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## Genome Sequencing of Rumen Bacteria Involved in Lignocellulose Digestion

A thesis presented in fulfilment of the requirements for the degree of

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Nikola Palevich

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#### Abstract

Determining the role of rumen microbes and their enzymes in plant polysaccharide breakdown is fundamental to understanding digestion and maximising productivity in ruminant animals. In order to learn more about lignocellulose degradation in pasturegrazed dairy cows under NZ conditions, twenty representative strains from five major phylotype clusters (Butyrivibrio fibrisolvens/hungatei cluster 383, Pseudobutyrivibrio xylanivorans clusters 247 and 245, Selenomonas ruminantium cluster 212, and Lachnospiraceae cluster 121), cultivated directly from the fibre-adherent rumen microbial fraction of dairy cows were selected. Genotypic and phenotypic analysis of these strains led to identification of Butyrivibrio sp. MB2003 that adheres to and efficiently degrades the plant fibre. The 3.3 Mb MB2003 genome was sequenced and annotated and found to consist of four replicons: a chromosome (7 contigs, in 1 super scaffold), a chromid (Bhu II), a megaplasmid (pNP144) and a small plasmid (pNP6). A novel feature of the MB2003 genome is the presence of a chromid (Bhu II) which is now the smallest chromid reported for all bacteria. The MB2003 polysaccharidedegrading enzymes, surface structures and predicted strategy for attachment to, and degradation of, complex polysaccharides was found to be comparable to that of the fibrolytic bacterium Butyrivibrio proteoclasticus B316. Both MB2003 and B316 are non-motile, despite the presence of flagellar gene clusters, and utilise a range of insoluble plant polysaccharides, but not cellulose. Xylan is the preferred insoluble substrate of MB2003 and its genome encodes a large repertoire of enzymes predicted to metabolise this complex polysaccharide. The MB2003 draft genome produced in this work is the first opportunity to conduct comparative analysis of two rumen bacteria belonging to the same genus. Although both MB2003 and B316 have similar phenotypic characteristics and occupy the same habitat, the genome of MB2003 is much smaller and contains fewer extracellular polysaccharide degrading enzymes. From this comparison it can be concluded that MB2003 is a secondary hemicellulose degrader, offering an alternate view of the genes required for a xylanolytic lifestyle in the rumen, and posing an interesting question about the purpose of the wider range of polysaccharide degrading enzymes found in B316.

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"Everything I do. I do it for you!" (Bryan Adams)

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### Abbreviations

bp, kb, Mbp	base pair(s), kilo base(s), mega base pair(s)			
CDS	Coding Sequences			
COGs	Clusters of Orthologous Groups			
DAPI	4', 6-diamidino-2-phenylindole			
EC	enzyme classification			
EDTA	ethylenediamine tetraacetic acid			
EPS	Extracellular Polysaccharides			
g	gram(s)			
hr	hour(s)			
mg	milligram(s)			
min	minute(s)			
ml	millilitre			
mM, M	milliMolar, Molar			
mV	milliVolts			
NDF	Neutral Detergent Fibre			
nt	nucleotide(s)			
ORFs	Open Reading Frames			
sec	second(s)			
TE	Tris-EDTA buffer			
v/v	volume : volume ratio			
w/v	weight : volume ratio			

# **Chapter 1** Literature Review

#### 1.1 The importance of ruminant animals to New Zealand agriculture

New Zealand agriculture differs from the rest of the world in that livestock are pasture fed, as opposed to being fed with grains or other high energy feed. The difference is in the elevated lignocellulose content of pasture that ruminants find difficult to degrade efficiently. Therefore, a great opportunity exists in New Zealand, to study and improve the efficiency of lignocellulose breakdown of forage-fed ruminant livestock leading to the increased productivity of animal products important to the New Zealand economy. In 2009 almost a third of the worlds' land area was devoted to agricultural pasture providing forage for more than 1.4 billion cattle, and 2.1 billion sheep and goats (FAOSTAT, 2007). The New Zealand dairy herd is continually expanding, in June 2009 the national herd amounted to 5.9 million head, and with 4.1 million beef cattle this brought the total New Zealand cattle herd to approximately 10 million. In the same year, the New Zealand sheep flock was estimated at 32.4 million head. When the two categories were combined 1.3 million tonnes of meat and approximately 15.2 million litres of milk was produced (FAOSTAT, 2007). The current value of agricultural products, including meat, milk, wool and velvet, to the New Zealand economy is approximately \$13.5 billion, and with the increase in population, demand for meat and milk products can only be expected to increase (FAOSTAT, 2007).

#### **1.2 Ruminants**

#### **1.2.1** The ruminant digestive tract

Ruminant animals belong to the order Artiodactyla which includes animals such as cattle, deer, sheep and goats along with many other wild ruminants (Figure 1.1). Ruminants digest plant material by initially chewing it and digesting it within the animal's first two stomachs (the reticulum and rumen, referred to collectively as the reticulorumen, or commonly just as "the rumen"). This is assisted by regurgitating the semi-digested material (known as the cud), and rechewing it. The word "ruminant" in fact comes from the Latin *ruminare*, which means "to chew over again". The cud is most accurately described as a bolus of semi-degraded food regurgitated from the reticulorumen of a ruminant, while the actual process of re-chewing the cud to further break down plant matter and stimulate digestion is called "rumination".

Most rumen microbiology studies to date have focused on the agriculturally important ruminants such as cattle and sheep that belong to the Bovidae family and deer belonging to the Cervidae family, as shown in Figure 1.1 below.

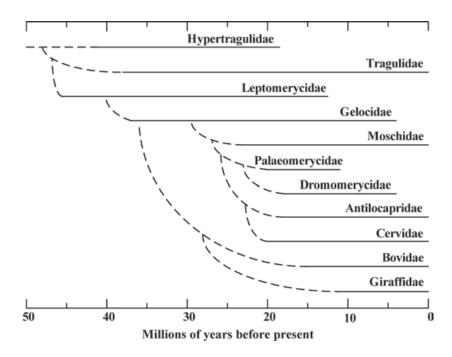
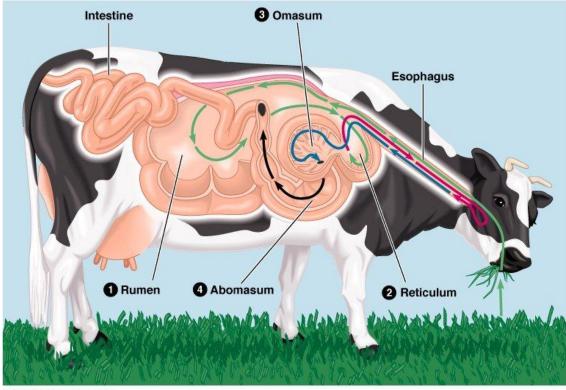


Figure 1.1. A phylogeny of ruminant families belonging to order Artiodactyla. Solid lines indicate age ranges documented in the fossil record and stippled lines indicate inferred age ranges and family relationships (Hackmann and Spain, 2010).

The typical digestive tract of a cow is shown in Figure 1.2. At approximately 100 L in cattle and up to 10 L in sheep, the rumen is the first and largest of the fore-stomach compartments. The reticulum is considered a simple rumen extension, and is connected to the omasum by a short tunnel-like structure called the reticulo-omasal orifice. The abomasum is the ruminant's true stomach; histologically it is similar to that of monogastric mammals (Flint *et al.*, 2008). In the rumen, plant material is mixed with saliva and separates into solid and liquid layers. The solid plant material clumps together and is buoyed up by trapped gas bubbles so that it floats to the surface of the reticulorumen to form a raft of material. The proximal location of the rumen facilitates the regurgitation of partially digested lignocellulose for further mastication. Occasionally, a portion of the solid raft material is regurgitated into the mouth, and chewed to assist in reducing its particle size. This process triggers the flow of copious amounts of saliva from the mouth to the fore-stomach, which under ideal conditions buffers the rumen at approximately pH 6.8 and is essential for efficient rumen function.



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Figure 1.2. Simplified schematic diagram of the ruminant digestive tract. The rumen is the first and largest fore-stomach compartment, and the primary site of microbial mediated lignocellulose degradation and fermentation. Digesta flows from the rumen to the reticulum, omasum and abomasum, respectively. (www.mun.ca/biology/scarr/Ruminant\_Digestion.htm)

#### 1.2.2 Ruminant-microbe symbiosis

A unique symbiosis exists between the ruminant and the microorganisms within the rumen environment. Ruminants are unable to digest lignocellulose, which makes up the main component of their diet. Lignocellulose is the most abundant organic material on Earth and consists of a matrix of cross-linked cellulose and hemicellulose networks, glycosylated proteins, and lignin polymers (Wang *et al.*, 2011). The microbes in the reticulorumen carry out lignocellulose degradation and fermentation within the rumen (Nocek and Russell, 1988), and in doing so generate large quantities of short chain volatile fatty acids (SCVFAs) which in turn support growth and cell turnover of the host animal. The main SCVFAs produced are acetic, propionic and butyric acids in an approximate ratio of 60:30:10 respectively. The host absorbs these SCVFAs across the rumen epithelium and transports them to the liver, where they are metabolised. Acetic acid is the major source of acetyl-CoA for lipid synthesis which is oxidised to generate

ATP in nearly all tissues of the ruminant. In order to produce energy from butyric acid,  $\beta$ -hydroxybutyric acid must be absorbed from the rumen epithelium and then undergoes oxidation in the appropriate tissues. Propionic acid is a major substrate for gluconeogenesis and is thus almost exclusively utilised in the liver. SCVFA production supplies more than 70% of the total energy requirements for the ruminant (Flint *et al.*, 2008). The ruminant obtains over half of its total protein requirements from the microbial biomass that is flushed from the rumen to the small intestine. Some of the ingested protein from plant material can be used directly by the ruminant if it by-passes degradation in the rumen (Ulyatt *et al.*, 1980), but most of the ingested plant protein is quickly broken down to peptides, amino acids and ammonia, which is then assimilated into microbial protein.

#### **1.2.3** Factors limiting digestion of forages in the rumen

Four main factorshave been recognised as restricting lignocellulose degradation in the rumen (Cheng *et al.*, 1991): (i) host factors that mediate the availability of nutrients through mastication, salivation and digesta kinetics (i.e. the fibre intake rate and extent of mastication by ruminants affects the rate of passage through the digestive tract, with higher intakes resulting in lower overall fibre digestion), (ii) the chemical composition and degradability of the insoluble component of plant material, (iii) the composition of the rumen microbial ecosystem and (iv) the polysaccharolytic capability of the rumen microbial ecosystem.

#### **1.2.4** The rumen microbial ecosystem

Culture-dependent studies on rumen microbiota have identified five fungal species, at least 370 bacterial and archeal species, and 40 protozoal species that work in concert to degrade and ferment lignocellulosic biomass (Orpin and Joblin, 1997). On the other hand, cultivation-independent molecular surveys looking at the microbial diversity within the rumen ecosystem have revealed thatonly 11% of the total bacterial taxa have been cultured (Tajima *et al.*, 1999; Edwards *et al.*, 2004; Shin *et al.*, 2004a; Shin *et al.*, 2004b; Shin *et al.*, 2004c; Cho *et al.*, 2006; Skillman *et al.*, 2006; Wright *et al.*, 2007). It is believed that the number of uncultivated individual species within the rumen range from some hundreds to thousands, with the majority categorised as being Gram-positive *Firmicutes* or the Gram-negative *Bacteroidetes* (Figure 1.3). Studies to date have shown

that the current cultured and completely characterised rumen microorganisms do not fully represent the principal and metabolically significant components of the rumen microbiota (Attwood *et al.*, 2008). As a result, our understanding of rumen fibre degradation and the enzyme systems involved in lignocellulose degradation is not fully developed. The discovery and complete characterisation of novel rumen microbes that are proficient at degrading lignocellulosic material will provide a much needed understanding of the metabolic processes involved in plant cell wall degradation.

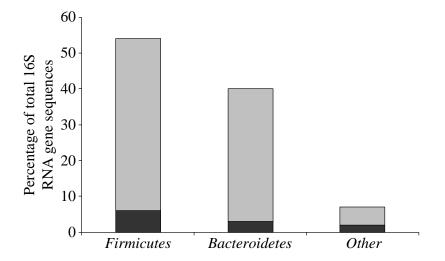


Figure 1.3. Bacterial diversity of the rumen microbial ecosystem. The percentage of 16S rRNA gene sequences represented by cultivated (black) and uncultivated (grey) bacteria is shown for the two predominant phyla, and minor or unknown phyla. Adapted from Edwards *et al.*, (2008).

#### **1.2.5** The fibre degrading rumen microbiome

The term rumen microbiome describes the set of rumen microbes, their genomes, and environmental interactions, and is composed of: (i) microbes found free living in the rumen liquor (planktonic phase), (ii) microbes loosely or tightly associated with ingested plant material (adherent phase) and (iii) microbes associated with the rumen epithelium. The adherence of microbes to plant material is crucial in order to maximise efficient degradation of plant cell wall polysaccharides (McAllister *et al.*, 1994). It has been shown that bacteria attach to plant material within minutes of ingestion (Bonhomme, 1990; Koike *et al.*, 2003a). Of the total microbial biomass in the rumen, ~80% are fibre adherent bacteria; they account for 90% of the total cellulase and xylanase activities, as well as ~70% of the amylase and protease activities in the rumen (Akin, 1980; Craig *et al.*, 1987; Minato *et al.*, 1993). Molecular surveys have demonstrated that *Bacteroidetes* mainly occupy the planktonic phase whereas *Firmicutes* account for up to 75% of the adherent bacterial population (Tajima *et al.*, 1999; Cho *et al.*, 2006).

#### **1.3** The Plant Cell Wall

The plant cell wall is the foremost source of nutrition for forage fed ruminants and constitutes approximately 80% of the dry weight of plant material. The cell wall is composed of a complex network of cellulose fibres surrounded by a matrix of non-cellulosic structural polysaccharides, proteins, phenolic compounds and lignin. The structures of the major cell wall polysaccharides are shown in Figure 1.4. Chemical composition varies greatly, depending on the plant species, age and the tissue type (Carpita and Gibeaut, 1993; Carpita, 1996).

#### 1.3.1 Type-I and Type-II plant cell walls

The primary cell wall of flowering plants can be separated into two classes, which differ significantly in their structural features and chemical composition. Type-I cell walls are made up of mainly cellulose microfibrils fixed in a xyloglucan (XyG)-rich hemicellulose, along with significant amounts of pectin and structural proteins (Table 1.1) (Carpita, 1996). They are abundant in both dicotyledonous and noncommelinoid monocotyledonous plants as well as in gymnosperms. Type-II cell walls are found only in commelinoid monocotyledonous plants (i.e. grasses) and differ in that they are comprised of cellulose embedded in significant amounts of verv glucuronoarabinoxylans (GAX) with mixed linkage glucans (MLGs), and modest levels of phenolic compounds (Carpita, 1996). In contrast to Type-I cell walls, Type II cell walls contain low levels of pectin and structural proteins. The secondary cell wall of grasses is mainly composed of cellulose, GAX, and lignin; it can contribute up to 50% of dry weight (Brown and Saxena, 2000). The two predominant plant types found in New Zealand pastures are perennial ryegrass and legumes (Woodfield, 1999). Perennial ryegrass is composed of Type-II cell walls with high levels of GAX and ferulic acid crosslinks, whereas legumes (clover and lucerne) have Type-I cell walls that are high in pectin and xyloglucans (Varner and Lin, 1989).

#### 1.3.2 Cellulose

The plant cell wall is comprised of approximately 40% cellulose, an energy rich structural polysaccharide (O'Sullivan, 1997). Cellulose is composed of  $\beta$ 1-4 linked glucose units that spontaneously form insoluble microfibrils (approximately 3-5 nm wide) of single strands of up to 15,000 glucose monomers (Figure 1.4, Vogel, 2008). Individual microfibrils contain variable numbers of cellulose chains and may also associate with other microfibrils to form a larger single microfiber (Pizzi and Eaton, 1985). These structures are held together via numerous inter- and intra-chain hydrogen bonds and van der Waals forces (Ioelovich, 2008). The exterior of cellulose microfibrils ismuch less rigid compared to the core regions due to the imperfections in bonds of the individual cellulose chains, the actual thickness of the microfibril or possibly through the interactions with other molecules surrounding the polymers (Ioelovich, 2008). The ability of cellulose toform strong bonds with a variety of non-cellulosic cell wall components accounts for the structural rigidity and tensile strength of the plant cell wall (Baskin, 2001).

Table 1.1 Estimated composition of Type-I and Type-II primary and secondary plant cell walls.

Cell wall component	Primary wall <sup>a</sup>		Secondary wall <sup>a</sup>	
	Type-I	Type-II	Type-I	Type-II
Cellulose	15-30 <sup>b,c,d</sup>	20-30 <sup>b,e</sup>	45-50 <sup>b</sup>	35-45 <sup>b,f</sup>
Hemicellulose				
Glucuronoarabinoxylans	5 <sup>b</sup>	20-40 <sup>c</sup>	20-30 <sup>b,g</sup>	40-50 <sup>b,g</sup>
Mixed linkage glucans	None	10-30 <sup>c</sup>	None	Minor
Xyloglucans	20-25	1-5 <sup>b,c</sup>	Minor	Minor
Mannans/glucomannans	5-10 <sup>c</sup>	Minor	3-5 <sup>g</sup>	Minor
Pectin	20-35 <sup>°</sup>	5 <sup>b</sup>	$0.1^{b}$	0.1 <sup>b</sup>
Structural proteins	10 <sup>c,d</sup>	1 <sup>c</sup>	Minor	Minor
Phenolic compounds	Minor	1-5 <sup>b,c</sup>	Minor	0.5-1.5 <sup>b</sup>
Lignin	Minor	Minor	7-10 <sup>b</sup>	20 <sup>b</sup>
Silica	None	None	Variable	5-15 <sup>b</sup>

<sup>a</sup> Values are the percentage of plant cell-wall dry weight. The table was adapted from (Vogel, 2008). Estimates were obtained from a number of sources as detailed. <sup>b</sup>(Ishii, 1997), <sup>c</sup>(O'Neil and York, 2003), <sup>d</sup>(Zablackis *et al.*, 1995), <sup>e</sup>(Mitchell *et al.*, 2007), <sup>f</sup>(Hatfield *et al.*, 1999) and <sup>g</sup>(Ebringerova *et al.*, 2005).

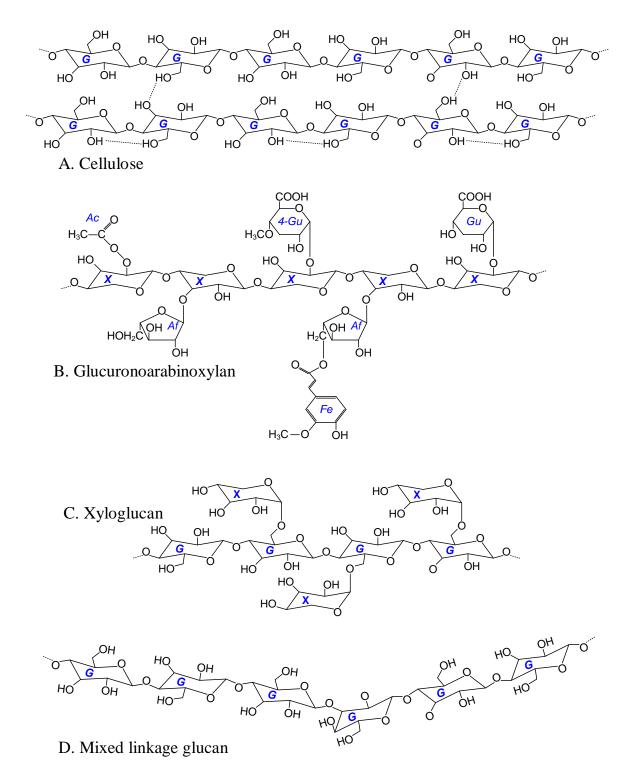


Figure 1.4. Simplified chemical structure of cellulose, glucuronoarabinoxylan, xyloglucan, and mixed linkage glucans. (A) Two chains of cellulose consisting of  $(1\rightarrow 4)$ - $\beta$ -D-glucose monomers with intra- and inter-chain hydrogen bonding (dotted lines). (B) The homopolymeric xylan backbone composed of  $(1\rightarrow 4)$ - $\beta$ -D-xylopyranose monomers with examples of the substituent side chains found in the cell wall of grasses. (C) The four residue repeating pattern of xyloglucan with examples of xylopyranose substituent groups. (D) A mixed linkage glucan chain comprised of two  $(1\rightarrow 4)$ - $\beta$ -cellotriose units connected by a  $(1\rightarrow 3)$ - $\beta$ -linkage. Ac, O-acetyl; Af,  $\alpha$ -L-arabinofuranose; Fe, ferulic acid; G, glucose; 4-Gu, 4-O-methyl-D-glucuronic acid; Gu, glucuronic acid; X, xylopyranose (xylose). Figure adapted from Vogel, 2008.

#### **1.3.3 Hemicellulose**

Hemicellulose is semi-soluble (i.e. unable to completely dissolve in water) and makes up 20%-35% of the total plant biomass. Unlike cellulose, it is a family of highly branched chemically heterogeneous polymers of pentoses, hexoses and sugar acids (Linder et al., 2003; Kabel et al., 2007). Hemicellulose interacts with neighbouring cellulose microfibrils (and other non-cellulosic cell wall structural polymers) in a structurally dependent manner, according to the sticky network model (Cosgrove, 2000). In this model, hemicelluloses are either tethered to the cellulose microfibrils by formation of multiple hydrogen bonds between the two polymers after deposition or become trapped during crystallisation. The two main representatives of hemicelluloses are GAX and xyloglucans (Figure 1.4). GAX in grasses is comprised of a  $(1\rightarrow 4)$ - $\beta$ -Dxylopyranose monomerbackbone (Aspinall and Preiss, 1980; Liab et al., 2000) that can be substituted with a number of different groups such as  $(1\rightarrow 2)-\alpha$ -linked and  $(1\rightarrow 3)-\alpha$ linked L-arabinofuranosyl groups, O-acetyl, and  $(1\rightarrow 2)-\alpha$ -D-glucuronic acid or 4-Omethyl-D-glucuronic acid groups to varying degrees (Borneman et al., 1990). The α-Larabinofuranosyl side groups may also form diferulic crosslinks with phenolic polymers such as ferulic acidby becoming esterified at the O-2 or O-5 positions. Xyloglucan is the main hemicellulose in the primary cell wall of many dicotyledonous plants and consists of a repeating pattern of four  $(1\rightarrow 4)$ - $\beta$ -D-glucose monomers substituted with  $(1\rightarrow 6)$ - $\alpha$ xylopyranose residues that are tightly hydrogen bonded to neighbouring cellulose microfibrils (Pauly et al., 1999).

#### 1.3.4 Pectin

Pectin is structurally the most intricate (i.e. complex and difficult to degrade) family of polysaccharides because it is involved in the control of the cell wall structure and expansion, cell-cell interactions and signalling, as well as in plant defence mechanisms (Jarvis, 1984). Pectin is mainly located in the primary cell wall, featuring in two distinct types of polysaccharides: homogalacturonan (HG) and rhamnogalacturonan I (RG-I). HG is a linear chain of  $(1\rightarrow 4)$ - $\alpha$ -D-galacturonic acid (GalA) residues that may be partially methylesterified or *O*-acetylated (Shibuya and Nakane, 1984; Carpita, 1989). Rhamnogalacturonan I (RG-I) is a more complex heteropolymer comprised of a backbone of repeating  $(1\rightarrow 2)$ - $\alpha$ -L-rhamnosyl- $(1\rightarrow 4)$ - $\alpha$ -D-GalA subunits, that can be profoundly substituted with complex side chains consisting of arabinofuranosyl units

and arabinogalactans (Saulnier and Thibault, 1999). Arabinogalactans are by nature heterogeneous but may consist of a backbone of  $(1\rightarrow3)$ - $\beta$ -linkedD-galactose residues substituted with  $(1\rightarrow6)$ - $\beta$ -D-galactose and/or  $(1\rightarrow3)$ - $\alpha$ -L-arabinofuranose. Furthermore, similar to GAX, the side chains of RG-I may be esterified with ferulic and *p*-coumaric acids (Nakamura *et al.*, 2002b; Coenen *et al.*, 2007). It is believed that pectic polysaccharides are covalently cross-linked to one another via their backbones. Thus it is possible that both HG and RG-I are very tightly associated with other plant cell wall polysaccharides including hemicellulose and cellulose (Nakamura *et al.*, 2002a).

#### 1.3.5 Lignin

Lignin is a crucial secondary cell wall component as it plays an important role in maintaining cell structure integrity, water transport and protecting against plant pathogens (Grabber, 2005). Lignin is not susceptible to enzymatic degradation by the rumen microbiota, and hence its presence in the cell wall is thought to be partly responsible for the recalcitrance of ruminant forages to breakdown in the rumen (Armstrong and Gilbert, 1985; McAllister *et al.*, 1994). In dicotyledonous plants, lignins contain mainly guaiacyl and syringyl subunits and a small quantity of *p*-hydroxyphenyl units (Campbell and Sederoff, 1996). An important attribute of grass lignins is the incorporation of diferulic acids during development by means of ether bonds linking the ferulic acid hydroxyl groups forming diferulic bonds (Scalbert *et al.*, 1985; Kondo *et al.*, 1990).

#### **1.4 Lignocellulose degradation**

For complete degradation of lignocellulosic material, the actions of three types of polysaccharide degrading enzymes (polysaccharidases) are required to work in concert. These enzymes are: (i) *O*-Glycosidehydrolases (GH), which hydrolyse glycosidic bonds between carbohydrate monomers or between carbohydrate and non-carbohydrate moieties and this activity takes place via general acid catalysis leading to an overall retention or inversion at the site of catalytic activity (Henrissat, 1991; Henrissat and Davies, 1997; Henrissat, 1998), (ii) Carbohydrate Esterases (CE), which hydrolyse the ester linkages of ferulic acid or acetate side chains and (iii) Polysaccharide Lyases (PL), which hydrolyse polysaccharide chains by  $\beta$ -elimination. Those lignocellulose-

degrading enzymes important for rumen forage degradation and their substrates are summarised in Table 1.2 and Figure 1.5.

Enzyme **Substrate** Endo- $\beta$ -1,4-xylanase  $(1\rightarrow 4)$ - $\beta$ -D-xylan Exo-β-1,4-xylosidase  $(1\rightarrow 4)$ - $\beta$ -D-xylooligomers, xylobiose  $(\beta$ -xylosidase)  $\alpha$ -L-arabinofuranosyl (1 $\rightarrow$ 2) or α-L-arabinofuranosidase  $(1 \rightarrow 3)$  xylooligomers 4-O-methyl-D-glucuronic acid α-Glucuronidase (substituted to xylan) O-acetyl xylan Acetyl xylan esterase Ferulic/p-coumaric acid esterified Ferulic/*p*-coumaric acid esterase arabinofuranosyl xylooligomers α-Galactosidase  $(1\rightarrow 6)$ - $\alpha$ -D-galactose Endo- $\beta$ -1,4-glucanase  $(1\rightarrow 4)$ - $\beta$ -D-glucan/cellulose Cellodextrinase Cellobiohydrolase  $(1\rightarrow 4)$ - $\beta$ -D-glucose/cellobiose  $(1\rightarrow 4)$ - $\beta$ -D-cellodextrins and cellobiose β-Glucosidase

lignocellulose degradation.

Table 1.2. Summary of the hemicellulolytic and cellulolytic enzymes important for

Descriptions and classifications from the CAZy database (Henrissat. et al., 2011).

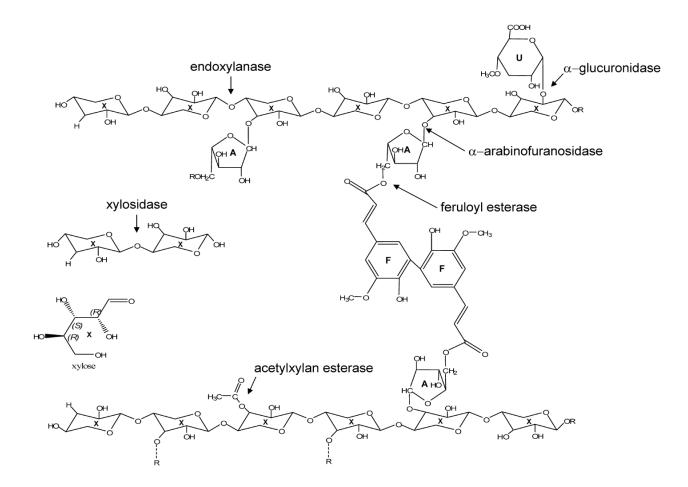


Figure 1.5. Schematic diagram illustrating the major linkages in the forage plant cell wall and the hemicellulolytic and cellulolytic enzymes important for lignocellulose degradation by ruminal microorganisms. A, arabinose; F, ferulic acid; U, 4-O-methylglucuronic acid; X, xylose; R, continuation of glycan chain. The major enzymes cleaving the plant cell wall include: endoxylanase, xylosidase, acetylxylan esterase,  $\alpha$ -arabinofuranosidase, feruloyl esterase,  $\alpha$ -glucuronidase.Modified image from Chesson and Forsberg, 1997.

#### **1.4.1** Hemicellulose degradation

Due to the complex nature and diverse chemical structure, hydrolysis of hemicelluloses requires a variety of enzymes. Endoxylanases ((1 $\rightarrow$ 4)- $\beta$ -D-xylanxylanohydrolases) cleave the internal linkages within the xylan backbone forming xylobiose and xylooligosaccharides. These end products are further degraded into xylobiose and/or xylose by  $\beta$ -D-xylosidases ((1 $\rightarrow$ 4)- $\beta$ -D-xylan-xylohydrolases). The diverse range of substituent's attached to hemicellulose are hydrolysed from the xylan backbone by the activity of  $\alpha$ -D-glucuronidases,  $\alpha$ -L-arabinofuranosidases, acetylxylan esterases, ferulic acid and *p*-coumaric acid esterases (Mackenzie *et al.*, 1987). Ferulic acid esterases may be vital in ruminant fibre degradation as they are thought to increase accessibility of hemicellulose to other fibre degrading enzymes by hydrolysing the ester bond between ferulic acids and hemicellulose (Black *et al.*, 1996; Janecek *et al.*, 2003).

#### 1.4.2 Cellulose degradation

Three types of enzymes catalyse cellulose hydrolysis to glucose: (i) Endo- $\beta$ -1,4glucanases cleave (1 $\rightarrow$ 4)- $\beta$ -D-glycosidic bonds at internal positions along the cellulose chain generating cellodextrins of variable chain lengths, (ii) Exoglucanases such as cellodextrinases and cellobiohydrolases act in a progressive manner on the reducing or non-reducing ends of cellulose to liberate glucose and cellobiose. Exoglucanases are also capable of degrading microcrystalline cellulose by stripping cellulose microfibrils from the microcrystalline structure (Teeri, 1997), and (iii)  $\beta$ -glucosidases complete the degradation process by hydrolysing soluble cellobiose and cellodextrins to glucose.

#### 1.4.3 Pectin degradation

Pectin degradation is facilitated by three classes of enzymes: (i) Depolymerases that act directly upon the pectin backbone, and are subdivided into various lyases (acting by  $\beta$ -elimination). Pectate lyases cleave  $(1\rightarrow 4)$ - $\alpha$ -linkages between galacturonic acids and may preferentially attack regions of unmethylated polygalacturonate (pectate), although they can act on regions with low levels of methylation (Tardy *et al.*, 1997). (ii) Hydrolases involved in pectin degradation include endopolygalacturonases, exopolygalacturonases and rhamnogalacturonases. Polygalacturonas are cleaved at random internal positions, and at the non-reducing

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chain ends in polygalacturonans. Rhamnogalacturonases hydrolyse bonds between Dgalacturonic acid and L-rhamnose in rhamnogalacturonan I (Sakai *et al.*, 1993). (iii) Esterases that hydrolyse acetyl, methyl or ferulic acids substituents from the main chains of the  $(1\rightarrow 4)$ - $\alpha$ -galacturonic acids. Acetylesterases remove C-2 and C-3 attached acetyl groups, and methylesterases act on methoxylated groups releasing methanol. Acetylesterase activity is enhanced when esterified pectins are pre-treated with methylesterase, suggesting there is an optimal sequence of esterase activities for pectin degradation (Shevchik and Hugouvieux-Cotte-Pattat, 2003).

#### 1.5 Rumen Microbial Genomics

#### **1.5.1** The fibrolytic rumen bacteria

To date our understanding of the various enzymatic processes that drive rumen forage degradation have been derived from molecular and biochemical analyses of single genes and/or gene products produced by microbes that have been grown in pure culture. Only a select few organisms areable to both efficiently breakdown and utilise the non-cellulosic components of the plant cell walls such as pectin and hemicellulose (Stewart *et al.*, 1997). Based on current knowledge, the predominant fibrolytic bacteria within the rumen of animals fed a high forage diet are summarised in Table 1.3 (Table adapted from Weimer, 1998). Genome sequence information concerning rumen microorganisms is scarce, as complete genomes are available for only four fibrolytic bacteria (Table 1.4). Many interesting discoveries have been made from the various fibrolytic bacterial genomes, among these are a large number of genes that code for proteins that facilitate breakdown of plant cell wall polysaccharides.

Dhylum	Species	Predominant Main fermentation		Defense	
Phylum	Species	Substrate	products	Reference	
	Butyrivibrio fibrisolvens			(Kopečný et al., 2003)	
	Butyrivibrio hungatei			(Kopečný et al., 2003)	
	Butyrivibrio proteoclasticus	X, P, S	hustanata (forma ata /lo atata	(Moon <i>et al.</i> , 2008)	
	Pseudobutyrivibrio ruminis		butyrate/formate/lactate	(Schoep and Gregg, 2007)	
Firmicutes	Pseudobutyrivibrio xylanovorans			(Kopečný et al., 2003)	
(Gram-positive)	Lachnospira sp.	Р		(Cotta and Forster, 2006)	
	Ruminococcus flavefaciens	С, Х	formate/succinate	(Ayers, 1958)	
	Ruminococcus albus	С, Х	formate/succinate	(Patterson et al., 1975)	
	Eubacterium cellulosolvens	C X la stata/farmata	1	(Anderson and Blair, 1996)	
	Clostridium sp.	С, Х	lactate/formate	(Kelly et al., 1987)	
Bacteroidetes	Prevotella ruminicola	X, S, P	propionate/succinate	(Purushe et al., 2010)	
(Gram-negative)	Prevotella bryantii	X, S, P	propionate/succinate	(Purushe et al., 2010)	
Fibrobacter	Fibrobacter succinogenes	С	formate/succinate	(Suen et al., 2011)	
(Gram-negative)	Fibrobacter intestinalis	С	formate/succinate	(Qi et al., 2005)	

Table 1.3. Summary of the major lignocellulose degrading bacteria of the bovine rumen.

X, xylan, S, starch, C, cellulose and P, pectin.

Organism	Contigs	Size (bp)	G+C%	Family	Sequencing Project*	Country	NCBI Number (NC)	Reference
Butyrivibrio proteoclasticus B316	1	3,555,059	40	Lachnospiraceae	AgResearch	NZ	014387	(Kelly et al., 2010)
	1	361,399	39				014389	
	1	302,355	40				014388	
	1	186,328	38				014390	
Prevotella ruminicola 23	1	3,619,559	47	Prevotellaceae	NACGFRB	USA	014033	(Purushe et al., 2010)
Fibrobacter succinogenes S85	1	3,842,635	48	Fibrobacteraceae	JGI/NACGFRB	USA	013410	(Suen et al., 2011)
Ruminococcus albus 7	1	3,685,408	44	Ruminococcaceae	JGI	USA	014833	Unpublished
	1	420,706	38				014824	
	1	352,646	44				014825	
	1	15,907	36				014826	
	1	7,420	42				014827	
Prevotella bryantii B14	98	3,592,947	39	Prevotellaceae	NACGFRB	USA	ADWO00000000	(Purushe et al., 2010)
Ruminococcus albus 8	245	4,373,730	46	Ruminococcaceae	NACGFRB	USA	ADKM00000000	Unpublished
Ruminococcus flavefaciens FD-1	119	4,573,608	45	Ruminococcaceae	NACGFRB	USA	ACOK00000000	(Miller et al., 2009)
Eubacterium cellulosolvens 6	107	3,260,436	48	Lachnospiraceae	JGI	USA	AEOA00000000	Unpublished

Table 1.4. Publicly available genome sequences from fibrolytic rumen bacteria.

\*NACGFRB, North American Consortium for the Genomics of Fibrolytic Rumen Bacteria. JGI, Joint Genome Institute. www.ncbi.nlm.nih.gov

#### 1.5.2 Butyrivibrio and Pseudobutyrivibrio

The genera Butyrivibrio and Pseudobutyrivibrio belong to the genetically diverse Lachnospiraceae family and previously were all called Butyrivibrio fibrisolvens. However they have been divided into two genera and several species (Orpin et al., 1985; Willems et al., 1996; Forster et al., 1997; Kopecny et al., 2001; Kopecny et al., 2003; Kim et al., 2011). Bacteria of the Butyrivibrio and Pseudobutyrivibrio assemblage are thought to be the main butyrate producers in the rumen and are considered amongst the most effective hemicellulose degraders (Diez-Gonzalez et al., 1999; Paillard *et al.*, 2007a). Xylans of different chemical and physical properties from a range of forages can be degraded by Butyrivibrio strains (Coen and Dehority, 1970; Miron and Benghedalia, 1993; Miron et al., 1994; Hespell and Cotta, 1995). Butyrivibrio strains are capable of growing on a range of simple sugars and plant polysaccharides such as pectins, mannans, starch and hemicelluloses. While they can produce a number of cellulose degrading enzymes, not all strains are able to utilise cellulose in vitro (Attwood and Reilly, 1995). Recent studies have shown that the bulk of the Butyrivibrio population in the rumen actually adheres to the solids fraction in rumen contents (Whitford et al., 1998; Tajima et al., 1999; Koike et al., 2003b), however the mechanisms responsible for fibre adhesion are currently not understood. Another key feature of *Butyrivibrio* species is their high proteolytic activity (Cotta and Hespell, 1986; Attwood and Reilly, 1995; Sales et al., 2000).

#### **1.5.3** Butyrivibrio proteoclasticus B316

*Butyrivibrio proteoclasticus* B316 was isolated from rumen contents of a New Zealand cow grazing a ryegrass-clover pasture (Attwood *et al.*, 1996). It was originally described as *Clostridium proteoclasticum*, however further taxonomic studies indicated that its reclassification into the genus *Butyrivibrio* (within the *Clostridial* subcluster XIVa) was more appropriate, as shown in Figure 1.6 (Attwood *et al.*, 1996; Moon *et al.*, 2008). The *B. proteoclasticus* B316 genome is 4.4 Mb in size and encodes 3813 coding sequences (CDSs) that are distributed across four replicons, consisting of the main chromosome (BPc1), two megaplasmids (pCY360 and pCY186) and a secondary chromosome, or chromid (BPc2). *B. proteoclasticus* has a Gram-positive cell wall structure even though cultures stain Gram-negative. Although cells have a single sub-polar flagellum, *B. proteoclasticus* is not motile (Kelly *et al.*, 2010).

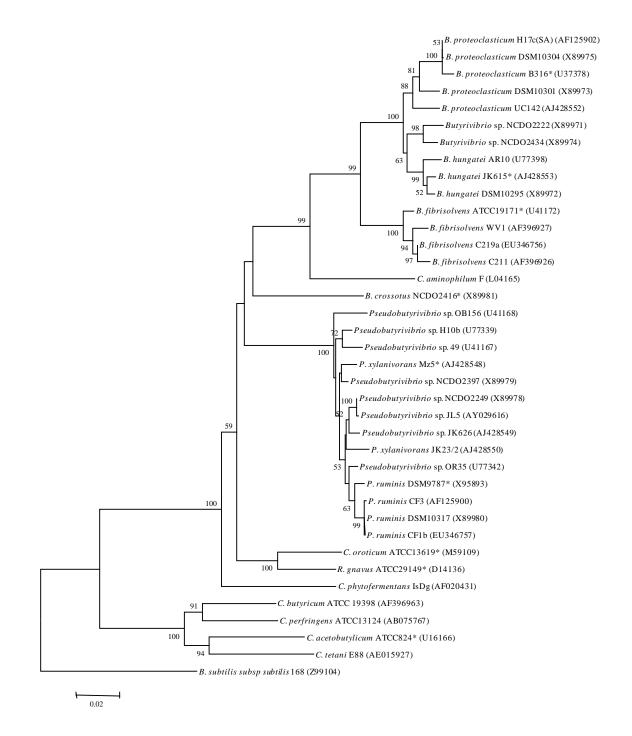


Figure 1.6. 16S rRNA gene phylogeny using near full-length sequences from Clostridial Cluster I and subcluster XIVa strains, with *Bacillus subtilis* sub sp. *subtilis* as an outgroup. Percentage bootstrap values were calculated from 10,000 replicates and are shown at nodes if >50 %. GenBank accession numbers are shown in parentheses. Bar, 0.02 nucleotide substitutions per site. \* indicates type strain. Figure adapted from Moon *et al.*, 2008.

*B. proteoclasticus* cells are slightly curved rods that form short chains or pairs but will occasionally also form long chains (Figure 1.7). *B. proteoclasticus* is prevalent in the rumen of animals grazing fresh pasture. Estimates of its populations via competitive PCR or real time PCR are ~2% and 9% respectively (Reilly and Attwood, 1998; Paillard *et al.*, 2007b). *B. proteoclasticus* produces butyrate, is highly xylanolytic and proteolytic and can also convert linoleic acid into stearic acid and thus may have an important role in biohydrogenation in the rumen (Attwood *et al.*, 1996).

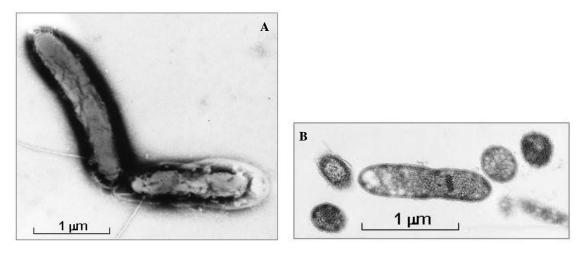


Figure 1.7. Ultrastructure of *B. proteoclasticus* B316 cells. Electron micrographs of negatively stained *B. proteoclasticus* cells showing the sub-polar flagellum (A), and thin-sectioned cells showing the gram-positive cell wall structure (B). Figure from Attwood *et al.*, 1996.

#### 1.6 Project Background

The AgResearch Research and Capability Fund (ARC; "Development of a functional metagenomics capability for the analysis of fibre-degrading rumen microbiota", contract number ARC0719) project was aimed at developing culture-independent methods to analyse the rumen microbiota, focusing on the fibre-adherent microbes. Three types of data were generated from this work: (i) 16S rRNA gene sequence that provided insight into the microbial community composition of the rumen, (ii) shotgun sequencing data that was used to gain an understanding of the genes present and the associated functions of these genes in the rumen community, and (iii) functional metagenomics was used to identify bioactivities involved in lignocellulose degradation (Moon *et al.*, 2010a; Moon*et al.*, 2010b). From the ARC project, plant-adherent rumen bacteria were obtained through fractionation of rumen contents, which is the process of separating bacteria that are tightly adhered to the plant matter from planktonic and loosely adherent

bacteria within the rumen contents. In the ARC project, two pasture-grazing cows (722 and 723) from AgResearch Grasslands, Palmerston North were sampled for rumen contents. The extraction of the plant-adherent (AD-adherent) fraction of rumen contents from pasture grazed cows was carried out using a modified protocol described by Larue *et al.*, (2005). Briefly, the rumen content was separated into solid and liquid fractions and the adherent bacteria were released by incubation of solid digesta in detergent. The extracted DNA from adherent bacteria was amplified using 16S primers (V3 region) and analysis of the resulting sequences revealed that in both animals the most prevalent phylum was Firmicutes, class Clostridia, order Clostridiales and the most prominent family was Lachnospiraceae.

The parallel New Economy Research Fund (NERF; "Accessing the uncultured rumen microbiome", contract number C10X0803) project aims to explore the uncultivated microbes of the rumen investigating the development of cultivation methods (Noel. S *et al.*, Unpublished) and culture-independent methods (metagenomics). Samantha Noel's PhD cultivation experiments used dilution theory to produce over a thousand cultured isolates from the adherent fraction of rumen contents collected from pasture-fed dairy cows over a 15 month period. From the cultured isolates, 16S rRNA gene sequences were obtained via Sanger sequencing for 141 isolates and incorporated into the ARC 16S dataset. The co-occurrence of these 16S rRNA gene sequences with the sequences from the ARC metagenomic project were determined by combining all these sequences and constructing a combined phylogenetic tree. Twenty sequences representing cultured isolates which grouped with the largest clusters of organisms were selected as the initial candidate list for genome sequencing.

