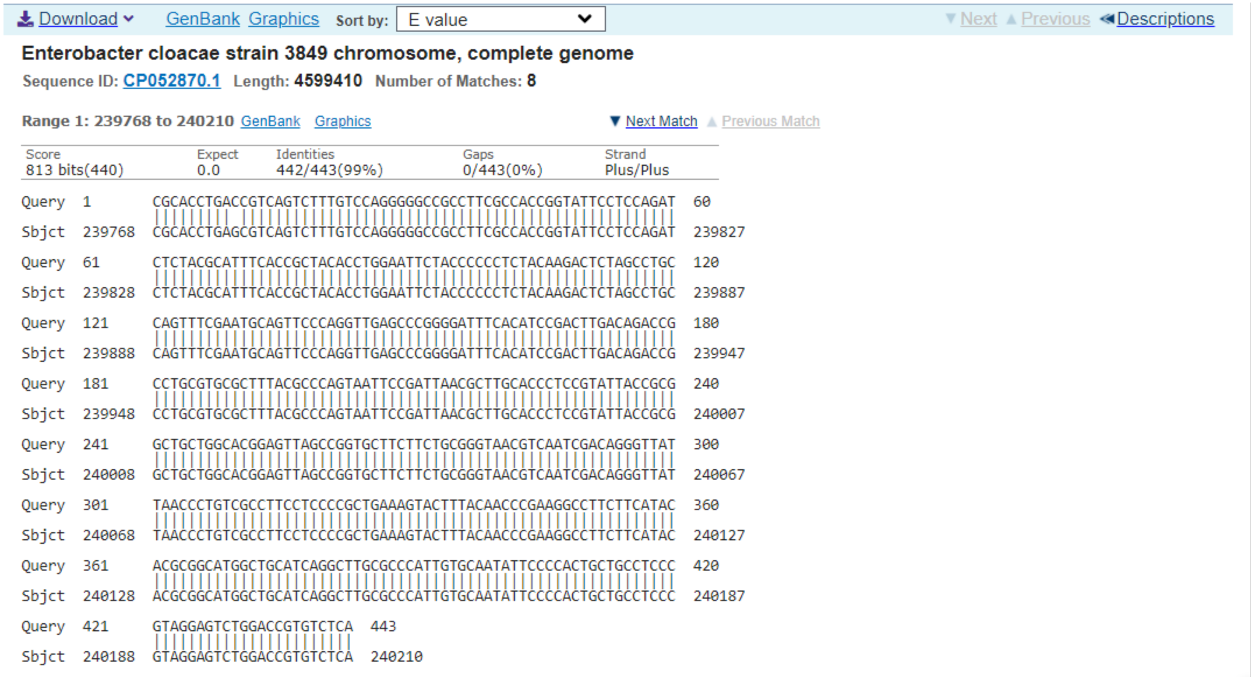


Sequences producing significant alignments

0 sequences selected

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	Enterobacter cloacae strain 3849 chromosome, complete genome	Enterobacter cl...	813	6459	100%	0.0	99.77%	4599410	CP052870.1
☐	Enterobacter cloacae strain BSN3 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	813	813	100%	0.0	99.77%	1428	MT310830.1
☐	Enterobacter hormaechei subsp. hoffmannii O143 gene for 16S ribosomal RNA, partial sequence	Enterobacter h...	813	813	100%	0.0	99.77%	1412	LC515572.1
☐	Enterobacter cloacae strain Varr_1bios 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	813	813	100%	0.0	99.77%	1058	MN135299.1
☐	Enterobacter sp. strain EUL361 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	813	813	100%	0.0	99.77%	1309	MT126447.1
☐	Enterobacter hormaechei strain ER46 16S ribosomal RNA gene, partial sequence	Enterobacter h...	813	813	100%	0.0	99.77%	1405	MT124571.1
☐	Enterobacter hormaechei strain PH5 16S ribosomal RNA gene, partial sequence	Enterobacter h...	813	813	100%	0.0	99.77%	1511	MT102423.1
☐	Enterobacter cloacae strain PE12 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	813	813	100%	0.0	99.77%	1464	MT102422.1
☐	Enterobacter cloacae strain CnLm-1 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	813	813	100%	0.0	99.77%	1403	MT074035.1
☐	Enterobacter hormaechei subsp. hoffmannii strain LB10 16S ribosomal RNA gene, partial sequence	Enterobacter h...	813	813	100%	0.0	99.77%	1424	MT071493.1
☐	Enterobacter hormaechei strain NK15 16S ribosomal RNA gene, partial sequence	Enterobacter h...	813	813	100%	0.0	99.77%	770	MT044306.1
☐	Enterobacter hormaechei strain NK8 16S ribosomal RNA gene, partial sequence	Enterobacter h...	813	813	100%	0.0	99.77%	770	MT044238.1
☐	Enterobacter hormaechei subsp. hoffmannii OIPH-N069 DNA, complete genome	Enterobacter h...	813	6503	100%	0.0	99.77%	4689117	AP019817.1
☐	Enterobacter hormaechei subsp. hoffmannii strain Eh1 chromosome, complete genome	Enterobacter h...	813	6498	100%	0.0	99.77%	4845040	CP034754.1
☐	Enterobacter cloacae strain EC 16S ribosomal RNA gene, partial sequence	Enterobacter cl...	813	813	100%	0.0	99.77%	1395	MN788615.1