#### 1.7 Project Aims

The overall purpose of the ARC and NERF research programmes is to improve our understanding of the polysaccharilytic capability of the rumen microbial ecosystem in pasture grazed cattle in New Zealand. A better understanding of the metabolic processes performed by the fibrolytic rumen microbiota is expected to generate new opportunities to enhance forage degradation, manipulate rumen function, and improve the productivity of the forage fed ruminants. Specifically the aims of this MSc project were to:

- Characterise a set of bacterial isolates obtained from the fibre-adherent rumen microbial fraction of dairy cows grazing on grass pastures (NERF programme), in order to identify strains that adhere to and efficiently degrade plant polysaccharides.
- 2. Sequence and annotate the genome of one bacterial isolate, identified in the first aim.
- 3. Identify the relevant genes encoding the polysaccharide-degrading enzymes of the organism and any surface structures involved in its attachment to the substrate.
- Compare the genome of the bacterial isolate to genomes of other fibrolytic rumen bacteria to gain insight into the genome organisation and modes of fibre degradation.

# Chapter 2 Materials and Methods

# 2.1 Materials

# 2.1.1 Bacterial strains

The bacterial strains used in this work are listed in Table 2.1.1.

Table 2.1. Bacterial strains.

Species	Strain	Culture collection accession number*	Source
Butyrivibrio fibrisolvens	D1 <sup>T</sup>	ATCC 19171	Rod Mackie, University of Illinois at Urbana-
Buryn viono jionisorvenis	DI		Champaign, IL, USA
Butyrivibrio hungatei	JK615	DSM 14810	Jan Kopecny, Institute of Animal Physiology
Bulynviono nungulei	JICOL	DDW114010	and Genetics, Prague, Czech Republic
Butyrivibrio	B316 <sup>T</sup>	DSM 14932	AgResearch, Grassland Research Centre,
proteoclasticus	<b>D</b> 510	DOM 14752	Palmerston North, New Zealand
			Paul Rainey, University of Auckland, School
Escherichia coli	DH5a	DSM 6897	of biological Sciences, Auckland, New
			Zealand
Fibrobacter	HM2	ATCC 43856	M.P.Bryant, University of Illinois at Urbana-
succinogenes	111112	ATCC 43650	Champaign, IL, USA
Pseudobutyrivibrio	$Mz5^{T}$	DSM 14809	Jan Kopecny, Institute of Animal Physiology
xylanivorans	IVIZ3	DSM 14009	and Genetics, Prague, Czech Republic
Ruminococcus	FD1	ATCC 19208	H. Flint, Rowett Inst. Scotland
flavefaciens	ΓDΙ	ATCC 19200	11. Find, Rowett Inst. Scottand
Streptococcus bovis	2B	ATCC 33317	A. Klieve, DPI, Brisbane, Australia

\* ATCC: American Type Culture Collection, USA; DSM: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Germany.

# 2.1.2 Buffers and reagents

# **dNTP** Solution

Deoxynucleotide triphosphates (dNTPs), dATP, dCTP, dGTP, and dTTP, were supplied separately, each at a concentration of 100 mM, (Invitrogen, Carlsbad, CA, USA). The dNTPs were mixed in equimolar concentrations and diluted in dH<sub>2</sub>O to give 20 mM stock solutions. Stock solutions were stored at -20°C until required.

# **EC Buffer**

EC buffer is composed of 100 mM EDTA, 1 M NaCl, 35 mM N-Lauryl-sarcosine (Sigma-Aldrich, St. Louis, MO, USA) and 6 mM Trizma base (Invitrogen, Carlsbad, CA, USA) dissolved in  $dH_2O$ . The buffer is adjusted to pH 7.6 with NaOH, then autoclaved at 121°C for 20 min.

#### **EDTA-Sarkosyl Solution**

EDTA-Sarkosyl solution is composed of 0.5 M ethylenediaminetetraacetic acid (EDTA) and 35 mM N-Lauryl-sarcosine dissolved in dH<sub>2</sub>O. The pH of the reagent is adjusted to pH 8.0 with NaOH, then autoclaved at 121°C for 20 min.

### **Glycerol Solution (40%)**

Glycerol solution is composed of 4.4 M glycerol (VWR International Ltd., Lutterworth, Leicestershire, U.K.) in water. The solution was mixed, boiled for 5 min, cooled to room temperature under  $O_2$ -free CO<sub>2</sub>, autoclaved at 121°C for 20 min and left to equilibrate for approximately 72 hr in an anaerobic chamber (Kenters *et al.*, 2010).

#### **Mineral Solution**

Mineral Solution is composed of 45 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>,10 mM (CaCl<sub>2</sub>.2H<sub>2</sub>O), 10 mM (MgSO<sub>4</sub>.7H<sub>2</sub>O), 200 mM NaCl and 45 mM KH<sub>2</sub>PO<sub>4</sub> (all supplied by VWR International Ltd., Lutterworth, Leicestershire, U.K). All components were dissolved in dH<sub>2</sub>O and the solution autoclaved at 121°C for 20 min (Kenters *et al.*, 2010).

#### **Modified Karnovsky's Fixative**

Modified Karnovsky's Fixative was made by heating paraformaldehyde (2 g per 100 ml) in dH<sub>2</sub>O to 60-70°C, and adding 1 M NaOH dropwise until the solution became clear. The solution was cooled in an ice bath and Buffer Salts (2.51 g Na<sub>2</sub>HPO<sub>4</sub>.12H<sub>2</sub>O and 0.41 g KH<sub>2</sub>PO<sub>4</sub>) and Glutaraldehyde Solution (12 ml of 25% glutaraldehyde in dH<sub>2</sub>O) were added. The fixative was stored at -20°C (Neinhuis and Edelmann, 1996).

#### **Phosphate-Buffered Saline (PBS, 10×) Solution**

 $10 \times$  PBS solutions is composed of 0.01 g CaCl<sub>2</sub> and 0.01 g MgCl<sub>2</sub> dissolved in 100 ml dH<sub>2</sub>O. The resulting solution was added to a solution containing 8.00 g NaCl, 0.20 g KCl, 1.44 g Na<sub>2</sub>HPO<sub>4</sub> and 0.24 g KH<sub>2</sub>PO<sub>4</sub> dissolved in 1000 ml dH<sub>2</sub>O. The combined solution was adjusted to pH 7.4, mixed well and autoclaved at 121°C for 20 min. The solution was used as a 10× stock (Neinhuis and Edelmann, 1996).

# Paraformaldehyde (PFA) Solution (4%)

PFA Solution is composed of 12 g PFA that was dissolved into 195 ml dH<sub>2</sub>O and heated to 60°C on a hotplate in a fume cupboard and 2 M NaOH was added until the solution became transparent. The solution was removed from the hotplate and 99 ml of 3x PBS solution was added and allowed to cool to room temperature. The pH was adjusted to

7.2 and the solution was filter sterilised. The PFA solution must be used within 24 hr or stored at -20°C in small aliquots (Neinhuis and Edelmann, 1996).

# Saline-EDTA Solution

Saline-EDTA Solution is composed of 10 mM EDTA (VWR International Ltd., Lutterworth, Leicestershire, UK) and 150 mM NaCl dissolved in dH<sub>2</sub>O. The pH of the solution was adjusted to 8.0, then autoclaved at 121°C for 20 min.

# **Selenite-Tungstate Solution**

Selenite-Tungstate solution is composed of 12.5 mM NaOH, 0.01 mM Na<sub>2</sub>SeO<sub>3</sub>·5H<sub>2</sub>O and 0.01 mM Na<sub>2</sub>WO<sub>4</sub>·2H<sub>2</sub>O dissolved in dH<sub>2</sub>O. The mixture was autoclaved at 121°C for 20 min (Tschech and Pfennig, 1984).

#### Sodium Dodecyl Sulphate (SDS) Solution (20% w/v)

SDS solution is composed of 200 g of SDS dissolved in 1.0 L of  $dH_2O$ . The pH of the solution was adjusted to 7.2, then filter sterilised into a sterile Schott bottle.

# **Substrate Solutions**

For carbon source utilisation experiments, 20% (w/v) stocks were made for 31 sugar substrates. Soluble sugars were made up in 20 ml of dH<sub>2</sub>O in N<sub>2</sub> filled Schott bottles by adding 4 g of each sugar substrate, dissolving, then autoclaving at 121°C for 20 min. The sugar substrates used were as follows: amygdalin, arabinose, cellobiose, cellulose, dextrin, esculin, fructose, galactose, glucose, glycerol, glycogen, myo-inositol, inulin, lactose, maltose, mannitol, mannose, melezitose, melibiose, pectin, raffinose, rhamnose, ribose, rutin, salicin, sorbitol, starch, sucrose, trehalose, xylan and xylose. The solutions were stored in the dark at room temperature until use (Leedle and Hespell, 1980).

#### Tris-Acetate-EDTA (TAE) Buffer (50× Stock solution)

TAE buffer (50×) is composed of 950 mM acetic acid (VWR International Ltd., Lutterworth, Leicestershire, UK), 50 mM EDTA and 2 M Trizma base (Invitrogen, Carlsbad, CA, USA) dissolved in dH<sub>2</sub>O. The pH was adjusted to 8.0 before autoclaving at 121°C for 20 min. A working solution (1×) was made by diluting the stock solution 1:50 in dH<sub>2</sub>O.

#### Tris-Borate-EDTA (TBE) Buffer (5× stock solution)

TBE buffer (5×) is composed of 445 mM  $B(OH)_3$  (VWR International Ltd., Lutterworth, Leicestershire, U.K), 10 mMEDTA and 445 mM Trizma base dissolved in dH<sub>2</sub>O and autoclaved at 121°C for 20 min. A working solution (0.5×) was made by diluting the stock solution 1:10 in dH<sub>2</sub>O.

# **Tris-EDTA (TE) Buffers**

Three types of TE buffer were used: TE buffer 10/0.1 (10 mM Trizma base and 0.1 mM EDTA), TE buffer 10/1 (10 mM Trizma base and 1 mM EDTA) and TE buffer 10/100 (10 mM Trizma base and 0.1 M EDTA). The buffer components were dissolved in  $dH_2O$  and the pH was adjusted to 8.0 before autoclaving at 121°C for 20 min.

#### **Tris-EDTA-Sucrose (TES) Buffer**

TES buffer is composed of 1 mM EDTA, 250 mM sucrose and 10 mM Trizma base dissolved in dH<sub>2</sub>O. The pH was adjusted to 7.5 before autoclaving at 121°C for 20 min.

#### Volatile Fatty Acid (VFA) Solution

VFA Solution is composed of 114 mM butyric acid, 28 mM *iso*-butyric acid, 24 mM *iso*-valeric acid, 24 mM *n*-valeric acid (all supplied by Sigma-Aldrich), 24 mM *D*,*L*-2methyl butyric acid, 202 mM propionic acid (both supplied by MERCK, Darmstadt, Germany) and 710 mM acetic acid in dH<sub>2</sub>O. The pH was adjusted to 7.5 with 1 M NaOH and the mixture was stored at -20°C (Attwood *et al.*, 1998).

#### Wash Solution for Pulse-Field Gel-Electrophoresis

Wash Solution for PFGE was composed of 2 M NaCl and 20 mM Trizma base dissolved in dH<sub>2</sub>O. The pH was adjusted to 7.6 with 6 M HCl then the solution was autoclaved at 121°C for 20 min.

#### 2.1.3 Media and media components

# **Rumen Fluid**

Rumen fluid was collected from rumen-cannulated cattle that had been fasted for 14-18 hr. The rumen contents were squeezed through 2 layers of cheesecloth and the liquid was collected and centrifuged twice at  $20,000 \times g$ , with the pelleted microbial and plant material being discarded each time. The resulting liquid was stored frozen at -20°C until required (Kenters *et al.*, 2010).

# **Clarified Rumen Fluid**

Frozen rumen fluid was thawed and centrifuged at  $20,000 \times g$  at 4°C for 15 min. The decanted liquid was bubbled with N<sub>2</sub> for 10 min, then autoclaved under N<sub>2</sub> at 121°C for 15 min (to inactivate viruses, etc) in serum vials closed with a butyl rubber stopper and crimp-sealed. The autoclaved liquid was allowed to cool and with stirring, 1.63 g of MgCl<sub>2</sub>·6H<sub>2</sub>O and 1.18 g of CaCl<sub>2</sub>·2H<sub>2</sub>O per 100 ml of rumen fluid was added. A heavy precipitate formed which was removed by centrifugation at 30,000×g at 4°C for 60 min. The resulting supernatant was collected and represents the Clarified Rumen Fluid (Kenters *et al.*, 2010).

# Cellobiose–Xylose–Arabinose–Lactate-Casamino acids–Peptone-Yeast extract-Rumen Fluid-Vitamins (GenRFV)

GenRFV is composed of the components listed in Table 2.2 added to 100 ml of Clarified Rumen Fluid.

Table 2.2.	GenRFV	components.
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Chemical	Volume
D-glucose	0.36 g
D-cellobiose	0.34 g
D-xylose	0.30 g
L-arabinose	0.30 g
Na L-lactate syrup	0.88 ml
Casamino acids	2 g
Bacto-Peptone	2 g
Yeast extract	2 g

The mixture was stirred and N<sub>2</sub> gas was bubbled through the mixture for 15 min. The mixture was transferred to a N<sub>2</sub>-flushed, sterile, serum vial through a 0.2  $\mu$ m pore size filter using a syringe and needle. For each 100 ml of GenRFV, 2ml of Vitamin Solution was added via syringe and needle. To achieve the final desired substrate and growth factor concentrations, 0.5 ml of GenRFV was added per 9.5 ml of medium. The final concentrations of each GenRFV component in the media were as follows: 5% (v/v) rumen fluid, 0.5 mM cellobiose, 1 mM each of glucose, xylose, and arabinose, 5 mM lactate, 4 mM each of Ca<sup>2+</sup> and Mg<sup>2+</sup>, and 1 g each of casamino acids, Bacto-Peptone, and yeast extract per L (Kenters *et al.*, 2010).

# No Substrate-Rumen Fluid-Vitamins (NoSubRFV)

NoSubRFV was prepared by adding 2 g of yeast extract to 100 ml of Clarified Rumen Fluid and bubbling with N<sub>2</sub> gas for 15 min. The mixture was transferred to a N<sub>2</sub>-flushed, sterile, serum vial through a 0.2  $\mu$ m pore size filter using a syringe and needle. Two ml of Vitamin Solution was added per 100 ml of mixture. To achieve final concentrations of 5% (v/v) rumen fluid, 4 mM each of Ca<sup>2+</sup> and Mg<sup>2+</sup>, and 1 g of yeast extract per litre, 0.5 ml of NoSubRFV was added to 9.5 ml of medium (Kenters *et al.*, 2010).

#### **Trace Element Solution**

The components listed in Table 2.3 were added and the solution was mixed well. The nitrilotriacetic acid was dissolved in  $dH_2O$  and the pH was adjusted to 6.5 using 1 M KOH before adding to the remaining solution. The mixture was autoclaved at 121°C for 20 min and stored at 4°C (Widdel *et al.*, 1983).

Chemical	Concentration
KAl(SO <sub>4</sub> ) <sub>2</sub> .12H <sub>2</sub> O	42 µM
$B(OH)_3$	162 μM
CaCl <sub>2</sub> .2H <sub>2</sub> O	680 µM
CoSO <sub>4</sub> .7H <sub>2</sub> O	640 μM
CuSO <sub>4</sub> .5H <sub>2</sub> O	40 µM
FeSO <sub>4</sub> .7H <sub>2</sub> O	360 µM
MnSO <sub>4</sub> .2H <sub>2</sub> O	2.24 mM
MgSO <sub>4</sub> .7H <sub>2</sub> O	12 mM
NaCl	17 mM
NiCl <sub>2.</sub> 6H <sub>2</sub> O	100 μM
Nitrilotriacetic acid	8 mM
Na <sub>2</sub> MoO <sub>4</sub> .2H <sub>2</sub> O	40 µM
Na <sub>2</sub> SeO <sub>3</sub> .5H <sub>2</sub> O	1 μM
ZnSO <sub>4</sub> .7H <sub>2</sub> O	625 µM

Table 2.3. Trace Element Solution components.

### Vitamin Solution

To make Vitamin Solution,  $dH_2O$  was boiled and allowed to cool to room temperature under O<sub>2</sub>-free CO<sub>2</sub>. All the components listed in Table 2.4 were added and O<sub>2</sub>-free CO<sub>2</sub> was allowed to bubble through the solution for a further 20 min before the solution was filter sterilised into Hungate tubes in 10 ml aliquots. The tubes were wrapped in aluminum foil to protect against light and stored either at -20°C, or kept at 4°C as working stocks (Kenters *et al.*, 2010).

Chemical	Concentration
Biotin	8 μΜ
D-Ca-pantothenate	23 µM
Folic acid	4.5 µM
Lipoic acid	24 µM
Nicotinic acid	40 µM
p-Aminobenzoic acid	36 µM
Pyridoxine-HCl	50 µM
Riboflavin	13 µM
Thiamine-HCl dihydrate	15 μM
Vitamin B <sub>12</sub>	75 nM

Table 2.4. Vitamin Solution components.

#### Basal Medium plus Yeast Extract (BY) Medium

BY Medium was prepared from the ingredients listed in Table 2.5 as follows: All components, except L-Cysteine-HCl and Vitamin Solution, were dissolved in 1 L of dH<sub>2</sub>O, and boiled to remove dissolved O<sub>2</sub>. The Vitamin Solution, NoSubRFV or GenRFV containing the Clarified Rumen Fluid were injected into each Hungate tube just prior to use. Resazurin was used to indicate that the solution was anoxic as it changed colour from red to colourless. The boiled colourless solution was allowed to cool on ice to approximately room temperature, while gassing with O<sub>2</sub>-free CO<sub>2</sub>. L-Cysteine-HCl was added and the resulting solution was distributed in 9.5 ml aliquots into CO<sub>2</sub>-flushed 10 ml Hungate tubes. The tubes were sealed and autoclaved at 121°C for 20 min (Leedle and Hespell, 1980).

Table 2.5. BY Medium components.

Medium component	Volume/1 L
NaCl	1 g
KH <sub>2</sub> PO <sub>4</sub>	0.5 g
$(NH_4)_2SO_4$	250 mg
CaCl.2H <sub>2</sub> O	130 mg
MgSO <sub>4</sub> .7H <sub>2</sub> O	200 mg
K <sub>2</sub> HPO <sub>4</sub>	1 g
Clarified Rumen Fluid	300 ml
dH <sub>2</sub> O	360 ml
NaHCO <sub>3</sub>	5 g
Resazurin (0.1%, w/v)	10 drops
L-cysteine-HCl	500 mg
Bacto Yeast extract	1 g
Trace Element Solution	1 ml

# RM02 Medium

RM02 medium was prepared as for BY Medium, but using the components listed in Table 2.6 (Kenters *et al.*, 2010).

Table 2.6.	RM02 Medium components.
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Medium component	Volume/ L
dH <sub>2</sub> O	950 ml
$(NH_4)_2SO_4$	0.6 g
$K_2HPO_4$	1.4 g
L-Cysteine-HCl	0.5 g
KCl	1.5 g
Resazurin (0.1% solution)	4 drops
NaHCO <sub>3</sub>	4.2 g
Selenite-Tungstate Solution	1 ml
Trace Element Solution	1 ml
Vitamin Solution	1%

# 2.1.4 Enzymes, Buffers and Reaction Conditions

# **DNA Degradase**

DNA Degradase (Zymo Research Corporation, Irvine, CA, USA) for degradation of DNA to deoxynucleotide monophosphates was supplied in a 10 U/ $\mu$ L stock solution that was prepared by dissolving 3  $\mu$ l of DNA Degradase in 7.5  $\mu$ l of 10× DNA Degradase Reaction Buffer and stored at -20°C.

# Lysozyme

Lysozyme (Boehringer Mannheim GmbH, Mannheim, Germany) was prepared as a 25 mg/ml stock solution by dissolving 125 mg lysozyme in 5 ml TE (10/1) Buffer and stored at -20°C.

# **Proteinase K**

Proteinase K (Roche Diagnostics, Basel, Switzerland) was used from a 10 mg/ml stock solution that was made by dissolving 50 mg of Proteinase K in 5 ml TE (10/1) Buffer and stored at -20°C.

### **Restriction Endonucleases**

All Restriction Endonucleases (REs), their reaction buffers and bovine serum albumin (BSA) were supplied by New England Biolabs, Beverley, MA, USA.

#### **Ribonuclease A (RNaseA)**

RNaseA (Sigma-Aldrich, St. Louis, MO, USA) was prepared as a 10 mg/ml stock solution as follows: 50 mg of RNaseA was combined with 5 ml of 10 mM Tris-HCl buffer. The solution was boiled for 15 min to degrade any contaminating DNase, and then allowed to cool to room temperature and stored at -20°C.

# 2.1.5 General Laboratory Equipment

The centrifuges used in this work are listed in Table 2.7. Centrifuge tubes were supplied in a variety of different capacities as listed in Table 2.8.

Brand	Vessels spun	Max RCF (×g)	Temp Control	Supplier
MiniSpin+	0.6 ml and 1.5 ml Eppendorf tubes	14,100	No	Eppendorf (Hamburg, Germany)
Biofuge Fresco	1.5 ml Eppendorf tubes	16,000	Yes	Heraeus (Hanau, Germany)
IEC Centra	15 ml, 50 ml Falcon tubes	3,500	Yes	Thermo Fisher Scientific, Inc. (Waltham, MA, USA)
Sorvall Evolution RC	50 ml Oakridge tubes, <sup>*</sup> 250 ml tubes	48,000 (SS34) 27,500 (GSA)	Yes	Thermo Fisher Scientific, Inc. (Waltham, MA, USA)

Table 2.7. Centrifuge specifications and suppliers.

Table 2.8. Centrifuge tubes and suppliers.

Brand	Capacity	Supplier
Eppendorf tubes	0.6 ml, 1.5 ml	Eppendorf (Hamburg, Germany)
Falcon tubes	15 ml,50 ml	Becton, Dickinson & Co. (Sparks, MD, USA)
Oakridge tubes	50 ml	Thermo Fisher Scientific, Inc. (Waltham, MA, USA)
Wide-mouth centrifuge bottles	250 ml	Nalgene (Rochester, NY, USA)

The Pulse-Field Gel-Electrophoresis (PFGE) unit used was a CHEF-DR® III system powered by a Powerpac Basic (Bio-Rad, Hercules, CA, USA). Electroporation was carried out using a Gene Pulser<sup>TM</sup> system (Bio-Rad, Hercules, CA, USA). Gas chromatography (GC) was carried out using an Aerograph 660 (Wilkens Instruments & Research, Inc., Walnut Creek, CA, USA). The gel tanks used for conventional agarose gel electrophoresis were a wide Mini-sub® cell GT and for PFGE, a CHEF electrophoresis cell was used (both supplied by Bio-Rad, Hercules, CA, USA). DNA gels (both conventional agarose and pulsed-field gels) were digitally photographed and analysed using a Gel Logic 200 Imaging System (Eastman Kodak Company, Rochester, NY, USA). An Olympus Vanox AHBT3 (Olympus America Inc., Center Valley, PA, USA) was used for light microscopy. The Polymerase Chain Reactions (PCRs) were carried out in a Px2 Thermal Cycler (ThermoHybaid, Sedanstr, Germany). The pH meter used to measure and adjust the pH of solutions and buffers was a PHM62 pH meter (Radiometer, Copenhagen, Sweden). Nitrogen and carbon dioxide gases were supplied at food grade while hydrogen was supplied either as a pure gas or an 80:20 (v/v) mixture with  $CO_2$  (BOC, Auckland, NZ).

# **Gel Migration Size Standards**

The Gel Migration Standards used in this thesis are listed in Table 2.9.

Table 2.9. Gel Migration Size Standards.

Standard	Range	Use <sup>*</sup>	Supplier
1 Kb+	100 bp – 12 Kb	GE	Invitrogen (Carlsbad, CA, USA)
Lambda (λ) ladder	48.5 Kb – 727.5 Kb	PFGE	New England Biolabs (Beverley, MA, USA)
Mid range marker I	15 Kb – 242.5 Kb	PFGE	New England Biolabs (Beverley, MA, USA)
Low range marker	2.03 Kb – 194 Kb	PFGE	New England Biolabs (Beverley, MA, USA)

<sup>\*</sup> GE: gel electrophoresis, PFGE: Pulse-field gel-electrophoresis.

# 2.1.6 Software

The software used in this thesis is listed in Table 2.10.

Table 2.10. Software used.

Software	Application	Source	Reference(s)
Artemis (v 7.0)	Genome sequence viewing and analysis	http://www.sanger.ac.uk/Software/Artemis/	(Rutherford et al., 2000)
ClustalW (v 2)	Global sequence alignment Circular and linear interactive genome	ftp://ftp.ebi.ac.uk/pub/software/clustalw2	(Thompson <i>et al.</i> , 1997)
DNAPlotter	visualization tool	http://www.sanger.ac.uk/resources/software/dnaplotter/	(Carver et al., 2009)
EMBOSS	Identification of DNA secondary structures	http://www.interactive- biosoftware.com/embosswin.html	(Rice et al., 2000)
GAMOLA	Automated genome sequence annotation	Supplied by the programmer Eric Altermann	(Altermann and Klaenhammer, 2003)
MEGA4	Sequence alignment and phylogenetic analysis tool	http://www.megasoftware.net/	(Kumar <i>et al.</i> , 2008)
MUMmer 3.0	Large-scale DNA and protein sequence alignment tool	http://mummer.sourceforge.net/	(Delcher et al., 2003)
Newbler (GS De Novo Assembler)	Genome assembly	http://www.454.com/	http://www.454.com/
Staden package (v 1.6.0)	DNA sequence assembly management	http://sourceforge.net/	(Staden et al., 2000)
Vector NTI advance package (v 9)	DNA sequence display and analysis	http://www.invitrogen.com/	(Lu and Moriyama, 2004)

# 2.2 Methods

#### 2.2.1 Bacterial isolate selection

The largest 16S rRNA gene sequence clusters (97% sequence identity) from the AgResearch Capability Fund project containing representative rumen bacterial cultures from the NERF project, were highlighted as the initial candidate cultures for this study. Twenty bacterial isolates, covering five different cluster groups were selected for this study. Among these, 9 isolates were from the *B. fibrisolvens* and *B. hungatei* cluster (Group 383), 9 from two *Pseudobutyrivibrio xylanivorans* cluster (7 from Group 247 and 2 from Group 245), and single isolates from the *Selenomonas ruminantium* cluster (Group 212) and the *Lachnospiraceae* cluster (Group 121).

# 2.2.2 Growth conditions

All Butyrivibrio and Pseudobutyrivibrio species, Selenomonas ruminantium and B. proteoclasticus B316, were cultured anaerobically in RM02 medium at 39°C unless otherwise specified. Where possible, cultures were transferred only for a limited number of sub-cultures before fresh cultures were revived from frozen stocks (-85°C), to avoid in-vitro culture-biased evolution (Papadopoulos et al., 1999). Culture purity was verified via wet mounts and Gram staining. Wet mounts were made by dropping  $\sim 25 \ \mu$ l of the culture onto a slide using a sterile 1 ml syringe and needle. A coverslip was laid across the culture and the resulting slide was subsequently examined using a light microscope under phase contrast illumination. Gram stains were carried out as follows: two drops of culture were applied to the surface of a glass slide and left to air dry next to a Bunsen burner. Once dry, the slide was passed through the flame several times to heat-fix the cells. The slide was stained in succession with Crystal Violet Solution (10% crystal violet (w/v) in ethanol) for 1 min, Iodine Solution (0.3% (w/v) iodine and 0.7% (w/v) potassium iodide in dH<sub>2</sub>O) for 1 min, and in acetone until the slide was decolourised. The slide was counter-stained with Safranine Solution (2.5% safranine (w/v) in ethanol). After each stage of treatment the slides were washed gently with water. After the final staining and wash the slide was blotted dry with tissue paper and examined using a light microscope.

#### **2.2.3** Bacterial growth curves

Fresh overnight bacterial cultures (0.5 ml inoculum) were used to inoculate Hungate tubes containing 9.5 ml of fresh, pre-warmed, RM02 medium, with cellobiose as the substrate and uninoculated RM02 medium as a blank. Optical density (OD) readings were taken using an Ultrospec 1100 Pro spectrophotometer (GE Healthcare, Buckinghamshire, England) at a wave length of 600 nm as previously described (Lambrecht, 1966; Beard *et al.*, 1995). OD<sub>600</sub> readings were measured at regular 2 hr intervals until stationary phase, and the initial reading taken after inoculation subtracted to calculate the change in OD.

#### 2.2.4 16S rRNA gene sequencing

Strains were grown as described in Section 2.2.2 using four 16S universal primers (fD1 al., forward 5'-gagtttgatcMtggctcag-3' (Justé et 2008), rD1 reverse 5'aaggaggtgatccaRccg-3' (Weisburg et al., 1991; Escalante et al., 2001), F1 forward 5'actcctacgggaggcagca-3' (Mrázek and Kopecný, 2001) and R3 reverse 5'ccagggtatctaatcctg-3') (PP and Rees, 1996), DNA was extracted (Section 2.2.13) and PCR products prepared for 16S rRNA sequencing at the Allan Wilson Centre Genome Sequencing Service at Massey University, Palmerston North (Section 2.2.14). The ABI trace files were processed using the Staden package. The ClustalW (Thompson et al., 1997) program was used to align the 16S rRNA sequences and phylogenetic analysis was performed using Molecular Evolutionary Genetics Analysis (MEGA4) software version 4.0 (Tamura et al., 2007).

#### 2.2.5 Carbon source utilisation

To test bacterial carbon source utilisation, fresh overnight cultures were used to inoculate Hungate tubes containing 31 different sugar substrates including seven insoluble polymer sugars (glycogen, pectin, inulin, cellulose, dextrin, starch and xylan).  $OD_{600}$  readings were measured initially after inoculation, and after 24 hr and 72 hr of incubation for soluble substrates (Moon *et al.*, 2008), while growth on insoluble substrates was assessed by microscopic examination and measurement of increased protein after growth.

#### 2.2.6 Culture Storage

Cultures were inoculated and grown overnight in 10 ml Hungate tubes containing 5 ml RM02 medium, 0.5 ml of culture inoculum, 0.5 ml of GenRFV. The cultures were supplemented with 3 ml of Glycerol Solution (40% v/v) then stored at - $85^{\circ}$ C.

# 2.2.7 Percentage Guanine plus Cysteine (%G+C) Content

%G+C content was determined for six bacterial strains as described by Ramsahoye. Genomic DNA of each bacterial strain (3 µg) was digested to deoxynucleotide monophosphates using DNA Degradase, and quantifiedusing a NanoDrop ® ND-1000 (NanoDrop Technologies, Inc., Wilmington, DE, USA). Samples were analysed by reversed-phase high-performance liquid chromatography (HPLC) as follows: Luna 5 µl C8 100A, 150 ×4.6 mm (OOF-4040-EO) column temp 6°C, flow rate 1 min, Solvent A = 50 mM (NH<sub>4</sub>)<sub>2</sub>HPO<sub>4</sub>, pH 4.1, Solvent B = 100% acetonitrile, isocratic solutions (97% Solvent A and 3% Solvent B), injection volume 50 µl, run time was 21 min between injections (Ramsahoye, 2002).

# 2.2.8 Volatile Fatty Acid (VFA) Analysis

To determine the VFA profile of bacterial strains, cultures were grown in RM02 medium supplemented with 0.5 ml GenRFV solution. After growth, cultures were centrifuged at  $10,000 \times g$  for 15 min at 4°C and the supernant was filtered through 0.45 µm polycarbonate filter (Nucleopore Corp., Pleasanton, CA, USA) into autosampler vials. The filtered samples were used immediately for chromatographic analysis (Ehrlich *et al.*, 1981) with the parameters described below: BioRad 2XHPX-87H column, column temperature was 45°C, solvent was 5 mM H<sub>2</sub>SO<sub>4</sub> (isocratic), flow rate was 0.8 ml/min (isocratic), and injection volume was 50 µl loop. The standards used for column calibration were 5 mM glucose, 10 mM succinic acid, 10 mM lactic acid, 20 mM formic acid, 20 mM acetic acid, 15 mM propionic acid, 20 mM ethanol, and 10 mM *n*-butyric acid (Attwood *et al.*, 1998).

# 2.2.9 Adhesion Assays

#### Visualising Bacterial Adherence with DAPI staining

The Adhesion Assay was used to visualise bacterial adherence to the insoluble carbohydrates sisal string (Donaghys, Christchurch, NZ) and ryegrass Neutral Detergent

Fibre (NDF) using Light Microscopy. Four bacterial strains were used as controls: *Fibrobacter succinogenes* HM2, *Ruminococcus flavefaciens* FD1, *Streptococcus bovis* 2B and *B. proteoclasticus* B316. All bacterial isolates (AB2010, MB2003, MA3014, AB3002, MA3010 and MB2006) and controls were grown in both BY and RM02 media using the GenRFV carbohydrate mix, containing either five strands of finely separated sisal or three strands of 10 mm NDF ryegrass fibre. The cultures were incubated overnight at 37°C. After 24 and 48 hr incubation, a few fibres were taken from each of the cultures and placed in 1.5 ml Eppendorf tubes, and fixed by adding 300  $\mu$ l PBS and 900  $\mu$ l of 4% PFA Solution (1:3 ratio of sample: PFA Solution). The samples were fixed for approximately 3-4 hr at 4°C then rinsed with 1 ml PBS.

# Staining

One ml of PBS containing 1 mg of 4', 6-diamidino-2-phenylindole (DAPI) was added to each tube and left to fix for approximately 10 min. Then samples were rinsed with 1 ml of PBS, three times in succession, inverting the fibres and mixing well. A single fibre was removed from each tube, placed on a glass microscope slide surrounded with PBS and a cover slip placed on top. The samples were observed under an Olympus Vanox AHBT3 Light Microscope (Olympus America Inc., Center Valley, PA, USA) using the default DAPI settings to visualise the fluorescent images (Hamada and Fujita, 1983).

#### 2.2.10 Scanning (SEM) and Transmission Electron Microscopy (TEM)

#### Preparation and fixation of NDF samples for SEM imaging

The NDF fraction was produced and prepared for experimental use as outlined by Maynard *et al* (Maynard *et al.*, 1979). Triplicate bacterial samples were grown in 10 ml BY medium (supplemented with 0.2 ml cellobiose 10% w/v) containing a single 10 mm ryegrass NDF strand (Van Soest *et al.*, 1991). Cultures were incubated at 37°C for 24 hr, the broths (along with the NDF strand) emptied into a sterile Petri dish. The NDF strands were separated and washed five times in 50 ml volumes of PBS with sterile forceps. Excess PBS was removed by flicking onto an adsorbent paper towel. The NDF samples from each bacterial strain were then fixed in 3 ml of Karnovsky's Fixative solution for 48 hr.

#### **Biological specimen processing for SEM**

Samples were fixed in TEM primary fixative (3% glutaraldehyde, 2% formaldehyde in 0.1 M Phosphate Buffer pH 7.2) for two days at room temperature. Three washes using PBS Buffer were carried out for 10-15 min each. Samples were dehydrated through a series of ethanol solutions: 25%, 50%, 75%, and 95% for 10-15 min each and  $2\times$  in 100% ethanol for approximately 1 hr. The samples were then Critical Point (CP) dried using liquid CO<sub>2</sub> as the CP fluid. The dried samples were mounted onto an aluminum specimen support stub using double-sided adhesive tape or conductive silver paint, sputter coated with gold, and observed via SEM (Neinhuis and Edelmann, 1996).

#### Negative Stain Method for Biological Specimen Processing for TEM

Triplicate bacterial samples were grown in 10 ml RM02 and BY medium (supplemented with 0.2 ml cellobiose 10% w/v) and incubated at 37°C for 24 hr. A drop of bacterial sample was placed onto a piece of parafilm followed by placement of a Formvar grid (shiny side down) on top of the drop of the sample. After 4 min, the liquid was drained from the grid with the edge of a piece of filter paper. The grid was placed on a drop of 2% phosphotungstic acid stain (or 2% (w/v) uranyl acetate in water for 4 min and drained with filter paper. The grid was allowed to dry, and observed under TEM (Bozzola and Russell, 1999).

#### 2.2.11 Motility Assay

To examine *Butyrivibrio* sp. MB2003 motility, a Motility Agar Stab Test was carried out using *B. proteoclasticus* B316 as a negative control. The motility test used 5 ml of 1% agar poured in a 10 ml Hungate tube and allowed to set. Freshly grown cells were stab-inoculated into the agar using a straightened inoculating pick, about two thirds of the way into the agar, ensuring to make the stab as straight as possible, as it was the amount of growth away from the stab that was to be examined. The cultures were incubated at 37°C for 24 to 48 hr and observed under a light source. Non-motile bacteria only grow where they were inoculated, whereas motile bacteria produce a diffuse or cloudy growth pattern a distance from the stab area (Tittsler and Sandholzer, 1936).

#### 2.2.12 Pulsed-field gel electrophoresis (PFGE)

#### **DNA extraction for PFGE**

To isolate genomic DNA for PFGE cultures were grown to approximately midexponential phase, and then heated to 70°C for 10 min to destroy heat-sensitive nucleases. Cells were transferred to 1.5 ml Eppendorf tubes and harvested by centrifugation at 5,000×g for 5 min. The supernatant was discarded and the harvested cells were subsequently resuspended in 1 ml Wash solution and harvested again by centrifugation at 5,000×g for 5 min. This step was repeated once more to give a total of two washes and cells were then resuspended in 150  $\mu$ l of the Wash Solution. The cell suspension was mixed 1:1 (v/v) with molten 2% Pulsed-Field Certified Low Melt Agarose (Bio-Rad, Hercules, CA, USA) in 125 mM EDTA equilibrated at 50°C. The resulting cell suspension was dispensed into 10-well reusable plug moulds (Bio-Rad, Hercules, CA, USA) and allowed to solidify at room temperature. Once solidified, plugs were transferred to Universal Bottles (up to 4 plugs per Universal) containing 4 ml of EC buffer containing 1 mg/ml lysozyme. Plugs were incubated on an Orbitech XL flask shaker with shaking (Infors HT) for 18-24 hr at 37°C to allow cell lysis to occur. The EC buffer/lysozyme solution was replaced with 4 ml of 0.5 M EDTA-Sarkosyl solution containing 0.5 mg/ml of Proteinase K. Plugs were incubated on the flask shaker for 16-24 hr at 37°C. Fresh EDTA-Sarkosyl/Proteinase K solution was added and the plugs were again incubated on the flask shaker for 16-24 hr at 37°C. The EDTA-Sarkosyl/Proteinase K solution was replaced with TE (10/1) containing 1 mM phenylmethylsulfonylfluoride (PMSF) to eliminate residual Proteinase K activity, and incubated on the flask shaker for 2 hr at 37°C. Plugs were washed once in TE (10/100) and stored at 4°C in the same solution (Yeoman, 2009).

# **Restriction Endonuclease digestion of PFGE gel plugs**

The appropriate gel plugs were cut to ~2.5 mm using a sterile scalpel, carefully transferred to a sterile Eppendorf tube containing 1 ml of TE 10/0.1 and allowed to equilibrate for 1 hr. The TE 10/0.1 buffer was removed, the plug immersed in an excess of the appropriate Restriction Endonuclease (RE) Buffer (and BSA where necessary), and the plug was allowed to equilibriate in this solution for 1 hr. The RE Buffer was removed and a fresh 100  $\mu$ l of the same buffer was added along with 0.2  $\mu$ l of the appropriate 1 U RE. The plug was incubated in this solution at the optimal temperature

of the RE for 16-24 hr. The RE buffer was removed and 500  $\mu$ l of TE 10/100 buffer was added. The plug was kept in this buffer at 4°C until PFGE was performed (Yeoman, 2009).

# PFGE

PGFE was carried out as described by Gardiner (Gardiner, 1991) using a Bio-Rad CHEF-DR® III system (Bio-Rad, Hercules, CA, USA). Pulsed-field Certified Agarose (Bio-Rad, Hercules, CA, USA) was mixed with 0.5x TBE buffer to give a final concentration of 1%. The mixture was boiled to dissolve the agarose and then allowed to cool to 50°C in a waterbath. Gels were cast in either a  $14 \times 13$  cm casting stand with a 1.5 mm thick 10 well comb, or a  $20.25 \times 14$  cm casting stand with a 1.5 mm thick 15 well comb. The gel was allowed to cool to room temperature and solidify. The appropriate agarose plugs were carefully transferred to the wells of the solidified gel. An appropriate DNA size ladder was added to the gel, typically the bordering wells. The plugs were then embedded in the gel with molten 1% Pulsed-field Certified Agarose in  $0.5 \times$  TBE. The gel was transferred to the Chef Electrophoresis cell containing 2 L of  $0.5 \times$  TBE. The TBE within the electrophoresis cell was maintained at 14°C by circulation through a Bio-Rad Model 1000 mini chiller using a variable speed pump set at 95%. The DNA fragments were separated by applying 5.5 volts/cm at 120° angles. Pulse switch times and electrophoretic duration were dependent upon the expected size range of the resulting RE fragments. The gel was stained with 0.5 µg/ml ethidium bromide for 40 min, then washed in water for 10 min and analysed by UV transillumination at  $\lambda$ =590 nm and photographed using a Gel Logic 200 system (Eastman Kodak Company, Rochester, NY, USA).

#### 2.2.13 Butyrivibrio sp. MB2003 Genome Project

# **Strain Information and Growth Conditions**

The strain chosen for whole genome sequencing was *Butyrivibrio* sp. MB2003 which was isolated from the rumen contents of grass-fed cattle (Noel. S *et al.*, Unpublished). The cultures were grown under anaerobic conditions at 39°C in RM02 medium broth supplemented with GenRFV.

#### **DNA extraction**

Genomic DNA was extracted using the method described by Saito and Miura (Saito and Miura, 1963). Briefly, 10 ml cultures were harvested at mid-exponential phase ( $OD_{600}$ = ~0.4) by centrifugation at 5,000×g for 5 min. The cell pellet was resuspended in 500  $\mu$ l Saline-EDTA Solution and harvested by centrifugation at 5000×g for 5 min. The cell pellet was resuspended in 500 µl of Saline-EDTA Solution containing 1 mg/ml lysozyme and 20 µg/ml Ribonuclease A (RNaseA). This solution was incubated for >1 hr at 37°C to allow the lysozyme to facilitate cell lysis, and the RNaseA to subsequently degrade RNA. Sodium dodecyl sulfate (SDS, 27 µl) solution, along with 11 µl of Proteinase K solution was added to give a final concentration of 1% (w/v) and 200 µg/ml respectively. The solution was incubated for 1.5 hr at 60°C to allow the Proteinase K to degrade cellular protein and inactivate nucleases. TE Buffer (10/1) (200 µl) was added and the mixture was extracted with phenol:chloroform. One volume of room temperature, buffer-saturated phenol was added to the DNA extraction and mixed by several inversions before precipitated protein and other organic material was fractionated by centrifugation at 13,000×g for 5 min. The supernatant was carefully transferred to a fresh Eppendorf tube and mixed with an equal volume of phenol:chloform:isoamyl alcohol mixture. The mixture was inverted several times before the phases were separated by centrifugation at 13,000×g for 5 min. The supernatant was transferred to a fresh eppendorf tube and this extraction step was repeated with an equal volume of chloroform to remove residual phenol. The supernatant was transferred to a fresh Eppendorf tube and 0.1 volumes 5 M ammonium acetate and 3 volumes of absolute ethanol were added and mixed. The mixture was left 16-24 hr at -20°C then centrifuged at 16,000×g for 30 min at 4°C. The supernatant was carefully removed using a pipette to avoid disturbing the DNA pellet. The pellet was washed in 200 µl of 70% ethanol and centrifuged again at 16,000×g for 15 min at 4°C. The supernatant was carefully removed using a pipette and allowed to dry at 37°C for 30 min. The DNA pellet was then dissolved in an appropriate volume of either sterile dH<sub>2</sub>O, TE (10/1) or 10 mM Tris-HCl, depending on the subsequent application. DNA concentration and purity was determined by spectrophotometry using the NanoDrop ® ND-1000 (NanoDrop Technologies, Inc., Wilmington, DE, USA). Absorbance readings were determined at  $\lambda$ =230 nm, 260 nm and 280 nm. DNA concentration was determined using the Beer-Lambert equation modified to use an extinction coefficient of 50 ngcm/ml for DNA and 40 ng-cm/ml for RNA (Petersen *et al.*, 2008). The purity of the samples was determined by analysis of the  $A_{260}/A_{280}$  and  $A_{260}/A_{230}$  ratios.

# Genome Sequencing and Assembly

The genome sequence of Butyrivibrio sp. MB2003 was determined using a pyrosequencing approach (Macrogen Corporation, Korea). A genomic DNA (gDNA) sample of high quality, double-stranded, non-degraded and purified by column purification protocols with an A<sub>260</sub>/A<sub>280</sub> ratio of approximately 1.8 was sent for sequencing at Macrogen Corporation, Korea for <sup>1</sup>/<sub>2</sub> plate of titanium paired-end (454 GS FLX-Titanium) pyrosequencing (Kircher and Kelso, 2010). Sequence data was received as a Standard Flowgram Format (SFF) file. Three separate programs were used to determine the baseline information from the SFF file. The SFFtools (www.454.com) program was utilised to generate a multifasta file of all the reads within the SFF input file. To count the number of reads within the newly generated multifasta file the GREP Unix function was used. The INFOSEQ program from the EMBOSS (Rice et al., 2000) package was utilised to analyse the length and distribution of the individual sequence reads. The read length and average %G+C content data for each read were processed and visualised using Microsoft Excel. Genome assembly of the SFF file was performed using the Newbler GS De novo Assembler software (www.454.com). The assembled contig fasta file was analysed using INFOSEQ to generate information regarding contig length and %G+C content, the results were summarised in Microsoft Excel spreadsheets.

### **Sequence Quality Control**

Any contigs within the DNA sequence found to have a %G+C of greater than 43% were removed from the assembled data. The total length and the average %G+C content of the remaining contigs were processed in INFOSEQ and summarised using Microsoft Excel.

# **Sequence Assembly Management**

The assembled sequence data was converted into an experimental (EXP) file format using the Pregap4 program of the Staden package. The EXP files were entered into the Gap4 program of the Staden package for further processing. Gap4 is a graphical interface program that enables visualisation and management of the assembled data.

#### **Contig Scaffolding**

Within Gap4, a list of contigs with their corresponding scaffolds (33 contigs arranged into 8 scaffolds) obtained from the Newbler scaffold file, was created and tabulated using Microsoft Excel. Basic Local Alignment Sequence Tool (BLAST) analysis of 800bp of sequence at each contig end was performed to identify super-scaffolds. The PERL script "get contig ends.pl" was used to extract 800 bp at both ends of each contig and outputted to a multi-FASTA file format. BLASTX compares translational sequence products of the nucleotide query to a protein database (http://www.ncbi.nlm.nih.gov/). The UNIX command below initiates a BLASTX of the modified multifasta file on the AgResearch IMPALA server:

/usr/local/blast/blastall –p blastx –d /data/databases/flatfile/illuminati\_blastdata/nr –i ContigsOfInterest.fasta –o ContigsOfInterest.fasta.nr –v5 –b5 &

The BLAST hits were analysed and the results summarised within Microsoft Excel, the top BLAST hit and corresponding accession number were recorded. BLAST results indicating contaminant contigs were identified and eliminated from the Gap4 database. The BLASTX results also produced information leading to the identification of three potential extrachromosomal elements within the *Butyrivibrio* sp. MB2003 genome. The three contigs were circularised using standard PCRs.

### 2.2.14 Gap Closure

#### **Primer Design**

The primer design function within the Gap4 program was used to design primers for gap closure of the *Butyrivibrio* sp. MB2003 genome project. For regions difficult to sequence, such as ribosomal rRNA operons, repeat regions and regions with possible stable secondary structures, the contigs of interest were visualised using Artemis (Rutherford *et al.*, 2000). BLASTN and BLASTX results for the coding ORFs in that region were examined. The information from the BLAST searches was used to select appropriate regions to allow design of suitable primers. Primers synthesized at 50 nM scale by IDT (Integrated DNA Technologies; http://eu.idtdna.com) were supplied desalted and lysophilized. Primers were reconstituted in sterile dH<sub>2</sub>O water at a concentration of 100  $\mu$ M and stored at -20°C. PCR reactions and subsequent preparations of PCR products were carried out for all gap closing reactions as described in sections below.

# **Polymerase Chain Reactions**

Polymerase Chain Reactions (PCR) were performed in 50  $\mu$ l volumes using a standard PCR protocol. Constituents were added to dH<sub>2</sub>O in a 0.2 ml thin wall PCR tube (Quality Scientific Plastics, Petaluma, CA, USA), in the order listed in Table 2.11, on ice. The solution was mixed using a P200 micropipetter (Thermo Labsystems, Waltham, MA, USA) and a sterile 200  $\mu$ l pipette tip and subsequently transferred to a PX2 Thermal Cycler (Thermo). The reaction was cycled through a 2 min denaturation at 94°C, followed by 35 cycles of:

- 94°C for 30 sec
- 56°C for 30 sec
- 72°C for 2 min

The reaction underwent a 2 min elongation at 72°C and was cooled to 4°C until examined by gel-electrophoresis.

PCR constituents	Amount per 1x Reaction	Final Concentration	
10x PCR Buffer, minus Mg	5 μL	1X	
10 mM dNTP mixture (each)	$4 \mu L$	0.2 mM each	
50 mM MgCl <sub>2</sub>	1.5 μL	1.5 mM	
Primer Mix (20 µm each 5'& 3')	$0.5 \mu\text{L}$ each	0.2 μM each	
Template DNA (diluted)	1 μĹ	(as required)	
Platinum Taq DNA Polymerase	0.2 μL	1.0 unit	
dH <sub>2</sub> O (autoclaved)	40.3 µL	N/A	
Total Volume	50 μL		

# Long Range PCR

Long Range PCR was performed using the Eppendorf Triple Master system (Eppendorf, Hamburg, Germany). The reaction was prepared as described in Table 2.12. The reaction was cycled through a 3 min denaturation at 93°C, followed by 35 cycles of:

- 93°C for 15 sec
- 56°C for 30 sec
- 68°C for 7 min

The reaction was cooled to 4°C until examined by gel-electrophoresis.

Table 2.12Long Range PCR assembly of reagents.

LR PCR constituents	Amount per 1x Reaction	<b>Final Concentration</b>	
10x HiFi PCR Buffer	5 μL	1X	
20 mM dNTP mixture (each)	2 µL	0.2 mM each	
50 mM MgSO <sub>4</sub>	2 µL	2.0 mM	
Primer Mix (20 µm each 5'& 3')	1.0 µL each	0.4 µM each	
Template DNA (diluted)	1 μL	(as required)	
HiFi Platinum Taq (5 units/µL)	0.2 µL	1.0 unit	
dH <sub>2</sub> O (autoclaved)	37.8 μL	N/A	
Total Volume	50 μL		

#### Agarose gel-electrophoresis

Agarose gel-electrophoresis was carried out using Bio-Rad equipment (Bio-Rad, Hercules, CA, USA). Agarose (Invitrogen, Carlsbad, CA, USA) or Low Melt Agarose (Progen, Heidelburg, Germany) was mixed with  $1 \times$  TAE buffer to give a final concentration of 1.5% w/v agarose or 1% w/v Low Melt Agarose, unless otherwise stated. The mixture was boiled to melt the agarose and then allowed to cool to 50°C in a waterbath. Gels were cast in a  $15 \times 10$  cm casting stand with either a 1.5 mm thick 15 well comb, or a 1.5 mm thick 20 well comb. The gel was allowed to cool to room temperature and solidify. The comb was removed and the gel tray was transferred to a wide Mini-sub® cell GT (Bio-Rad) and immersed in 1× TAE buffer. Unless otherwise stated, 9 µl of each PCR-amplified product was dispensed on to a small square of Parafilm M (American National Can, Chicago, IL, USA), combined with 1 µl of 10× BlueJuice<sup>TM</sup> (Invitrogen, Carlsbad, CA, USA) and carefully transferred to a separate well. Also, 8 µl of the 1 Kb+ ladder (Invitrogen, Carlsbad, CA, USA) was added typically to bordering wells. The DNA fragments were separated using a Powerpac Basic applying 80 volts (5  $^{1}/_{3}$  volts/cm) for 60 min. The gel was stained with 0.5 µg/ml ethidium bromide for 40 min, then washed in water for 10 min and analysed by UV transillumination at  $\lambda$ =590 nm and photographed using a Gel Logic 200 system (Eastman Kodak Company, Rochester, NY, USA).

# PCR clean up

DNA fragments resulting from PCR reactions were purified using a QIAquick® PCR purification kit (Qiagen, Hilden, Germany). Binding (PB) Buffer from the kit (5 volumes) were mixed with the product of each PCR reaction and the solution was applied to a QIAquick spin column and subjected to centrifugation for 60 sec at  $13,000 \times g$ . During this process, DNA of 0.1 - 10 Kb binds to the column, while all other constituents of the reaction flow through. The flow through was discarded and 750 µl of Elution (PE) Buffer from the kit was applied to the column and centrifuged for 60 sec at  $13,000 \times g$ . This washing step was repeated once more, discarding the flow–through each time. The column was centrifuged for an additional 1 min at  $13,000 \times g$  to remove any residual PE buffer, and 30 µl of sterile dH<sub>2</sub>O was added to the centre of the QIAquick column and incubated at room temperature for 5 min. The eluate was transferred to a fresh sterile Eppendorf tube by centrifugation at  $13,000 \times g$  for 60 sec.

# **PCR Product Sequencing**

All DNA sequencing reactions of PCR products were conducted by the Allan Wilson Centre Genome Sequencing Service at Massey University, Palmerston North. This service included fluorescent labeling of PCR products using the Big Dye<sup>TM</sup> Terminator (Version 3.1), a Ready Reaction Cycle Sequencing Kit, subsequent removal of unincorporated fluorescent dideoxy NTPs (ddNTPs) by cleanup and precipitation of products and capillary separation on an ABI3730 Genetic Analyzer (Applied Biosystems Inc., Carlsbad, California). Results were received as ABI tracefiles that were analysed using Trev (Ewing *et al.*, 1998; Bonfield *et al.*, 2002), a DNA trace visualization and editing tool from the Staden package.

#### **Gap Closure**

The *Butyrivibrio* sp. MB2003 ABI trace files received from sequencing of the PCR products were entered into the Gap4 database. The ABI files were pre-processed as summarised in Figure 2.1 and the process were repeated until gaps were closed.

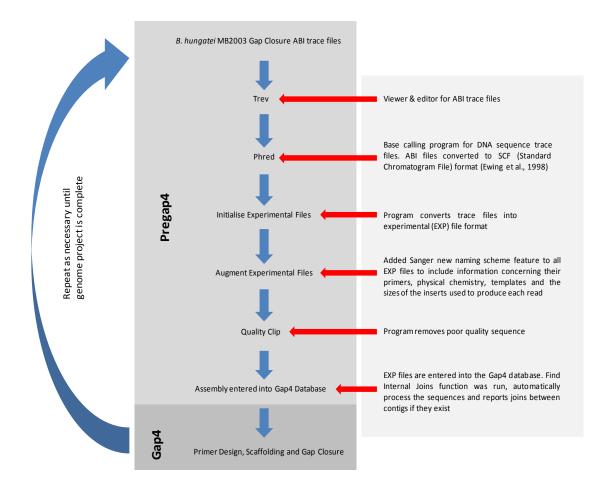


Figure 2.1. Outline of the pre-processing and assembly of the *Butyrivibrio* sp. MB2003 gap closure sequences.

#### 2.2.15 Annotation of the Butyrivibrio sp. MB2003 genome

#### **Gene Prediction**

The GAMOLA (Global Annotation of Multiplexed On-site bLasted DNA-sequences) (Altermann and Klaenhammer, 2003) software was used to predict protein-coding Open Reading Frames (ORFs) and provide an automated annotation of the generated gene model. To determine ORFs present within each input DNA sequence GAMOLA utilises the gene finding programs: GLIMMER3.0 (Gene Locator and Interpolated Markov ModelER) (Delcher et al., 1999), CRITICA (Coding Region Identification Tool Invoking Comparative Analysis) (Badger and Olsen, 1999), and PRODIGAL (Prokaryotic Dynamic Programming Genefinding Algorithm) (Hyatt et al., 2010) to create an additive gene model. Preliminary annotation and functional characterisation of the ORFs in the MB2003 genome were made based on analysis of BLASTP and BLASTX results against the NCBI (National Center for Biotechnology Information) NR (non-redundant) database (Sayers et al., 2011). The search results were presented in a report that places the results with the lowest "e-value" at the top along with their general description, along with the local alignment. The BLAST hit with lowest e-value for a particular sequence was determined as the initial "auto" annotation for that ORF. The HMMER3 program (Release 24) was utilised for Protein Family (PFam) analysis (Eddy, 1998). The InterPro database (2007/2008 release) was also incorporated into the analysis of PFams as an additional source of information regarding PFams, and was also utilised in the analysis of TIGRfams. TIGRfams (Version 9) were used to provide useful information for identifying functionally related proteins based on sequence similarity (Haft et al., 2003). COGs (Clusters of Orthologous Groups of proteins) were used to represent proteins or clusters of genes that correspond to a conserved domain (Tatusov et al., 2000). The Rfam database provides information on the non-coding RNA (ncRNA) elements (Gardner et al., 2009). The INFERNAL (INFERence of RNA Alignment) package was utilised for annotation of Rfams (Version 9.1) (Eddy, 2002). The SignalP database was used to predict presence of signal peptides (including their respective cleavage sites) based on artificial neural networks and HMMs (Dyrløv Bendtsen et al., 2004). The TMHMM database was used to predict and describe transmembrane helices for individual protein domains based on HMMs (Krogh et al., 2001). Upon completion of the annotation process, the Artemis program (Rutherford et

al., 2000) was used to visualise, analyse and interpret the results produced by GAMOLA.

#### **Manual Curation**

After completion of GAMOLA analysis, manual annotation of the predicted ORFs was carried out to verify annotations or make alterations to the start and stop of each predicted Coding Sequence (CDS) if necessary. Each ORF was analysed individually via Artemis and annotated based on the best possible BLASTP hit for that particular sequence, the e-value of the corresponding protein hit, and the e-value of the corresponding PFam result. Significant similarity to a characterised homolog was an alignment with at least 30% amino acid sequence identity and 50% sequence similarity across at least 70% of both ORFs. Another factor in determining correct annotation of a CDS was the associated TIGR domain classification. TIGRFams differ from PFams in that they provide more accurate functional assignments to the genes they describe, whereas PFams use names which represent only a small subset of the functions of the genes which they describe. Ribosomal RNA (rRNA) genes were identified based on their BLASTN analysis and were annotated manually. ORFs smaller than 50 amino acids that lacked a significant match to any previously described gene and gave no trusted hits to known HMMs were eliminated. Putative functions were assigned based upon the bioinformatic analyses and where possible identified by the appropriate Gene Ontologies and/or Enzyme Commission (EC) number(s). ORFs displaying no significant sequence similarity to any previously described gene were annotated as "hypothetical" proteins, whereas those displaying significant sequence similarity to a gene of unknown function were annotated as "conserved hypothetical" proteins. Any alterations to the beginning and/or end of the amino acid sequence for each ORF were made based on sequence data and protein comparisons. Manual annotation was first performed on the three extrachromosomal elements, the chromosome was annotated last. Gap closure continued during the annotation process and currently 7 rounds of gap closure have been completed for this work.

# 2.2.16 Analysis of sequence data

# **MUMmer Plot**

The software MUMmer 3 (Delcher *et al.*, 2003) was used to generate a synteny plot of the *Butyrivibrio* sp. MB2003 chromosome versus the *B. proteoclasticus* B316 chromosome to allow genome wide comparisons to be made. The Gsview (Lang, 2002) program was used to visualise the generated MUMmer plot.

# **Circular Plot**

DNAPlotter (Carver *et al.*, 2009) was used to display the sequence information of the four replicons of *Butyrivibrio* sp. MB2003 as circular plots. The program also illustrates the %G+C content and %GC skew information as part of the circular plot. The resulting images were saved as PostScript format files and visualised using the Gsview program.

# Genes involved in Polysaccharide Breakdown

Comparative analysis of the total number of glycoside hydrolases, polysaccharide lyases, carbohydrate esterases and carbohydrate-binding proteins was performed for *Butyrivibrio* sp. MB2003 and *B. proteoclasticus* B316. The genes encoding polysaccharide degrading enzymes involved in the breakdown of plant cell walls were derived from GAMOLA output and the CAZy (Carbohydrate-Active enZYmes) database (Henrissat. *et al.*, 2011), and were tabulated using Microsoft Excel.

# Chapter 3 Results

# 3.1 Bacterial isolate selection

Prior to the start of this project, work within a NERF program had isolated a range of rumen bacteria from the plant-adherent fraction of rumen contents from pasture-grazed dairy cows (Noel. S *et al.* Unpublished). The relative abundance of these organisms was assessed by comparing their partial 16S rRNA gene sequences (500bp, V1-V3 region) with sequences obtained from high-throughput pyrosequencing of 16S rRNA genes amplified from DNA extracted from rumen contents of pasture-fed dairy cows in a parallel ARC project. The sequences of the freshly isolated bacteria were analysed and clustered into groups within a phylogenetic tree. The phylogenetic tree was composed of 347 OTUs with 3,870 different representative 16S rRNA gene sequences from the V1-V3 region, of which 151 culturable isolates were available for study. The co-clustering of sequences from cultured organisms with large groups of sequences derived directly from rumen contents DNA was used as an indicator of their abundance in the rumen and by inference, their importance in the plant fibre degradation process.

Altogether, 20 isolates covering five large clusters were selected for study. The *B. fibrisolvens/hungatei* family (cluster group 383) contained 9 isolates. The *P. xylanivorans* cluster consisted of two separate groups (247 and 245); the 247 cluster group contained 7 isolates while the 245 cluster group contained 2 isolates. A single isolate associated with the *Selenomonas ruminantium* cluster (cluster group 212) and one isolate clustered with the *Lachnospiraceae* family AB2031 (cluster group 121) were chosen for study, giving a total of 20 candidate isolates for study (Figure 3.1 and Table 3.1).

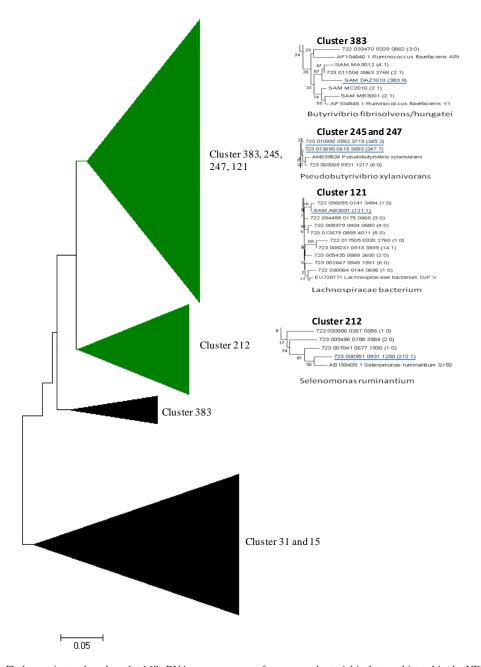


Figure 3.1. Phylogenetic tree based on the 16S rRNA gene sequences from rumen bacterial isolates cultivated in the NERF study, plant-adherent rumen microbial communities isolated in the ARC study, and a selection of reference rumen bacteria. The raw 16S rRNA pyrosequence dataset from the ARC study (V3 region) was pre-processed using the Ribosomal Database Project (RDP) Release 9 pyrosequencing pipeline (Cole et al., 2009), then combined with 16S rRNA sequences (V1-V3 region) from bacterial isolates cultivated in the NERF study (Noel. S et al. Unpublished). In RDP, the sequences were aligned using the Infernal aligner (Nawrocki and Eddy, 2007) and 97% sequence identity clusters were generated using the Complete Linkage Clustering tool, resulting in 306 clusters. A representative sequence from each cluster was selected using the Dereplicate and FASTA sequence selection tools, and aligned with 16S rRNA gene sequences from 54 reference rumen bacterial isolates using the Infernal aligner. The resulting alignment consisted of a total of 360 sequences and 1807 positions. The alignment was imported into MEGA4 (Tamura et al., 2007) for phylogenetic analysis. The phylogeny shown was determined using the Neighbour Joining method (Saitou and Nei, 1987), with evolutionary distances computed using the Kimura 2-parameter method (Kimura, 1980). The sum of branch lengths = 15.6573; the tree is drawn to scale with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. All positions containing alignment gaps and missing data were eliminated only in pairwise sequence comparisons. For simplicity, the four major clades that comprise the tree are represented by triangles, and the locations of the most abundant clusters containing cultivated representatives are indicated to the right of these four clades. The triangles in green represent clades containging the most abundant clusters with cultivated representatives selected for study, the triangles in black represent clades containing other remaining clusters. The subtrees to the right underline the specific cluster groups from which candidate isolates were selected. The first number in brackets corresponds to the number of ARC sequences in the cluster, and the second is the number of cultivated NERF sequences in the cluster. The reference isolate description for each specific cluster group is given below each subtree. \*Isolate codes: The first two letters of the isolate designation correspond to month (May or August), and to cow (cows A, B, C, D, E were located at Lye farm, Dairy NZ, Hamilton). The first number designates the dilution factor of the inoculum for the culture and the remaining 3 numbers indicate the culture number. The DAZ notation refers to a cow located at the AgResearch, Grasslands campus in Palmerston North used in preliminary experiments.

Clusters	Number of sequences in cluster	16S Reference sequence					Isolates*					Total
1	383	Butyrivibrio fibrisolvens/hungatei	AB2010	MB2006	DAZ1011	MA3006	MB2003	DAZ1010	MA2014	MB2014	MB3002	9
2	247	Pseudobutyrivibrio xylanivorans	DAZ1012	MA3010	DAZ2006	DAZ1009	AB2006	MA2017	DAZ1006			7
3	245	Pseudobutyrivibrio xylanivorans	MA2006	MA3014								2
4	212	Selenomonas ruminantium	AB3002									1
5	121	Lachnospiraceae	AB2031									1

Table 3.1. Summary of occurrence of all 20 isolates within large clusters of 16S rRNA gene sequences derived from pasture-fed cows.

Each isolate is grouped according to their closest relative deduced via 16S rRNA sequence. \*Isolate codes: The first two letters of the isolate designation correspond to month (May or August), and to cow (cows A, B, C, D, E were located at Lye farm, Dairy NZ, Hamilton). The first number designates the dilution factor of the inoculum for the culture and the remaining 3 numbers indicate the culture number. The DAZ notation refers to a cow located at the AgResearch, Grasslands campus in Palmerston North used in preliminary experiments.

# 3.2 Characterisation of candidate isolates

Initial characterisation of the 20 original isolates was based on: co-occurrence in large clusters of 16S rRNA gene sequences retrieved from rumen contents, individual 16S rRNA gene sequences and PFGE patterns (Figure 3.2). From these characterisation results, 6 isolates were selected for further phenotypic characterisation.

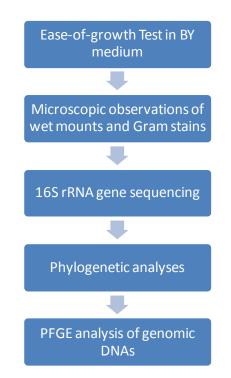


Figure 3.2. Outline of the initial phenotypic characterisation experiments of the 20 original isolates.

The 20 isolates selected for analysis were revived from frozen stocks by inoculating 0.5 ml of the thawed culture into BY medium and incubating overnight at 37°C. Thirteen cultures grew after overnight incubation and displayed similar optical densities. Isolates AB3002, DAZ1009, MA2017 and DAZ1011 formed sediment at the bottom of the tube after overnight growth but, when inverted displayed even turbidity. Isolate MB2003 displayed the best growth after overnight incubation and the culture displayed rope-like consistency once inverted. Isolates AB2031 and DAZ2006 did not grow overnight and were incubated for a longer period. Isolate AB2031 displayed a small amount of growth after two days of incubation while DAZ2006 did not grow in BY medium, after three repetitions of the ease-of-growth test. Thus isolates AB2031 and DAZ2006 were eliminated from further study based on their failure to meet the ease of growth requirement.

# 3.2.1 Microscopic observations of wet mounts and Gram stains

All of the isolates (except DAZ2006) were inoculated onto RM02 medium and incubated overnight at 37°C. Wet mounts were prepared for each isolate and observed using phase contrast microscopy (Table 3.2).

Table 3.2. Microscopic observations of isolates.

Isolate	Cell characteristics			
Isolate	Cen characteristics			
AB2006	medium length rod, slightly curved, mainly form pairs and few long chains	- ve		
AB2010	small length rod, slightly curved, mainly single cells	- ve		
AB2031	medium length rod, slightly curved, mainly form pairs and few clusters	- ve		
AB3002	large length rod, curved, mainly single cells, few pairs	- ve		
DAZ1006	medium length rod, slightly curved, mainly form pairs	- ve		
DAZ1009	medium length rod, slightly curved, mainly single cells, few pairs and few clusters	- ve		
DAZ1010	medium length rod, straight, mainly single cells, some pairs	- ve		
DAZ1011	small length rod, slightly curved, mainly form pairs and few chains	- ve		
DAZ1012	small length rod, slightly curved, predominantly single cells	- ve		
MA2006	medium length rod, slightly curved, mainly form pairs and few large chains	- ve		
MA2014	small length rod, slightly curved, mainly form clusters	+ ve		
MA2017	small length rod, slightly curved, mainly form pairs	- ve		
MA3006	medium length rod, slightly curved, mainly form pairs	- ve		
MA3010	medium length rod, slightly curved, mainly form pairs and few large chains, cocci may also be present possibly contaminated	- ve		
MA3014	small length rod, slightly curved, mainly form large chains and few clusters	- ve		
MB2003	small length rod, curved, mainly forms pairs and few large chains and clusters	- ve		
MB2006	small length rod, slightly curved, mainly form pairs and few chains	- ve		
MB2014	small length rod, slightly curved, mainly form pairs	- ve		
MB3002	medium length rod, slightly curved, mainly single cells, few pairs	- ve		

The samples were very similar in their morphological characteristics and varied only in their size and tendency to form chains, pairs or to exist as single cells. All cultures stained Gram negative, except for MA2014 which stained Gram positive. Overnight cultures in RM02 medium were streaked onto RM02 agar plates and allowed to grow overnight, anaerobically. Individual, well separated colonies were restreaked and checked for purity via microscopic examination. Pure cultures of each isolate were stored at -85°C in 10 ml Hungate tubes containing 5 ml RM02 medium supplemented with 40% v/v glycerol.

#### 3.2.2 16S rRNA gene sequencing

Genomic DNAs were extracted from each of the bacterial isolates and their 16S rRNA genes amplified using 16S rRNA primers (see 2.2.4) and sequenced by the Alan Wilson Centre at Massey University. All isolates produced single, clear PCR product bands when analysed by agarose gel electrophoresis, with concentrations of approximately 40-92 ng/µl. The purified PCR products were sent for 16S rRNA sequencing with four 16S rRNA gene primers (fD1, rD1, F1 and R3) which generate almost full length 16S rRNA gene sequences. The sequence analysis results are shown in Table 3.3. Seventeen of the bacterial isolate sequences matched closely with *Butyrivibrio* or *Pseudobutyrivibrio* 16S rRNA gene sequences. One isolate, AB3002, matched most closely with *Selenomonas ruminantium*. Isolates AB2006 and DAZ1012 produced poor quality sequences from two separate sequencing attempts. Searches with these sequences against both the RDP and BLASTN databases produced inconsistent results, thus isolates AB2006 and DAZ1012 were excluded as candidates for further study.

#### **3.2.3** Phylogenetic analyses

The 16S rRNA sequences of the remaining 16 candidate isolates were aligned using ClustalW and their phylogenetic relationships determined using MEGA4 software and shown as a tree (Figure 3.3). The bottom portion of the tree shows that 9 isolates grouped with the *B. hungatei* species. The isolates MA2006, MA3014, MA3010, and DAZ1009 grouped with the *Pseudobutyrivibrio* sp. and two isolates (MA2017 and DAZ1006) grouped with the *P. ruminis*. Isolate AB3002 clustered close to *Selenomonas ruminantium*.

Table 3.3. RDP and BLASTN search results for 16S rRNA gene sequences of each bacterial isolate.

Isolate	RDP <sup>a</sup>	NCBI nr <sup>b</sup>		
AB2006 (1)	Butyrivibrio fibrisolvens; M55 (0.701)	Butyrivibriofibrisolvens isolate M55 (100%)		
AB2006 (2) (poor)	bacterium YE59 (0.596)	Uncultured bacterium clone SJTU_D_12_11 (100%)		
AB2010	Butyrivibrio fibrisolvens; M55 (0.966)	Butyrivibrio fibrisolvens isolate M55 (99%)		
AB3002	Selenomonas ruminantium; S206; (0.881)	Selenomonas ruminantium strain: S206 (98%)		
DAZ1006	Pseudobutyrivibrio ruminis; pC-XS7; (0.999)	Pseudobutyrivibrio ruminis strain pC-XS7 (100%)		
DAZ1009	Pseudobutyrivibrio ruminis; pC-XS7 (0.949)	Pseudobutyrivibrio ruminis strain pC-XS7 (98%)		
DAZ1010	Butyrivibrio fibrisolvens; M55 (0.968)	Butyrivibrio fibrisolvens isolate M55 (99%)		
DAZ1011	Butyrivibrio fibrisolvens; NCDO 2398 (0.969)	Butyrivibrio fibrisolvens (strain NCDO 2398) (99%)		
DAZ1012 (1) (poor)	Butyrivibrio fibrisolvens; M55 (0.880)	Butyrivibrio fibrisolvens isolate M55 (100%)		
DAZ1012 (2) (poor)	Butyrivibrio fibrisolvens; M55 (0.754)	Butyrivibrio fibrisolvens isolate M55 (98%)		
MA2006	Butyrivibrio fibrisolvens; 1.230 (0.950)	Pseudobutyrivibrio ruminis strain pC-XS7 (98%)		
MA2014	Butyrivibrio fibrisolvens; M55 (0.966)	Butyrivibrio fibrisolvens isolate M55 (99%)		
MA2017	Pseudobutyrivibrio ruminis; pC-XS7 (0.964)	Pseudobutyrivibrio ruminis strain pC-XS7 (99%)		
MA3006	Butyrivibrio fibrisolvens; M55 (0.968)	Butyrivibrio fibrisolvens isolate M55 (99%)		
MA3010	Pseudobutyrivibrio ruminis; pC-XS7 (0.974)	Pseudobutyrivibrio ruminis strain pC-XS7 (99%)		
MA3014	Butyrivibrio fibrisolvens; 1.230 (0.957)	Butyrivibrio fibrisolvens (100%)		
MB2003	Butyrivibrio fibrisolvens; NCDO 2398 (0.895)	Butyrivibriofibrisolvens (strain NCDO 2398) (99%)		
MB2006	Butyrivibrio fibrisolvens; M55 (0.966)	Butyrivibrio fibrisolvens isolate M55 (100%)		
MB2014	Butyrivibrio fibrisolvens; M55 (0.964)	Butyrivibrio fibrisolvens isolate M55 (99%)		
MB3002	Butyrivibrio fibrisolvens; M55 (0.960)	Butyrivibrio fibrisolvens isolate M55 (100%)		

<sup>a</sup>The RDP database was searched using the SEQ MATCH algorithm. Numbers in brackets indicate percentage similarity values. <sup>b</sup>The NCBI nr (http://blast.ncbi.nlm.nih.gov/Blast) database was searched using the BLASTN algorithm. Numbers in brackets indicate % identity.

# 3.2.4 PFGE analysis of genomic DNAs

Pulse-Field Gel Electrophoresis (PFGE) was carried out on restriction enzyme digests of DNAs isolated from 18 isolates (all except DAZ2006 and AB2031) to examine genome differences among the bacterial isolates. Genomic DNAs digested with ApaI (recognition site GGGCC|C) showed that all isolates have different restriction digestion profiles or patterns. Ten samples that had the clearest bands and produced the highest quality PFGE profiles were selected for further study. These 10 isolates were: MA3010, MA3014, DAZ1011, MB2003, MB2014, DAZ1010, AB2010, MB3002, MB2006 and MA2014 (Figure 3.4). The remaining 8 samples produced poor PFGE profiles and were eliminated as candidates for further study after multiple attempts. PFGE plugs of the 10 best samples were run uncut, on a 1% agarose gel to determine if there was evidence of extra chromosomal elements such as plasmids, megaplasmids and secondary chromosomes (Figure 3.5). All samples except MB2014 produced a band near the top of the gel which represents uncut chromosomal DNA. In addition, MB2003 produced two clear bands below the chromosomal band which, possibly represent megaplasmids. MA3010 also produced two additional bands, while MA3014 produced one band. DAZ1011 also produced a single band however the DNA preparation was partially degraded and produced a smeared appearance in the gel.

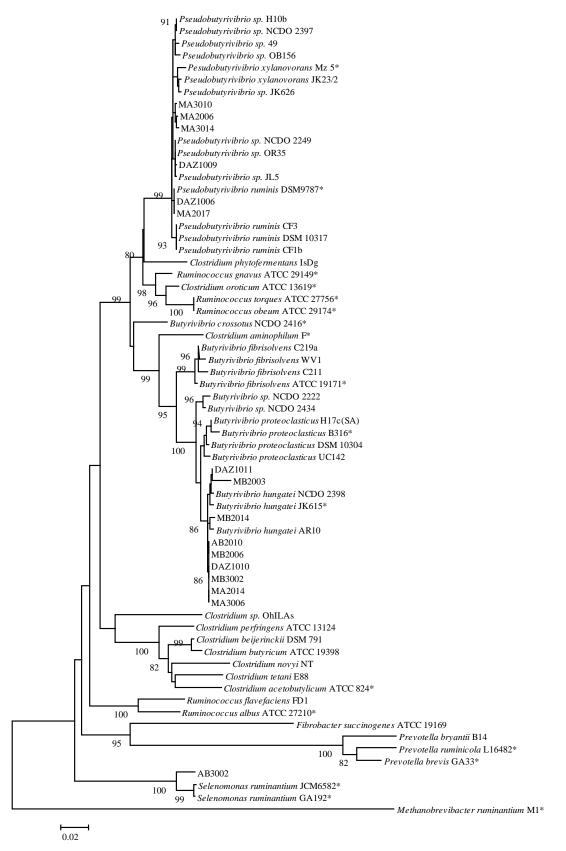


Figure 3.3. Phylogenetic tree based on 16S rRNA sequence data showing the 16 remaining isolates. \*Indicates type strain. 16S rRNA gene phylogeny was inferred using the Neighbor-Joining method (Saitou and Nei, 1987) with distances calculated using the Kimura 2-parameter method (Kimura, 1980) and implemented in MEGA4 (Tamura *et al.*, 2007). *M. ruminantium* M1 was used as an outgroup. Percentage bootstrap values were calculated from 10,000 replicates (Felsenstein, 1985) and are shown at nodes if >80%.

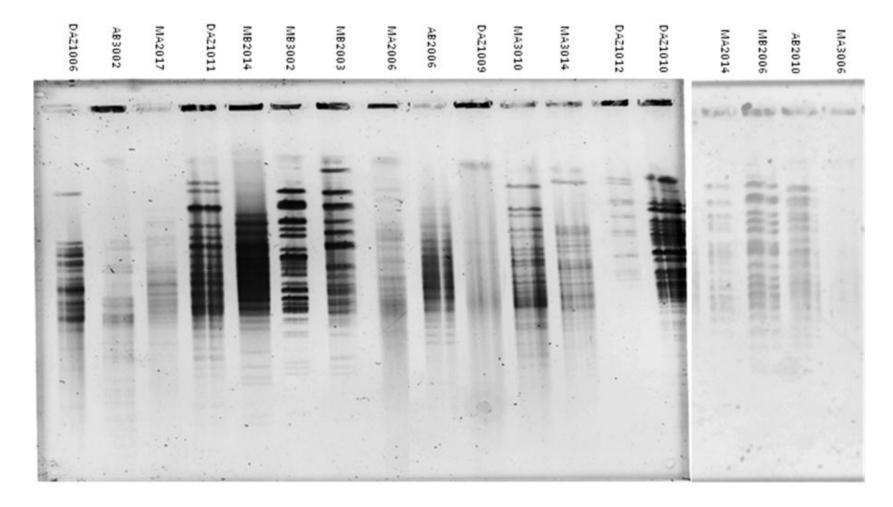


Figure 3.4. 1% Agarose PFGE gels of 18 candidate isolates. DNAs were digested with *Apa*1. The gel was run for 20 hr with the pulse time ramped from 1 to 30 sec.

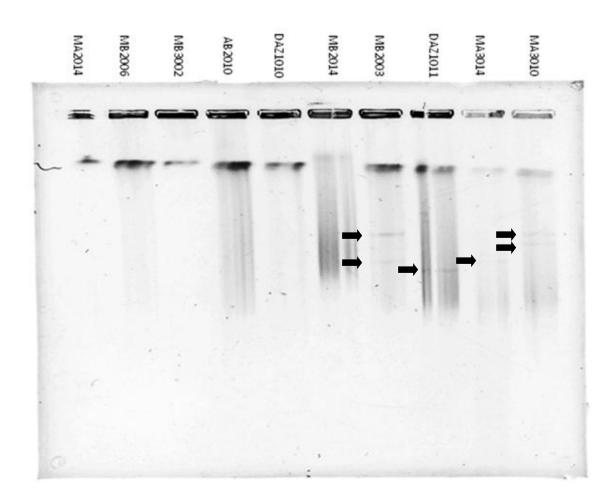


Figure 3.5. 1% Agarose PFGE gel of uncut genomic DNA from 10 selected isolates. The gel was run for 20 hr with the pulse time ramped from 1 to 30 sec. Arrows represent putative megaplasmids.

# **3.3** Final strain selection and phenotypic characterisation

From the original 20 strains, the list of candidate isolates was narrowed down to 6 strains based on; ease of growth, co-occurrence in large clusters of 16S rRNA gene sequences retrieved from rumen contents, individual 16S rRNA gene sequences and PFGE patterns. The isolates selected for further phenotypic characterisation were MB2006, AB2010, MB2003, MA3014, MA3010 and AB3002. Phenotypic characterisation was divided into four main experiments that provided sufficient information to choose two final candidate isolates for whole-genome sequencing.

# 3.3.1 Carbon source utilisation

Experiments were performed to determine carbon-source utilisation for each of the bacterial isolates (Table 3.4). Overall cultures displayed optimal growth on cellobiose and sucrose, and all cultures were able to utilise arabinose, dextrin, glucose, and pectin to achieve some level of growth. Substrates that all cultures could not utilise include: myo-inositol, mannitol and sorbitol.

Substrate	Buty	rivibrio hun	gatei		butyrivibrio nivorans	Selenomonas ruminantium
	AB2010	MB2003	MB2006	MA3010	MA3014	AB3002
Amygdalin	++	+	-	++	++	++
Arabinose	++	++	+	++	+	+
Cellobiose	++	++	++	++	++	++
Dextrin	++*	++*	++*	++*	++*	++*
Fructose	++	-	++	++	++	++
Galactose	+	++	-	++	++	++
Glucose	++	++	++	++	++	++
Glycerol	+	-	-	+	-	+
Glycogen	_*	_*	_*	_*	_*	_*
myo- Inositol	-	-	-	-	-	-
Inulin	+*	++*	++*	++*	++*	++*
Lactose	-	++	-	-	+	++
Maltose	+	++	+	++	++	++
Mannitol	-	-	-	-	-	-
Mannose	-	-	+	+	+	++
Melezitose	+	-	-	+	-	+
Melibiose	+	-	-	++	++	++
Pectin	++*	++*	++*	++*	++*	++*
Raffinose	+	-	-	++	++	++
Rhamnose	+	-	-	+	-	+
Ribose	+	-	-	+	-	+
Salicin	++	++	++	++	++	+
Sorbitol	-	-	-	-	-	-
Starch	++*	+*	+*	+*	++*	++*
Sucrose	++	++	++	++	++	++
Trehalose	++	-	++	-	-	++
Xylan	+	++*	+*	+*	++	++*
Xylose	++	++	++	++	++	+

Table 3.4.	Carbon	source	utilisation	of the	six	candidate isolates.

Positive controls were individual strains grown in RM02 with the GenRFV supplemental mixture. Growth: ++, 0.5-1.0  $\Delta OD_{600}$  reading, +, 0.2-0.5  $\Delta OD_{600}$  reading and -, 0-0.2  $\Delta OD_{600}$  reading. \*Insoluble substrates.

#### 3.3.2 Insoluble substrate utilisation

Several of the substrates commonly utilised by rumen bacteria are insoluble which prevents estimation of their use by measurement of change in optical density. To assess utilisation of the insoluble substrates glycogen, pectin, inulin, cellulose, dextrin, starch and xylan, cultures containing these substrates were assessed for growth using visual and microscopic examination (Table 3.5). Isolates MB2003, MA3014 and AB3002 were able to grow well on xylan, MB2003, MA3014, MA3010, MB2006 and AB3002 were all able to grow on all insoluble substrates except glycogen. AB2010 did not grow in glycogen and displayed poor growth in all other insoluble substrates.

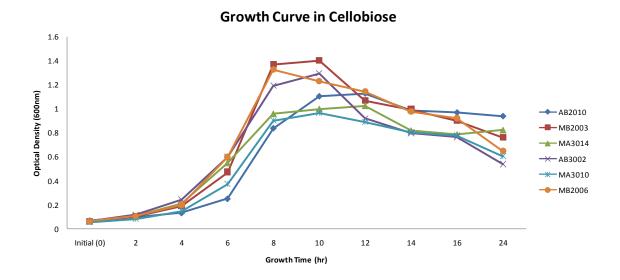
Table 3.5. Wet mount observations of insoluble carbon source utilisation of the six candidate isolates.

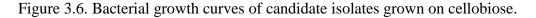
			Isolates ob	servations*		
Substrate	AB2010	MB2003	MA3014	AB3002	MA3010	<b>MB2006</b>
Glycogen	DC, -, P	DC, -, P	DC, -, P	DC, -, P	DC, -, P	DC, -, P
Pectin	+, P	++, P	++, P	++, P	++, P	++, P
Inulin	+, P	++, P	+, P	++, P	++, P	++, P
Cellulose	+, P	+, P	+, P	+, P	+, P	+, P
Dextrin	+, P	++, P	++, P	++, P	+, P	+, P
Starch	+, P	++, P	++, P	++, P	++, P	++, P
Xylan	+, P	++, P	++, P	++, P	+, P	+, P

\*DC, dead cells, (cells appeared shrivelled and disfigured, and showed no movement) -, no growth, +, poor growth, ++, good growth and P, pure culture.

#### **3.3.3** Growth curves for six candidate isolates on optimal substrate (cellobiose)

The carbon-source utilisation experiments indicated that all the bacterial strains grew well on cellobiose. Therefore cellobiose was used as substrate to examine growth of the isolates over a 24 hr period. All six cultures followed very similar growth patterns. The exponential phase of growth for all cultures was between 4 and 8 hr of growth. Maximum cell density for all cultures was reached at 8 to 10 hr. Isolates MB2003, MB2006 and AB3002 displayed the highest maximum ODs among the six cultures. The stationary phase was from 10 to 24 hr (Figure 3.6).





# 3.3.4 VFA analysis

VFA analysis was carried out to determine the fermentation end products of each of the isolates and to help confirm their taxonomic placement (Table 3.6). The *B. hungatei* isolates (MB2003, MB2010 and MB2006) all produced large amounts of formic acid (approximately 15-20 mM), and acetic and *n*-butyric acids both at approximately 5 mM. *P. xylanivorans* isolates (MA3014 and MA3010) produced similar amounts of *n*-butyric acid, less than 5 mM of formic acid, and substantial lactic acid. The characteristic differentiation between *Butyrivibrio* sp. and *Pseudobutyrivibrio* sp. is that *Pseudobutyrivibrio* sp. produce large amounts of lactic acid (approximately 10 mM) as opposed to large amounts of formic acid. The *Selenomonas ruminantium* produced approximately 15 mM of lactic acid and 2 mM of succinic acid, which differ from other two groups and is characteristic for *Selenomonas ruminantium* species (Martin and Dean, 1989).

			VFA concen	tration (mM)		
Isolates	Formic	Acetic	Propionic	n-Butyric	Succinic	Lactic
AB2010	20.9	4.0	0.0	7.0	0.0	0.4
MB2003	16.4	3.6	0.1	4.7	0.0	0.1
MB2006	17.2	3.3	0.0	5.0	0.0	0.5
MA3014	4.3	0.0	0.1	5.4	0.0	8.2
MA3010	2.4	0.0	0.0	5.3	0.0	9.8
AB3002	0.0	0.0	0.0	0.0	2.1	14.6

Table 3.6. VFA analysis for the six candidate isolates. VFA concentrations are expressed as the average of two duplicate cultures.

# 3.3.5 Moles %G+C content

The moles %G+C content of the DNA of each of the isolates was determined to help assign them to a taxonomic group. The %G+C content for five of the six isolates corresponded well to their taxonomic position assigned by 16S rRNA gene sequencing. The *B. hungatei* isolates (MB2003, MB2010 and MB2006) all produced moles % G+C contents of 38-39% which are typical of *Butyrivibrio* species. Isolate MA3014 gave 38% G+C content that is typical of *Pseudobutyrivibrio* species. The AB3002 isolate gave a moles %G+C content of 51% that is consistent with that of *Selenomonas ruminantium* (Table 3.7). However no data could be generated for MA3010 due to sample error.

Table 3.7. Moles %G+C content for the six candidate strains.