Enterobacter cloacae strain 3849 chromosome, complete genome

Sequence ID: CP052870.1 Length: **4599410** Number of Matches: **8**

Range 1: 239768 to 240210 GenBank Graphics

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813 bits(440)  0.0      442/443(99%)    0/443(0%)   Plus/Plus

Query  1       CGCACCTGACCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGAT  60
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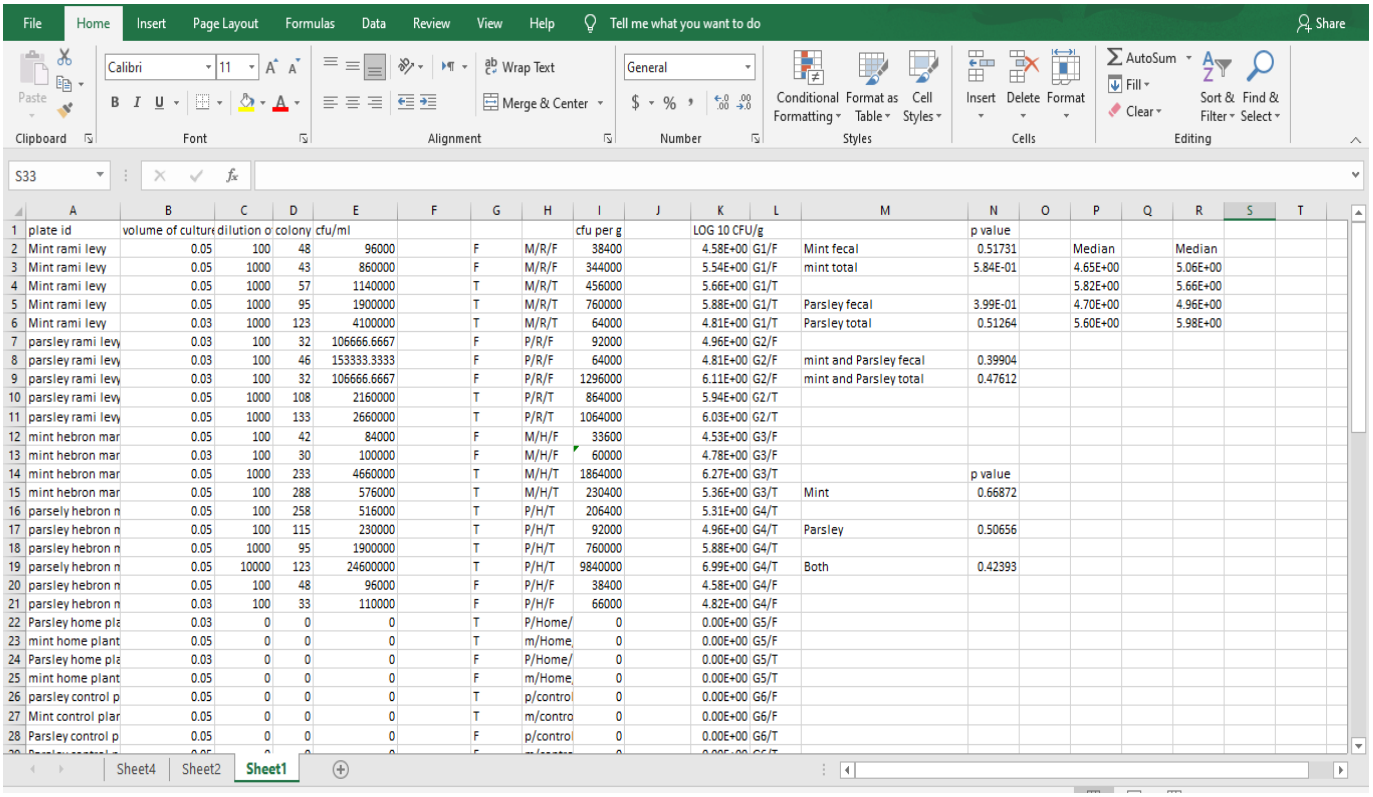
Appendix D:

Data

Plate id	Volume of culture plated (ml)	Dilution factor	Colony count	CFU/g	Pate type	LOG 10 CFU/g
Mint rami levy	0.05	100	48	38400	F*	4.58E+00
Mint rami levy	0.05	1000	43	344000	F	5.54E+00
Mint rami levy	0.05	1000	57	456000	T*	5.66E+00
Mint rami levy	0.05	1000	95	760000	T	5.88E+00
Mint rami levy	0.03	1000	123	64000	T	4.81E+00
Parsley rami levy	0.03	100	32	92000	F	4.96E+00
Parsley rami levy	0.03	100	46	64000	F	4.81E+00
Parsley rami levy	0.03	100	32	1296000	F	6.11E+00
Parsley rami levy	0.05	1000	108	864000	T	5.94E+00
Parsley rami levy	0.05	1000	133	1064000	T	6.03E+00
Mint Hebron	0.05	100	42	33600	F	4.53E+00
Mint Hebron	0.03	100	30	60000	F	4.78E+00
Mint Hebron	0.05	1000	233	1864000	T	6.27E+00
Mint Hebron	0.05	100	288	230400	T	5.36E+00
Parsley Hebron	0.05	100	258	206400	T	5.31E+00
parsley Hebron	0.05	100	115	92000	T	4.96E+00
parsley Hebron	0.05	1000	95	760000	T	5.88E+00
parsley Hebron	0.05	10000	123	9840000	T	6.99E+00
parsley Hebron	0.05	100	48	38400	F	4.58E+00
parsley Hebron	0.03	100	33	66000	F	4.82E+00
Parsley home	0.03	0	0	0	T	0.00E+00
Mint home	0.05	0	0	0	T	0.00E+00
Parsley home	0.03	0	0	0	F	0.00E+00
Mint home	0.05	0	0	0	F	0.00E+00
Parsley control	0.05	0	0	0	T	0.00E+00
Parsley control	0.05	0	0	0	F	0.00E+00

*F (Fecal coliform) *T (Total coliform)

Data



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
1	plate id	volume of culture	dilution o	colony	cfu/ml				cfu per g		LOG 10 CFU/g			p value						
2	Mint rami levy	0.05	100	48	96000		F	M/R/F	38400		4.58E+00	G1/F	Mint fecal	0.51731		Median		Median		
3	Mint rami levy	0.05	1000	43	860000		F	M/R/F	344000		5.54E+00	G1/F	mint total	5.84E-01		4.65E+00		5.06E+00		
4	Mint rami levy	0.05	1000	57	1140000		T	M/R/T	456000		5.66E+00	G1/T				5.82E+00		5.66E+00		
5	Mint rami levy	0.05	1000	95	1900000		T	M/R/T	760000		5.88E+00	G1/T	Parsley fecal	3.99E-01		4.70E+00		4.96E+00		
6	Mint rami levy	0.03	1000	123	4100000		T	M/R/T	64000		4.81E+00	G1/T	Parsley total	0.51264		5.60E+00		5.98E+00		
7	parsley rami levy	0.03	100	32	106666.6667		F	P/R/F	92000		4.96E+00	G2/F								
8	parsley rami levy	0.03	100	46	153333.3333		F	P/R/F	64000		4.81E+00	G2/F	mint and Parsley fecal	0.39904						
9	parsley rami levy	0.03	100	32	106666.6667		F	P/R/F	1296000		6.11E+00	G2/F	mint and Parsley total	0.47612						
10	parsley rami levy	0.05	1000	108	2160000		T	P/R/T	864000		5.94E+00	G2/T								
11	parsley rami levy	0.05	1000	133	2660000		T	P/R/T	1064000		6.03E+00	G2/T								
12	mint hebron mar	0.05	100	42	84000		F	M/H/F	33600		4.53E+00	G3/F								
13	mint hebron mar	0.03	100	30	100000		F	M/H/F	60000		4.78E+00	G3/F								
14	mint hebron mar	0.05	1000	233	4660000		T	M/H/T	1864000		6.27E+00	G3/T		p value						
15	mint hebron mar	0.05	100	288	576000		T	M/H/T	230400		5.36E+00	G3/T	Mint	0.66872						
16	parsely hebron n	0.05	100	258	516000		T	P/H/T	206400		5.31E+00	G4/T								
17	parsley hebron n	0.05	100	115	230000		T	P/H/T	92000		4.96E+00	G4/T	Parsley	0.50656						
18	parsley hebron n	0.05	1000	95	1900000		T	P/H/T	760000		5.88E+00	G4/T								
19	parsely hebron n	0.05	10000	123	24600000		T	P/H/T	9840000		6.99E+00	G4/T	Both	0.42393						
20	parsley hebron n	0.05	100	48	96000		F	P/H/F	38400		4.58E+00	G4/F								
21	parsley hebron n	0.03	100	33	110000		F	P/H/F	66000		4.82E+00	G4/F								
22	Parsley home pla	0.03	0	0	0		T	P/Home/	0		0.00E+00	G5/F								
23	mint home plant	0.05	0	0	0		T	m/Home,	0		0.00E+00	G5/F								
24	Parsley home pla	0.03	0	0	0		F	P/Home/	0		0.00E+00	G5/T								
25	mint home plant	0.05	0	0	0		F	m/Home,	0		0.00E+00	G5/T								
26	parsley control p	0.05	0	0	0		T	p/control	0		0.00E+00	G6/F								
27	Mint control plar	0.05	0	0	0		T	m/contro	0		0.00E+00	G6/F								
28	Parsley control p	0.05	0	0	0		F	p/control	0		0.00E+00	G6/T								