Isolate	Moles %G+C
AB2010	$39 \pm 0.04$
MB2003	38±0.06
MB2006	39±0.06
MA3014	38±0.01
MA3010	N/A
AB3002	51±0.02

#### 3.3.6 Adherence

One of the main prerequisites for plant cell wall degradation is that the bacteria physically adhere to the plant material. Two methods of microscopy were used to visualise the adherence of the isolates MB2003 and MA3014 on plant material; observation of bacteria (stained with DAPI under a light microscope) grown with neutral detergent fraction (NDF) or sisal string, and Scanning Electron Microscopy of bacteria adherent to NDF. *B. hungatei* MB2003 displayed good growth in BY media in the presence of NDF (Figure 3.7 A and B) and showed adherence to the ends of the NDF material. There were signs that the NDF plant material had been degraded.

Light microscopy and SEM images of *P. xylanivorans* MA3014 grown in BY media in the presence of NDF (Figure 3.7 C and D, and Figure 3.9) showed that MA3014 adheres to the ends of NDF material, where the disintegration of the structure of the NDF edges was much greater than observed with MB2003. The images indicate degradation of NDF plant material as the MA3014 bacteria have colonised and formed a coat around the isolated piece of NDF resulting in breakdown of the plant material. Figure 3.7 E and F displays *B. proteoclasticus* B316 cultures adhered to the ends of the NDF plant material. The NDF structures appear more intact compared to the MB2003 and MA3014 cultures.

SEM was carried out as outlined in Methods Section 2.2.10. Figure 3.8 A and B show the adherence of MB2003 at the ends of the NDF material. A higher magnification (Figure 3.8 C and D) clearly illustrate observed adherence. The images also show the medium length, and slightly curved rod shape of MB2003 cells.

Compared to the MB2003 cultures, MA3014 appears to grow better in BY media, and attach more prominently at the ends of the NDF fibres (Figure 3.9 A and B). A large amount of material associated with the MA3014 cells can be clearly seen as a stringy dense matrix (Fig 3.9 C and D). The MA3014 cells appear shorter in length, less curved and thicker than the MB2003 cells. No cells were observed attached to the NDF plant material in negative controls.

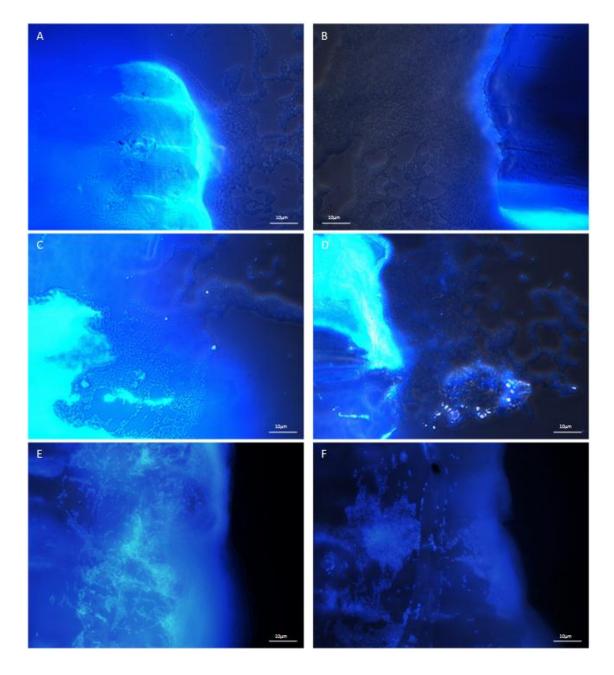


Figure 3.7. Fluorescence microscopy images of DAPI-stained MB2003 (A, B), MA3014 (C, D) and *B. proteoclasticus* B316 (E, F) cultures grown on BY media containing NDF plant material (100× magnification).

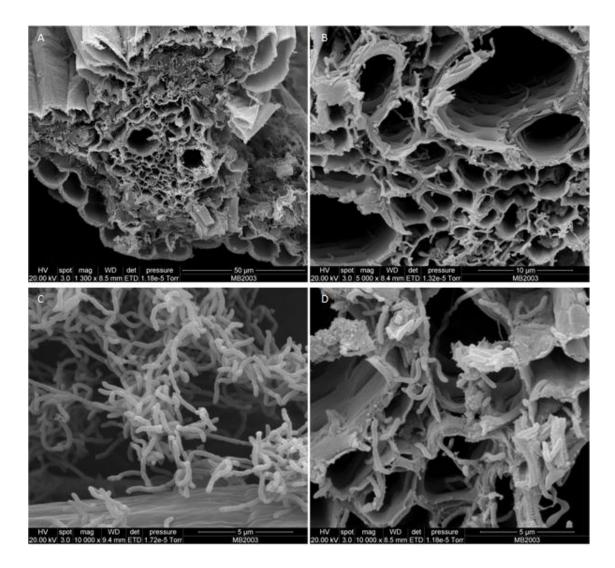


Figure 3.8. Scanning Electron Microscopy images of MB2003 cultures grown on BY media on NDF plant material. A,  $1,300 \times$  magnification, B,  $5,000 \times$  magnification, C and D,  $10,000 \times$  magnification.

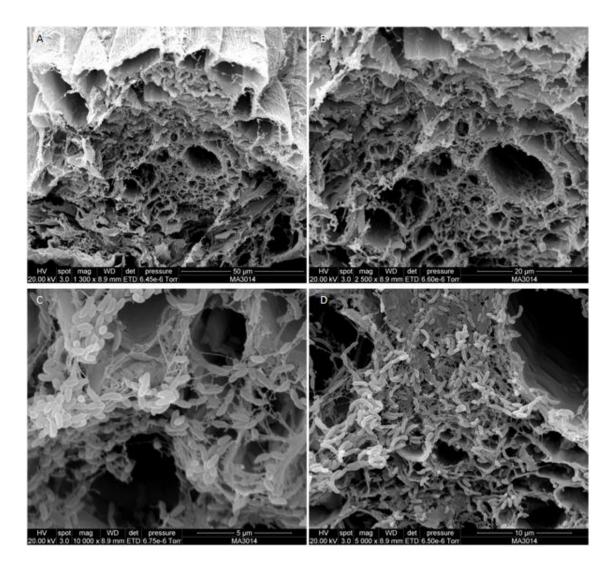


Figure 3.9. Scanning Electron Microscopy images of MA3014 cultures grown on BY media containing NDF plant material. A,  $1,300 \times$  magnification, B,  $2,500 \times$  magnification, C,  $10,000 \times$  magnification and D,  $5,000 \times$  magnification.

# 3.3.7 Taxonomic assignment

Two bacterial strains (MB2003 and MA3014) were selected for genome sequencing based on their phenotypic properties. These strains were identified as *Butyrivibrio hungatei* MB2003 and *Pseudobutyrivibrio xylanivorans* MA3014 by comparison of their properties with the taxonomic descriptions reported by Kopecny *et al.*, (2003).

# 3.4 Whole-genome sequencing of MB2003

Based on the phenotypic characterisation results, MA3014 and MB2003 were selected as the final genome sequencing candidates. Genomic DNA was extracted from both MA3014 and MB2003 as described in Methods Section 2.2.13. DNA purity and quality were checked and organism identities were confirmed by re-sequencing their 16S rRNA genes. High quality gDNA (1 mg) was shipped to Macrogen sequencing facility (Korea) and pyrosequenced using 454 Titanium paired-end sequencing technology. Initial examination of the sequence assembly information indicated that the MB2003 genome was smaller and contained fewer contigs (31 contigs in MB2003 compared to 116 in MA3014) arranged into fewer scaffolds compared to MA3014 (7 scaffolds in MB2003 and 13 in MA3014). Due to time constraints, MB2003 was chosen for further sequence assembly, gap closure and annotation.

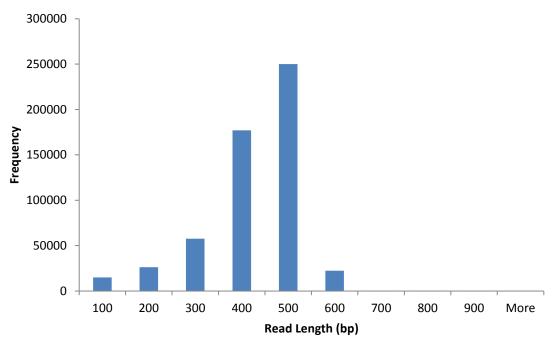
#### **3.4.1** Sequence statistics

The sequence statistics for the <sup>1</sup>/<sub>2</sub> plate of 454 Titanium paired-end sequencing obtained for MB2003 via Macrogen's whole-genome sequencing service are shown in Table 3.8.

Table 3.8. MB2003 sequence statistics.

Sequence characteristic	bp/%G+C
Average read length	377
Min read length	40
Max read length	891
Total number of reads	548373
Total base pairs sequenced	206681869
Ave. %G+C of the reads	39

The read length frequency graph is shown in Figure 3.10. The highest read length frequency was for read lengths of ~500 bp in length. The assembly of the sequence reads (sff file) was carried out in a one-step assembly using Newbler software (GC de novo Assembler). The initial assembly of the MB2003 sequence data resulted in 937 contigs (Table 3.9) which was an unusually high number of contigs. The contigs had an average %G+C content of 55%, while the experimentally determined %G+C content for MB2003 was 38.2%. The assembly results appeared to be inconsistent with a genome of approximately 4 Mb with a 38.2% G+C content, so we investigated the composition of the contigs further.



# **Frequency vs. Read Length**

Figure 3.10. Bar chart of read length frequency for input files for  $\frac{1}{2}$  plate of 454 Titanium paired-end sequencing.

Table 3.9. MB2003 contig statistics.

Contig characteristic	Contig Length (bp)
Sum of contigs	4096761
Min	500
Max	368100
Average %G+C	55
Contig Number	937

A distribution of contig length showed that the vast majority of the 937 contigs were approximately 1000 bp in size (Figure 3.11). Furthermore, Macrogen informed us that there may have been a cross contamination of *Brucella* DNA from their sequencing facility into our samples, which may explain the large amount of small contigs and the unusually high %G+C content of 55%.

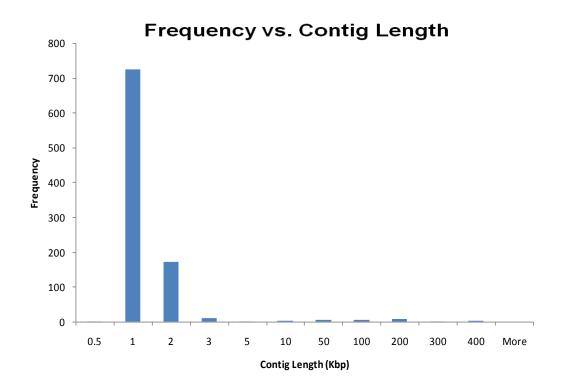


Figure 3.11. Distribution of contig length.

To identify contaminant contigs from the sequence assembly, a three-part analysis procedure was applied to all 937 contigs. Firstly, an arbitrary cut-off of 43% or above %G+C content was made for each contig. This identified 904 contigs (56% average %G+C content and an average size of 814 bp in length) as potential Brucella contig contaminants. Brucella species have %G+C contents ranging from 56 to 58% (Morgan and Corbel, 1976). Secondly, scaffold information obtained from the paired-end sequencing data was used to identify any contigs present in scaffolds. Contigs present in scaffold information are likely to represent the dominant MB2003 assembly. However, four contigs (contig02327, contig02328, contig01185 and 01186) that subsequently were identified as Brucella contamination were present in scaffold 121 and 77, respectively (BLASTX analysis see below). Thirdly, a BLASTX analysis against the NR database was carried out on all contigs to confirm the presence of Brucella sequence. Based on the combined results of the three approaches described above, 904 contigs identified as Brucella contaminated contigs were removed from the raw assembly. This contamination accounted for 734,762 bp in total which represents 17.9% of the original MB2003 sequencing data.

The arrangement of the 31 remaining MB2003 contigs into their appropriate scaffolds was determined by further analysis of the paired-end data information. Contigs were paired with their corresponding scaffolds which resulted in 4 major scaffolds and 3 single scaffolds containing all 31 contigs. These 7 scaffolds were arranged into the predicted order by carrying out BLAST searches of the ends of each of the contigs (800 bp) using the *B. proteoclasticus* B316 genome sequence as the scaffolding template.

By comparing the locus tags from BLAST analyses, the contigs at the ends of the scaffolds could be determined and thus the initial hypothetical order of scaffold arrangement was generated (Table 3.11). The top BLAST results for the ends of contig 00005f and 00005r were for bpr\_III136 and III139 respective locus tags that are present in the *B. proteoclasticus* B316 chromid. The top BLAST hits for the ends of contig 00009f and contig 02243f were for plasmid replication proteins RepB. Thus contigs 00005, 00009 and 02243 appear to represent extrachromosomal elements. Combinations of PCRs were carried out for contigs at the end of each scaffold in order to determine the orientation of each scaffold to each other and also to close sequence gaps. PCR products from the reactions were sequenced and the new sequence added to the contig end. New primers were then designed near the new end of the contigs and the gap closure procedure was repeated.

After seven rounds of gap closure, the MB2003 draft genome contained a main chromosome with 7 gaps remaining, three of which correspond to rRNA regions (Figure 3.11), plus a 91 kb chromid (Bhu II), a small 6.3 kb plasmid (pNP6) and a 144 kb megaplasmid (pNP144). The three extrachromosomal replicons have all been closed and their sequence confirmed using PCRs. Once the genome is closed, an *in silico* restriction enzyme map will be carried out for MB2003 and assembly will be verified by PFGE.

Scaffold Number	Contig Name	Contig Size (bp)	% G+C
scaffold001	contig00005	90577	37.6
scaffold002	contig00007	345280	39.9
scaffold002	contig00008	196580	41.9
scaffold003	contig00009	6344	35.7
scaffold115	contig02243	143881	36.9
scaffold116	contig02282	8953	38.9
scaffold116	contig02283	7091	42.7
scaffold116	contig02284	59856	41.1
scaffold116	contig02285	222644	40.3
scaffold116	contig02286	28584	40.8
scaffold116	contig02287	233430	39.5
scaffold116	contig02288	52481	39.7
scaffold116	contig02289	53306	40
scaffold116	contig02290	30640	40.1
scaffold121	contig02327	1686	53.1
scaffold121	contig02328	1136	50.6
scaffold121	contig02329	124873	40.8
scaffold121	contig02330	184603	39.8
scaffold122	contig02337	139170	39.1
scaffold122	contig02338	1097	40.7
scaffold122	contig02339	9032	39.3
scaffold122	contig02340	182228	38.1
scaffold122	contig02341	24938	38.6
scaffold122	contig02342	71625	38.8
scaffold122	contig02343	130003	39.2
scaffold122	contig02344	86794	39.3
scaffold122	contig02345	35293	40.4
scaffold122	contig02346	23544	39.8
scaffold122	contig02347	366544	39.7
scaffold122	contig02348	368100	39.8
scaffold122	contig02349	125618	40.2

Table 3.10. Arrangement of MB2003 contigs into scaffolds.

Contig Name	Accession	Locus_tag	Top blast Hit	Organism	% ID	E-value Score
contig00005f	YP_003832404.1	bpr_III136	GNAT family acetyltransferase/NUDIX domain- containing protein	Butyrivibrio proteoclasticus B316	100	3.00E-63
contig00005r	YP_003832407.1	bpr_III139	TetR family transcriptional regulator	Butyrivibrioproteoclasticus B316	93	1.00E-96
contig00007r	YP_003829901.1	bpr_I0574	Acetyltransferase	Butyrivibrioproteoclasticus B316	70	4.00E-46
contig00008f	ZP_02073755.1		hypothetical protein CLOL250_00503	Clostridium sp. L2-50	64	5.00E-23
contig00009f	YP_002286760.1		plasmid recombination protein	Butyrivibrio fibrisolvens OB157	41	4.00E-04
contig00009r	AAA23031.1		Replicase	Campylobacter hyointestinalis	34	2.00E-13
contig01185r	ZP_05955688.1		LOW QUALITY PROTEIN: outer membrane autotransporter barrel domain-containing protein	Brucella pinnipedialis B2/94	79	0
contig01186f	ZP_05189756.1		intimin/invasin family protein	Brucella abortus bv. 4 str. 292	100	e-147
contig02243f	YP_003832274.1	bpr_III001	replication initiation protein RepB1	Butyrivibrio proteoclasticus B316	55	1.00E-44
contig02243r	ZP_04455084.1		hypothetical protein GCWU000342_01100	Shuttleworthia satelles DSM 14600	48	6.00E-34
contig02282r	CBK94202.1		Helix-turn-helix.	Eubacterium rectale M104/1	47	7.00E-22
contig02290f	YP_003830557.1	bpr_I1236	hypothetical protein bpr_I1236	Butyrivibrio proteoclasticus B316	55	3.00E-51
contig02327r	ZP_03294132.1		hypothetical protein CLOHIR_02084	Clostridium hiranonis DSM 13275	90	3.00E-53
contig02330f	ZP_03801676.1		hypothetical protein COPCOM_03977	Coprococcus comes ATCC 27758	73	1.00E-04
contig02337r	YP_003830558.1	bpr_I1237	chemotaxis protein CheW	Butyrivibrio proteoclasticus B316	97	e-101
contig02349f	no hit					

Table 3.11. Summary of BLASTX search results of contig ends (800bp) for MB2003 genome. Red indicates contaminant contigs.

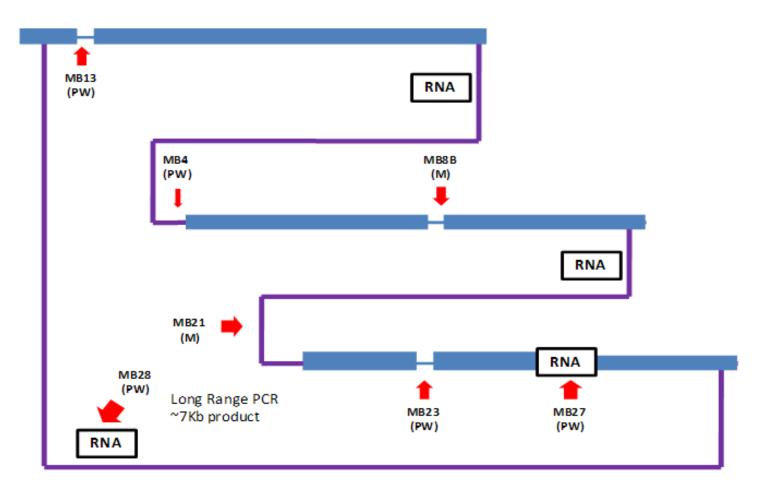


Figure 3.12. Diagrammatic representation of the MB2003 draft genome. Seven rounds of gap closure were completed for the MB2003 chromosome resulting in 1 super-scaffold representing 7 contigs and 7 gaps remaining to close. The total chromosome size is 3,129,625bp and total chromosome %G+C content is 39.86% (based on GAMOLA analysis). The blue boxes represent the contigs of the MB2003 chromosome. The purple lines show where the contigs are predicted to be attached to each other (not to scale). The RNA boxes indicate the positions of rRNA regions. The red arrows and associated MB labels indicate the positions of the gaps that are still to be closed, where PW indicates primer walking and M indicates that new primers need to be designed for these gap regions.

# 3.5 Comparison of the MB2003 genome to *B. proteoclasticus* B316

# 3.5.1 MUMmer plot

A MUMmer plot was used to align the incomplete draft MB2003 chromosome with the B316 complete chromosome. MUMmer is a whole genome alignment program that compares the genome of one organism with another by generating an alignment of their genomes in the form of a dot plot diagram. The plots reveal regions of conservation between the two genomes under comparison.

In a MUMmer plot the reference genome is plotted along the x-axis (in this case *B. proteoclasticus* B316) and the query genome is on the y-axis (MB2003 draft genome). Wherever the two sequences match a coloured dot is plotted on the chart, the forward matches are displayed in red and the reverse matches are displayed in blue. A straight line of dots starting from bottom left to the top right means that the two regions are exactly identical. The B316 vs MB2003 genome plot shows the presence of dots (blue and red combined) on a diagonal indicating that the two genomes contain many similar sequences and thus their genomes share many similar genes.

The plot also showed an X-shaped pattern known as an X-alignment (Figure 3.13). This X-shape is symmetrical about the putative origin of replication of the MB2003 and *B. proteoclasticus* B316 genomes and indicates that matching sequences tend to occur at the same distance from the origin/terminus of replication but not necessarily on the same side of the origin.

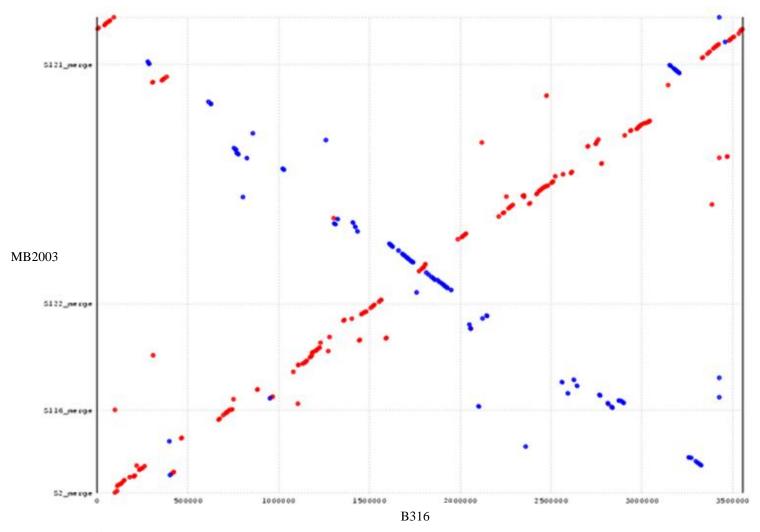


Figure 3.13. MUMmer plot of versus *B. proteoclasticus* B316 chromosomes.

# 3.6 Multi-replicon genome architecture

The draft *B. hungatei* MB2003 genome is currently in four replicons: the chromosome, chromid (Bhu II), megaplasmid (pNP144) and a small plasmid (pNP6). A comparison with *B. proteoclasticus* B316 and the draft MA3014 genome are shown in Table 3.12. The %G+C content for all four MB2003 replicons is similar, and is similar to the %G+C content of the *B. proteoclasticus* B316 replicons and the draft MA3014 genome. In total the MB2003 genome is more than 1 Mbp smaller than *B. proteoclasticus* B316, chromosome 400,000 bp smaller, the chromid is approximately 200,000 bp smaller and the megaplasmids and plasmid are both smaller in size.

Genome	Status	Organization	Contig No.	Size (bp)	GC %
Butyrivibrio proteoclasticus B316	Complete	Chromosome	1	3,554,804	40
		Chromid	1	302,358	40
		Megaplasmid	1	361,399	39
		Megaplasmid	1	186,325	38
				4,404,886	
Butyrivibrio hungatei MB2003	Draft	Chromosome	7	3,137,803	40
		Chromid	1	91,836	38
		Megaplasmid	1	143,881	37
		Plasmid	1	6,344	36
				3,374,113	
Pseudobutyrivibrio sp. MA3014	Draft	Nd	116	3,458,205	39

Table 3.12. Structure of *Butyrivibrio* and *Pseudobutyrivibrio* genomes.

# 3.7 Butyrivibrio hungatei MB2003 genome annotation

Genome annotation was carried out as described in Methods Section 2.2.15. The draft *B. hungatei* MB2003 genome was run through GAMOLA, where autoannotation was carried out for all 2,982 genes in the four replicons.

### 3.7.1 MB2003 Chromid Bhu II

A chromid is an extrachromosomal element containing essential genes (Harrison *et al.*, 2010). *B. proteoclasticus* B316 was found to contain a single chromid but in general these elements are rare in Gram positive bacteria. The MB2003 chromid is the third largest replicon in this bacterium at 91,836 bp and 38% G+C content (Figure 3.14 and Table 3.13). The total coding percentage for the megaplasmid is 88% with 88 predicted genes in total. The chromid has the only copies of genes involved in fatty acid biosynthesis that are theoretically essential to the growth and survival of MB2003. The MB2003 chromid also contains four genes involved in carbohydrate degradation including a  $\beta$ -galactosidase (Bga42A), a  $\beta$ -glucosidase (Bgl3A), a feruloyl esterase (Est1A) and a polysaccharide deacetylase (Est4A). A full list of genes from the chromid is shown in Appendix I (Table A1).

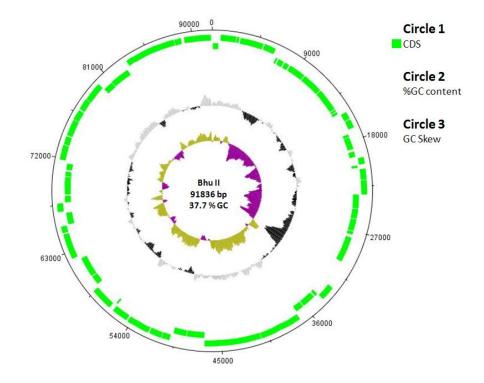


Figure 3.14. Circular plot of the MB2003 Bhu II chromid. The green colour coding of the genomic features in circle 1 represent Coding Sequence (CDS), %G+C content is shown in circle 2 and GC skew in circle 3.

Table 3.13. Sequence information of the MB2003 Bhu II chromid.

Total coding (bps)	80909
Total (bps)	91836
Coding %	88
Total number of genes	88

### 3.7.2 MB2003 Plasmid pNP6

The MB2003 pNP6 plasmid is the smallest of the four replicons at 6,344 bp and has a G+C content of 36% (Figure 3.15 and Table 3.14). The plasmid encodes only five genes, all of which appear to be involved in plasmid replication. pNP6 does not encode any genes involved in polysaccharide degradation. A full list of genes from the plasmid is shown in Appendix I (Table A2).

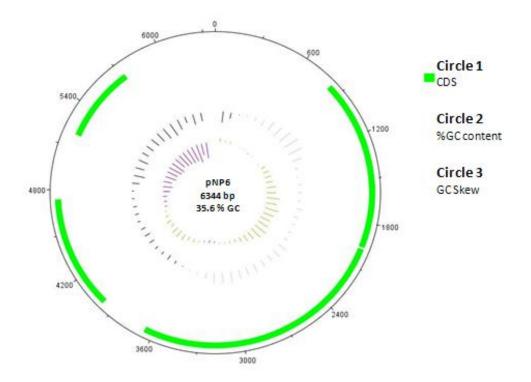


Figure 3.15. Circular plot of the MB2003 pNP6 plasmid. The green colour coding of the genomic features in circle 1 represent Coding Sequence (CDS), %G+C content is shown in circle 2 and GC skew in circle 3.

Table 3.14. Sequence information of the MB2003 pNP6 plasmid.

Total coding (bps)	4135
Total (bps)	6344
Coding %	65
Total number of genes	5

# 3.7.3 MB2003 Megaplasmid pNP144

The pNP144 megaplasmid is the second largest replicon at 143,881 bp and has a %G+C content of 37% (Figure 3.16 and Table 3.15). The total coding percentage for the megaplasmid is 80% with 154 predicted genes in total. Approximately 120 pNP144 genes encode hypothetical proteins and have no assigned function. None of the pNP144 genes are predicted to be involved in lignocellulose degradation. A full list of genes from the megaplasmid is shown in Appendix I (Table A3).

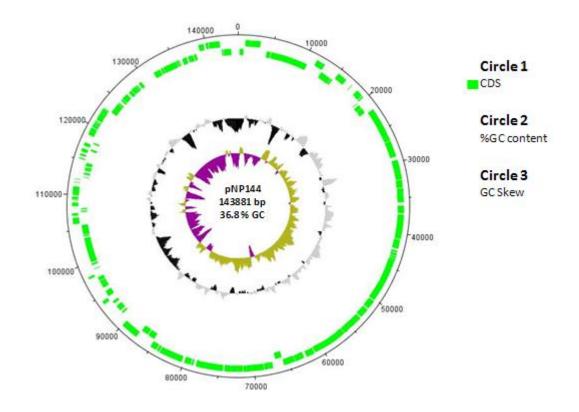


Figure 3.16. Circular plot of the MB2003 pNP144 megaplasmid. The green colour coding of the genomic features in circle 1 represent Coding Sequence (CDS), %G+C content is shown in circle 2 and GC skew in circle 3.

Table 3.15. Sequence information of the MB2003 pNP144 megaplasmid.

Total coding (bps)	116441
Total (bps)	144530
Coding %	80
Total number of genes	154

### 3.7.4 MB2003 Chromosome

The chromosome is the largest of the four replicons in the MB2003 genome with a provisional size of 3,137,803 bp and a %G+C content of 40%. The draft chromosome encodes a total of 2,735 genes and it is currently made up of 7 contigs arranged into 1 scaffold (Figure 3.17 and Table 3.16). All genes on the chromosome have been manually annotated and a full list of genes is shown in Appendix I (Table A4).

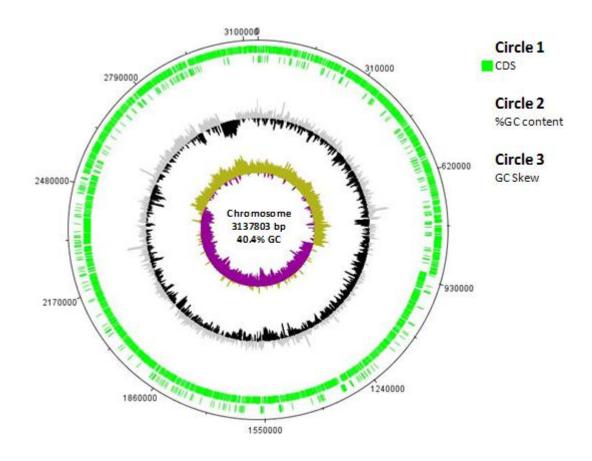


Figure 3.17. Circular plot of the draft MB2003 chromosome. The green colour coding of the genomic features in circle 1 represent Coding Sequence (CDS), %G+C content is shown in circle 2 and GC skew in circle 3.

Table 3.16. Sequence information of the MB2003chromosome.

Total coding (bps)	2750638
Total (bps)	3137803
Coding %	88
Total number of genes	2735

# 3.8 Genes involved in polysaccharide breakdown

The main aim of sequencing the MB2003 genome was to identify genes involved in the breakdown of plant cell walls. Therefore the Carbohydrate-Active enZYmes (CAZy) database was used to identify glycoside hydrolases, glycosyl transferases, polysaccharide lyases, carbohydrate esterases and carbohydrate-binding protein families within the MB2003 glycobiome. The genes involved in polysaccharide breakdown are summarised in Table 3.17. A total of 90 genes were identified that encode either secreted or intracellular proteins that are involved in the breakdown of polysaccharides.

Proteins		Predicted Catalytic Domain*			
	GH	CE	PL	CBP	
Predicted Secreted	16	2	-	1	
Predicted Intracellular	60	10	1	-	
Total	76	12	1	1	

Table 3.17. MB2003 genes predicted to encode secreted or intracellular proteins involved in polysaccharide breakdown.

\*GH, glycoside hydrolase, CE, carbohydrate esterase, PL, polysaccharide lyase and CBP, carbohydrate binding protein.

A comparison of the secreted and intracellular polysaccharide degrading genes of MB2003 with those from *B. proteoclasticus* B316 was made and is summarised in Table 3.18 and Table 3.19. Out of the 19 secreted genes in MB2003 involved in polysaccharide degradation, only two, lysozyme Lyc25B and feruloyl esterase Est1A, do not have a corresponding match with a gene in B316. These two secreted proteins are encoded by the MB2003 chromid (Bhu II).

The intracellular proteins involved in polysaccharide degradation predicted from the MB2003 genome were compared with homologues in the *B. proteoclasticus* B316 genome (Table 3.19). The majority (59) of MB2003 genes involved in polysaccharide breakdown excluding glycosyl transferases, had corresponding homologues in *B. proteoclasticus* B316. Three of the genes encoding intracellular proteins were found in the Bhu II chromid: a  $\beta$ -glucosidase (Bgl3A), a  $\beta$ -galactosidase (Bga42A) and a polysaccharide deacetylase (Est4A).

Table 3.18. Secreted polysaccharide degrading genes in MB2003 compared with their homologues in *B. proteoclasticus* B316.

MB2003 gene name	Size (aa)	Catalytic domains	Binding domains	Homologue in B316	% Match id/sim
β-N-acetylhexosaminidase Bhx3A	427	GH3		Bhx3B	48 /64
β-glucosidase Bgl3D	982	GH3	C- terminal TMH	Bgl3D	83 /89
endo-1,4-β-glucanase Cel5C	543	GH5	CBM2a	Cel5C	69 /81
endo-1,4-β-glucanase/xylanase Cel5A	417	GH5		Cel5A	55 /67
endo-1,4-β-xylanase Xyn10B	425	GH10		Xyn10E	68 /77
endo-1,4-β-xylanase Xyn10A	451	GH10		Xyn10A	80 /87
α-amylase Amy13B	536	GH13		Amy13B	58 /71
chitinase Chi18A	567	GH18		Chi18A	72 /82
lysozyme Lyc25A	362	GH25		Lyc25A	71 /84
lysozyme Lyc25B	515	GH25		Lyc25D	70 /83
lysozyme Lyc25C	561	GH25		Lyc25C	66 /79
lysozyme Lyc25D	242	GH25			
glycoside hydrolase family 30 Gh30A	575	GH30		Gh30A	69 /80
xylosidase/arabinofuranosidase Xsa43A	543	GH43	CBM6	Xsa43A	70 /79
arabinogalactan endo-1,4-β- galactosidase Agn53A	439	GH53		Agn53B	60 /74 *
4-α-glucanotransferase Mal77A	506	GH77		Mal77A	80 /88
feruloyl esterase Est1A	351	CE1		Est1C	69 /79
polysaccharide deacetylase Est4C	280	CE4		Est4C	60 /72
carbohydrate binding protein	983		CBM2a (x1), CBM6 (x5)		

\*, not full length, % id, percentage identified amino acids, % sim, percentage similar amino acids with corresponding BLAST scores. Genes in blue are encoded in the chromid (Bhu II).

Table 3.19. Intracellular polysaccharide degrading genes in MB2003 compared with their homologues in *B. proteoclasticus* B316.

	Size	Catalytic	Binding	Homologue	% Match
MB2003 gene name	(aa)	domains	domains	in B316	id/sim
mannasa 6 phasphata isamarasa/glyaasida		GH1,			
mannose 6-phosphate isomerase/glycoside hydrolase family 1 protein	765	PMI			
nyurolase family i protein		typeI			
β-galactosidase Bga2A	1034	GH2		Bga2A	76 /86
β-galactosidase Bga2C	714	GH2			
β-galactosidase Bga2B	825	GH2		Bga2B	70 /83
glycoside hydrolase family 2 Gh2B	641	GH2		Gh2B	77 /88
glycoside hydrolase family 2 Gh2A	912	GH2		Gh2F	48 /63
glycoside hydrolase family GH2C	776	GH2			
β-glucosidase Bgl3A	803	GH3		Bgl3C	57 /71
β-glucosidase Bgl3B	808	GH3		Bgl3E	83 /90
β-glucosidase Bgl3C	671	GH3			
β-xylosidase Xyl3A	707	GH3		Xyl3A	82 /87
reducing end xylose-releasing exo-	383	GH8		Xyn8A	76 /83
oligoxylanase Xyn8A				-	10705
cellodextrinase Cel9B	552	GH9	CelD	Cel9B	72 /83
1,4-α-glucan branching enzyme GlgB2	824	GH13	CBM48	GlgB2	76 /87
	024	01115	(x2)	Gigb2	10/07
1,4-α-glucan branching enzyme GlgB1	663	GH13	CBM48	GlgB1	88 /94
α-amylase Amy13C	434	GH13		Amy13C	88/94
α-amylase Amy13A	697	GH13		Amy13E	70 /82
α-amylase Amy13D	511	GH13		Amy13G	73 /83
glycogen debranching enzyme GlgX1	726	GH13	CBM48	GlgX1	85 /91
glycogen debranching enzyme GlgX2	648	GH13		GlgX2	63 /76
sucrose phosphorylase Suc13P	553	GH13		Suc13P	88 /92
lysozyme Lyc25E	1213	GH25	Big2 (x2)	Lyc25E	54 /66
α-galactosidase Aga27A	577	GH27		Aga27A	65 /77
glycoside hydrolase family 27 Gh27A	442	GH27		Gh27A	73 /85
polygalacturonase Pg128A	531	GH28			
polygalacturonase Pgl28B	519	GH28		Pgl28B	76 /87
α-L-fucosidase Fuc29A	475	GH29		Fuc29A	49 /67
glycoside hydrolase family 31 Gh31A	756	GH31		Gh31A	58 /74
glycoside hydrolase family 31 Gh31C	674	GH31		Gh31C	81 /89
glycoside hydrolase family 31 Gh31B	635	GH31		Gh31D	83 /91
sucrose-6-phosphate hydrolase Scr32A	493	GH32		Scr32A	89 /94
β-galactosidase Bga35A	622	GH35		Bga35A	84 /90
β-galactosidase Bga35B	735	GH35		Bga35B	64 /76
α-galactosidase Aga36A	782	GH36		Aga36A	72 /82
α-galactosidase Aga36B	620	GH36		Aga36B	54 /71
α-galactosidase Aga36C	730	GH36		Aga36C	73 /85
α-mannosidase Man38A	1053	GH38		Man38A	55 /68
β-galactosidase Bga42A	673	GH42			
xylosidase/arabinofuranosidase Xsa43B	301	GH43		Xsa43I	45 /63
xylosidase/arabinofuranosidase Xsa43C	302	GH43			
xylosidase/arabinofuranosidase Xsa43D	517	GH43		Xsa43D	55 /69

xylosidase/arabinofuranosidase Xsa43E	352	GH43			
xylosidase/arabinofuranosidase Xsa43G	312	GH43		Xsa43G	85 /91
xylosidase/arabinofuranosidase and esterase Xsa43F	925	GH43, CE10		Xsa43H	72 /80
$\alpha$ -L-arabinofuranosidase Arf51C	630	GH51	CBM9		
$\alpha$ -L-arabinofuranosidase Arf51A	502	GH51	CBM_X	Arf51A	56 /72
$\alpha$ -L-arabinofuranosidase Arf51B	502 504	GH51	CDINI_II	Arf51B	87 /92
$\alpha$ -D-glucuronidase Agu67A	662	GH67		Agu67A	70 /79
unsaturated glucuronyl hydrolase Ugl88A	385	GH88		Ugl88A	64 /76
unsaturated glucuronyl hydrolase Ugl88B	383	GH88		Ugl88B	43 /60
cellobiose phosphorylase Cbp94A	814	GH94		Cbp94A	89 /94
glycoside hydrolase family 95 Gh95A	734	GH95		Gh95A	43 /58
unsaturated rhamnogalacturonyl hydrolase					
Gh105A	349	GH105		Gh105A	93 /97
unsaturated rhamnogalacturonyl hydrolase Gh105B	363	GH105		Gh105C	77 /85
				lacto-N-	
1. A. N. L'AND LAND AND AND A	700	CU1112		biose	70 /07
lacto-N-biose phosphorylase	722	GH112		phosphoryla	78 /87
				se	
α-glucuronidase Gh115A	947	GH115		Gh115A	72 /85
xylosidase Xyl120A	861	GH120		Gh120A	72 /81
xylosidase Xyl120B	664	GH120		Gh120B	57 /70
glycoside hydrolase	340	GH		NC	
glycoside hydrolase	389	GH		NC	
feruloyl esterase Est1B	243	CE1		Est1E	53 /71
acetyl-xylan esterase Est2A	372	CE2		Est2A	68 /79
polysaccharide deacetylase Est4A	207	CE4			
polysaccharide deacetylase Est4D	274	CE4		Est4D	70 /86
polysaccharide deacetylase Est4B	244	CE4		Est4E	57 /77
N-acetylglucosamine-6-phosphate	371	CE9		NagA	50 /68
deacetylase NagA				-	50700
acetyl-xylan esterase Est10A	275	CE10		Est10A	66 /79
carbohydrate esterase family 12 Est12A	584	CE12		Est12A	52 /66
carbohydrate esterase family 12 Est12B	244	CE12			
polysaccharide lyase Pl11A	746	PL11			
glycogen phosphorylase GlgP1	769	GT35		GlgP	92 /96
glycogen phosphorylase GlgP2	824	GT35		GlgP2	87 /93
acetyl-xylan esterase	626			acetyl-xylan	58 /73
	-			esterase	

\*, not full length, % id, percentage identified amino acids, % sim, percentage similar amino acids with corresponding BLAST scores, NC, not classified. Genes in blue are encoded in the chromid (Bhu II).

# 3.9 Xylan degradation in MB2003

MB2003 is able to grow on xylan and the genome encodes numerous enzymes predicted to be involved in this process. These include endo-1, 4- $\beta$ -xylanases (GH5 and GH10), xylosidases (GH3, GH8, GH30, GH43 and GH120), arabinofuranosidases (GH43 and GH51),  $\alpha$ -glucuronidases (GH67 and GH115), feruloyl esterases (CE1) and acetyl xylan esterases (CE2, CE4 and CE10) (Figure 3.18). As yet, no functional data is available for any of these enzymes, however comparisons can be made with the *B. proteoclasticus* B316 genome. Microarray analysis of *B. proteoclasticus* B316 (Kong, 2007) showed that two clusters of genes were significantly upregulated in cells grown on wheat arabinoxylan. These gene clusters were designated polysaccharide utilisation loci (PUL). Figure 3.19 shows that a very similar gene arrangement occurs in MB2003.

However, the MB2003 genes form a single PUL, containing genes predicted to have xylanase, xylosidase, xylosidase/arabinofuranosidase,  $\alpha$ -glucuronidase and acetyl-xylan esterase activity. In *B. proteoclasticus* B316 a gene encoding a secreted feruloyl esterase is also present (Est1C). The equivalent gene is missing from this location in MB2003 but a close match (Est1A) is found on the chromid (Bhu II). Est1A is the only feruloyl esterase predicted to be secreted by MB2003. Also located in the MB2003 PUL is a gene encoding xylose isomerase (ORF530) which catalyses the first step in intracellular xylose metabolism via the pentose phosphate pathway.

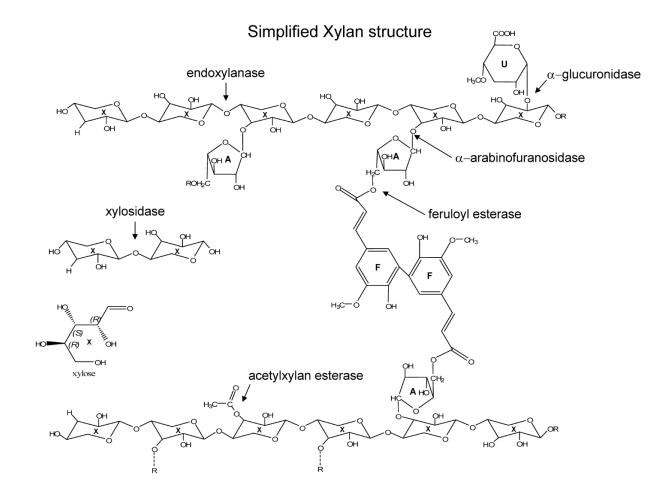
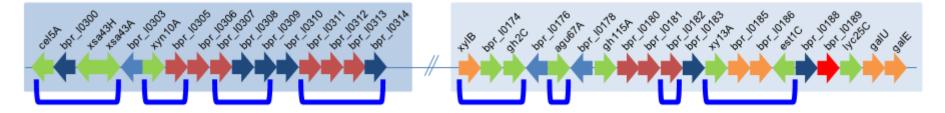


Figure 3.18. Diagrammatic representation of xylan, showing linkages attacked by hemicellulose-degrading enzymes. A, arabinose; F, ferulic acid; U, 4-*O*-methylglucuronic acid; X, xylose; R, continuation of glycan chain. Modified image from Chesson and Forsberg (1997).

Butyrivibrio proteoclasticus B316



Butyrivibrio sp. MB2003

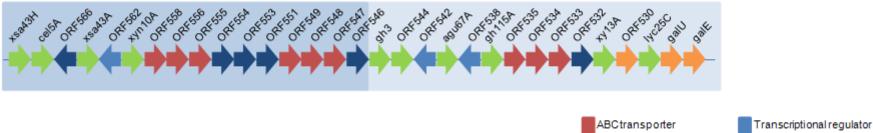




Figure 3.19. Comparison of PUL in B. hungatei MB2003 and B. proteoclasticus B316.

#### 3.10 Motility

Upon completion of annotation and analysis of the MB2003 genome, several genes were uncovered that were thought to encode flagella. To investigate the possibility of the presence of functional flagella in MB2003, a simple motility assay was carried out. Soft agar medium was stabbed with cultures and observed after overnight inoculation at 37°C. The motility assay revealed that *B. hungatei* MB2003 and *B. proteoclasticus* B316 (described previously as non-motile (Attwood et al., 1996)) were non-motile whereas the *P. xylanovorans* MA3014 displayed a motile phenotype (Figure 3.20 A).

The performance of a bacterium in a motility assay does not however imply the absence of a flagellum, as it is known that *B. proteoclasticus* B316 contains a flagellum but is non-motile. Thus an analysis of the region encoding the flagella genes and the order of these genes for all three cultures was carried out. The chromosomal region starting at *flg*E and ending with *mot*B genes revealed that the size of the *flg*E gene is the same for MB2003 and B316 but much smaller in MA3014, and that two extra genes were present in MB2003 (Ion channel and *flb*D) and B316 (*est*1B and *flb*D) but were absent in the MA3014 genome (Figure 3.20 B). The *flb*D genes are the same size in both MB2003 and B316 and the *est*1B and Ion channel genes are also approximately the same size in their respective genomes. The *mot*A and *mot*B genes are present in all three chromosomes and are approximately the same in size and do not appear to differ from one another. The MA3014 flagellar biosynthetic loci appear uninterrupted whereas in *B. hungatei* MB2003 and *B. proteoclasticus* B316 they appear to have insertions in flagella genes that might result in impaired motility.

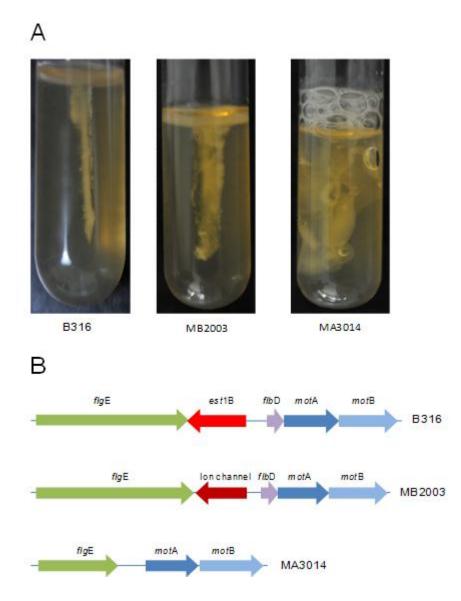


Figure 3.20. Motility assays and flagella biosynthesis operons in MB2003, MA3014 and B316. A, Motility assay; B, Genes encoded in the flagella biosynthesis operon.

# 3.11 Transmission Electron Microscopy (TEM)

To look for flagella, TEM was carried out on B. hungatei MB2003, B. proteoclasticus B316 and P. xylanivorans MA3014. All cultures were grown in RM02 and BY media overnight at 37°C with the GenRFV supplement, and electron microscopy grids were prepared as outlined in the Methods Section 2.2.10. Images in Figure 3.21 A and B show MB2003 cells in RM02 medium. In Figure 3.21 A there appears to be a long flagellum protruding from the middle of the bottom cell that stretches out and past the upper cell. This particular image is one of few found to contain such a structure; the majority of TEM images of MB2003 cells did not contain any apparent surface structures (Figure 3.21 B). There were no flagella detected on any of the MA3014 cells observed. Most MA3014 cells appeared shriveled and dehydrated (Figure 3.21 C). An interesting observation was the presence of unusual structures on the surface of some MA3014 cells (Figure 3.21 D). From a previous study, B316 have been shown to possess a single flagellum but they are non-motile. When grown in RM02 the B316 bacteria did not contain a single flagellum and appeared shriveled and dehydrated. However the RM02 media does not contain many of the substrates that encourage optimal growth for ruminant bacteria and thus the same TEM protocol was carried out on the three cultures grown in BY media.

The TEM images for all three cultures grown in BY media produced the same results as in the RM02 medium (Figure 3.22). The morphology of all three different bacteria was identical to those in RM02 and the MA3014 displayed inclusion bodies on the surface of the cells (Figure 3.22 D). There were no signs of flagella on any cell in any of the three cultures. The background staining on the TEM images was due to the negative stain binding to all of the molecules in the substrate rich BY media. All of the samples prepared for TEM imaging in both RM02 and BY were not centrifuged or had any kind of modification done to improve the quality of the image. Thus more work needs to be done with TEM imaging to completely rule out the possibility of visualising flagella in these particular cultures.

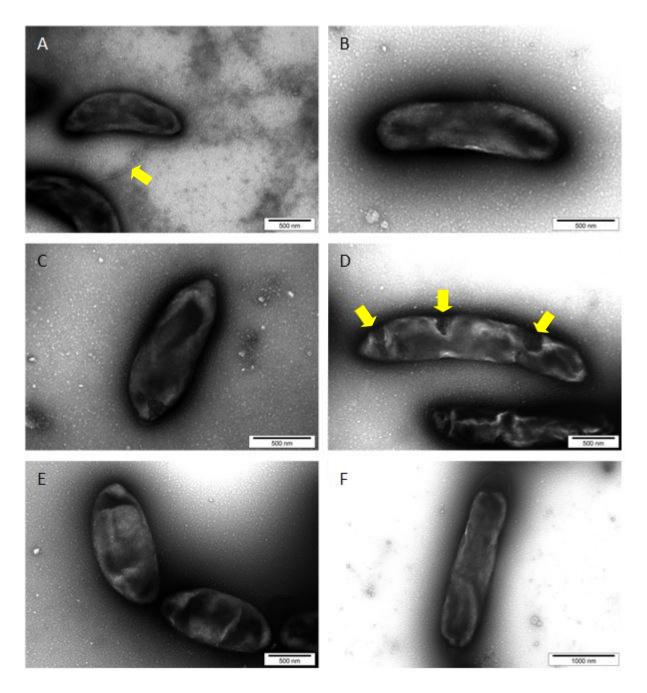


Figure 3.21. Transmission Electron Microscopy images of MB2003, MA3014 and B316 cells from cultures grown on RM02 media after overnight incubation. A and B, MB2003; C and D, MA3014; E and F, B316.

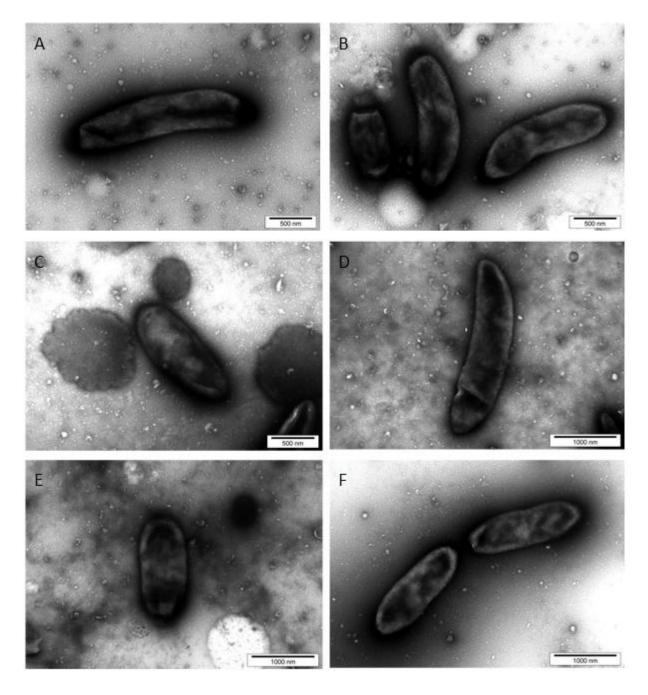


Figure 3.22. Transmission Electron Microscopy images of MB2003, MA3014 and B316 planktonic cells from cultures grown on BY media after overnight incubation. A and B, MB2003; C and D, MA3014; E and F, B316.

# Chapter 4 Discussion

The work described in this thesis forms part of larger ARC and NERF programmes focused on understanding the role of plant adherent bacteria in the breakdown of plant cell wall polysaccharides in the rumen of pasture grazed cattle in New Zealand. These programs include novel cultivation approaches to isolate plant adherent bacteria coupled with metagenomic analyses to assess bacterial diversity, and genomic analysis of individual bacteria which are described here. The aim of this MSc was to select representative plant-adherent bacterial cultures based an analysis of metagenomic 16S rRNA sequence data, to determine their phenotypic and general genomic characteristics and to genome sequence isolates in order to learn more about their lignocellulose degradation systems.

The bacteria that adhere to plant material are thought to be the main fibrolytic bacteria in the rumen (Weimer et al., 1993), with the best studied organisms being Fibrobacter succinogenes, Prevotella sp., Ruminococcus flavefaciens, Ruminococcus albus and Butyrivibrio sp. (Tajima et al., 1999; Russell and Rychlik, 2001; Koike et al., 2003b). However, the rumen harbours a dense bacterial population and the diversity of organisms involved in plant polysaccharide breakdown in the rumen is only now beginning to be revealed. A recent meta-analysis of all the curated 16S rRNA gene (rrn) sequences deposited in the RDP database (Kim et al., 2011), has provided insight into the composition of the rumen bacterial microbiome. A total of 13,478 bacterial sequences of rumen origin were analysed with nineteen bacterial phyla represented. Firmicutes, Bacteroidetes and Proteobacteria were the predominant phyla accounting for 57.8%, 26.7% and 6.9% of the total bacterial sequences, respectively. Approximately 90.6% of the Firmicutes sequences were assigned to class Clostridia (Whitford et al., 1998; Tajima et al., 1999; Tajima et al., 2000), with the largest families (Lachnospiraceae and Ruminococcaceae) accounting for 23.8% and 25.8% of the sequences. The predominant genera were Butyrivibrio, Acetovibrio, Ruminococcus, Succiniclasticum and Pseudobutyrivibrio. An important finding from this study was that a large number of the Firmicutes sequences have not been classified to any existing family, order or genus within the Clostridia class.

Data from the metagenomic analysis of 16S rRNA gene sequences performed in the ARC project showed similar results. The most prevalent organisms in the plant adherent fraction were from the family Lachnospiraceae within the Firmicutes phylum, with

*Butyrivibrio*, and *Pseudobutyrivibrio* the most common genera. Consequently, these bacteria are predicted to be predominant in the rumen and the isolation and classification of novel strains belonging to these groups will greatly improve our knowledge of rumen function and our understanding of plant polysaccharide breakdown within the rumen.

A total of 141 bacterial isolates cultivated through NERF programme (Noel. S et al., Unpublished) had their 16S rRNA genes sequenced and this information was combined with the sequences from the ARC metagenomic project into a single phylogenetic tree. 16S rRNA gene sequences of isolates corresponding to large clusters of gene sequences retrieved directly from rumen contents were selected as cultivated representatives of those clusters. In all, twenty isolates representing 5 major clusters were selected as candidates for genome sequencing. Genomic DNA was extracted from each isolate and used to produce full length 16S rRNA sequences to confirm their original classification. PFGE was performed to determine if there were differences within the cluster representatives at the genome level and to establish whether they contained extra chromosomal elements. Phenotypic characterisation experiments examined carbon source utilisation (both soluble and insoluble substrates), VFA production, and made observations of bacterial adherence to plant material using DAPI staining and SEM. These characterisations led to the description of *B. hungatei* MB2003 and *P.* xylanivorans MA3014 strains and were selected for whole-genome sequencing. Because of time constraints only the MB2003 genome analysis is reported here.

#### 4.1 MB2003 general genome features

The *B. hungatei* MB2003 genome sequence was found to consist of four replicons: a chromosome (currently in 7 contigs arranged into one super scaffold), a chromid (Bhu II), a megaplasmid (pNP144) and a small plasmid (pNP6; Table 3.12). This is very similar genome architecture to the multi-replicon genome of *B. proteoclasticus* B316 (Kelly *et al*, 2010). For many MB2003 genes, the closest homologues were to B316 genes. This is not surprising as B316 is the only other *Butyrivibrio* species genome sequenced. A MUMmer plot comparing the main chromosomes of MB2003 with B316 produced an X-shaped alignment. The most likely explanation for such an X-alignment is inversions of the chromosomes that cause the reversal of genomic sequence symmetry around the origin/terminus of DNA replication.

The main difference between MB2003 and B316 is in the size of the four replicons. The *B. proteoclasticus* B316 genome contains two megaplasmids of 360 Kb and 186 Kb compared to MB2003 which contains only one megaplasmid of 144 Kb. Megaplasmids in *Butyrivibrio* species are predicted to encode genes important for survival in the rumen, but no genes have been identified that contribute to the breakdown of lignocellulose (Yeoman, 2009).

The small MB2003 plasmid, pNP6 is unusual as extrachromosomal DNAs in *Butyrivibrio* are usually large. The pNP6 plasmid appears to encode only genes involved in its own replication and transfer and has no functional role in the degradation of polysaccharides. Its small size opens the possibility of development as a potential vector for *Butyrivibrio* species. First attempts at producing shuttle vectors for *Butyrivibrio* species (Ware *et al.*, 1992; Whitehead, 1992), produced poorly selectable plasmids that had problems with poor transformation efficiency and plasmid stability. Beard *et al.*, (1995) reported the construction of a stable 9.5 Kb shuttle vector, pBHerm, based on the *B. fibrisolvens* plasmid pRJF1 capable of successful transfer, replication and selection in both *E. coli* and *B. fibrisolvens*. The pBHerm system was demonstrated to be a highly stable transformation system and a practical tool for genetic alterations to *Butyrivibrio* species. A study by Gregg *et al.*, (1998) used the pBHerm shuttle vector augmented by the addition of a fluoroacetate dehalogenase gene attached to a copy of the erythromycin-resistance gene promoter to produce a *Butyrivibrio* strain capable of detoxifying fluoroacetate, and demonstrated this with *in vivo* experiments in sheep.

A novel feature of both the MB2003 and *B. proteoclasticus* B316 genomes is the presence of chromids or secondary chromosomes. Chromids are replicons that have %G+C content similar to that of their main chromosome, but have plasmid type maintenance and replication systems, and are smaller than the chromosome but usually larger than any other plasmids present. Chromids contain genes essential for growth and maintenance of the organism along with several core genus-specific genes that can be found on the chromosome in other species of bacteria (Harrison *et al.*, 2010). The Bhu II replicon has most of these characteristics and therefore has been designated as a chromid of MB2003. Since the Bhu II chromid of *B. hungatei* MB2003 is smaller than the BPc2 chromid of B316, it is now the smallest chromid reported for bacteria. The chromid description was developed for replicons found in a wide range of Gram

negative bacteria. The replicons found in *Butyrivibrio* species are smaller in size and warrant further investigation to determine if similar extrachromosomal elements occur in other Gram positive bacteria.

#### 4.2 Polysaccharide Degradation

The ability to adhere to plant material is an essential characteristic for plant polysaccharide degrading bacteria within the rumen. Using light microscopy and SEM, MB2003 was observed to adhere to plant material (Figures 3.7 and 3.8). The mechanisms involved in rumen bacterial adherence to plant material are not fully understood. MB2003 contains genes for flagellum biosynthesis, exopolysaccharide (EPS) production and for a single carbohydrate-binding protein containing, CBM2 and CBM6 domains. However, only two of the polysaccharide degrading proteins, that are predicted to be secreted, have CBM domains. MB2003 has numerous genes predicted to encode proteins involved in production of exopolysaccharides. MB2003 produces large amounts of ropey filaments that could potentially be exopolysaccharide covering the cells, which can be seen under SEM observation of MB2003 and even more so in MA3014 grown in BY medium on NDF plant material (Figures 3.8 C, D and 3.9C, D). B316 has several potential mechanisms for adhesion to plant cell walls including a large number of CBM-containing proteins, and genes encoding for exopolysaccharide production, a single flagellum, pili and several cell surface proteins with a likely role in adhesion.

Both MB2003 and B316 are non-motile, while *P. xylanivorans* MA3014 displayed motility as shown using a motility assay (Figure 3.20 A and Attwood *et al.*, (1996)). Analysis of the genes in the flagella biosynthesis operon revealed the absence of two gene insertions in MA3014 (Figure 3.20 B). Flagellar gene organization is almost identical for both MB2003 and B316. The cluster of genes that encode for the flagellum structure and are responsible for motility functions are disrupted in both bacteria. It is hypothesised that these insertions impair motility in both MB2003 and B316. The TEM images from this study could not produce clear evidence of flagella for either MB2003 or B316 on NDF plant material (Figure 21 A, B, E and F and Figure 22 A, B, E and F). However it is possible that both bacteria use their flagellum for adherence rather than motility (Shimoyama *et al.*, 2009). From previous work it is known that B316 possesses

an flagella but is non-motile (Attwood *et al.*, 1996). MB2003 may be the same, however further investigation is required to resolve the flagellum issue.

Approximately 3% of the MB2003 genome (90 CDSs) is predicted to encode proteins dedicated to polysaccharide degradation (Table 3.18 and 3.19), similar to that found in B316. In total, MB2003 has 76 glycoside hydrolase and 86 glycosyl transferase genes (Table A4 in Appendix I), whereas *B. proteoclasticus* B316 has 113 GHs and 121 GTs (Kelly *et al.*, 2010). The numbers of GHs and GTs in MB2003 are comparable to B316 in terms of the number of genes relative to genome size.

Xylan is the preferred insoluble substrate that MB2003 utilises for growth and the genome encodes 29 enzymes predicted to metabolise this complex polysaccharide (Figure 4.1). Among these 7 are secreted: Cel5A (GH5), Xyn10A/B (GH10), Gh30A (GH30), Xsa43A (GH43), Est1A (CE1) and Est4C (CE4) (Table 3.18). All have significant matches to B316. The feruloyl esterase Est1A is the only gene encoding xylan degradation found on the chromid (Bhu II) of MB2003. The intracellular genes encoding proteins involved in xylan degradation and their catalytic domains are: Est10A (CE10), Xyl120A/B (GH120), Est1B (CE1), Xsa43B-G (GH43), Xyn8A (GH8), Xyl3A (GH3), Agu67A (GH67), Arf51A-C (GH51), Gh115A (GH115), Est2A (CE2), Est4A, B, D, and an unclassified acetyl-xylan esterase (Table 3.19). Of these all have significant matches to B316 except Xsa43C, Xsa43E, Arf51C and Est4A. Furthermore observation of the clusters of genes encoding xylan degradation in B316 and MB2003 (Figure 3.19) show similar arrangements. The difference is that the genes in MB2003 are found in a single cluster, whereas in B316 they form two separate clusters. In B316 genes from both clusters have been shown by microarray analysis to be strongly upregulated in xylan grown cells (Kong, 2007).

Both MB2003 and B316 are unable to degrade cellulose but are able to utilise a range of other insoluble plant polysaccharides. The foundation of the B316 catalytic capability for the breakdown of pectin, starch and xylan is predicted to be centered around nine large cell-associated proteins (Amy13A, Agn53A, Est12B, Lic16A, Pel1A, Pme8B, Xsa43J, Xyn10B, and Bpr\_I0264, (Kelly *et al.*, 2010)). These proteins contain multiple cell wall binding repeat domains at their C-termini that are predicted to anchor them to the peptidoglycan cell wall. MB2003 does not contain any genes encoding cell wall binding repeats and is thus markedly different from B316. As mentioned above

MB2003 prefers to utilise xylan as the primary growth substrate whereas the major sources of pyruvate for central metabolism in B316 are derived from breakdown products of both xylan and pectin, where pectin is the preferred growth substrate. B316 is thus a more versatile degrader of plant cell wall polysaccharides than MB2003 as it is able to utilise a wide range of insoluble polysaccharides for growth and metabolism.

When comparing the predicted number of secreted enzymes involved in polysaccharide degradation in Figures 4.2 and 4.3, there are many differences between the 44 enzymes of B316 and the 19 of MB2003. The overall size of the secreted enzymes in B316 (average 880 aa) are much larger than enzymes secreted by MB2003 (average 510 aa). B316 has nine enzymes larger than 1,000 aa and three larger than 2,000 aa whereas MB2003 has no secreted enzyme larger than 1,000 aa in size.

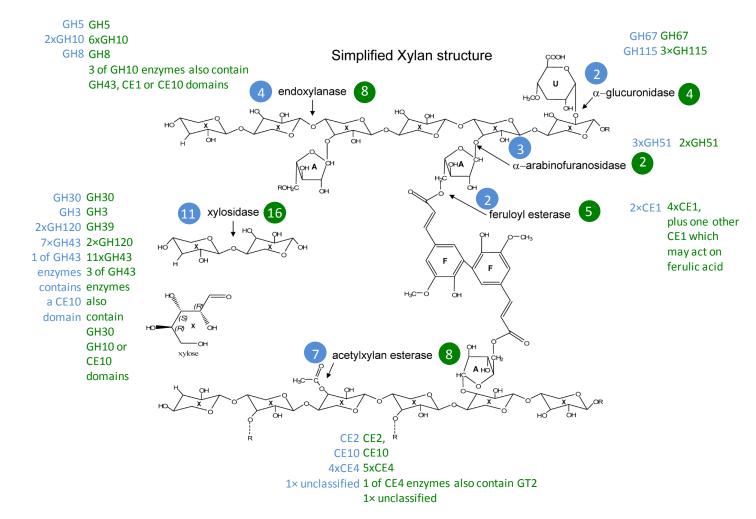


Figure 4.1. Diagrammatic representation of xylan, showing linkages attacked by hemicellulose-degrading enzymes in *B. hungatei* MB2003 (n =blue) and *B. proteoclasticus* B316 (n = green). A, arabinose; F, ferulic acid; U, 4-*O*-methylglucuronic acid; X, xylose; R, continuation of glycan chain. Modified image from Chesson and Forsberg (1997).

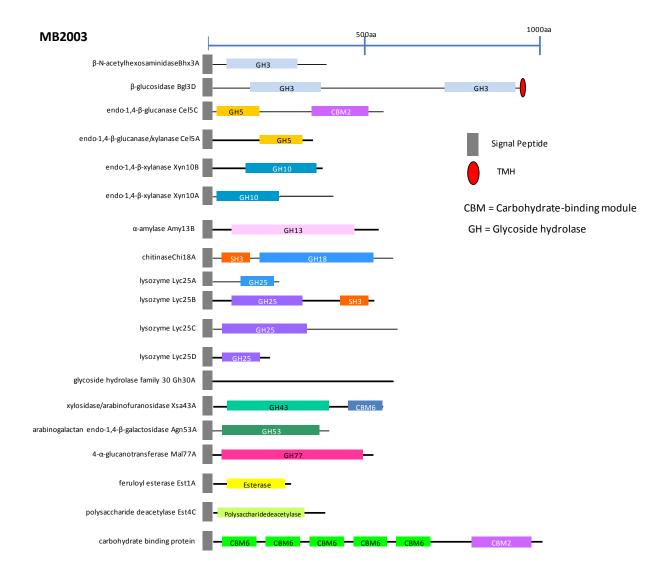


Figure 4.2. Predicted domain architectures (PFAM) of secreted enzymes encoded by genes involved in polysaccharide breakdown in *B. hungatei* MB2003.

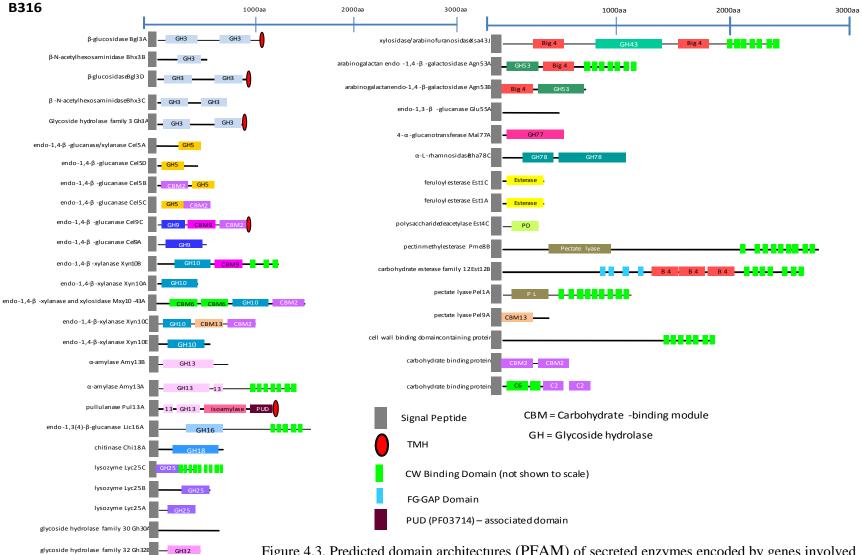


Figure 4.3. Predicted domain architectures (PFAM) of secreted enzymes encoded by genes involved in polysaccharide breakdown in *B. proteoclasticus* B316.

xylosidase/arabinofuranosidase Xsa43A

xylosidase/arabinofuranosidase Xsa43F

- GH43 - CBM6

GH43

#### 4.3 Comparison of polysaccharide-degrading strategies in ruminal bacteria

Genome sequence information is now available for *B. hungatei* MB2003, *B. proteoclasticus* B316 and for two well-studied cellulolytic rumen bacteria, *Fibrobacter succinogenes* S85 (Suen *et al.*, 2011) and *Ruminococcus flavefaciens* FD-1 (Miller *et al.*, 2009). These strainshave a large repertoire of genes predicted to encode polysaccharide-degrading enzymes. In the current opinion these species are thought to work in synergy in the rumen to degrade plant biomass while using different approaches to breakdown polysaccharides (Flint *et al.*, 2008).

#### Butyrivibrio sp.

B. hungatei MB2003 is capable of degrading and utilising hemicellulose as the main substrate, but not cellulose. Similarly B. proteoclasticus B316 is unable to degrade cellulose, but can degrade and utilise hemicellulose, and pectin (Kelly et al. 2010). For both, MB2003 and B316, enzymes that initiate polysaccharide breakdown are secreted, but the majority of the enzymes involved in carbohydrate metabolism are predicted to be intracellular. This suggests a model of plant cell wall breakdown in which secreted enzymes generate a variety of complex oligosaccharides that are transported into the cell for further metabolism. In B316, the clustering of genes encoding intracellular polysaccharide degrading enzymes with genes for transporters, transcriptional regulators and environmental sensors in several polysaccharide utilisation loci (Kelly et al., 2010) supports this model. Clustering of polysaccharide-degrading enzymes around transporters could be a possible mechanism to reduce competition by limiting the amount of readily useable polysaccharide products in the surrounding environment that other microbes can utilise. Both B316 and MB2003 are able to adhere to plant material which together with their polysaccharide-degrading capabilities implicates that they are typical of plant colonisers in the rumen environment. However, given that B316 has more extensive polysaccharide-degrading capabilities than MB2003 it is possible that B316 is an initial coloniser and degrader of plant material in the rumen, whereas MB2003 may best be described as a secondary degrader.

#### Fibrobacter succinogenes

F. succinogenes S85 is a cellulose-degrading specialist in the rumen. Although it has the ability to produce a variety of enzymes capable of hydrolyzing plant cell wall polysaccharides, it uses these enzymes solely to gain access to cellulose. The genome lacks the genes necessary to transport and metabolise non-cellulose polysaccharides, resulting in utilisation of only cellulose as an energy source. The carbohydrates not used by F. succinogenes should be available to support the growth of a variety of other bacteria. Three unique models have been proposed for cellulose degradation by F. succinogenes. One model describes the growth of F. succinogenes as a biofilm on the cellulose surface, similar to a case reported for ruminococci (Costerton, 1992). Fibroslime proteins (Gong et al., 1996; Jun et al., 2007a) and Type IV pilin structures (Jun et al., 2007b) are hypothesised to initiate cellulose breakdown by facilitating cell-surface attachment to the substrate and mediating GH and CBM containing enzyme interactions polysaccharides. A phylogenetically-related bacterium, Cytophaga with the hutchinsonii, is known to strongly associate with cellulose and has been proposed to degrade cellulose by disrupting cellulose fibers and absorbing through the outer cell membrane (Wilson, 2009). It is predicted to do this by cleaving the individual cellulose chains using various endoglucanases, thus enabling direct access to the hydrolytic products of cellulose (e.g. glucose, cellobiose, and cellodextrins). Lastly, a model similar to that proposed for the  $\alpha$ -proteobacterium Sphingomonas sp. A1 (Hashimoto et al., 2005a; Hashimoto et al., 2005b) may apply, where the organism forms "pits" over its cell membrane acting as channels that can import the products of cellulose via highaffinity periplasmic proteins coupled with ABC transporters. In this model the degradation of the glucose, cellobiose, and cellodextrins would occur in the cytoplasm.

#### Ruminococcus flavefaciens

*R. flavefaciens* FD-1 can utilise a range of plant cell wall polysaccharides and produces a multi-enzyme cellulosome complex in which enzymes are linked to a non-catalytic scaffold structure via dockerin domains. FD-1 secretes at least 75% of its GHs and most of these are predicted to be cellulosome-associated, implying that most polysaccharide breakdown occurs extracellularly. The cellulosome organization in FD-1 is extremely complex and more than 200 dockerin-containing proteins have been identified from the draft genome sequence (Miller *et al.*, 2009).

#### 4.4 Conclusion

The work described in this thesis was the first opportunity to conduct comparative genome analysis of two rumen bacteria belonging to the same genus and cultivated directly from the rumen microbial fraction of New Zealand cattle. The preliminary genotypic and phenotypic analysis of cultured representatives of large clusters of rumen organisms, confirmed *Butyrivibrio* and *Pseudobutyrivibrio* as important rumen bacteria under pasture grazed conditions. These characterisations led to the selection of *Butyrivibrio hungatei* MB2003, a strain that adheres to plant fibre and efficiently degrades xylan as the prime candidate for genome sequencing.

The finding that *Butyrivibrio hungatei* MB2003 has a multi-replicon genome, similar to that found in *B. proteoclasticus* B316 and the observation of other extrachromosomal DNAs in PFGE analyses, indicates that this type of genome arrangement is common among rumen *Butyrivibrio* species. Most of the genes encoding core metabolic processes in both these species are encoded on the chromosome or chromid, but the megaplasmids and plasmid are largely cryptic, which leaves a question mark as to the role of these extrachromosomal elements in *Butyrivibrio*, especially the large megaplasmids which encode a significant proportion of the genome.

The MB2003 genome encodes a large repertoire of enzymes predicted to metabolise hemicellulose which is consistent with its ability to grow well on xylan. Although both MB2003 and B316 have similar phenotypic characteristics and occupy the same habitat, the genome of MB2003 is significantly smaller and is predicted to contain much fewer extracellular polysaccharide degrading enzymes.

This comparison offers an alternate view of the genes required for a xylan/hemicellulose-degrading lifestyle in the rumen and poses an interesting question about the purpose of the greater range of polysaccharide degrading enzymes found in B316. It can be concluded that MB2003 is likely to be a secondary hemicellulose degrader in the rumen, relying on organisms such as B316 for enzymatic cleavage of polysaccharide linkages that it does not encode itself.

#### 4.5 Future work

There are several areas identified in this thesis where future work is justified. The remaining gaps in the *B. hungatei* MB2003 genome will be closed and the final sequence will be reanalysed via GAMOLA to confirm the gene annotations and will be prepared for NCBI submission. Similarly, the draft *P. xylanivorans* MA3014 genome will be closed and fully annotated, to allow an in depth investigation into the polysaccharide degradation machinery of this bacterium. Genome comparisons of *Pseudobutyrivibrio* MA3014 will then be possible with MB2003, B316 and the human strain *Pseudobutyrivibrio* (*B. fibrisolvens*) 16/4 genomes which will hopefully offer new insights into the polysaccharide-degrading activities of this important group of rumen bacteria.

The adherence of MB2003 and MA3014 to plant substrates warrants further investigation along with the further attempts to visualise flagella. A better understanding of the metabolic capacity of *Butyrivibrio* and *Pseudobutyrivibrio* species would certainly be assisted via a side-by-side comparison of their growth on a range of soluble substrates in parallel with whole genome gene and protein expression profiling, coupled with end-product and metabolite analyses. The development of shuttle vectors using the pNP6 plasmid would also be useful to allow gene manipulation studies to be conducted in MB2003 and related strains in the future.

## Appendix I

### Gene Lists

Table A1. Summary of manual annotation of the genes within the chromid (Bhu II) of MB2003.

Gene number	Start	Stop	Size of gene (bp)	Gene Annotation
1	71	655	584	transcriptional regulator TetR family
4	820	2307	1487	radical SAM domain-containing protein
5	2397	2582	185	>hypothetical protein<
7 9	2745	4958	2213	GGDEF/EAL domain-containing protein
10	5086 6598	6171 6798	1085	tyrosine recombinase XerC hypothetical protein
10	6888	7478	590	hypothetical protein
12	7590	8072	482	HTH domain-containing protein
13	8222	8827	605	transcriptional regulator TetR family
14	8830	9909	1079	conserved hypothetical protein
15	10019	12040	2021	beta-galactosidase Bga42A
16	12111	13622	1511	PAP2 family protein
17	13619	14356	737	acyltransferase
18	14487	14666	179	hypothetical protein
19 21	14736 15247	15020 15918	284 671	DNA-binding protein hypothetical protein
21	16015	16851	836	degV family protein
25	17246	17542	296	anti-sigma factor antagonist
26	17578	18777	1199	hypothetical protein
27	19014	19619	605	hypothetical protein
28	19773	20411	638	orotate phosphoribosyltransferase PyrE
29	20456	20692	236	hypothetical protein
30	20905	21888	983	phosphate acetyltransferase Pta
33	21993	23348	1355	MATE efflux family protein
34	23339	24745 25779	1406	GGDEF domain-containing protein
35 36	24832 25849	25779	947 1193	hydrogenase accessory protein HypB
30	25849	27042	341	hypothetical protein hydrogenase nickel insertion protein HypA
39	27736	29043	1307	AAA family ATPase
40	29085	30251	1166	replication initiation protein RepB1
42	32881	33708	827	plasmid partitioning protein ParA
43	33708	34241	533	hypothetical protein
44	34289	34573	284	DNA-binding protein
46	34718	36088	1370	MATE efflux family protein
48	36138	36986	848	MerR family transcriptional regulator
49 50	37101 37339	37322 38271	221 932	acyl carrier protein
51	38282	39217	935	enoyl-(acyl-carrier-protein) reductase FabK malonyl CoA-acyl carrier protein transacylase FabD
52	39210	39950	740	3-oxoacyl-(acyl-carrier-protein) reductase FabG
53	39943	41175	1232	3-oxoacyl-(acyl-carrier-protein) synthase FabF
54	41188	41610	422	acetyl-CoA carboxylase biotin carboxyl carrier protein AccB
55	41622	42062	440	beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ
57	42064	43404	1340	acetyl-CoA carboxylase biotin carboxylase AccC
58	43395	44225	830	acetyl-CoA carboxylase carboxyl transferase beta subunit AccD
59 60	44248 45009	45003 46670	755 1661	acetyl-CoA carboxylase carboxyl transferase alpha subunit AccA acetyl-CoA synthetase AscA
61	45009	48463	1763	methyl-accepting chemotaxis protein McpA
62	48476	49777	1301	sugar ABC transporter substrate-binding protein
63	49979	50347	368	response regulator domain-containing protein
64	50383	50787	404	ACT domain-containing protein
65	50814	52001	1187	aminotransferase
67	52119	52370	251	GIY-YIG domain-containing protein
68	52371	53411	1040	S-adenosyl-methyltransferase MraW family protein
69 71	53424 54501	54347 56024	923 1523	radical SAM domain-containing protein SPFH domain/band 7 family protein
71 72	56085	56264	1525	hypothetical protein
72	56472	58616	2144	UvrD/REP family ATP-dependent DNA helicase
75	58926	59843	917	CorA-like Mg2+ transporter protein
76	59887	60537	650	potassium uptake protein TrkA family protein
79	60548	61915	1367	potassium uptake protein TrkH family protein
81	62276	64687	2411	beta-glucosidase Bgl3A
84	64842	65066	224	hypothetical protein
85	65087	65476	389	UBA/TS-N domain-containing protein
86 87	65547 66894	66725 67661	1178 767	Na+/H+ antiporter hypothetical protein
87	67751	68392	641	hypothetical protein
89	68502	70067	1565	hypothetical protein
90	70070	70282	212	HTH domain-containing protein
91	70299	70775	476	hypothetical protein
92	71001	71624	623	polysaccharide deacetylase Est4A
93	71880	72545	665	phosphoglycerate mutase family protein
94	72565	73281	716	hypothetical protein
95	73346	74134	788	metallo-beta-lactamase family protein
96 97	74226	75773	1547	lysozyme Lyc25A
	75829	76830	1001	GNAT family acetyltransferase

98	76979	78034	1055	feruloyl esterase Est1A
99	78077	79900	1823	ABC transporter ATP-binding protein
100	79902	80906	1004	sugar ABC transporter substrate-binding protein
103	80921	82918	1997	methyl-accepting chemotaxis protein McpB
104	83321	83977	656	hypothetical protein
105	83970	85907	1937	transposase
106	85911	86909	998	hypothetical protein
108	86893	88218	1325	hypothetical protein
109	88297	88557	260	hicA family protein
110	88554	88901	347	hicB family protein
111	89181	90107	926	GNAT family acetyltransferase/NUDIX domain- containing protein
112	90140	90508	368	CrcB-like protein
113	90555	91757	1202	MFS transporter

Table A2. Summary of manual annotation of the genes within the plasmid (pNP6) of MB2003.

Gene number	Start	Stop	Size of gene (bp)	Gene Annotation
2	826	1563	737	>plasmid mobilization protein<
3	1535	1966	431	hypothetical protein
8	3980	4735	755	hypothetical protein
11	5194	5724	530	plasmid replication protein
4	1976	3658	1682	TraG/TraD family protein

Table A3. Summary of manual annotation of the genes within the megaplasmid (pNP144) of MB2003.

Gene number	Start	Stop	Size of gene (bp)	Gene Annotation
1	283	852	569	signal peptidase I LepB
3	1066	1710	644	hypothetical protein
5	1707	3152	1445	hypothetical protein
7	4284	4853	569	restriction endonuclease
8	4876	5628	752	hypothetical protein
9	5606	6814	1208	hypothetical protein
10	6817	7668	851	hypothetical protein
11	7668	10469	2801	TraG/TraD family protein
12	11476	12288	812 458	partitioning protein ParA
13	12281 12783	12739 14399	458	hypothetical protein hypothetical protein
14	12785	14399	197	hypothetical protein
10	14950	16395	1445	hypothetical protein
19	17410	17568	158	hypothetical protein
21	18430	19395	965	hypothetical protein
22	19557	19721	164	hypothetical protein
23	19799	19951	152	hypothetical protein
25	20131	20754	623	hypothetical protein
26	20826	21566	740	hypothetical protein
29	21782	25969	4187	cell surface protein
30	25969	26799	830	sortase B family protein
31	26857	29181	2324	ATPase involved in pili biogenesis
32	29650	31032	1382	cell surface protein
33	31045	31446	401	hypothetical protein
34	31465	32433	968	hypothetical protein
35	32488	33564	1076	hypothetical protein
37 38	33655 34689	34617 35657	962 968	hypothetical protein
39	34689	37207	1136	hypothetical protein hypothetical protein
40	37318	40824	3506	hypothetical protein
40	40918	40324 42189	1271	hypothetical protein
42	42469	42780	311	hypothetical protein
43	42824	43195	371	hypothetical protein
44	43260	43598	338	hypothetical protein
45	43631	43972	341	hypothetical protein
46	43972	45048	1076	hypothetical protein
48	45060	47414	2354	hypothetical protein
51	47426	50071	2645	hypothetical protein
52	50204	51418	1214	hypothetical protein
53	51703	53022	1319	hypothetical protein
54	53177	53686	509	hypothetical protein
55	53676	54167	491	hypothetical protein
56	54182	55150	968 1022	hypothetical protein
57 58	55178 56251	56200 57315	1022	hypothetical protein hypothetical protein
59	57334	58536	1202	hypothetical protein
60	58563	61085	2522	hypothetical protein
61	61226	61564	338	hypothetical protein
62	61567	62457	890	hypothetical protein
63	62775	64124	1349	transposase
64	64147	64458	311	hypothetical protein
65	64458	65510	1052	hypothetical protein
66	65507	65764	257	hypothetical protein
67	65821	66819	998	hypothetical protein
68	67400	67624	224	hypothetical protein
69	67596	67892	296	hypothetical protein
70	67906	68568	662	hypothetical protein
71	68641	70317	1676	hypothetical protein
72	70314	71078	764	hypothetical protein
73	71075	71524	449	hypothetical protein
74 75	71589 72331	72320 73203	731	ThiF family protein hypothetical protein
75	72331 73224	73203	872 1001	hypothetical protein hypothetical protein
78	73224 74419	76809	2390	ATP-dependent DNA helicase UvrD/REP family
78	76858	77757	899	DNA polymerase III, delta subunit
79	77788	78228	440	single-stranded DNA binding protein Ssb1
81	78604	78831	227	hypothetical protein
82	78936	79907	971	hypothetical protein
83	80264	81208	944	hypothetical protein
84	81205	81924	719	DNA polymerase III delta' subunit
85	81943	83601	1658	DNA polymerase III gamma and tau subunits DnaX
87	83723	84004	281	>hypothetical protein<
88	0.110.1	05002	899	phage integrase family protein
00	84194	85093	899	phage integrase failing protein
88 89 90	84194 85186 86400	85093 86250 87395	1064 995	phage integrase family protein transglutaminase domain-containing protein

91	87492	89993	2501	hypothetical protain
93	91145	91441	296	hypothetical protein hypothetical protein
94	91641	92600	959	hypothetical protein
95	93021	93449	428	hypothetical protein
96	93816	94082	266	hypothetical protein
97	94075	94272	197	hypothetical protein
98	94407	95306	899	hypothetical protein
99	95775	96323	548	hypothetical protein
100	96394	96567	173	hypothetical protein
101	96646	96879	233	hypothetical protein
101	96986	97603	617	hypothetical protein
102	97828	98172	344	hypothetical protein
103	98876	98998	122	hypothetical protein
105	99505	99765	260	CRISPR-associated protein Cas2
107	99940	103689	3749	hypothetical protein
109	103849	104133	284	hypothetical protein
110	104172	105584	1412	archaeal ATPase family protein
111	105820	106776	956	hypothetical protein
112	107017	107427	410	hypothetical protein
113	107479	107745	266	Fic/DOC family protein
113	107862	108056	194	hypothetical protein
115	108408	108767	359	DNA-binding protein
115	108760	108945	185	hypothetical protein
118	109226	109381	155	hypothetical protein
118	109220	109531	293	hypothetical protein
119	109380	110082	293	hypothetical protein
120	110082	111152	1070	hypothetical protein
125	111762	111875	113	hypothetical protein
125	112214	112333	115	hypothetical protein
120	112214	112333	143	hypothetical protein
130	112040	112783	254	hypothetical protein
130	113356	113508	152	hypothetical protein
131	113530	113952	341	HTH domain-containing protein
132	113966	113732	173	hypothetical protein
133	114136	114270	134	hypothetical protein
134	114130	114270	554	hypothetical protein
135	114270	115301	230	
130	115561	115301	230	hypothetical protein DNA-binding protein
139	116160	116579	419	
140	116633	116875	242	hypothetical protein hypothetical protein
140	117027	117476	449	hypothetical protein
141	117027	117470	179	hypothetical protein
143	118695	119750	1055	HD-GYP domain-containing protein
147	119903	120274	371	hypothetical protein
148	120329	120274	224	hypothetical protein
150	12052)	120333	197	hypothetical protein
150	120032	121651	629	DNA replication protein DnaD
151	121663	122043	380	hypothetical protein
152	1221003	122330	230	hypothetical protein
155	122323	122802	479	hypothetical protein
154	122323	122002	167	hypothetical protein
155	122041	123691	611	hypothetical protein
150	123080	123071	413	hypothetical protein
157	123711 124148	124124	413	hypothetical protein
159	124143			appointent proton
160		24971	227	hypothetical protein
		124921 125577	227 290	hypothetical protein hypothetical protein
	125287	125577	227 290 932	hypothetical protein
160 161 162			290	hypothetical protein phosphoadenosine phosphosulfate reductase family protein
161 162	125287 125606 126913	125577 126538 127470	290 932 557	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein
161 162 163	125287 125606 126913 127484	125577 126538 127470 128017	290 932 557 533	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein hypothetical protein
161 162 163 164	125287 125606 126913	125577 126538 127470 128017 128316	290 932 557 533 302	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein hypothetical protein hypothetical protein
161 162 163 164 165	125287 125606 126913 127484 128014 128335	125577 126538 127470 128017 128316 128610	290 932 557 533	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
161 162 163 164 165 167	125287 125606 126913 127484 128014 128335 128885	125577 126538 127470 128017 128316 128610 129292	290 932 557 533 302 275 407	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
161 162 163 164 165 167 169	125287 125606 126913 127484 128014 128335 128885 131535	125577 126538 127470 128017 128316 128610 129292 132215	290 932 557 533 302 275 407 680	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
161 162 163 164 165 167	125287 125606 126913 127484 128014 128335 128885 131535 132215	125577 126538 127470 128017 128316 128610 129292 132215 132505	290 932 557 533 302 275 407	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
161           162           163           164           165           167           169           170	125287 125606 126913 127484 128014 128335 128885 131535	125577 126538 127470 128017 128316 128610 129292 132215	290 932 557 533 302 275 407 680 290	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
161           162           163           164           165           167           169           170           171           172	125287 125606 126913 127484 128014 128335 128885 131535 132215 132215 132529 132680	125577 126538 127470 128017 128316 128610 129292 132215 132505 132669 133057	290 932 557 533 302 275 407 680 290 140	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
161           162           163           164           165           167           169           170           171           172           174	125287 125606 126913 127484 128014 128335 128885 131535 132215 132529 132680 133135	125577 126538 127470 128017 128316 128610 129292 132215 132205 132669 133057 135129	290 932 557 533 302 275 407 680 290 140 377 1994	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein
161           162           163           164           165           167           169           170           171           172           174	125287 125606 126913 127484 128014 128035 128885 131535 132215 132529 132680 133135 135144	125577 126538 127470 128017 128316 128610 129292 132215 132505 132669 133057 135129 135278	290 932 557 533 302 275 407 680 290 140 377 1994 134	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein
161           162           163           164           165           167           169           170           171           172           174	125287 125606 126913 127484 128014 128335 128885 131535 132215 132529 132680 133135 135144 135305	125577 126538 127470 128017 128316 128610 129292 132215 132505 132669 133057 135129 135278 135619	290 932 557 533 302 275 407 680 290 140 377 1994	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein
161           162           163           164           165           167           169           170           171           172           174           175           176           177	125287 125606 126913 127484 128014 128335 138885 131535 132215 132225 132529 132680 133135 135144 135305 135633	125577 126538 127470 128017 128316 128610 129292 132215 132505 132669 133057 135129 135278 135619 135830	290 932 557 533 302 275 407 680 290 140 377 1994 134 314 197	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein
161           162           163           164           165           167           169           170           171           172           174           175           176           177           178	125287 125606 126913 127484 128014 128335 138355 132155 132215 132529 132680 133135 135144 135305 135633 136150	125577 126538 127470 128017 128316 128610 129292 132215 132505 132669 133057 135129 135278 1355619 135830 136920	290 932 557 533 302 275 407 680 290 140 377 1994 134 314 197 770	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein
161           162           163           164           165           167           169           170           171           172           174           175           176           177	125287 125606 126913 127484 128014 128335 131535 132215 132529 132680 133135 135144 135305 135633 136150 137109	125577 126538 127470 128017 128316 128610 129292 132215 132265 1322669 133057 135129 135578 135619 1355619 1356920 137396	290 932 557 533 302 275 407 680 290 140 377 1994 134 314 197 770 287	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein
161           162           163           164           165           167           169           170           171           172           174           175           176           177           178           179	125287 125606 126913 127484 128014 128335 132885 131535 132215 132225 132259 132680 133135 135144 135305 135633 136150 137109 137397	125577 126538 127470 128017 128316 128610 129292 132215 132505 132669 133057 135129 135278 1355619 135830 136920	290 932 557 533 302 275 407 680 290 140 377 1994 134 314 197 770	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein
161           162           163           164           165           167           169           170           171           172           174           175           176           177           178           179           180	125287 125606 126913 127484 128014 128035 128885 131535 132215 132529 132680 133135 135144 135305 135144 135305 135633 136150 137109 137397	125577 126538 127470 128017 128316 128610 129292 132215 132505 132669 133057 135129 1355129 1355129 135578 135619 135830 136920 137396 137843 138409	290 932 557 533 302 275 407 680 290 140 377 1994 134 314 197 770 287 446 437	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein
161           162           163           164           165           167           169           170           171           172           174           175           176           177           178           179           180           181	125287 125606 126913 127484 128014 128335 128885 131535 132215 132529 132680 133135 135144 135305 135633 136150 137109 137397 137972 138964	125577 126538 127470 128017 128316 128610 129292 132215 132505 132669 133057 135129 135578 135619 135578 135619 135830 136920 137396 137843 138409 139761	290 932 557 533 302 275 407 680 290 140 377 1994 134 314 197 770 287 446 437 797	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein
161           162           163           164           165           167           169           170           171           172           174           175           176           177           178           179           180           181           182           183	125287 125606 126913 127484 128014 128335 128885 131535 132215 132529 132680 133135 135144 135305 135633 136150 137109 137397 133977 1339772 138964 140028	125577 126538 127470 128017 128316 128610 129292 132215 132505 132669 133057 135129 135278 135619 1355278 135619 135830 136920 137396 137843 138409 139761 140342	290 932 557 533 302 275 407 680 290 140 377 1994 134 314 197 770 287 446 437 797 314	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein
161           162           163           164           165           167           169           170           171           172           174           175           176           177           178           179           180           181	125287 125606 126913 127484 128014 128335 128885 131535 132215 132529 132680 133135 135144 135305 135633 136150 137109 137397 137972 138964	125577 126538 127470 128017 128316 128610 129292 132215 132505 132669 133057 135129 135578 135619 135578 135619 135830 136920 137396 137843 138409 139761	290 932 557 533 302 275 407 680 290 140 377 1994 134 314 197 770 287 446 437 797	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein
161           162           163           164           165           167           169           170           171           172           174           175           176           177           178           179           180           181           182           183           184	125287 125606 126913 127484 128014 128335 128885 131535 132215 132529 132680 133135 135144 135305 135633 136150 137109 137397 137972 138964 140028 140420	125577 126538 127470 128017 128316 128610 129292 132215 132265 1322669 133057 135129 1355278 135619 1355278 135619 135830 136920 137396 137843 138409 139761 140342 142033	290 932 557 533 302 275 407 680 290 140 377 1994 134 314 197 770 287 446 437 797 314 1613	hypothetical protein phosphoadenosine phosphosulfate reductase family protein hypothetical protein

Table A4. Summary of manual annotation of the genes within the chromosome of MB2003.

Gene number	Start	Stop	Size of gene (bp)	Annotation
1	349	744	395	HTH domain-containing protein
1	399	1505	1106	hypothetical protein
1	15	140	125	hypothetical protein
1	462 138	1538 5288	1076 5150	hypothetical protein
1	4	483	479	hypothetical protein hypothetical protein
1	7	903	896	prolipoprotein diacylglyceryl transferase Lgt
1	498	854	356	hypothetical protein
1	792	1355	563	phosphoglycerate mutase family protein
1	222	1562	1340	hypothetical protein
2	550	3024	2474	1,4-alpha-glucan branching enzyme GlgB
2	836	1969	1133	hypothetical protein
2	1526	2194	668	L-serine dehydratase beta subunit SdhB
2 2	438 351	881 650	443 299	hypothetical protein hypothetical protein
2	509	1954	1445	hypothetical protein
2	1557	2657	1100	class II aldolase/adducin family protein
2	5441	5812	371	DtxR family transcriptional regulator
2	916	2013	1097	GTP-binding protein YchF
2	1410	2600	1190	AAA family ATPase
2	237	1115	878	AraC family transcriptional regulator
2	98	2221	2123	hypothetical protein
2	1233	1700	467	acetyltransferase
3	2203	3090	887	L-serine dehydratase alpha subunit SdhA
3	943 2020	2247 3114	1304 1094	23S rRNA methyltransferase hypothetical protein
3	1299	2204	905	chemotaxis protein CheW
3	439	1071	632	hypothetical protein
3	3058	4317	1259	hypothetical protein
3	2682	3923	1241	gamma-glutamyl phosphate reductase ProA
3	5936	7480	1544	HD/KH domain-containing protein
3	2378	2599	221	hypothetical protein
3	1111	2625	1514	hypothetical protein
3	2793	3239	446	hypothetical protein
3	1610 1257	2941 2348	1331 1091	MatE efflux family protein GDP-mannose 4,6-dehydratase gmd
3	2047	2445	398	hypothetical protein
3	1757	2863	1106	glycosyl transferase GT4 family protein
4	2160	3968	1808	threonyl-tRNA synthetase ThrS
4	784	2592	1808	Carboxylesterase type B
4	3143	3883	740	hypothetical protein
4	2311	3126	815	hypothetical protein
4	4402	5571	1169	D-3-phosphoglycerate dehydrogenase SerA
4 4	4095 7651	4664 8262	569 611	5-formyltetrahydrofolate cycloligase recombination regulator RecX
4	3286	4152	866	NAD-dependent epimerase/dehydratase
4	3248	3721	473	cNMP binding domain-containing protein
4	2357	3310	953	NAD-dependent epimerase/dehydratase
4	2518	3771	1253	hypothetical protein
4	2242	3447	1205	flavin containing amine oxidoreductase family protein
4	2883	3545	662	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase IspD
5	4175	4864	689	hypothetical protein
5	2460 3922	3428 5514	968 1592	hypothetical protein hypothetical protein
5	5571	6653	1082	phosphoserine aminotransferase SerC
5	705	1364	659	deoxyribose-phosphate aldolase DeoC
5	2624	3220	596	hypothetical protein
5	2701	3687	986	L-asparaginase AnsA
5	3728	5230	1502	AAA family ATPase
5	3790	4854	1064	aldose 1-epimerase
5	3444	4151	707	glycosyl transferase GT2 family protein
5	3872	5014	1142	glycoprotease family protein
6	4871 3110	4981 4132	110 1022	hypothetical protein alvcosyl transferase GT2 family protein
6	3916	4132 4707	791	glycosyl transferase GT2 family protein hypothetical protein
6	2779	4281	1502	glycerol kinase GlpK
6	5538	8468	2930	peptidase M16 family protein
6	7063	8589	1526	YkuD domain-containing protein
6	4677	6560	1883	hypothetical protein
6	8316	9383	1067	DNA recombination protein RecA
6	1461	2822	1361	citrate synthase cit
6	3549	4322	773	SAM-dependent methyltransferase
6	3695	4054 4760	359 518	hypothetical protein
6	4242 3365	3784	419	phosphoglycerate mutase family protein SCP domain-containing protein
U	5505	2704	717	ber domain containing protein

1	1051	5452	500	
6	4864 4218	5463 7415	599 3197	recombinational DNA repair protein RecR
6	4218 5025	5786	761	isoleucyl-tRNA synthetase IleS hypothetical protein
6				
7	4286	4792	506	thioesterase superfamily protein
7	4737	5813	1076	hypothetical protein
7	4302	5750	1448	glycerol-3-phosphate dehydrogenase GlpA
7	8485	9441	956	GTP-binding protein Era
7	3210	5444	2234	hypothetical protein
7	2672	3892	1220	tyrosyl-tRNA synthetase TyrS
7	8603	10291	1688	acetolactate synthase large subunit IlvB
7	6629	8296	1667	FAD dependent oxidoreductase
7	2846	3112	266	hypothetical protein
7	4577	6424	1847	beta-lactamase family protein
7	4184	4804	620	hypothetical protein
7	4937	5533	596	hypothetical protein
7	5275	6624	1349	hypothetical protein
7	4012	5802	1790	hypothetical protein
7	5463	5810	347	hypothetical protein
7	5922	6503	581	hypothetical protein
8	3929	5662	1733	alpha-galactosidase Aga27A
8	5100	5579	479	hypothetical protein
8	4937	5857	920	phosphate butyryltransferase ptb
8	5923	6465	542	hypothetical protein
8	5747	7015	1268	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
8	9451	10098	647	
			647	DNA repair protein RecO
8	5495	6112		imidazole glycerol phosphate synthase glutamine amidotransferase subunit HisH
8	8628	9854	1226	FAD dependent oxidoreductase
8	9629	10165	536	hypothetical protein
8	3198	4691	1493	threonine synthase ThrC
8	6485	7036	551	hypothetical protein
8	5100	6764	1664	methyl-accepting chemotaxis protein Mcp
8	5582	6469	887	hypothetical protein
8	6682	10014	3332	TPR domain-containing protein
8	5838	6293	455	hypothetical protein
8	5814	7412	1598	DNA polymerase III gamma and tau subunits DnaX
8	6518	7444	926	ribonuclease Z
9	6505	8163	1658	cellodextrinase Cel9B
9	5741	6559	818	metallo-beta-lactamase family protein
9	5860	6924	1064	butyrate kinase buk
9	7027	7392	365	hypothetical protein
9	10212	10766	554	hypothetical protein
9	6125	6886	761	imidazole glycerol phosphate synthase cyclase subunit HisF
9	5681	6070	389	hypothetical protein
9	10328	12016	1688	dihydroxy-acid dehydratase IIvD
9	10328	10581	392	hypothetical protein
9	4811	5608	797	hypothetical protein
9	7049	7651		
9			602	hypothetical protein
	6514	6897	383	glyoxalase family protein
9	6306	7175	869	dTDP-4-dehydrorhamnose reductase rfbD
9	7453	8526	1073	6-phosphofructokinase PfkA
9	7757	8443	686	MIP family transporter
9	7448	8662	1214	glycoprotease family protein
10	6931	8082	1151	reducing end xylose-releasing exo-oligoxylanase Xyn8A
10	8652	10211	1559	polygalacturonase Pgl28B
10	6662	7507	845	GNAT family acetyltransferase/NUDIX domain-containing protein
10	8152	9090	938	PAP2 family protein
10	7611	8999	1388	argininosuccinate lyase ArgH
10	10788	12227	1439	glycyl-tRNA synthetase glyS
10	6893	7570	677	uracil-DNA glycosylase Ung
10	6235	6594	359	ArsR family transcriptional regulator
10	9857	11494	1637	hypothetical protein
10	10598	11329	731	hypothetical protein
10	5609	6490	881	hypothetical protein
10	6909	7445	536	phosphoglycerate mutase family protein
10	10161	11003	842	AraC family transcriptional regulator
10	7233	8405	1172	hypothetical protein
10	8954	10168	1214	hypothetical protein
10	8675	9112	437	hypothetical protein
10	7511	10078	2567	preprotein translocase SecA subunit secA
11	9183	9683	500	hypothetical protein
11	9183	10214	1085	aspartate-semialdehyde dehydrogenase Asd
11	12256	10214 14910	2654	
				alaninetRNA ligase alaS
11	7657	8943	1286	diaminopimelate decarboxylase LysA
11		6848	218	heavy metal associated domain-containing protein
11	6630			hypothetical protein
11 11	12023	13717	1694	
11 11 11	12023 11511	13717 12014	503	hypothetical protein
11 11 11 11	12023 11511 11611	13717 12014 11937	503 326	hypothetical protein hypothetical protein
11 11 11 11 11 11	12023 11511 11611 7825	13717 12014 11937 8403	503 326 578	hypothetical protein hypothetical protein xanthine phosphoribosyltransferase Xpt
11 11 11 11 11 11 11 11	12023 11511 11611 7825 8309	13717 12014 11937 8403 8626	503 326 578 317	hypothetical protein hypothetical protein xanthine phosphoribosyltransferase Xpt thioredoxin
11 11 11 11 11 11 11 11	12023 11511 11611 7825 8309 7462	13717 12014 11937 8403 8626 7713	503 326 578 317 251	hypothetical protein hypothetical protein xanthine phosphoribosyltransferase Xpt thioredoxin hypothetical protein
11 11 11 11 11 11 11 11 11 11	12023 11511 11611 7825 8309 7462 8461	13717 12014 11937 8403 8626 7713 8724	503 326 578 317 251 263	hypothetical protein hypothetical protein xanthine phosphoribosyltransferase Xpt thioredoxin hypothetical protein phosphocarrier HPr family
11 11 11 11 11 11 11 11	12023 11511 11611 7825 8309 7462	13717 12014 11937 8403 8626 7713	503 326 578 317 251	hypothetical protein hypothetical protein xanthine phosphoribosyltransferase Xpt thioredoxin hypothetical protein

12	7568	8845	1277	endo-1,4-beta-xylanase Xyn10E
12	6595	7878	1283	beta-N-acetylhexosaminidase Bhx3B
12	10156	11298	1142	peptide chain release factor 2 prfB
12	15035	15211	176	ribosomal protein S21 rpsU
12	6865	8766	1901	heavy metal translocating P-type ATPase
12	13692	14795	1103	3-isopropylmalate dehydrogenase LeuB
12	11995	13206	1211	hypothetical protein
12	8703	9743	1040	hypothetical protein
12	7770	8387	617	hypothetical protein
12	10993	12621	1628	hypothetical protein
12	8726	10075	1349	phosphoglucosamine mutase glmM
12	10190	11071	881	aldose 1-epimerase family protein
12	11358	11828	470	GAF domain-containing protein
13	11389	12447 10483	1058	LacI family transcriptional regulator
13	9695 10248	11624	788 1376	hypothetical protein archaeal ATPase family protein
13	15352	16884	1532	Na+/H+ antiporter
13	14871	15245	374	preprotein translocase subunit YajC
13	13209	14234	1025	PhoH family protein
13	12045	13106	1061	HD-GYP domain-containing protein
13	8636	9874	1238	serine hydroxymethyltransferase GlyA
13	8445	9437	992	ABC transporter permease
13	9752	10537	785	hypothetical protein
13	10094	11116	1022	YbbR family protein
13	11133	11882	749	hypothetical protein
13	11922	12866	944	oligopeptide ABC transporter ATP-binding protein
13	10410	11504	1094	HD-GYP domain-containing protein
14	12674	13594	920	sugar ABC transporter permease
14	11617	13776	2159	DNA topoisomerase III TopB
14	8772	10712	1940	beta-lactamase family protein
14	15310	16437	1127	queuine tRNA-ribosyltransferase Tgt
14	14244	14726	482	hypothetical protein
14	13107	14408	1301	penicillin-binding protein PbpA
14	10000	10971	971	diacylglycerol kinase family protein
14	10555 8528	12618 9148	2063 620	2-enoate reductase
14	11368	12117	749	hypothetical protein hypothetical protein
15	10488	11030	542	hypothetical protein
15	13791	14480	689	acetyltransferase
15	17020	17826	806	metallophosphoesterase
15	8964	10706	1742	hypothetical protein
15	16503	17633	1130	D-alanyl-D-alanine carboxypeptidase VanY
15	14728	15753	1025	MORN repeat-containing protein
15	9437	10537	1100	ABC transporter permease
15 15	9437 12618	10537 13421	1100 803	ABC transporter permease phospholipase
15	12618	13421	803	phospholipase
15 15 15 15	12618 9292 12662 12251	13421 9729	803 437	phospholipase cytidine deaminase Cdd
15 15 15 15 15	12618 9292 12662 12251 11956	13421 9729 13582 13192 13026	803 437 920 941 1070	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein hypothetical protein
15 15 15 15 15 15 15	12618           9292           12662           12251           11956           12850	13421 9729 13582 13192 13026 13986	803 437 920 941 1070 1136	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD
15 15 15 15 15 15 15 15	12618 9292 12662 12251 11956 12850 11541	13421 9729 13582 13192 13026 13986 12830	803 437 920 941 1070 1136 1289	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
15 15 15 15 15 15 15	12618           9292           12662           12251           11956           12850	13421 9729 13582 13192 13026 13986 12830 14520	803 437 920 941 1070 1136	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD
15 15 15 15 15 15 15 15 16 16	12618 9292 12662 12251 11956 12850 11541 13606 11199	13421           9729           13582           13192           13026           13986           12830           14520           11951	803 437 920 941 1070 1136 1289 914 752	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA
15 15 15 15 15 15 15 16 16 16	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321	803 437 920 941 1070 1136 1289 914 752 692	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein
15           15           15           15           15           15           16           16           16           16           16	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577	803           437           920           941           1070           1136           1289           914           752           692           749	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA
15 15 15 15 15 15 15 15 16 16 16 16 16	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690	803 437 920 941 1070 1136 1289 914 752 692 749 893	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD
15           15           15           15           15           15           16           16           16           16           16	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797 17703	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812	803           437           920           941           1070           1136           1289           914           752           692           749	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase A roC
15           15           15           15           15           15           16           16           16           16           16           16           16           16	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690	803 437 920 941 1070 1136 1289 914 752 692 749 893 1109	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD
15           15           15           15           15           16           16           16           16           16           16           16           16           16           16           16           16           16	12618 9292 12662 12251 11956 11850 11541 13606 11199 14629 17828 10797 17703	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3
15           15           15           15           15           15           16           16           16           16           16           16           16           16           16           16           16           16           16           16           16           16           16           16	12618 9292 12662 12251 11956 12850 11541 13606 111541 13606 11199 14629 17828 10797 17703 15913	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosime recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA
15           15           15           15           15           16	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797 17703 15913 14527 11035	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AToC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein
15           15           15           15           15           16	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797 17703 15913 14527 11035	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein
15           15           15           15           15           15           16	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797 17703 15913 14527 11035 10540 14896	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18877           11690           18812           17298           15897           11760           12072           15390	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPI-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein
$     \begin{array}{r}       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       16 \\$	12618 9292 12662 12251 11956 11956 11541 13606 11199 14629 17828 10797 17703 15913 14527 11703 15913 14527 11035 10540 14896 10180 13197 13103	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein hypothetical protein
$     \begin{array}{r}       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       16 \\$	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797 17703 15913 14527 11035 10540 14896 10180 13197 13103	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
$     \begin{array}{r}       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       16 \\       17 \\       17 \\       17 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       17 \\       17 \\       10 \\       17 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       10 \\       17 \\       10 \\$	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797 17703 15913 14527 11035 10540 14896 10180 13197 13103 13994	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18877           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein bypothetical protein hypothetical protein
$     \begin{array}{r}       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       16 \\       17 \\       17 \\       17 \\       17 \\       17 \\       17 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       17 \\$	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797 17703 15913 14527 11035 10540 14896 10180 13197 13103 13994 14588 12017	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein ABC transporter ATP-binding protein hypothetical protein
$     \begin{array}{r}       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       17 \\       17 \\       17 \\       17 \\       17 \\       17 \\       17 \\       17 \\       17 \\       17 \\       17 \\       17 \\       17 \\       15 \\       15 \\       15 \\       16 \\       16 \\       16 \\        16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       17 $	12618 9292 12662 12251 11956 11850 11541 13606 11199 14629 17828 10797 17703 15913 14527 11035 10540 14896 10180 13197 13103 13994 14588 12017	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein ABC transporter ATP-binding protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein hypothetical protein oligopeptide ABC transporter substrate-binding protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
$     \begin{array}{r}       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       16 \\       17 \\$	12618           9292           12662           12251           11956           12850           11541           13606           11199           14629           17703           15913           14527           11035           10540           14896           10180           13197           13103           13994           14588           12017           15344	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363           19150	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein oligopeptide ABC transporter permease protein OppC sugar ABC transporter substrate-binding protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein bypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
$     \begin{array}{r}       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       17 \\$	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797 17703 15913 14527 11035 10540 14896 10180 13197 13103 13994 14588 12017 15344 18581 11710	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363           19150           13020	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569           1310	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein oligopeptide ABC transporter permease protein OppC sugar ABC transporter substrate-binding protein hypothetical protein
$     \begin{array}{r}       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       17 \\$	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797 17703 15913 14527 11035 10540 14896 10180 13197 13103 13197 13103 13994 14588 12017 15344 18581 11710 18914	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18877           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363           19150           13020           19978	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569           1310           1064	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter Permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein oligopeptide ABC transporter permease protein OppC sugar ABC transporter substrate-binding protein hypothetical protein oligopeptide ABC transporter permease protein OppC sugar ABC transporter substrate-binding protein hypothetical protein chromosome segregation and condensation protein B scpB aminotransferase domain-containing protein 6-phosphogluconolactonase
$     \begin{array}{r}       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       15 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       16 \\       17 \\$	12618           9292           12662           12251           11956           12850           11541           13606           11199           14629           17828           10797           17703           15913           14527           11035           10540           13197           13103           13197           13103           13994           14588           12017           15344           18581           11710           18914           17328	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363           19150           13020           19978           18203	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569           1310           1064	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein bypothetical protein bypothetical protein hypothetical protein bypothetical protein bypothetical protein bypothetical protein bypothetical protein bypothetical protein bypothetical protein bypothetical protein bypothetical protein chromosome segregation and condensation protein B scpB aminotransferase domain-containing protein
$     \begin{array}{r} 15 \\             15 \\             15 \\           $	12618           9292           12662           12251           11956           12850           11541           13606           11199           14629           17703           15913           14527           11035           10540           13197           13103           13994           14588           12017           15344           18581           11710           18914           17328	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363           19150           13020           19978           18203           18139	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569           1310           1064           875           2237	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein NdA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein bypothetical protein hypothetical protein hypothetical protein bypothetical protein hypothetical protein hypothetical protein hypothetical protein bypothetical protein hypothetical protein hypothetical protein bypothetical protein hypothetical protein hypothetical protein hypothetical protein bypothetical protein hypothetical protein protein fo-phosphogluconolactonase oxidoreductase NAD-binding domain-containing protein peptidase U32 family protein
$     \begin{array}{r} 15 \\             15 \\             15 \\           $	12618           9292           12662           12251           11956           12850           11541           13606           11199           14629           17703           15913           14527           100540           13197           13103           13994           14588           12017           15344           18581           11710           18914           17328           15902	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363           19150           13020           19978           18203           18139           13434	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569           1310           1064           875           2237           1262	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein ABC transporter ATP-binding protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein oligopeptide ABC transporter substrate-binding protein hypothetical protein hypothetical protein oligopeptide ABC transporter substrate-binding protein hypothetical protein bypothetical protein chromsome segregation and condensation protein B scpB aminotransferase domain-containing protein 6-phosphogluconolactonase oxidoreductase NAD-binding domain-containing protein peptidase U32 family protein
$     \begin{array}{r} 15 \\             15 \\             15 \\           $	12618           9292           12662           12251           11956           12850           11541           13606           11199           14629           17828           10797           17703           15913           14527           11035           10540           14896           10180           13103           13994           14588           12017           15344           18581           11710           18914           17328           15902           12172           13546	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363           19150           13020           19978           18139           13434           15126	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569           1310           1064           875           2237           1262           1580	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein hypothetical protein hypothetical protein bypothetical protein hypothetical protein beta
$     \begin{array}{r} 15 \\             15 \\             15 \\           $	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797 17703 15913 14527 11035 10540 14896 10180 13197 13103 13197 13103 13994 14588 12017 15344 18581 11710 18914 17328 15902 12172	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363           19150           13020           19978           18203           18139           13434           15126	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569           1310           1064           875           2237           1262	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter Permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein oligopeptide ABC transporter permease protein OppC sugar ABC transporter substrate-binding protein hypothetical protein oligopeptide ABC transporter permease protein SpA typothetical protein chromosome segregation and condensation protein hypothetical protein chromosome segregation and condensation protein hypothetical protein chromosome segregation and condensation protein hypothetical protein hypothetical protein chromosome segregation and condensation protein B scpB aminotransferase domain-containing protein peptidase U32 family protein EAL domain-containing protein EAL domain-containing protein
$     \begin{array}{r} 15 \\             15 \\             15 \\           $	12618           9292           12662           12251           11956           11541           13606           11199           14629           17828           10797           17703           15913           14527           11035           10540           14896           10180           13197           13031           13994           14588           12017           15344           18581           11710           18914           17328           15902           12172           13546           11059	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18877           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363           19150           13020           19978           18203           18139           13434           15126           11658           14849	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569           1310           1064           875           2237           1262           1580           599	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter Permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein bypothetical protein oligopeptide ABC transporter permease protein OppC sugar ABC transporter substrate-binding protein hypothetical protein bypothetical protein chromosome segregation and condensation protein bypothetical protein Brng family protein Brng family protein EAL domain-containing protein hypothetical protein
$     \begin{array}{r} 15 \\             15 \\             15 \\           $	12618 9292 12662 12251 11956 12850 11541 13606 11199 14629 17828 10797 17703 15913 14527 11035 10540 14896 10180 13197 13103 13197 13103 13994 14588 12017 15344 18581 11710 18914 17328 15902 12172	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363           19150           13020           19978           18203           18139           13434           15126	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569           1310           1064           875           2237           1262           1580           599           1187	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter Permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein oligopeptide ABC transporter permease protein OppC sugar ABC transporter substrate-binding protein hypothetical protein oligopeptide ABC transporter permease protein SpA typothetical protein chromosome segregation and condensation protein hypothetical protein chromosome segregation and condensation protein hypothetical protein chromosome segregation and condensation protein hypothetical protein hypothetical protein chromosome segregation and condensation protein B scpB aminotransferase domain-containing protein peptidase U32 family protein EAL domain-containing protein EAL domain-containing protein
$     \begin{array}{r} 15 \\             15 \\             15 \\           $	12618           9292           12662           12251           11956           12850           11541           13606           11199           14629           17828           10797           17703           15913           14527           11035           10540           14896           10180           13197           13103           13994           14588           12017           15344           18581           11710           18914           17328           15902           12172           13546           11059           13662           13602	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363           19150           13020           19978           18203           18139           13434           15126           11658           14849           14027	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569           1310           1064           875           2237           1262           1580           599           1187           425	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein hypothetical protein onrithine carbamoyltransferase Arg hypothetical protein hypothetical protein oligopeptide ABC transporter permease protein OppC sugar ABC transporter permease protein OppC sugar ABC transporter permease protein Mapothetical protein hypothetical protein bypothetical protein fo-phosphogluconolactonase oxidoreductase NAD-binding domain-containing protein Brup family protein EAL domain-containing protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
$     \begin{array}{r} 15 \\             15 \\             15 \\           $	12618           9292           12662           12251           11956           12850           11541           13606           11199           14629           17703           15913           14527           1035           10540           14896           10180           13197           13103           13994           14588           12017           15344           18581           11710           18914           17328           15902           12172           13546           11059           13662           13662	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16363           19150           13020           19978           18203           18139           13434           15126           11658           14849           14027           13940	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569           1310           1064           875           2237           1262           1580           599           1187           425           557	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein ABC transporter ATP-binding protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein oligopeptide ABC transporter permease protein OppC sugar ABC transporter aprotein hypothetical protein hypothetical protein bypothetical protein hypothetical protein bypothetical protein hypothetical protein bypothetical protein bypothetical protein hypothetical protein bypothetical protein hypothetical protein bypothetical protein bypothetical protein bypothetical protein hypothetical protein bypothetical protein
$     \begin{array}{r} 15 \\             15 \\             15 \\           $	12618           9292           12662           12251           11956           12850           11541           13606           11199           14629           17703           15913           14527           100540           13197           13103           13994           14588           12017           15344           18581           11710           18914           17328           15902           12172           13546           11059           13662           13383           15075	13421           9729           13582           13192           13026           13986           12830           14520           11951           15321           18577           11690           18812           17298           15897           11760           12072           15390           11001           13592           13408           15073           16240           13633           16363           19150           13020           19978           18203           18139           13434           15126           11658           14849           14027           13940           16010	803           437           920           941           1070           1136           1289           914           752           692           749           893           1109           1385           1370           725           1532           494           821           395           305           1079           1652           1616           1019           569           1310           1064           875           2237           1262           1580           599           1187           425           557           935	phospholipase cytidine deaminase Cdd hypothetical protein hypothetical protein oligopeptide ABC transporter ATP-binding protein OppD UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA sugar ABC transporter permease tRNA pseudouridine synthase A TruA hypothetical protein chromosome segregation and condensation protein ScpA tyrosine recombinase XerD chorismate synthase AroC NADPH-dependent glutamate synthase GltA3 rod shape-determining protein RodA PAP2 family protein ABC transporter ATP-binding protein hypothetical protein ornithine carbamoyltransferase Arg hypothetical protein oligopeptide ABC transporter permease protein OppC sugar ABC transporter substrate-binding protein hypothetical protein hypothetical protein bypothetical protein hypothetical protein Bran family protein EAL domain-containing protein hypothetical protein

18	16488	17933	1445	GGDEF domain-containing protein
18	19371	20723	1352	methylmalonyl-CoA decarboxylase alpha subunit mmdA
18	13083	14111	1028	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase
18	11551	12381	830	purine-nucleoside phosphorylase DeoD
18	20196	21269	1073	spermidine/putrescine ABC transporter ATP-binding protein PotA
18	18304	19752	1448	TPR domain-containing protein
18	18202	18609	407	cell division protein ZapA
18	11813	12790	977	glycosyl transferase GT2 family protein
18	13807	15546	1739	ABC transporter ATP-binding/permease protein
18	11715	12368	653	5'-nucleotidase domain-containing protein
18	14891	15799	908	diacylglycerol kinase family protein
18	14033	14713	680	comF family protein
18	13955	14362	407	hypothetical protein
18	16088 12919	17782 14409	1694 1490	oligopeptide ABC transporter substrate-binding protein OppA metallopeptidase M23 family protein
18	12919	16137	662	hypothetical protein
19	17936	19342	1406	GGDEF domain-containing protein
19	20741	21607	866	sodium ion-translocating decarboxylase gamma subunit
19	12403	13707	1304	amidohydrolase
19	19766	20626	860	methylenetetrahydrofolate dehydrogenase/cyclohydrolase FolD
19	18660	19670	1010	holliday junction DNA helicase RuvB
19	12845	13480	635	hypothetical protein
19	15543	17162	1619	ABC transporter ATP-binding/permease protein
19	16600	17157	557	GNAT family acetyltransferase
19	12499	13080	581	phosphoglycerate mutase family protein
19	15796	16995	1199	hypothetical protein
19	14739	16988	2249	exodeoxyribonuclease V alpha subunit RecD
19	14359	14883	524	RNA polymerase sigma factor sigma-70 family protein
19	17935	18060	125	conserved hypothetical
19	14532	14972	440	hypothetical protein
20	16314	17795	1481	sucrose-6-phosphate hydrolase Scr32A
20	16375 21621	17217 21980	842 359	polysaccharide deacetylase Est4
20	14198	16369	2171	biotin attachment domain-containing protein
20	13711	15384	1673	adenine-specific DNA methylase
20	21256	22080	824	MutS domain-containing protein spermidine/putrescine ABC transporter permease PotB
20	20721	22397	1676	formate-tetrahydrofolate ligase Fhs
20	13548	14573	1025	DNA polymerase III delta subunit HolA
20	17281	18744	1463	cobalt ABC transporter ATP-binding protein CbiO
20	17180	17347	167	hypothetical protein
20	13103	14020	917	ribosome small subunit-dependent GTPase A Rsg
	17075	17457	202	
20	17065	17457	392	hypothetical protein
20	17065	17457 15456	419	hypothetical protein HIT domain-containing protein
20	15037	15456	419	HIT domain-containing protein
20 20 20 21	15037 18403	15456 19635	419 1232	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein
20 20 20 21 21	15037 18403 15268 17799 17232	15456 19635 15921 18767 18251	419 1232 653 968 1019	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein
20 20 20 21 21 21 21	15037 18403 15268 17799 17232 19567	15456 19635 15921 18767 18251 20007	419 1232 653 968 1019 440	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfcD family protein
20 20 21 21 21 21 21 21	15037 18403 15268 17799 17232 19567 22031	15456 19635 15921 18767 18251 20007 23173	419 1232 653 968 1019 440 1142	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit
20 20 21 21 21 21 21 21 21 21	15037 18403 15268 17799 17232 19567 22031 16170	15456 19635 15921 18767 18251 20007 23173 17276	419 1232 653 968 1019 440 1142 1106	HIT domain-containing protein hypothetical protein ReIA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfcD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter
20 20 21 21 21 21 21 21 21 21 21	15037 18403 15268 17799 17232 19567 22031 16170 15384	15456 19635 15921 18767 18251 20007 23173 17276 15878	419 1232 653 968 1019 440 1142 1106 494	HIT domain-containing protein hypothetical protein ReIA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H
20 20 21 21 21 21 21 21 21 21 21 21	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700	15456 19635 15921 18767 18251 20007 23173 17276 15878 20416	419 1232 653 968 1019 440 1142 1106 494 716	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA
20 20 21 21 21 21 21 21 21 21 21 21 21	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427	419 1232 653 968 1019 440 1142 1106 494 716 686	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ
20 20 21 21 21 21 21 21 21 21 21 21	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700	15456 19635 15921 18767 18251 20007 23173 17276 15878 20416	419 1232 653 968 1019 440 1142 1106 494 716	HIT domain-containing protein         hypothetical protein         RelA/SpoT domain-containing protein         carbohydrate kinase PfkB family protein         hypothetical protein         NfeD family protein         sodium ion-translocating decarboxylase beta subunit         CDF family transporter         ribonuclease H         holliday junction DNA helicase RuvA         cobalt ABC transporter permease protein CbiQ         hypothetical protein
20 20 21 21 21 21 21 21 21 21 21 21 21 21	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397	15456 19635 15921 18767 18251 20007 23173 17276 15878 20416 19427 17876	419 1232 653 968 1019 440 1142 1106 494 716 686 479	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ
20 20 21 21 21 21 21 21 21 21 21 21 21 21 21	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 15384 19700 18741 17397 14028	15456 19635 15921 18767 18251 20007 23173 17276 15878 20416 19427 17876 16067	419 1232 653 968 1019 440 1142 1106 494 716 686 479 2039	HIT domain-containing protein           hypothetical protein           RelA/SpoT domain-containing protein           carbohydrate kinase PfkB family protein           hypothetical protein           hypothetical protein           NED family protein           sodium ion-translocating decarboxylase beta subunit           CDF family transporter           ribonuclease H           holliday junction DNA helicase RuvA           cobalt ABC transporter permease protein CbiQ           hypothetical protein           PASTA domain-containing serine/threonine protein kinase
20 20 21 21 21 21 21 21 21 21 21 21 21 21 21	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509	419 1232 653 968 1019 440 1142 1106 494 716 686 479 2039 488	HIT domain-containing protein         hypothetical protein         RelA/SpoT domain-containing protein         carbohydrate kinase PfkB family protein         hypothetical protein         NfcD family protein         sodium ion-translocating decarboxylase beta subunit         CDF family transporter         ribonuclease H         holliday junction DNA helicase RuvA         cobalt ABC transporter permease protein CbiQ         hypothetical protein         PASTA domain-containing serine/threonine protein kinase         dihydrofolate reductase FolA
20 20 21 21 21 21 21 21 21 21 21 21 21 21 21	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266	419 1232 653 968 1019 440 1142 1106 494 716 686 479 2039 488 794	HIT domain-containing protein         hypothetical protein         RelA/SpoT domain-containing protein         carbohydrate kinase PfkB family protein         hypothetical protein         NfeD family protein         sodium ion-translocating decarboxylase beta subunit         CDF family transporter         ribonuclease H         holliday junction DNA helicase RuvA         cobalt ABC transporter permease protein CbiQ         hypothetical protein         PASTA domain-containing serine/threonine protein kinase         dihydrofolate reductase FolA         flagellar basal-body rod protein FlgG
20 20 21 21 21 21 21 21 21 21 21 21 21 21 21	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185	419 1232 653 968 1019 440 1142 1106 494 716 686 479 2039 488 794 701	HIT domain-containing protein         hypothetical protein         RelA/SpoT domain-containing protein         carbohydrate kinase PfkB family protein         hypothetical protein         NfeD family protein         sodium ion-translocating decarboxylase beta subunit         CDF family transporter         ribonuclease H         holliday junction DNA helicase RuvA         cobalt ABC transporter permease protein CbiQ         hypothetical protein         PASTA domain-containing serine/threonine protein kinase         dihydrofolate reductase FolA         flagellar basal-body rod protein FlgG         LytTR/response regulator domain-containing protein
20 20 20 21 21 21 21 21 21 21 21 21 21 21 21 21	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 15384 19700 18741 17397 14028 17021 17472 15484 19686 15932 18781	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863	419 1232 653 968 1019 440 1142 1106 494 716 686 479 2039 488 794 701 668 682 929 1082	HIT domain-containing protein         hypothetical protein         RelA/SpoT domain-containing protein         carbohydrate kinase PfkB family protein         hypothetical protein         NED family protein         sodium ion-translocating decarboxylase beta subunit         CDF family transporter         ribonuclease H         holliday junction DNA helicase RuvA         cobalt ABC transporter permease protein CbiQ         hypothetical protein         PASTA domain-containing serine/threonine protein kinase         dihydrofolate reductase FoIA         flagellar basal-body ord protein FlgG         LytTR/response regulator domain-containing protein         hypothetical protein         glycosyl transferase GT2 family protein         GGDEF domain-containing protein
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20           20           20           21           22	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484 17021 17472 15484 18278 20010 23201 15895 22080 22398	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843	HIT domain-containing protein           hypothetical protein           RelA/SpoT domain-containing protein           carbohydrate kinase PfkB family protein           hypothetical protein           NED family protein           sodium ion-translocating decarboxylase beta subunit           CDF family transporter           ribonuclease H           holliday junction DNA helicase RuvA           cobalt ABC transporter permease protein CbiQ           hypothetical protein           PASTA domain-containing serine/threonine protein kinase           dihydrofolate reductase FolA           flagellar basal-body rod protein FlgG           LytTR/response regulator domain-containing protein           glycosyl transferase GT2 family protein           GGDEF domain-containing protein           uridylate kinase PyrH           SPFH domain/containing protein           oxaloacetate decarboxylase alpha subunit oadA           metallophosphoesterase           spermidine/putrescine ABC transporter permease PotC           FtsK/SpoIIIE family protein
20           20           20           21           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484 19686 15932 18781 18278 20010 23201 15895 22080 22398 20424	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049	HIT domain-containing protein hypothetical protein ReIA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine/threonine protein kinase dihydrofolate reductase FoIA flagellar basal-body rod protein FlgG LytTR/response regulator domain-containing protein glycosyl transferase GT2 family protein GGDEF domain-containing protein uridylate kinase PyrH SPFH domain/band 7 family protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoesterase spermidine/putrescine ABC transporter permease PotC FtsK/SpOIIIE family protein branched-chain amino acid aminotransferase IIvE
20           20           20           21           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22	15037 18403 15268 17799 17232 19567 22031 16170 15384 17397 14028 17021 17472 15484 19686 15932 18781 18278 20010 23201 15895 22080 22398 20424 14650	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965	419 1232 653 968 1019 440 1142 1106 494 716 686 479 2039 488 794 701 668 929 1082 695 917 1412 632 788 2843 1049 2315	HIT domain-containing protein         hypothetical protein         RelA/SpoT domain-containing protein         carbohydrate kinase PfkB family protein         hypothetical protein         hypothetical protein         NfeD family protein         sodium ion-translocating decarboxylase beta subunit         CDF family transporter         ribonuclease H         holliday junction DNA helicase RuvA         cobalt ABC transporter permease protein CbiQ         hypothetical protein         PASTA domain-containing serine/threonine protein kinase         dihydrofolate reductase FolA         flagellar basal-body rod protein FlgG         LytTR/response regulator domain-containing protein         glycosyl transferase GT2 family protein         glycosyl transferase GT2 family protein         GGDEF domain/band 7 family protein         oxaloacetate decarboxylase alpha subunit oadA         metallophosphoesterase         spermidine/putrescine ABC transporter permease PotC         FtsK/SpOIIIE family protein         branched-chain amino acid aminotransferase IIvE         DNA internalization-related competence protein ComEC
20           20           20           21           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22	15037 18403 15268 17799 17799 17732 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484 19686 15932 18781 18278 20010 23201 15895 22080 22398 20424 14650 17869	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965           18330	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049           2315           461	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine/threonine protein kinase dihydrofolate reductase FolA flagellar basal-body rote protein FlgG LytTR/response regulator domain-containing protein glycosyl transferase GT2 family protein GGDEF domain-containing protein uridylate kinase PyrH SPFH domain-containing protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoesterase spermidine/putrescine ABC transporter permease PotC FtsK/SpoIIIE family protein branched-chain amino acid aminotransferase IIVE
20           20           20           21           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 17472 17472 15484 19686 15932 18781 18278 20010 23201 15895 22080 22398 20424 14650 17869 16060	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965           18330           16650	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049           2315           461	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine/threonine protein kinase dihydrofolate reductase FoIA flagellar basal-body rod protein FlgG LytTR/response regulator domain-containing protein glycosyl transferase GT2 family protein GGDEF domain-containing protein uridylate kinase PyrH SPFH domain-containing protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoesterase spermidine/putrescine ABC transporter permease PotC FtsK/SpoIIIE family protein DNA internalization-related competence protein ComEC NUDIX domain-containing protein
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20           20           20           21           22	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484 19000 18741 17397 14028 17021 17472 15484 19950 22010 23201 15895 22080 22398 20424 14650 17869 16060 18423 16206	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965           18330           16650           19253           16961	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049           2315           461           590           830           755	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NED family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine/threonine protein kinase dihydrofolate reductase FoIA flagellar basal-body rod protein FlgG LytTR/response regulator domain-containing protein glycosyl transferase GT2 family protein GGDEF domain-containing protein uridylate kinase PyrH SPFH domain/band 7 family protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoesterase spermidine/purtescine ABC transporter permease PotC FtsK/SpoIIIE family protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein serine/threonine protein protein flgG hypothetical protein FlgG
20           20           20           21           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484 19686 15932 18781 18278 20010 23201 15895 22080 22398 20424 14650 17869 16060 18423 16206 19956	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965           18330           16650           19253           16961           21005	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049           2315           461           590           830           755           1049	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine/threonine protein kinase dihydrofolate reductase FoIA flagellar basal-body rod protein FlgG LytTR/response regulator domain-containing protein glycosyl transferase GT2 family protein GGDEF domain/containing protein uridylate kinase PyrH SPFH domain/band 7 family protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoesterase spermidine/putrescine ABC transporter permease PotC FtsK/SpOIIIE family protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein serine/threonine protein flgG
20           20           20           21           22	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484 19000 18741 17397 14028 17021 17472 15484 19950 22010 23201 15895 22080 22398 20424 14650 17869 16060 18423 16206	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965           18330           16650           19253           16961	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049           2315           461           590           830           755	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NED family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine/threonine protein kinase dihydrofolate reductase FoIA flagellar basal-body rod protein FlgG LytTR/response regulator domain-containing protein glycosyl transferase GT2 family protein GGDEF domain-containing protein uridylate kinase PyrH SPFH domain/band 7 family protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoesterase spermidine/purtescine ABC transporter permease PotC FtsK/SpoIIIE family protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein serine/threonine protein protein flgG hypothetical protein FlgG
20           20           20           21           22           22           22           22           22           22           22           22           22           22           22           22           22           23	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484 19686 15932 18781 18278 20010 23201 15895 22080 22398 20124 14650 17869 16060 18423 16206 19956 19001	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965           18330           16650           19253           16961           21005           19552	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049           2315           461           590           830           755           1049           551	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine//hreonine protein kinase dihydrofolate reductase FoIA flagellar basal-body rot protein FlgG LytTR/response regulator domain-containing protein glycosyl transferase GT2 family protein GGDEF domain-containing protein glycosyl transferase GT2 family protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoesterase spermidine/putrescine ABC transporter permease PotC FtsK/SpoIIIE family protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein serine//hreonine protein FlgG hypothetical protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein serine/hreonine protein FlgG hypothetical protein hypothetical protein flagellar basal-body rod protein FlgG
20           20           20           21           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484 19686 15932 18781 18278 20010 23201 15895 22080 22398 20424 14650 17869 16060 18423 16206 19956	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965           18330           16650           19253           16961           21005           19552           18669	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049           2315           461           590           830           755           1049           551           1343	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine/threonine protein kinase dihydrofolate reductase FolA flagellar basal-body rod protein FlgG LytTR/response regulator domain-containing protein glycosyl transferase GT2 family protein GGDEF domain-containing protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoesterase spermidine/putrescine ABC transporter permease PotC FtsK/SpoIIIE family protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein serine/threonine protein FlgG hypothetical protein flagellar basal-body rod protein flgG ftsK/SpoIIIE family protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein serine/threonine protein flgG hypothetical protein hypothetical protein flagellar basal-body rod protein FlgG
20           20           20           21           22	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484 19686 15932 18781 18278 20010 23201 15895 22080 22398 20424 14650 17869 16060 18423 16206 19956 19956	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965           18330           16650           19253           16961           21005           19552           18669           17518	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049           2315           461           590           830           755           1049           551           1343           1001	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine/threonine protein kinase dihydrofolate reductase FolA flagellar basal-body rod protein FlgG LyfTR/response regulator domain-containing protein glycosyl transferase GT2 family protein GGDEF domain-containing protein uridylate kinase PyrH SPFH domain/band 7 family protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoesterase spermidine/putrescine ABC transporter permease PotC FtsK/SpoIIIE family protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDDIX domain-containing protein serine/threonine protein flgG hypothetical protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDDIX domain-containing protein hypothetical protein serine/threonine protein plosphatase flagellar basal-body rod protein FlgG hypothetical protein hypothetical protein hypothetical protein hypothetical protein
20           20           20           21           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           22           23           23           23	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 15384 19700 18741 17397 14028 17021 17472 15484 17021 17472 15484 18278 20010 23201 15895 22080 22398 20424 14650 17869 16060 18423 16206 19956 19001 17326 16517 22858	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965           18330           16650           19253           16961           21005           19552           18669           17518           23928	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049           2315           461           590           830           755           1049           551           1343           1001           1070	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfcD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine/threonine protein kinase dihydrofolate reductase FoIA flagellar basal-body rod protein FlgG LytTR/response regulator domain-containing protein glycosyl transferase GT2 family protein GGDEF domain-containing protein uridylate kinase PyrH SPFH domain/band 7 family protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoesterase spermidine/putrescine ABC transporter permease PotC FtsK/SpoIIIE family protein serine/threonine protein flgG hypothetical protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein serine/threonine protein flgG hypothetical protein flagellar basal-body rod protein FlgG hypothetical protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein hypothetical protein hypothetical protein flgG
20           20           20           21           22           22           22           22           22           22           22           22           22           22           22           23           23           23           23           23           23	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484 19686 15932 18781 18278 20010 23201 15895 22080 22398 20424 14650 17869 16060 18423 16206 19956 19001 17326 16517 22858 25410 21529 16986	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965           18330           16650           19253           16961           21005           19552           18669           17518           23928           22944           17849	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049           2315           461           590           830           755           1049           551           1343           1001           1070           572           1415	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine/threonine protein kinase dihydrofolate reductase FoIA flagellar basal-body rod protein FlgG LytTR/response regulator domain-containing protein glycosyl transferase GT2 family protein GGDEF domain/band 7 family protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoseterase spermidine/putrescine ABC transporter permease PotC FtsK/SpOIIE family protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein serine/htreonine protein flgG hypothetical protein flagellar basal-body rod protein FlgG flagellar basal-body rod protein flgG flagellar basal-body rod protein glycosyl transferase GT2 family protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoseterase spermidine/putrescine ABC transporter permease PotC FtsK/SpOIIE family protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein serine/htreonine protein phosphatase flagellar basal-body rod protein FlgG hypothetical protein hypothetical protein tryptophanyl-tRNA synthetase trpS spermidine/putrescine ABC transporter substrate-binding protein PotD hypothetical protein
20           20           20           21           22           22           22           22           22           22           22           22           22           22           23           23           23           23           23           23           23	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484 19686 15932 18781 18278 20010 23201 15895 22080 22398 20424 14650 17869 16060 18423 16206 19957 19956 19	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965           18330           16650           19253           16961           21005           19552           18669           17518           23928           22944           17849           19170	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049           2315           461           590           830           755           1049           551           1343           1001           1070           572           1415           863           719	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfcD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine/threonine protein kinase dihydrofolate reductase FoIA flagellar basal-body rod protein FlgG LytTR/response regulator domain-containing protein glycosyl transferase GT2 family protein glycosyl transferase GT2 family protein glycosyl transferase GT2 family protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoesterase spermidine/putrescine ABC transporter permease PotC FtsK/SpOIIIE family protein serine/threonine rotein flgG hypothetical protein figgellar basal-body rod protein FlgG furtice transporter permease PotC ftsK/SpOIIIE family protein oxaloacetate decarboxylase alpha subunit oadA metallophosphoesterase spermidine/putrescine ABC transporter permease PotC ftsK/SpOIIIE family protein serine/threonine protein flgG hypothetical protein hypothetical protein flagellar basal-body rod protein FlgG hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
20           20           21           22           22           22           22           22           22           22           22           22           22           23           23           23           23           23	15037 18403 15268 17799 17232 19567 22031 16170 15384 19700 18741 17397 14028 17021 17472 15484 19686 15932 18781 18278 20010 23201 15895 22080 22398 20424 14650 17869 16060 18423 16206 19956 19001 17326 16517 22858 25410 21529 16986	15456           19635           15921           18767           18251           20007           23173           17276           15878           20416           19427           17876           16067           17509           18266           16185           20354           16861           19863           18973           20927           24613           16527           22868           25241           21473           16965           18330           16650           19253           16961           21005           19552           18669           17518           23928           22944           17849	419           1232           653           968           1019           440           1142           1106           494           716           686           479           2039           488           794           701           668           929           1082           695           917           1412           632           788           2843           1049           2315           461           590           830           755           1049           551           1343           1001           1070           572           1415	HIT domain-containing protein hypothetical protein RelA/SpoT domain-containing protein carbohydrate kinase PfkB family protein hypothetical protein NfeD family protein sodium ion-translocating decarboxylase beta subunit CDF family transporter ribonuclease H holliday junction DNA helicase RuvA cobalt ABC transporter permease protein CbiQ hypothetical protein PASTA domain-containing serine/threonine protein kinase dihydrofolate reductase FoIA flagellar basal-body rod protein FlgG LytTR/response regulator domain-containing protein glycosyl transferase GT2 family protein glycosyl transferase GT2 family protein oxaloacetate decarboxylase lapha subunit oadA metallophosphoesterase spermidine/putrescine ABC transporter permease PotC FtsK/SpoIIIE family protein branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein serine/threonine protein flgG branched-chain amino acid aminotransferase IIvE DNA internalization-related competence protein ComEC NUDIX domain-containing protein serine/threonine protein protein flgG hypothetical protein flagellar basal-body rod protein FlgG hypothetical protein serine/threonine protein phosphatase flagellar basal-body rod protein FlgG hypothetical protein hypothetical protein

23 23 23 24 24 24 24 24	19317 20344 16957 21098	20309 21015 17880	992 671	thymidylate synthase thyA cell shape determining protein MreB hypothetical protein
23 24 24 24 24	16957		671	hypothetical protein
24 24 24 24		17880		nypotietietii protein
24 24	21098	21000	923	cell envelope-related transcriptional attenuator
24		22099	1001	glycosyl transferase GT2 family protein
	20974	22791	1817	ABC transporter ATP-binding/permease
24	17602	18255	653	transaldolase
24 24	24173 26040	24859	686	hypothetical protein
24 24	26040	27908 23798	1868 827	glucosamine-fructose-6-phosphate aminotransferase GlmS hypothetical protein
24	17918	19312	1394	two component system histidine kinase
24	19451	20134	683	hypothetical protein
24	19214	19339	125	hypothetical protein
24	17905	19257	1352	rRNA small subunit methyltransferase B Sun
24	18436	20040	1604	RNA-metabolising metallo-beta-lactamase
24	21031	21945	914	hypothetical protein
24	17955	18284	329	hypothetical protein
25	24742	26922	2180	glycogen debranching enzyme GlgX
25	22099	23136	1037	CDP-glucose 4,6-dehydratase rfbG
25	19556	20281	725	undecaprenyl pyrophosphate synthase UppS
25	18965	20536	1571	beta-lactamase family protein
25 25	18540	22781 24816	4241 1001	CnaB domain-containing cell-surface protein
25	23815 19432	24816	680	glycosyl transferase GT2 family protein two component system response regulator
25	20187	20999	812	hypothetical protein
25	20187	21353	1145	hypothetical protein
25	20474	23350	2876	excinuclease ABC subunit A uvrA
25	17004	17948	944	hypothetical protein
25	21942	22316	374	hypothetical protein
26	23149	24495	1346	DegT/DnrJ/EryC1/StrS family aminotransferase
26	20306	21130	824	phosphatidate cytidylyltransferase CdsA
26	22956	24605	1649	ABC transporter ATP-binding/permease
26	26909	27514	605	hypothetical protein
26	20580	21149	569	hypothetical protein
26	22768	23382	614	sortase family protein
26 26	27987 24907	28790 25395	803 488	glutamate 5-kinase ProB
26	20131	20778	647	3-isopropylmalate dehydratase small subunit LeuD competence protein ComE
26	19320	19835	515	DNA topology modulation protein FlaR-related protein
26	19311	20585	1274	Na+dependent transporter SNF family
26	23396	25393	1997	excinuclease ABC subunit B uvrB
26	17990	18646	656	NUDIX domain-containing protein
26	18382	19788	1406	exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase
27	21364	23358	1994	xylosidase
27	24497	25405	908	NAD-dependent epimerase/dehydratase
27	24612	25514	902	metallophosphoesterase
27	27532	28209	677	two component system response regulator
27	21431	22978	1547	cysteine protease C1 family protein
27	25414	26685	1271	3-isopropylmalate dehydratase large subunit LeuC
27 27	20825 19891	22267 20343	1442 452	sugar ABC transporter substrate-binding protein
27	20689	20343	560	hypothetical protein hypothetical protein
27	21369	221249	755	hypothetical protein
27	25464	25703	239	hypothetical protein
27	22682	26167	3485	GGDEF/EAL domain-containing protein
27	19785	20756	971	glycosyl transferase GT2 family protein
28	25414	26952	1538	glycosyl transferase GT2 family protein
28	21322	22464	1142	1-deoxy-D-xylulose-5-phosphate reductoisomerase Dxr
28	25539	26021	482	hypothetical protein
28	23082	23372	290	hypothetical protein
28	23475	25028	1553	SSS family transporter
28	29470	30648	1178	acyltransferase
28 28	26771 22324	29233	2462	hypothetical protein
28	22324 21429	23523 22361	932	acetylornithine aminotransferase ArgD methionyl-tRNA formyltransferase fmt
28	21429 25700	26656	932	serine/threonine protein kinase
28	18750	19559	809	FRG domain-containing protein
28	20760	22163	1403	glycosyl transferase GT2 family protein
29	27065	27694	629	hypothetical protein
29	22472	23524	1052	peptidase M50 family protein
29	26389	26673	284	chaperonin GroES
29	28280	29722	1442	two component system histidine kinase
29	23725	24912	1187	cobalamin biosynthesis protein CbiD
29	30684	31154	470	SsrA-binding protein SmpB
29	29302	30330	1028	ketol-acid reductoisomerase IlvC
	23385	24242	857	sugar ABC transporter permease
29	22469	23344	875	amino acid ABC transporter substrate-binding protein
29	22272		584	hypothetical protein
29 29	23272	23856		
29 29 29	26659	27408	749	serine/threonine protein phosphatase
29 29	26659 19702	27408 20484		serine/threonine protein phosphatase hypothetical protein
29 29 29 29 29	26659	27408	749 782	serine/threonine protein phosphatase

30	23541	24599	1058	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase IspG
30	26726	28348	1622	chaperonin GroEL
30	29734	30615	881	hypothetical protein
30	24934	26379	1445	glycogen synthase ADP-glucose type GlgA
30	25040	25510	470	GNAT family acetyltransferase
30	30545	31048	503	acetolactate synthase small subunit IlvH
30	23545	24441	896	acetylglutamate kinase ArgB
30	24242	25153	911	hypothetical protein
30	23390	24130	740	amino acid ABC transporter ATP-binding protein
30	20561	22123	1562	sugar ABC transporter substrate-binding protein
30	27604	28740	1136	AAA family ATPase
30	24009	26063	2054	glycosyl transferase GT2 family protein
31	25566	26000	434	ACT domain-containing protein
31	31319	32629	1310	hypothetical protein
31	20528	22057	1529	GDSL-family lipase/acylhydrolase
31	27504	28769	1265	C-terminal processing peptidase prc
31	28773	30431	1658	hypothetical protein
31	26079	28190	2111	glycosyl transferase GT2 family protein
32	28504	29691	1187	UDP-galactopyranose mutase glf
32 32	24635	29164	4529	DNA polymerase III C PolC
32	28778 31345	30226 31452	1448 107	arginine decarboxylase SpeA
				hypothetical protein
32 32	26389 26038	28041 27339	1652 1301	polysaccharide biosynthesis protein phenylacetyl-CoA ligase PaaK
32	31173	33632	2459	ribonuclease R Rnr
32	31173	33369	752	hypothetical protein
32	24452	25690	1238	arginine biosynthesis bifunctional protein ArgJ
32	24432	22616	515	hypothetical protein
32	24143	24817	674	amino acid ABC transporter permease
32	23971	25338	1367	potassium uptake protein TrkH family protein
32	28794	30026	1232	metallopeptidase M23 family protein
32	22184	23014	830	sugar ABC transporter permease
32	28202	29137	935	SAM-dependent methyltransferase
33	29861	31165	1304	flagellar hook-associated protein FliD
33	29744	30199	455	hypothetical protein
33	30428	31300	872	spermidine synthase SpeE
33	28474	29391	917	hypothetical protein
33	27366	27944	578	indolepyruvate ferredoxin oxidoreductase beta subunit IorB
33	33716	33958	242	hypothetical protein
33	25690	26133	443	GNAT family acetyltransferase
33	25285	26745	1460	sugar ABC transporter substrate-binding protein
33	22713	23156	443	hypothetical protein
33	24858	25364	506	peptide deformylase def
33	25420	26781	1361	potassium uptake protein TrkA family protein
33	30491	31687	1196	flavodoxin/beta-lactamase domain-containing protein
33	29113	30360	1247	SAM-dependent methyltransferase
34	30331	31335	1004	beta-lactamase family protein
34	29442	29720	278	hypothetical protein
34	27948	29702	1754	indolepyruvate ferredoxin oxidoreductase alpha subunit IorA
34	34046	35593	1547	2,3-bisphosphoglycerate-independent phosphoglycerate mutase GpmA
34	33530	37234	3704	hypothetical protein
34	26157	27221	1064	N-acetyl-gamma-glutamyl-phosphate reductase ArgC
34	23153 23011	23566 23901	413 890	hypothetical protein
34	31707	34802	3095	sugar ABC transporter permease
34	30380	34802 31705	1325	two component system histidine kinase/response regulator hybrid protein polysaccharide ABC transporter ATP-binding protein
35	31283	33157	1874	hypothetical protein
35	31535	31999	464	molecular chaperone Hsp
35	31404	32666	1262	carboxynorspermidine dehydrogenase
35	29892	31526	1634	AMP-binding enzyme
35	27461	28699	1238	argininosuccinate synthase ArgG
35	23846	24439	593	MFS transporter
35	25505	27751	2246	primosomal protein N' pri
35	26923	27465	542	flavodoxin family protein
35	30019	30765	746	cell division permease FtsX
35	23898	25004	1106	sugar ABC transporter ATP-binding protein
35	34823	36193	1370	sugar ABC transporter substrate-binding protein
35	31779	32768	989	polysaccharide ABC transporter permease
36	33280	33429	149	ribosomal protein L33 rpmG
36	32821	33879	1058	hypothetical protein
36	29899	30945	1046	glutamyl aminopeptidase M42 family
36	31871	32191	320	hypothetical protein
36	37677	38159	482	acetolactate synthase small subunit IlvH
36	27498	28100	602	hypothetical protein
36	30905	31645	740	cell division ATP-binding protein FtsE
36	25020	25190	170	hypothetical protein
36	36222	36737	515	hypothetical protein
36	32777	33322	545	dTDP-4-dehydrorhamnose 3,5-epimerase RfbC2
37	33461	33739	278	preprotein translocase subunit secE
	32079	32903	824	hypothetical protein
37			101	
37 37	33881	34075	194	hypothetical protein
37			194 1865 2597	hypothetical protein fibronectin-binding A domain-containing protein heavy metal translocating P-type ATPase

37         35738         37459         1721         hypothetical pr           37         38202         39827         1625         acetolactate synthase larg           37         27771         29258         1487         UDP-N-acetylmuramoylalanyl-D-glutamate           37         31659         32741         1082         hypothetical pr           37         25187         25519         332         hypothetical pr           37         36748         37251         503         transcription elongation fa           37         36748         37251         503         transcription elongation fa           37         3350         33811         461         hypothetical pr           38         34100         34828         728         ABC transporter ATP-b           38         34833         35270         437         dUTP diplosphat           38         27115         28101         986         AraC family transcriptic           38         29416         31212         1796         ssDNA exonuclea           38         28114         29724         1610         hypothetical pr           38         32970         33158         188         hypothetical pr <td< th=""><th>ge subunit IIvB -2,6- diaminopimelate ligase Mur otein otein ctor GreA/GreB2 otein inding protein ase Dut onal regulator use RecJ</th></td<>	ge subunit IIvB -2,6- diaminopimelate ligase Mur otein otein ctor GreA/GreB2 otein inding protein ase Dut onal regulator use RecJ
37         31659         32741         1082         hypothetical pr           37         25187         25519         332         hypothetical pr           37         36748         37251         503         transcription elongation fa           37         36748         37251         503         transcription elongation fa           37         33350         33811         461         hypothetical pr           38         34100         34828         728         ABC transporter ATP-b           38         34833         35270         437         dUTP diphosphat           38         27115         28101         986         AraC family transcriptio           38         29416         31212         1796         ssDNA exonuclea           38         28114         29724         1610         hypothetical pr           38         32970         33158         188         hypothetical pr           38         25532         27070         1538         2Fe-2S iron-sulfur cluster binding d           38         37323         38186         863         fructose-1,6-bisphosphate	otein otein tor GreA/GreB2 otein inding protein ase Dut onal regulator use RecJ
37         25187         25519         332         hypothetical pr           37         36748         37251         503         transcription elongation fac           37         33350         33811         461         hypothetical pr           38         34100         34828         728         ABC transporter ATP-b           38         34833         35270         437         dUTP diphosphat           38         27115         28101         986         AraC family transcription           38         29416         31212         1796         ssDNA exonuclea           38         28114         29724         1610         hypothetical pr           38         32970         33158         188         hypothetical pr           38         32532         27070         1538         2Fe-2S iron-sulfur cluster binding d           38         3732	otein tor GreA/GreB2 otein inding protein ase Dut onal regulator use RecJ
37         36748         37251         503         transcription elongation fac           37         33350         33811         461         hypothetical pr           38         34100         34828         728         ABC transporter ATP-b           38         34833         35270         437         dUTP diphosphat           38         27115         28101         986         AraC family transcription           38         29416         31212         1796         ssDNA exonuclea           38         28114         29724         1610         hypothetical pr           38         32970         33158         188         hypothetical pr           38         32532         27070         1538         2Fe-2S iron-sulfur cluster binding d           38         37323         38186         863         fructose-1,6-bisphosphate	ctor GreA/GreB2 otein inding protein ase Dut onal regulator se RecJ
37         33350         33811         461         hypothetical pr           38         34100         34828         728         ABC transporter ATP-b           38         34833         35270         437         dUTP diphosphat           38         24833         35270         437         dUTP diphosphat           38         24115         28101         986         AraC family transcriptic           38         29416         31212         1796         ssDNA exonuclea           38         28114         29724         1610         hypothetical pr           38         32970         33158         188         hypothetical pr           38         2532         27070         1538         2Fe-2S iron-sulfur cluster binding d           38         37323         38186         863         fructose-1,6-bisphosphate	otein inding protein ase Dut onal regulator se RecJ
38         34100         34828         728         ABC transporter ATP-b           38         34833         35270         437         dUTP diphosphat           38         24813         35270         437         dUTP diphosphat           38         27115         28101         986         AraC family transcripti           38         29416         31212         1796         ssDNA exonuclea           38         28114         29724         1610         hypothetical pr           38         32970         33158         188         hypothetical pr           38         25532         27070         1538         2Fe-2S iron-sulfur cluster binding d           38         37323         38186         863         fructose-1,6-bisphosphate	inding protein ase Dut onal regulator se RecJ
38         34833         35270         437         duTP diphosphat           38         27115         28101         986         AraC family transcription           38         29416         31212         1796         ssDNA exonuclea           38         28114         29724         1610         hypothetical pr           38         32970         33158         188         hypothetical pr           38         25532         27070         1538         2Fe-2S iron-sulfur cluster binding d           38         37323         38186         863         fructose-1,6-bisphosphate	ase Dut onal regulator se RecJ
38         27115         28101         986         AraC family transcriptic           38         29416         31212         1796         ssDNA exonuclea           38         28114         29724         1610         hypothetical pr           38         32970         33158         188         hypothetical pr           38         25532         27070         1538         2Fe-2S iron-sulfur cluster binding d           38         37323         38186         863         fructose-1,6-bisphosphate	onal regulator ise RecJ
38         29416         31212         1796         ssDNA exonuclea           38         28114         29724         1610         hypothetical pr           38         32970         33158         188         hypothetical pr           38         25532         27070         1538         2Fe-2S iron-sulfur cluster binding d           38         37323         38186         863         fructose-1,6-bisphosphate	ise RecJ
38         28114         29724         1610         hypothetical pr           38         32970         33158         188         hypothetical pr           38         25532         27070         1538         2Fe-2S iron-sulfur cluster binding d           38         37323         38186         863         fructose-1,6-bisphosphate	
38         32970         33158         188         hypothetical pr           38         25532         27070         1538         2Fe-2S iron-sulfur cluster binding d           38         37323         38186         863         fructose-1,6-bisphosphate	
38         25532         27070         1538         2Fe-2S iron-sulfur cluster binding d           38         37323         38186         863         fructose-1,6-bisphosphate	
38         37323         38186         863         fructose-1,6-bisphosphate	
, <b>1</b> 1	01
38 33867 34736 869 glucose-1-phosphate thymidy	
39         38274         40367         2093         alpha-amylase Ar	
39         33756         34379         623         transcription termination/antiter	
39         32915         33574         659         two component system res	
39 33020 34519 1499 altronate oxidoreduc	
39 35353 36816 1463 glutamyl-tRNA synth	
39 29017 29781 764 response regulator domain-c	
39 28128 30449 2321 hypothetical pri	otein
39 32331 34616 2285 protein-export membrane	
39 33206 34132 926 CAAX amino terminal prote	ase family protein
39 34758 35843 1085 dTDP-glucose 4,6-deby	
40 34506 34931 425 ribosomal protein I	
40 36797 38725 1928 UvrD/REP family ATP-deper	
40 39846 42287 2441 methionine synthat	
40 29875 30711 836 degV family pr	
40 30461 31159 698 hypothetical pr	
40 34637 36073 1436 radical SAM domain-con	
40 29797 31680 1883 threonyl-tRNA synth	
40 34142 34990 848 hypothetical pro-	
40 27205 28365 1160 hypothetical pr	
41 34945 35634 689 ribosomal protein	
41 33604 34458 854 hypothetical pr	
41 34572 36131 1559 ABC transporter ATP-b	
41         37478         38671         1193         CDF family trans           41         42284         43336         1052         hypothetical pr	*
41         30729         31214         485         hypothetical pr           41         31191         31670         479         hypothetical pr	
41         35005         35739         734         acyl-ACP thioes	
41         40568         42427         1859         ATP-dependent metallop	
41 35876 37267 1391 Hypothetical pr	
42 39194 41140 1946 glycogen debranching e	
42 34706 35356 650 PAP2 family pr	
42 34818 36431 1613 hypothetical pr	
42 38668 39339 671 thiamine pyrophosp	bhokinase
42 43333 43821 488 hypothetical pr	otein
42 31220 31579 359 Hpt domain-containi	ng protein
42 31876 32307 431 hypothetical pr	otein
42 31771 32250 479 SEC-C domain-contai	
42 42452 42976 524 hypoxanthine phosphoribos	yltransferase Hpt
43 37349 40990 3641 lysozyme Ly	
43 35812 36954 1142 capsule biosynthesi	-
43 36492 37655 1163 carboxynorspermidine deca	
43 41137 42381 1244 tripeptide aminopept	-
43         39339         40703         1364         hypothetical pr           43         43872         44297         425         ATP synthase F1 epsilon	
43         31670         32737         1067         peptide chain release fi           43         32405         32926         521         hypothetical pr	
43         32405         32926         521         hypothetical pr           43         32588         33415         827         hypothetical pr	
43         5238         53413         827         hypothetical pr           43         28388         29434         1046         hypothetical pr	
43         2336         27434         1040         hypothetical picture           43         42981         44393         1412         tRNA(Ile)-lysidine syn	
43         4251         4435         1412         Hittage           44         37167         37742         575         ribosomal protein I	
44         37687         38925         1238         agmatine deiminas	-
44         42385         43827         1442         tRNA-thiotransferase e	
44         44301         45665         1364         ATP synthase F1 beta s	-
44 32785 33624 839 methyltransferase	
44 33121 33876 755 hypothetical pr	
44 36391 37671 1280 hypothetical pr	
44 33501 34727 1226 L,L-diaminopimelate am	inotransferase
44 35996 38107 2111 glutamine synthetase tr	ype III GlnA
44 44455 44766 311 septum formation init	iator DivIC
45 35353 36699 1346 MatE efflux family	y protein
45 38944 39843 899 N-carbamoylputrescine amic	dohydrolase AguB
45 36191 38299 2108 hypothetical pr	
45 40930 41574 644 sugar-phosphate isomerase L	
45 45679 46542 863 ATP synthase F1 gamma	
45 33631 34689 1058 hypothetical pr	
45 37695 38009 314 L-rhamnose 1-epim	
45 38206 39372 1166 peptidase U32 famil	ly protein

45	20456	20246	800	hymothesisal protein
45	29456 44835	30346 45074	890 239	hypothetical protein RNA-binding S4 domain-containing protein
43	44833	43529	1892	Alpha-L-arabinofuranosidase
46	37814		377	*
		38191		ribosomal protein L7/L12 rplL
46 46	36831	37745	914 569	LysR family transcriptional regulator
	38375	38944		hypothetical protein
46 46	43857	46535	2678	DNA mismatch repair protein MutS
-	46598	48391	1793	ATP synthase F1 alpha subunit AtpA
46	34770	34976	206	ribosomal protein L31 RpmE
46	38033	39298	1265	histidyl-tRNA synthetase his
46	35006	35917	911	diaminopimelate epimerase dapF
46	39441	40088	647	O-methyltransferase
46	41116	42621	1505	hypothetical protein
47	37951	38886	935	cysteine synthase CysK
47	39877	40698	821	hypothetical protein
47	38975	39889	914	hypothetical protein
47	46536	48458	1922	DNA mismatch repair protein MutL
47	43546	44400	854	HAD superfamily hydrolase
47	48384	48875	491	ATP synthase F0 B subunit AtpF
47	35086	35709	623	RNA polymerase sigma factor sigma-70 family protein
47	33876	35204	1328	hypothetical protein
47	39372	40952	1580	EAL domain-containing protein
47	36165	38033	1868	ABC transporter ATP binding/permease
47	40078	40569	491	hypothetical protein
47	45075	46658	1583	PEGA domain-containing protein
48	38530	42351	3821	DNA-directed RNA polymerase beta subunit rpoB
48	40695	41930	1235	hypothetical protein
48	48455	49393	938	tRNA delta(2)-isopentenylpyrophosphate transferase MiaA
48	44393	45607	1214	ion transport protein
48	35715	36464	749	rRNA methylase SpoU family protein
48	41327	43279	1952	EAL domain-containing protein
48	30407	32185	1778	GGDEF domain-containing protein
48	46785	48143	1358	tRNA nucleotidyltransferase Cca
48	42655	44067	1412	hypothetical protein
49	42396	46133	3737	DNA directed RNA polymerase beta-prime subunit RpoC
49	39067	39975	908	LysR family transcriptional regulator
49	40091	41815	1724	hypothetical protein
49	49386	50669	1283	aluminum resistance protein
49	48890	49108	218	ATP synthase F0 C subunit AtpE
49	36480	36917	437	ribonuclease III family protein
49	43303	43605	302	hypothetical protein
49	38035	39843	1808	ABC transporter ATP binding/permease
49	32196	33869	1673	GGDEF domain-containing protein
49	44182	44526	344	hypothetical protein
50	46278	46697	419	ribosomal protein S12 rpsL
50	41985	42872	887	molecular chaperone Hsp33
50	42103	42951	848	hypothetical protein
50	50749	51462	713	DNA repair protein RadC
50	39936	40598	662	two component system histidine kinase
51	43654	45861	2207	beta-galactosidase Bga35
51	46817	47332	515	ribosomal protein S7 rpsG
51	40005	40907	902	AraC family transcriptional regulator
51	43469	44932	1463	Type I restriction-modification system methyltransferase subunit
51	51472	52476	1004	rod shape-determining protein MreB
51	45635	47479	1844	RNA helicase DEAD/DEAH box family protein
51	49655	49795	140	hypothetical protein
51	36902	38326	1424	cysteinyl-tRNA synthetase CysS
51	40603	41301	698	two component system response regulator
51	40591	42270	1679	RNA-metabolising metallo-beta-lactamase
51	33871	34398	527	hypothetical protein
51	48222	49940	1718	GGDEF domain-containing protein
51	44523	44906	383	hypothetical protein
52	47435	49504	2069	translation elongation factor G fusA
52	40982	42361	1379	MatE efflux family protein
52	44956	46140	1184	hypothetical protein
52	52477	53346	869	rod shape-determining protein MreC
52	47508	48050	542	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase PgsA
52	49130	49873	743	ATP synthase F0 A subunit AtpB
52	38352	38897	545	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase IspF
52	41314	42150	836	SAM-dependent methyltransferase
52	42332	42607	275	hypothetical protein
52	44912	45883	971	hypothetical protein
53	43061	44782	1721	methyl-accepting chemotaxis protein Mcp
53	53352	53876	524	rod shape-determining protein MreD
53	48050	49408	1358	MiaB-like tRNA modifying enzyme
53	38947	39222	275	branched-chain amino acid transport protein AzID
53	45887	46900	1013	LacI family transcriptional regulator
53	42154	42627	473	small multi-drug export family transporter
53	42621	43040	419	holliday junction resolvase YqgF
53	34452	35189	737	hypothetical protein
53	45899	47008	1109	hypothetical protein
54	44916	47654	2738	glycoside hydrolase family 2 Gh2F
54	49643	50833	1190	translation elongation factor Tu tufA
5.				

54	42452	44201	1749	humothotical mastein
54	42453	44201	1748	hypothetical protein
54 54	49405 49961	49683 52270	278 2309	DNA-directed RNA polymerase omega subunit RpoZ
				hypothetical protein
54	46915	47775	860	sugar ABC transporter permease
54	42627	43682	1055	histidinol-phosphate transaminase hisC
54	43054	43329	275	hypothetical protein
54 54	35291	36001	710	hypothetical protein
-	49933	51618	1685	GGDEF domain-containing protein
55	50949	51083	134	hypothetical protein
55	44265	45167	902	hypothetical protein
55	53869	56727	2858	penicillin-binding protein PbpA
55	49724	50347	623	guanylate kinase Gmk
55	52313	52633	320	hypothetical protein
55	39245	39961	716	branched-chain amino acid transport protein AzlC
55	47799	49199	1400	sugar ABC transporter permease
55	43411	44763	1352	MiaB-like tRNA modifying enzyme MiaB
56	51127	51684	557	hypothetical protein
56	45183	46157	974	D-isomer specfic 2-hydroxyacid dehydrogenase
56	47764	48402	638	CoA-binding domain-containing protein
56	46398	47408	1010	phage integrase family protein
56	56740	57864	1124	rod shape-determining protein RodA
56	50337	50507	170	hypothetical protein
56	52856	55375	2519	hypothetical protein
56	39985	41202	1217	alanyl-tRNA synthetase family protein
56	49295	50620	1325	sugar ABC transporter substrate-binding protein
56	44856	45086	230	hypothetical protein
56	36017	37003	986	hypothetical protein
56	51625	53058	1433	prolyl-tRNA synthetase ProS
57	51732	52151	419	GNAT family acetyltransferase
57	48419	49081	662	hypothetical protein
	48419 47408			hypothetical protein
57 57	47408 57869	48226 58264	818 395	
				methylglyoxal synthase MgsA
57	50593	51507	914	hypothetical protein
57	55407	55814	407	anti-sigma regulatory factor
57	41279	41797	518	CarD family transcriptional regulator
57	50880	52037	1157	DNA protecting protein Dpr
57	44254	44961	707	bacterial sugar transferase
57	37073	37390	317	hypothetical protein
57	47047	48507	1460	MBOAT family acyltransferase
58	52246	52389	143	NUDIX domain-containing protein
58	49155	50711	1556	carbohydrate kinase family protein
58	48266	49378	1112	hypothetical protein
58	58239	59213	974	D-alanyl-D-alanine carboxypeptidase DacA
58	51566	52930	1364	hypothetical protein
58	55882	56559	677	hypothetical protein
58	41938	42492	554	GNAT family acetyltransferase
58	52027	53607	1580	Mg chelatase-like protein
58	45192	46394	1202	thiamine biosynthesis/tRNA modification protein Thil
58	37488	38033	545	hypothetical protein
58	53655	54206	551	anaerobic ribonucleoside triphosphate reductase activating protein NrdG
58	48609	49322	713	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase IspD
59	52386	52928	542	hypothetical protein
59	47036	47800	764	
59	50712	51869	1157	alanine racemase Alr
59	59285	59704	419	hypothetical protein
59	56593	57639	1046	thiamin biosynthesis lipoprotein ApbE
59	42494	42931	437	
				hypothetical protein
59	44986	45717	731	hypothetical protein
59	46409	47566	1157	cysteine desulfurase IscS
59	38033	38593	560	hypothetical protein
59	54296	56527	2231	anaerobic ribonucleoside triphosphate reductase NrdD
59	49342	50184	842	LicD family protein
60	57636	59906	2270	glycoside hydrolase family 31 Gh31A
60	53049	53924	875	metallophosphoesterase
60	48797	49258	461	hypothetical protein
60	49412	52765	3353	Type I site-specific restriction- modification system R (restriction) subunit and related
				helicases
60	59758	61365	1607	hypothetical protein
60	52954	53226	272	ACT domain-containing protein
60	53771	54832	1061	twitching motility protein pil
60	45740	46414	674	sortase B family protein
60	47571	48323	752	hypothetical protein
60	38628	39107	479	YbaK family protein
60	56647	57465	818	glutamate racemase MurI
60	50367	51158	791	hypothetical protein
61	59923	62127	2204	glycoside hydrolase family 95 Gh95A
61	49299	50441	1142	transcription termination factor NusA
61	52810	53493	683	hypothetical protein
61	61446	61973	527	hypothetical protein
61	53315	54112	797	metallo-beta-lactamase family protein
61	42928	44757	1829	EAL domain-containing protein
61	54851	55936	1085	HD-GYP domain-containing protein
	46488	47546	1085	cell envelope-related transcriptional attenuator
61				

61         3413         approx         334         mode SM           61         5158         358         by Octoccal prosin           61         5110         5581         100         by Octoccal prosin           62         5110         653         160         by Octoccal prosin           62         5010         663         100         by Octoccal prosin           62         5080         5680         100         by Octoccal prosin           63         5081         5580         100         by Octoccal prosin           64         4593         5680         100         by Octoccal prosin           65         4641         100         12 Motoccal prosin         by Octoccal prosin           66         4641         1144         00         by Octoccal prosin         by Octoccal prosin           67         44114         1144         00         by Octoccal prosin         by Octoccal prosin           68         5403         5501         132         by Octoccal prosin         by Octoccal prosin           68         5403         5501         132         by Octoccal prosin         by Octoccal prosin           68         5403         5503         100	61	48323	49360	1037	ribosomal protein L11 methyltransferase prmA
64         5110         5121         1921         1922         apply plasmasker ALDB           62         4518         4614         131         apply plasmasker ALDB           63         4580         4614         131         apply plasmasker ALDB           64         4580         5660         130         apply plasmasker ALDB           64         5610         5660         130         by plasmasker ALDB           64         5610         5660         730         by plasmasker ALDB           64         5610         5660         730         by plasmasker ALDB           64         5611         5602         740         by plasmasker ALDB           64         5611         5603         741         marker ALDB           65         5613         5604         747         marker ALDB           64         5613         5513         567         7561         by plasmasker ALDB           65         5613         5513         137         by plasmasker ALDB         by plasmasker ALDB           64         4569         7578         1313         by plasmasker ALDB         by plasmasker ALDB           64         5661         5513         137         by					
64         5110         5121         1011         bypechacia proxim           62         62116         6622         1852         Apbig stackaster AgADB           63         54606         5606         5606         5607         1919           64         55016         5606         5607         1919         hypechacia proxim           64         55016         5506         1919         hypechacia proxim         hypechacia proxim           62         55016         5502         450         1919         hypechacia proxim         hypechacia proxim           63         55016         5502         450         450         1910         hypechacia proxim         hypechacia proxim           64         55017         5502         4501         1910         hypechacia proxim         hypechacia proxim           64         55012         5504         1610         hypechacia proxim         hypechacia proxim           64         55103         5507         1510         hypechacia proxim         hypechacia proxim           63         5610         5511         1171         oxpechacia proxim         hypechacia proxim           64         5610         5512         1417         hypechacia proxim					01
62         4480         4494         1330         John State         John	61	51180	52481	1301	hypothetical protein
62         5468         55780         229         Physobelicial porein           62         55816         5463         100         3. debuschant container Acid           62         55816         5463         100         3. debuschant container Acid           62         6233         6233         5238         100         Statistic porein           63         6438         1013         between porein         Data Statistic porein           64         6434         4144         595         membrane stanport porein faulty transporter           62         5586         4113         obtain statistic porein         and the stanport porein faulty transporter           63         5571         5586         411         obtain statistic porein         and the stanport porein faulty transporter           64         6514         5573         5563         322         bypolaticla porein         bypolaticla porein           63         6514         5573         5583         obtain transport porein faulty transporter           64         6561         75781         1179         obtain transport porein         faulty transporter           64         5671         75781         1373         bypolaticla porein         faulty transporter <tr< td=""><td>62</td><td>62161</td><td>64023</td><td>1862</td><td>alpha-galactosidase Aga36B</td></tr<>	62	62161	64023	1862	alpha-galactosidase Aga36B
62         5546         5547         5546         5547         5546         5547         5556         55576 <th< td=""><td>62</td><td>44890</td><td>46194</td><td>1304</td><td>alpha-amylase Amy13C</td></th<>	62	44890	46194	1304	alpha-amylase Amy13C
62         5366         5463         100         Separating protein           62         67184         68140         56612         590         HD Assumic constanting protein           63         6844         56612         590         HD Assumic constanting protein           64         6841         5964         5966         5976         5976           63         5956         5976         5976         5976         5976           63         5956         5976         5976         5976         5976           63         5956         5976         5976         5976         5976           63         5956         5976         5976         5976         5976           63         5971         5576         5971         5576         5976           63         6181         6700         177         segate prifision II as the segate	62	54086	54580		hypothetical protein
62         6331         63146         1103         3-46-9/deplopment syshue Aroll           62         6356         48050         641         Big Systum consisting contain           62         6356         48050         641         Big Systum constant           62         6341         5352         15360         777         method Sit Aroma constant           63         5352         15360         777         method Sit Aroma constant         787           64         5354         15549         617         method Sit Aroma constant         788           63         5454         15549         1610         Ipportant protein         7A           63         5451         1519         response protein protein         7A           63         6411         6507         179         segment protein         7A           63         6411         6507         179         segment protein         7A           64         6507         5781         1717         segment protein         7A           64         6507         5791         1579         hipportant protein         7A           64         6507         5791         1579         hipportant protein         7A <td>-</td> <td></td> <td>50700</td> <td></td> <td>hypothetical protein</td>	-		50700		hypothetical protein
62         996         HD Jonume containing proton           62         4756         4850         464         Bypolerical proton           62         4013         4110         4969         member receipt protin Endly transporter           63         4013         4111         4969         member receipt protin Endly transporter           64         4013         4111         4969         member receipt protin Endly transporter           65         4574         4576         4576         4576           66         45771         4556         4576         4576           63         4514         4570         4576         4576           64         4513         4570         4576         4576           63         4514         4570         4577         4576         4576           64         45761         1178         polyacherink by objectical proton         458           63         3579         5576         1477         Hypotherical proton         458           64         5573         1487         Hypotherical proton         458         458           64         5570         1487         Hypotherical proton         458         458         4597					
62         9756         9870         9441         Storage           62         6414         41144         459         membrase trajport provise fundily transport           63         5767         5860         713         babterial Strike domain-screating fundily transport           63         5964         5256         617         middle linana UA           63         5974         5860         713         middle linana UA           63         5974         5503         1237         middle linana UA           63         5371         5503         132         hypohetical protein           63         6371         5570         133         bage protein ILapA           63         6488         5672         113         orgene-hipotechar Shafing protein           64         5681         1760         mage ACP runnoper and shafing shafing protein         middle hipotechar protein           63         5571         5791         133         orgene-hipotechar protein         middle hipotechar protein           64         5642         5790         113         orgene-hipotechar protein         middle hipotechar protein           64         5643         5670         orgene-hipotechar protein         middle hipotechar protein </td <td></td> <td></td> <td></td> <td></td> <td></td>					
62         49441         5002         1181         characterization of the second s					
60         44143         41164         979         membrane tracking protein family transporter           62         5592         5540         417         statistic formit containing protein           63         55444         5501         1501         hypothetical protein           63         55744         5501         2501         hypothetical protein           63         55744         5500         257         hypothetical protein           63         5571         5500         157         hypothetical protein           63         55873         57931         1176         usymethypothetic protein           63         4589         47902         103         hypothetical protein           63         55873         57931         1178         usymethypothetic protein           63         55873         57931         1178         usymethypothetic protein           64         55973         57931         1178         usymethypothetic protein           63         5580         1683         hypothetical protein         usymethypothetics protein           64         56973         59700         1683         hypothetical protein           64         569710         6698         722					
62         57947         5860         713         Internal SLI Domain containing presen           62         55022         55369         617         windle Klause Usk           63         5643         5624         1610         hypothecial protein           63         5771         55401         323         hypothecial protein           64         6510         5597         hypothecial protein           63         46111         6509         hypothecial protein           63         46111         6509         hypothecial protein           63         46111         6509         hypothecial protein           63         4609         47902         113         hypothecial protein           63         55071         51516         1141         hypothecial protein           64         55071         51516         11417         hypothecial protein           64         55071         51516         11417         hypothecial protein           64         55071         51516         1147         hypothecial protein           64         55071         631         degrammers         hypothecial protein           64         45081         49066         722					
62         5302         5504         610         untue lame UA           63         5504         5503         1610         hopathstal potein         1.7A           63         5571         55001         332         hopathstal potein         1.7A           63         6181         65700         539         sign Apptale ILpot         1.6A           63         6181         65700         1.79         upper ALA         1.6A         1.6A           63         6418         56071         5711         1.78         upper ALA         1.6A					
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61         5974         5500         372         Productal protein           63         6316         63700         539         signal protage II LpA           63         6316         63700         539         signal protage II LpA           63         6411         64581         729         cell division protein           63         64581         7402         113         bypotherial protein           63         64589         47902         113         bypotherial protein           63         64593         46592         833         polymechnic bypotherial protein           64         5451         5509         1059         hypotherial protein           64         5451         5509         1059         hypotherial protein         hypotherial protein           64         5451         5509         1059         hypotherial protein         hypotherial protein           64         5451         5509         1059         hypotherial protein         hypotherial protein           64         4503         6600         867         signal protein         hypotherial protein           64         4503         6600         120         hypotherial protein         hypotherial protein	-				
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63         611         6700         5.90         signal peptiduse I LapA,           63         6411         6584         1760         sugar AIC transports substate heining protein ItAA           63         6473         57851         1178         oxygen independent coproperly vingen III AV           63         56673         57851         1178         oxygen independent coproperly vingen III AV           63         55001         5002         1330         Interedotati           63         5501         5002         Byothetic protein         Interedotati           64         6533         5502         1803         Interedotati         Interedotati           64         6534         5740         1804         Coprometer protein Dax         Interedotati           64         6533         58601         9871         1804         Coprometer protein Dax           64         41101         41490         8194         Coprometer Dax         Coprometer Dax           64         41101         41494         8194         Coprometer Dax         Coprometer Dax           64         41010         41940         8194         Coprometer Dax         Coprometer Dax           65         56118         50702 <t< td=""><td></td><td></td><td></td><td></td><td>-</td></t<>					-
63         5118         5047         2190         cell division protein Pi-A           63         6489         47002         1313         uppotential protein           63         6489         47002         1313         oxyges-histopendic opportspringent III oxidus: Hem           63         48893         48872         833         polystochrick flossynthesis protein           63         5580         55126         1447         hypothetical protein           64         5642         55126         1447         hypothetical protein           64         5641         55106         630         diplosopic-CoA kinas: Coal           64         5642         55106         630         diplosopic-CoA kinas: Coal           64         5642         55106         630         diplosopic-CoA kinas: Coal           64         5602         46000         839         Antermotype more protein bick           64         5602         5244         isochristamate kinding protein           65         6700         65429         929         postechristic homity byrothesin           65         6731         53118         644         chaporan protein bick           65         4683         67382         932					
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64         59/42         32.64         1904         Chapter provide Dark           64         41101         41940         859         ArxG family transcription proglutor           64         59021         59674         653         1804 Arymines-N7: methy hydrolase           65         55166         58070         524         Bioschorizantes family hydrolase           65         65013         66429         292         peacolarizing synthase RbA family protein           65         66851         67776         93318         644         chaptora protein           65         49637         93329         692         polyaschuide hosynthesis protein           65         49637         93338         644         chaptora protein           65         59744         53138         644         chaptora protein           66         59759         79049         14218         1469         D-lamic crabysprotein State           66         59750         79049         14217         denosmisse deminase Add           66         59751         79040         polyaschuid protein           66         59752         79040         2888         ramshation initiation fange protein           66         597637	64	65933	66820	887	sugar ABC transporter permease
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66         56972         59086         2114         DNA polymerase I PolA           66         48365         49504         1139         hypothetical protein           66         57851         59659         1808         GTP-binding protein Lep           66         43302         54393         1031         heat-inducible transcription repressor HrcA           66         42973         43824         851         aninoglycoside 6-adenylytransferase           67         590069         59287         218         hypothetical protein           67         590069         59287         218         hypothetical protein           67         59109         59432         323         hypothetical protein           67         70441         72750         2309         two component system response regulator           67         49675         50169         494         hypothetical protein           67         54611         55117         506         hypothetical protein           67         43853         44647         794         SAM-dependent methyltransferase           67         64133         5417         506         hypothetical protein           67         64234         62172         938 <td></td> <td></td> <td></td> <td></td> <td></td>					
66         48365         49504         1139         hypothetical protein           66         57851         59659         1808         GTP-binding protein Lep           66         57362         54393         1031         heat-inducible transcription repressor HrA           66         42973         43824         851         aminoglycoside 6-adenylytransferase           67         59069         59287         218         hypothetical protein           67         57799         58359         560         hypothetical protein           67         65527         66111         584         hypothetical protein           67         70441         72750         2309         two component system response regulator           67         49675         50169         494         hypothetical protein           67         49675         50169         494         hypothetical protein           67         54611         55117         506         hypothetical protein           67         6124         62172         938         exonuclease family protein           67         6124         62172         938         exonuclease family protein           68         62188         63015         827	66			2114	
66         57851         59659         1808         GTP-binding protein Lep           66         53362         54393         1031         heat-inducible transcription repressor HrcA           66         42973         43824         851         aminoglycoside - 3denylyttransferase           67         59069         59287         218         hypothetical protein           67         57799         58359         560         hypothetical protein           67         65527         66111         584         hypothetical protein           67         65527         66111         584         hypothetical protein           67         59109         59432         323         hypothetical protein           67         70441         72750         2309         two component system response regulator           67         49675         50169         494         hypothetical protein           67         48675         50117         506         hypothetical protein           67         43853         44647         794         SAM-dependent methyltransferase           67         61234         62172         938         exonuclease family protein           68         62188         63015         827<	66	48365	49504	1139	* *
66         42973         43824         851         aminoglycoside 6-adenylyltransferase           67         59069         59287         218         hypothetical protein           67         59799         58359         560         hypothetical protein           67         65527         66111         584         hypothetical protein           67         59109         59432         323         hypothetical protein           67         70441         72750         2309         two component system response regulator           67         70441         72750         2309         two component system response regulator           67         49675         50169         494         hypothetical protein           67         49675         50169         494         hypothetical protein           67         54611         55117         506         hypothetical protein           67         54351         44647         794         SAM-dependent methyltransferase           67         61234         62172         938         econuclease family protein           68         62188         63015         827         acetyl-sylan esterase Est10A           68         59255         6530         1235<	66	57851	59659	1808	
67         59069         59287         218         hypothetical protein           67         57799         58359         560         hypothetical protein           67         65527         66111         584         hypothetical protein           67         59109         59432         323         hypothetical protein           67         70441         72750         2309         two component system response regulator           67         70441         72750         2309         two component system response regulator           67         70441         72750         2309         two component system response regulator           67         54611         55117         506         hypothetical protein           67         54611         55117         506         hypothetical protein           67         64234         62172         938         exonuclease family protein           67         5555         57539         944         glycosyl transferase GT2 family protein           68         62188         63015         827         actyl-xylan esterase Est10A           68         59295         60530         1235         hypothetical protein           68         58505         58720	66	53362	54393	1031	heat-inducible transcription repressor HrcA
67         57799         58359         560         hypothetical protein           67         65527         66111         584         hypothetical protein           67         59109         59432         323         hypothetical protein           67         70441         72750         2309         two component system response regulator           67         49675         50169         494         hypothetical protein           67         49675         50169         494         hypothetical protein           67         54611         55117         506         hypothetical protein           67         54611         55117         506         hypothetical protein           67         64611         55117         506         hypothetical protein           67         64214         62172         938         exonuclease family protein           67         56595         57539         944         glycosyl transferase GT2 family protein           68         62188         63015         827         actyl-xylan esterase Es10A           68         58505         58720         215         hypothetical protein           68         59550         60530         1235         hypothetical	66	42973	43824	851	aminoglycoside 6-adenylyltransferase
67         65527         66111         584         hypothetical protein           67         59109         59432         323         hypothetical protein           67         70441         72750         2309         two component system response regulator           67         49675         50169         494         hypothetical protein           67         43853         44647         794         SAM-dependent methyltransferase           67         61234         62172         938         exonuclease family protein           68         62188         63015         827         acetyl-xylan esterase Est10A           68         62188         63015         827         acetyl-xylan esterase Est10A           68         53957         54394         437         ribosome-binding factor A RbfA           68         54505         58720         215         hypothetical protein           68         59550         60998         1448	67	59069	59287	218	hypothetical protein
67         59109         59432         323         hypothetical protein           67         70441         72750         2309         two component system response regulator           67         49675         50169         494         hypothetical protein           67         49675         50169         494         hypothetical protein           67         59871         60134         263         ribosomal protein S20 rps           67         54611         55117         506         hypothetical protein           67         43853         44647         794         SAM-dependent methyltransferase           67         61234         62172         938         exonuclease family protein           68         56595         57539         944         glycosyl transferase GT2 family protein           68         63105         827         acetyl-xylan esterase Ex10A           68         53957         54394         437         ribosome-binding factor A RbfA           68         53957         54394         437         ribosome-binding factor A RbfA           68         59505         60530         1235         hypothetical protein           68         59550         60998         1448         <	67	57799	58359	560	hypothetical protein
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67         59871         60134         263         ribosomal protein S20 rps           67         54611         55117         506         hypothetical protein           67         43853         44647         794         SAM-dependent methyltransferase           67         61234         62172         938         exonuclease family protein           67         61234         62172         938         exonuclease family protein           67         56595         57539         944         glycosyl transferase GT2 family protein           68         62188         63015         827         acetyl-xylan esterase Est10A           68         59295         60530         1235         hypothetical protein           68         53957         54394         437         ribosome-binding factor A RbfA           68         58505         58720         215         hypothetical protein           68         66175         67185         1010         phage integrase family protein           68         59550         60998         1448         sugar transporter GPH family protein           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         57510         <					
67         54611         55117         506         hypothetical protein           67         43853         44647         794         SAM-dependent methyltransferase           67         61234         62172         938         exonuclease family protein           67         61234         62172         938         exonuclease family protein           67         56595         57539         944         glycosyl transferase GT2 family protein           68         62188         63015         827         acetyl-xylan esterase Est10A           68         59295         60530         1235         hypothetical protein           68         53957         54394         437         ribosome-binding factor A RbfA           68         58505         58720         215         hypothetical protein           68         66175         67185         1010         phage integrase family protein           68         59550         60998         1448         sugar transporter GPH family protein           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         57610         59187         1577         flavin containing protein           68         57610					
67         43853         44647         794         SAM-dependent methyltransferase           67         61234         62172         938         exonuclease family protein           67         56595         57539         944         glycosyl transferase GT2 family protein           68         62188         63015         827         acetyl-xylan esterase Est 10A           68         59295         60530         1235         hypothetical protein           68         59295         60530         1235         hypothetical protein           68         53957         54394         437         ribosome-binding factor A RbfA           68         58505         58720         215         hypothetical protein           68         66175         67185         1010         phage integrase family protein           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         57510         59187         1577         flavin containing amine oxidoreductase           69         54391         5531         950         DHH domain-containing protein           69         58					
67         61234         62172         938         exonuclease family protein           67         56595         57539         944         glycosyl transferase GT2 family protein           68         62188         63015         827         acetyl-xylan esterase Ext10A           68         59295         60530         1235         hypothetical protein           68         53957         54394         437         ribosome-binding factor A RbfA           68         53957         54394         437         ribosome-binding factor A RbfA           68         538505         58720         215         hypothetical protein           68         66175         67185         1010         phage integrase family protein           68         59550         60998         1448         sugar transporter GPH family protein           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         55257         56447         1190         aspartate/tyrosine/aromatic aminotransferase           68         57610         59187         1577         flavin containing motein           69         54391         55341         950         DHH domain-containing protein           69					
67         56595         57539         944         glycosyl transferase GT2 family protein           68         62188         63015         827         acctyl-xylan esterase Est 10A           68         59295         60530         1235         hypothetical protein           68         59295         60530         1235         hypothetical protein           68         53957         54394         437         ribosome-binding factor A RbfA           68         58505         58720         215         hypothetical protein           68         66175         67185         1010         phage integrase family protein           68         66175         67185         2621         ATP-dependent chaperone protein ClpB           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         55257         56447         1190         aspartate/tyrosine/aromatic aminotransferase           68         44674         45105         431         NUDIX domain-containing protein           69         54391         55341         950         DIHH domain-containing protein           69<					
68         62188         63015         827         acetyl-xylan esterase Est10A           68         59295         60530         1235         hypothetical protein           68         53957         54394         437         ribosome-binding factor A RbfA           68         53957         54394         437         ribosome-binding factor A RbfA           68         58505         58720         215         hypothetical protein           68         66175         67185         1010         phage integrase family protein           68         59550         60998         1448         sugar transporter GPH family protein           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         55257         56447         1190         aspartate/tyrosine/aromatic aminotransferase           68         44674         45105         431         NUDIX domain-containing protein           69         54391         55341         950         DHH domain-containing protein           69         58743         59060         317         HNH endonuclease domain-containing protein					
68         59295         60530         1235         hypothetical protein           68         53957         54394         437         ribosome-binding factor A RbfA           68         58505         58720         215         hypothetical protein           68         66175         67185         1010         phage integrase family protein           68         66175         67185         1010         phage integrase family protein           68         66175         67185         1010         phage integrase family protein           68         59550         60998         1448         sugar transporter GPH family protein           68         5957         56447         1190         aspartate/tyrosine/aromatic aminotransferase           68         44674         45105         431         NUDIX domain-containing protein           68         57610         59187         1577         flavin containing amine oxidoreductase           69         54391         55341         950         DHH domain-containing protein           69         62470         1472         hypothetical protein           69         60998         62470         1472         hypothetical protein           69         60208         61221					
68         53957         54394         437         ribosome-binding factor A RbfA           68         58505         58720         215         hypothetical protein           68         66175         67185         1010         phage integrase family protein           68         66175         67185         1010         phage integrase family protein           68         59550         60998         1448         sugar transporter GPH family protein           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         50737         53358         2621         MTP-dependent chaperone protein ClpB           68         55257         56447         1190         aspartate/tyrosine/aromatic aminotransferase           68         44674         45105         431         NUDIX domain-containing protein           68         57610         59187         1577         flavin containing amine oxidoreductase           69         54391         55341         950         DHH domain-containing protein           69         60998         62470         1472         hypothetical protein           69         72957         75764         2807         pyruvate phosphate dikinase PpdK					
68         58505         58720         215         hypothetical protein           68         66175         67185         1010         phage integrase family protein           68         59550         60998         1448         sugar transporter GPH family protein           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         55257         56447         1190         aspartate/tyrosine/aromatic aminotransferase           68         44674         45105         431         NUDIX domain-containing protein           68         57610         59187         1577         flavin containing amine oxidoreductase           69         54391         55341         950         DHH domain-containing protein           69         58743         59060         317         HNN endonuclease domain-containing protein           69         60998         62470         1472         hypothetical protein           69         72957         75764         2807         pyruvate phosphate dikinase PpdK           69         60208         61221         1013         hypothetical protein           69         60208         61221         1013         hypothetical protein           69 </td <td></td> <td></td> <td></td> <td></td> <td></td>					
68         66175         67185         1010         phage integrase family protein           68         59550         60998         1448         sugar transporter GPH family protein           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         55257         56447         1190         aspartate/tyrosine/aromatic aminotransferase           68         54647         45105         431         NUDIX domain-containing protein           68         54647         45105         431         NUDIX domain-containing protein           68         57610         59187         1577         flavin containing amine oxidoreductase           69         54391         55341         950         DHH domain-containing protein           69         58743         59060         317         HNH endonuclease domain-containing protein           69         60998         62470         1472         hypothetical protein           69         72957         75764         2807         pyruvate phosphate dikinase PpdK           69         60208         61221         1013         hypothetical protein           69         5431         54576         1145         cobalamin adenosyltransferase CobA					÷
68         59550         60998         1448         sugar transporter GPH family protein           68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         55257         56447         1190         aspartate/tyrosine/aromatic aminotransferase           68         44674         45105         431         NUDIX domain-containing protein           68         57610         59187         1577         flavin containing amine oxidoreductase           69         54391         55341         950         DHH domain-containing protein           69         58743         59060         317         HNH endonuclease domain-containing protein           69         60998         62470         1472         hypothetical protein           69         72957         75764         2807         pyruvate phosphate dikinase PpdK           69         60208         61221         1013         hypothetical protein           69         53431         54576         1145         cobalamin adenosyltransferase CobA           69         56624         57577         953         hypothetical protein           69         63171         63713         542         glutathione peroxidase					
68         50737         53358         2621         ATP-dependent chaperone protein ClpB           68         55257         56447         1190         aspartate/tyrosine/aromatic aminotransferase           68         44674         45105         431         NUDIX domain-containing protein           68         57610         59187         1577         flavin containing amine oxidoreductase           69         54391         55341         950         DHH domain-containing protein           69         58743         59060         317         HNH endonuclease domain-containing protein           69         60998         62470         1472         hypothetical protein           69         72957         75764         2807         pyruvate phosphate dikinase PpdK           69         60208         61221         1013         hypothetical protein           69         53431         54576         1145         cobalamin adenosyltransferase CobA           69         56624         57577         953         hypothetical protein           69         63171         63713         542         glutathione peroxidase					
68         55257         56447         1190         aspartate/tyrosine/aromatic aminotransferase           68         44674         45105         431         NUDIX domain-containing protein           68         57610         59187         1577         flavin containing amine oxidoreductase           69         54391         55341         950         DHH domain-containing protein           69         58743         59060         317         HNH endonuclease domain-containing protein           69         60998         62470         1472         hypothetical protein           69         72957         75764         2807         pyruvate phosphate dikinase PpdK           69         60208         61221         1013         hypothetical protein           69         53431         54576         1145         cobalamin adenosyltransferase CobA           69         56624         57577         953         hypothetical protein           69         63171         63713         542         glutathione peroxidase					
68         44674         45105         431         NUDIX domain-containing protein           68         57610         59187         1577         flavin containing amine oxidoreductase           69         54391         55341         950         DHH domain-containing protein           69         58743         59060         317         HNH endonuclease domain-containing protein           69         60998         62470         1472         hypothetical protein           69         72957         75764         2807         pyruvate phosphate dikinase PpdK           69         60208         61221         1013         hypothetical protein           69         53431         54576         1145         cobalamin adenosyltransferase CobA           69         56624         57577         953         hypothetical protein           69         63171         63713         542         glutathione peroxidase					
68         57610         59187         1577         flavin containing amine oxidoreductase           69         54391         55341         950         DHH domain-containing protein           69         58743         59060         317         HNH endonuclease domain-containing protein           69         60998         62470         1472         hypothetical protein           69         72957         75764         2807         pyruvate phosphate dikinase PpdK           69         60208         61221         1013         hypothetical protein           69         53431         54576         1145         cobalamin adenosyltransferase CobA           69         56624         57577         953         hypothetical protein           69         63171         63713         542         glutathione peroxidase					
69         54391         55341         950         DHH domain-containing protein           69         58743         59060         317         HNH endonuclease domain-containing protein           69         60998         62470         1472         hypothetical protein           69         72957         75764         2807         pyruvate phosphate dikinase PpdK           69         60208         61221         1013         hypothetical protein           69         53431         54576         1145         cobalamin adenosyltransferase CobA           69         56624         57577         953         hypothetical protein           69         63171         63713         542         glutathione peroxidase					
69         58743         59060         317         HNH endonuclease domain-containing protein           69         60998         62470         1472         hypothetical protein           69         72957         75764         2807         pyruvate phosphate dikinase PpdK           69         60208         61221         1013         hypothetical protein           69         53431         54576         1145         cobalamin adenosyltransferase CobA           69         56624         57577         953         hypothetical protein           69         63171         63713         542         glutathione peroxidase					-
69         60998         62470         1472         hypothetical protein           69         72957         75764         2807         pyruvate phosphate dikinase PpdK           69         60208         61221         1013         hypothetical protein           69         53431         54576         1145         cobalamin adenosyltransferase CobA           69         56624         57577         953         hypothetical protein           69         63171         63713         542         glutathione peroxidase					
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69         60208         61221         1013         hypothetical protein           69         53431         54576         1145         cobalamin adenosyltransferase CobA           69         56624         57577         953         hypothetical protein           69         63171         63713         542         glutathione peroxidase					
69         53431         54576         1145         cobalamin adenosyltransferase CobA           69         56624         57577         953         hypothetical protein           69         63171         63713         542         glutathione peroxidase	69	60208	61221	1013	
69 63171 63713 542 glutathione peroxidase	69			1145	
	69	56624	57577	953	hypothetical protein
69 59349 60581 1232 GDSL-family lipase/acylhydrolase		63171	63713	542	glutathione peroxidase
	69	59349	60581	1232	GDSL-family lipase/acylhydrolase

50	(0720	<1.45 <b>7</b>	707	
70 70	60720	61457	737 956	RelA/SpoT domain-containing protein
70	55411 59106	56367 59447	341	tRNA pseudouridine synthase B TruB
				ArsC family protein
70	67347	68492	1145	D-alanyl-D-alanine carboxypeptidase DacA
70	75986	76810	824	glycerophosphoryl diester phosphodiesterase
70	50433	51287	854	hypothetical protein
70	61251	62210	959	cobalamin biosynthesis protein Cob
70	45255	46208	953	hypothetical protein
70	63720	64529	809	RNA-binding S4 domain-containing protein
70	60711	61946	1235	polysaccharide biosynthesis protein
71	61570	63798	2228	hypothetical protein
71	59507	60142	635	hypothetical protein
71	68613	70136	1523	DHH domain-containing protein
71	62629	63714	1085	HD-GYP domain-containing protein
71	77100	77744	644	hypothetical protein
71	51284	52909	1625	hypothetical protein
71	62217	63431	1214	cobalamin biosynthesis protein Cob
71	54577	55182	605	hypothetical protein
71	57850	58956	1106	hypothetical protein
71	64531	65106	575	NUDIX domain-containing protein
71	61936	62904	968	glycosyl transferase GT2 family protein
72	63918	65249	1331	capsule biosynthesis protein
72	56378	57286	908	riboflavin biosynthesis protein RibF
72	70194	70610	416	LysM domain-containing protein
72	63904	64500	596	NUDIX domain-containing protein
72	52890	53507	617	hypothetical protein
72	63499	65373	1874	hypothetical protein
72	55236	56033	797	thiamine biosynthesis protein ThiF
72	55256	59276	323	
72			323	hypothetical protein
	46780	48330		GMP synthase GuaA
73	65378	66184	806	hypothetical protein
73	57305	58243	938	membrane transport protein family transporter
73	60415	60645	230	hypothetical protein
73	70784	71404	620	LexA repressor
73	64708	65010	302	hypothetical protein
73	77816	79255	1439	MBOAT family acyltransferase
73	65560	66054	494	heptaprenyl diphosphate synthase component I family protein
73	48480	49796	1316	NLPC/P60 domain-containing protein
73	65744	67618	1874	cysteine protease C11 family protein
74	66268	66789	521	peptidyl-prolyl cis-trans isomerase cyclophilin- type
74	58304	59998	1694	phosphoglucomutase/phosphomannomutase family protein
74	60704	61153	449	hypothetical protein
74	71451	71786	335	hypothetical protein
74	79318	80799	1481	hypothetical protein
74	53821	54147	326	hypothetical protein
74	66074	66466	392	hypothetical protein
74	56119	56718	599	GTP-binding protein
74	59425	60339	914	hypothetical protein
74	49842	51233	1391	asparaginyl-tRNA synthetase AsnS
74	67679	67927	248	hypothetical protein
75	60157	60354	197	PspC domain-containing protein
75	71821	72405	584	HD domain-containing protein
75	65007	667.42	1646	
75	65097	66/43	2069	hypothetical protein
75	80830	82899		
75	66557	67342	785	chemotaxis protein methyltransferase Che
75	60339	61583	1244	hypothetical protein
75	51259	52485	1226	peptidyl-prolyl cis-trans isomerase FKBP-type
75	63010	64872	1862	hypothetical protein
76	60509	61600	1091	hypothetical protein
76	61361	62218	857	hypothetical protein
76	72402	73010	608	nicotinate (nicotinamide) nucleotide adenylyltransferase NadD
76	66843	68573	1730	ABC transporter ATP-binding/permease
76	83026	84444	1418	GGDEF domain-containing protein
76	67496	68638	1142	ribosomal protein S1 rps
76	56772	58553	1781	ABC transporter ATP-binding/permease
76	52659	53132	473	hypothetical protein
76	64894	65913	1019	radical SAM domain-containing protein
77	67842	69044	1202	hypothetical protein
77				
77	62257	63366	1109	hypothetical protein
			1109 311	hypothetical protein hypothetical protein
77	62257	63366		
77 77	62257 73041	63366 73352	311	hypothetical protein
	62257 73041 68570	63366 73352 70294	311 1724	hypothetical protein ABC transporter ATP-binding/permease
77	62257 73041 68570 54150	63366 73352 70294 55667	311 1724 1517 854	hypothetical protein ABC transporter ATP-binding/permease hypothetical protein hydroxymethylbutenyl pyrophosphate reductase Isp
77 77 77 77	62257 73041 68570 54150 68619 58553	63366 73352 70294 55667 69473 60238	311 1724 1517 854 1685	hypothetical protein ABC transporter ATP-binding/permease hypothetical protein hydroxymethylbutenyl pyrophosphate reductase Isp ABC transporter ATP-binding/permease
77 77 77 77 77	62257 73041 68570 54150 68619 58553 61675	63366           73352           70294           55667           69473           60238           62097	311 1724 1517 854 1685 422	hypothetical protein ABC transporter ATP-binding/permease hypothetical protein hydroxymethylbutenyl pyrophosphate reductase Isp ABC transporter ATP-binding/permease hypothetical protein
77 77 77 77 77 77	62257 73041 68570 54150 68619 58553 61675 53160	63366           73352           70294           55667           69473           60238           62097           53612	311 1724 1517 854 1685 422 452	hypothetical protein ABC transporter ATP-binding/permease hypothetical protein hydroxymethylbutenyl pyrophosphate reductase Isp ABC transporter ATP-binding/permease hypothetical protein hypothetical protein
77 77 77 77 77 77 77 77	62257 73041 68570 54150 68619 58553 61675 53160 68399	63366 73352 70294 55667 69473 60238 62097 53612 68839	311 1724 1517 854 1685 422 452 440	hypothetical protein ABC transporter ATP-binding/permease hypothetical protein hydroxymethylbutenyl pyrophosphate reductase Isp ABC transporter ATP-binding/permease hypothetical protein hypothetical protein hypothetical protein
77 77 77 77 77 77 77 77 77	62257 73041 68570 54150 68619 58553 61675 53160 68399 65954	63366           73352           70294           55667           69473           60238           62097           53612           68839           67447	311 1724 1517 854 1685 422 452 452 440 1493	hypothetical protein ABC transporter ATP-binding/permease hypothetical protein hydroxymethylbutenyl pyrophosphate reductase Isp ABC transporter ATP-binding/permease hypothetical protein hypothetical protein hypothetical protein hypothetical protein
77 77 77 77 77 77 77 77 78	62257 73041 68570 54150 68619 58553 61675 53160 68399 65954 69397	63366           73352           70294           55667           69473           60238           62097           53612           68839           67447           69639	311 1724 1517 854 1685 422 452 440 1493 242	hypothetical protein ABC transporter ATP-binding/permease hypothetical protein hydroxymethylbutenyl pyrophosphate reductase Isp ABC transporter ATP-binding/permease hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
77 77 77 77 77 77 77 77 77 78 78	62257 73041 68570 54150 68619 58553 61675 53160 68399 65954 69397 61604	63366           73352           70294           55667           69473           60238           62097           53612           68839           67447           69639           62209	311 1724 1517 854 1685 422 452 440 1493 242 605	hypothetical protein ABC transporter ATP-binding/permease hypothetical protein hydroxymethylbutenyl pyrophosphate reductase Isp ABC transporter ATP-binding/permease hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
77 77 77 77 77 77 77 77 78 78 78 78 78	62257 73041 68570 54150 68619 58553 61675 53160 68399 65954 69397 61604 63366	63366           73352           70294           55667           69473           60238           62097           53612           68839           67447           69639           62209           64604	311 1724 1517 854 1685 422 452 440 1493 242 605 1238	hypothetical protein ABC transporter ATP-binding/permease hypothetical protein hydroxymethylbutenyl pyrophosphate reductase Isp ABC transporter ATP-binding/permease hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
77 77 77 77 77 77 77 77 77 78 78	62257 73041 68570 54150 68619 58553 61675 53160 68399 65954 69397 61604	63366           73352           70294           55667           69473           60238           62097           53612           68839           67447           69639           62209	311 1724 1517 854 1685 422 452 440 1493 242 605	hypothetical protein ABC transporter ATP-binding/permease hypothetical protein hydroxymethylbutenyl pyrophosphate reductase Isp ABC transporter ATP-binding/permease hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein

70	04574	05001	1207	
78 78	84574 55792	85881 56712	1307 920	MFS transporter hypothetical protein
78	69482	70141	659	cytidylate kinase cmk
78		61883	1277	
	60606			ATP-dependent Clp protease ATP-binding subunit ClpX
78 78	62253	63245	992	hypothetical protein
	53625	54494	869	4-diphosphocytidyl-2C-methyl-D-erythritol kinase IspE
79 79	69728	70270	542	hypothetical protein
	62369	62635	266	ribosomal protein S15 RpsO
79	64626	65018	392	hypothetical protein
79	74765	75052	287	ribosomal protein L27 RpmA
79	56949	57251	302	hypothetical protein
79	70161	71426	1265	FAD dependent oxidoreductase
79	61905	62507	602	ATP-dependent Clp protease proteolytic subunit ClpP
80	70284	71345	1061	hypothetical protein
80	62870	64960	2090	polyribonucleotide nucleotidyltransferase
80	65345	66265	920	peptidyl-prolyl cis-trans isomerase FKBP-type
80	75056	75385	329	hypothetical protein
80	85908	87548	1640	hypothetical protein
80	57251	57586	335	hypothetical protein
80	63375	63989	614	CAAX amino terminal protease family protein
80	54668	55291	623	hypothetical protein
81	57928	59391	1463	endo-1,4-beta-glucanase Cel5C
81	71503	72531	1028	CAAX amino terminal protease family protein
81	75407	75715	308	ribosomal protein L21 RplU
81	88069	88956	887	degV family protein
81	71438	72379	941	HTH/SIS domain-containing protein
81	63986	64234	248	hypothetical protein
81	69246	70016	770	hypothetical protein
81	67482	68735	1253	hypothetical protein
82	72609	74219	1610	alpha-amylase Amy13B
82	65235	66839	1604	peptide chain release factor 3 PrfC
82	66439	68229	1790	ABC transporter ATP-binding protein
82	89002	89250	248	hypothetical protein
82	59724	61769	2045	UvrD/REP family ATP-dependent DNA helicase
82	72376	72927	551	TetR family transcriptional regulator
82	62719	63318	599	hypothetical protein
82	64221	64772	551	hypothetical protein
82	55367	56272	905	dihydroorotate dehydrogenase PyrD
82	70032	70733	701	hypothetical protein
82	68790	70112	1322	mannose-6-phosphate isomerase/mannose-1-phosphate guanylyl transferase
83	74397	75068	671	HAD superfamily hydrolase
83	66978	68291	1313	hypothetical protein
83	68456	69964	1508	ABC transporter permease protein
83	75801	76967	1166	ribonuclease Rne/Rng family
83	89374	91032	1658	GGDEF/EAL domain-containing protein
83	73047	73676	629	MgtC family protein
				olioo and an antida an an E
84	75092	76891	1799	oligoendopeptidase pepF
84	75092 68354	68728	374	hypothetical protein
84 84	75092 68354 76960	68728 77688	374 728	hypothetical protein hypothetical protein
84 84 84	75092 68354 76960 61835	68728 77688 62812	374 728 977	hypothetical protein
84 84 84 84	75092 68354 76960 61835 63438	68728 77688 62812 64946	374 728 977 1508	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig
84 84 84	75092 68354 76960 61835	68728 77688 62812	374 728 977	hypothetical protein hypothetical protein CAAX amino terminal protease family protein
84 84 84 84 84 84 84	75092 68354 76960 61835 63438 64917 70548	68728 77688 62812 64946 65636 71687	374 728 977 1508 719 1139	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig hypothetical protein DegT/Dnrl/EryC1/StrS family aminotransferase
84 84 84 84 84 84 84 85	75092 68354 76960 61835 63438 64917 70548 76905	68728 77688 62812 64946 65636 71687 77522	374 728 977 1508 719 1139 617	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig hypothetical protein DegT/DnrJ/EryC1/StrS family aminotransferase flavin reductase domain-containing protein
84 84 84 84 84 84 85 85	75092 68354 76960 61835 63438 64917 70548 76905 68744	68728 77688 62812 64946 65636 71687 77522 69148	374 728 977 1508 719 1139 617 404	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig hypothetical protein DegT/DnrJ/EryC1/StrS family aminotransferase flavin reductase domain-containing protein transcription antitermination factor NusB
84 84 84 84 84 85 85 85 85 85	75092 68354 76960 61835 63438 64917 70548 76905 68744 77681	68728 77688 62812 64946 65636 71687 77522 69148 79561	374 728 977 1508 719 1139 617 404 1880	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig hypothetical protein DegT/DrrJ/EryCI/StrS family aminotransferase flavin reductase domain-containing protein transcription antitermination factor NusB radical SAM domain-containing protein
84 84 84 84 84 85 85 85 85 85 85	75092 68354 76960 61835 63438 64917 70548 76905 68744 77681 91222	68728 77688 62812 64946 65636 71687 77522 69148 79561 91500	374 728 977 1508 719 1139 617 404 1880 278	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig hypothetical protein DegT/Dnr/EryC1/StrS family aminotransferase flavin reductase domain-containing protein transcription antitermination factor NusB radical SAM domain-containing protein DNA-binding protein
84           84           84           84           84           84           85           85           85           85           85           85           85	75092 68354 76960 61835 64917 70548 76905 68744 77681 91222 62918	68728 77688 62812 64946 65636 71687 77522 69148 79561 91500 63523	374 728 977 1508 719 1139 617 404 1880 278 605	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig hypothetical protein DegT/DnrJ/EryC1/StrS family aminotransferase flavin reductase domain-containing protein transcription antitermination factor NusB radical SAM domain-containing protein DNA-binding protein YkuD domain-containing protein
84 84 84 84 84 85 85 85 85 85 85 85 85 85	75092 68354 76960 61835 63438 64917 70548 76905 68744 77681 91222 62918 74063	68728 77688 62812 64946 65536 71687 77522 69148 79561 91550 63523 76621	374 728 977 1508 719 1139 617 404 1880 278 605 2558	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig hypothetical protein DegT/DnrJ/EryC1/StrS family aminotransferase flavin reductase domain-containing protein transcription antitermination factor NusB radical SAM domain-containing protein DNA-binding protein YkuD domain-containing protein GGDEF/EAL domain-containing protein
84           84           84           84           84           85           85           85           85           85           85           85           85           85           85           85           85	75092 68354 76960 61835 63438 64917 70548 76905 68744 77681 91222 62918 74063 65258	68728 77688 62812 64946 65636 71687 77522 69148 79561 91500 63523 76621 65656	374 728 977 1508 719 1139 617 404 11880 278 605 2558 398	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig hypothetical protein DegT/DnrJ/EryC1/StrS family aminotransferase flavin reductase domain-containing protein transcription antitermination factor NusB radical SAM domain-containing protein DNA-binding protein YkuD domain-containing protein GODEF/EAL domain-containing protein
84           84           84           84           84           84           85           85           85           85           85           85           85           85           85           85           85           85           85           85           85	75092 68354 76960 61835 63438 64917 70548 76905 68744 77681 91222 62918 74063 65258 65715	68728 77688 62812 64946 65636 71687 77522 69148 79561 91500 63523 76621 65656 67448	374 728 977 1508 719 1139 617 404 1880 278 605 2558 398 1733	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig hypothetical protein DegT/DnrJ/EryC1/StrS family aminotransferase flavin reductase domain-containing protein transcription antitermination factor NusB radical SAM domain-containing protein DNA-binding protein YkuD domain-containing protein GGDEF/EAL domain-containing protein GNAT family acetyltransferase ABC transporter ATP-binding/permease
84           84           84           84           84           84           85           85           85           85           85           85           85           85           85           85           85           85           85           85           85           85           85           85	75092 68354 76960 61835 63438 64917 70548 76905 68744 77681 91222 62918 74063 65258 65715 56288	68728 77688 62812 64946 65636 71687 77522 69148 79561 91500 63523 76621 65656 67448 57088	374 728 977 1508 719 1139 617 404 1880 278 605 2558 398 1733 800	hypothetical protein           hypothetical protein           CAAX amino terminal protease family protein           trigger factor tig           hypothetical protein           DegT/DnrJ/EryCl/StrS family aminotransferase           flavin reductase domain-containing protein           transcription antitermination factor NusB           radical SAM domain-containing protein           DNA-binding protein           YkuD domain-containing protein           GGDEF/EAL domain-containing protein           GNAT family acetyltransferase           ABC transporter ATP-binding/permease           dihydroorotate dehydrogenase electron transfer subunit
84           84           84           84           84           85	75092 68354 76960 61835 64917 70548 76905 68744 77681 91222 62918 74063 65258 65715 56288 71050	68728 77688 62812 64946 65636 71687 77522 69148 79561 91500 63523 76621 65656 67448 57088 71757	374 728 977 1508 719 617 404 1880 278 605 2558 398 1733 800 707	hypothetical protein           hypothetical protein           CAAX amino terminal protease family protein           trigger factor tig           hypothetical protein           DegT/DnrJ/EryCl/StrS family aminotransferase           flavin reductase domain-containing protein           transcription antitermination factor NusB           radical SAM domain-containing protein           DNA-binding protein           YkuD domain-containing protein           GGDEF/EAL domain-containing protein           GNAT family acetyltransferase           ABC transporter ATP-binding/permease           dihydroorotate dehydrogenase electron transfer subunit           HTH domain-containing protein
84           84           84           84           84           85	75092 68354 76960 61835 63438 64917 70548 76905 68744 77681 91222 62918 74063 65258 65715 56288 71050 71792	68728 77688 62812 64946 65536 71687 77522 69148 79561 91500 63523 76621 65556 67448 57088 71757 72727	374 728 977 1508 719 1139 617 404 1880 278 605 2558 398 1733 800 707 935	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig hypothetical protein DegT/DnrJ/EryC1/StrS family aminotransferase flavin reductase domain-containing protein transcription antitermination factor NusB radical SAM domain-containing protein DNA-binding protein YkuD domain-containing protein GGDEF/EAL domain-containing protein GGDEF/EAL domain-containing protein dihydroorotate dehydrogenase dihydroorotate dehydrogenase electron transfer subunit HTH domain-containing protein glycosyl transferase
84           84           84           84           84           85           86	75092 68354 76960 61835 63438 64917 70548 76905 68744 77681 91222 62918 74063 65258 65715 56288 65715 56288 71050 71792 69186	68728 77688 62812 64946 65636 71687 77522 69148 79561 91500 63523 76621 65656 67448 57088 71757 72727 70364	374 728 977 1508 719 1139 617 404 1880 278 605 2558 398 1733 800 707 935 1178	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig hypothetical protein DegT/DnrJ/EryC1/StrS family aminotransferase flavin reductase domain-containing protein transcription antitermination factor NusB radical SAM domain-containing protein DNA-binding protein DNA-binding protein GGDEF/EAL domain-containing protein GGDEF/EAL domain-containing protein GNAT family acetyltransferase ABC transporter ATP-binding/permease dihydroorotate dehydrogenase electron transfer subunit HTH domain-containing protein glycosyl transferase exodeoxyribonuclease VII large subunit XseA
84           84           84           84           84           85	75092 68354 76960 61835 63438 64917 70548 76905 68744 77681 91222 62918 74063 65258 65715 56288 71050 71792	68728 77688 62812 64946 65536 71687 77522 69148 79561 91500 63523 76621 65556 67448 57088 71757 72727	374 728 977 1508 719 1139 617 404 1880 278 605 2558 398 1733 800 707 935	hypothetical protein           hypothetical protein           CAAX amino terminal protease family protein           trigger factor tig           hypothetical protein           DegT/DnrJ/EryC1/StrS family aminotransferase           flavin reductase domain-containing protein           transcription antitermination factor NusB           radical SAM domain-containing protein           DNA-binding protein           YkuD domain-containing protein           GGDEF/EAL domain-containing protein           GNAT family acetyltransferase           dihydroorotate dehydrogenase electron transfer subunit           HTH domain-containing protein           glycosyl transferase           exodeoxyribonuclease VII large subunit XseA           hypothetical protein
84           84           84           84           84           85           86           86	75092 68354 76960 61835 63438 64917 70548 76905 68744 77681 91222 62918 74063 65258 65715 56288 71050 71792 69186 69946	68728 77688 62812 64946 65536 71687 77522 69148 79561 91500 63523 76621 65556 67448 57088 71757 72727 70364 70539	374 728 977 1508 719 1139 617 404 1880 278 605 2558 398 1733 800 707 935 1178 593	hypothetical protein           hypothetical protein           CAAX amino terminal protease family protein           trigger factor tig           hypothetical protein           DegT/DnrJ/EryC1/StrS family aminotransferase           flavin reductase domain-containing protein           transcription antitermination factor NusB           radical SAM domain-containing protein           VkuD domain-containing protein           GGDEF/EAL domain-containing protein           GNAT family acetyltransferase           ABC transporter ATP-binding/permease           dihydroorotate dehydrogenase electron transfer subunit           HTH domain-containing protein           glycosyl transferase           exodeoxyribonuclease VII large subunit XseA           hypothetical protein           bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase
84           84           84           84           84           84           85           86           86           86	75092 68354 76960 61835 64917 70548 76905 68744 77681 91222 62918 74063 65258 65715 56288 71050 71792 69186 69946 79571	68728           77688           62812           64946           65636           71687           77522           69148           79561           91500           63523           76621           65556           67448           57088           71757           72277           70364           70539           80788	374           728           977           1508           719           1139           617           404           1880           278           605           2558           398           1733           800           707           935           1178           593           1217	hypothetical protein           hypothetical protein           CAAX amino terminal protease family protein           trigger factor tig           hypothetical protein           DegT/DnrJ/EryCl/StrS family aminotransferase           flavin reductase domain-containing protein           transcription antitermination factor NusB           radical SAM domain-containing protein           DNA-binding protein           YkuD domain-containing protein           GGDEF/EAL domain-containing protein           GRDEF/EAL domain-containing protein           GRDEF/EAL domain-containing protein           GNAT family acetyltransferase           ABC transporter ATP-binding/permease           dihydroorotate dehydrogenase electron transfer subunit           HTH domain-containing protein           glycosyl transferase           exodeoxyribonuclease VII large subunit XseA           hypothetical protein           bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase
84           84           84           84           84           84           85           86           86           86           86	75092 68354 76960 61835 63438 64917 70548 76905 68744 77681 91222 62918 74063 65258 65715 56288 71050 71792 69186 69946 79571 91645	68728           77688           62812           64946           65536           71687           77522           69148           79561           91500           63523           76621           65556           67448           57088           71757           72727           70364           70539           80788           92904	374           728           977           1508           719           1139           617           404           1880           278           605           2558           398           1733           800           707           935           1178           593           1217           1259	hypothetical protein hypothetical protein CAAX amino terminal protease family protein trigger factor tig hypothetical protein DegT/DnrJ/EryC1/StrS family aminotransferase flavin reductase domain-containing protein transcription antitermination factor NusB radical SAM domain-containing protein DNA-binding protein NA-binding protein YkuD domain-containing protein GGDEF/EAL domain-containing protein GGDEF/EAL domain-containing protein GGDEF/EAL domain-containing protein gGNAT family acetyltransferase ABC transporter ATP-binding/permease dihydroorotate dehydrogenase electron transfer subunit HTH domain-containing protein glycosyl transferase exodeoxyribonuclease VII large subunit XseA hypothetical protein bifunctional phosphoribosyl-ATP pyrophosphatase protein HisIE
84           84           84           84           84           84           85           86           86           86	75092 68354 76960 61835 64917 70548 76905 68744 77681 91222 62918 74063 65258 65715 56288 71050 71792 69186 69946 79571	68728           77688           62812           64946           65636           71687           77522           69148           79561           91500           63523           76621           65556           67448           57088           71757           72277           70364           70539           80788	374           728           977           1508           719           1139           617           404           1880           278           605           2558           398           1733           800           707           935           1178           593           1217	hypothetical protein           hypothetical protein           CAAX amino terminal protease family protein           trigger factor tig           hypothetical protein           DegT/DnrJ/EryCl/StrS family aminotransferase           flavin reductase domain-containing protein           transcription antitermination factor NusB           radical SAM domain-containing protein           DNA-binding protein           YkuD domain-containing protein           GGDEF/EAL domain-containing protein           GRDEF/EAL domain-containing protein           GRDEF/EAL domain-containing protein           GNAT family acetyltransferase           ABC transporter ATP-binding/permease           dihydroorotate dehydrogenase electron transfer subunit           HTH domain-containing protein           glycosyl transferase           exodeoxyribonuclease VII large subunit XseA           hypothetical protein           bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase
84           84           84           84           84           84           85           85           85           85           85           85           85           85           85           85           85           85           85           85           85           85           86           86           86           86           86           86           86           86           86           86           86           86           86           86           86           86           86	75092 68354 76960 61835 63438 64917 70548 76905 68744 77681 91222 68744 77681 91222 62918 74063 65258 65715 56288 71050 71792 69186 69946 79571 91645 63646 76607	68728           77688           62812           64946           65636           71687           77522           69148           79561           91500           63523           76621           65656           67448           57088           71757           72277           70364           70539           80788           92904           64986           77137	374           728           977           1508           719           1139           617           404           1880           278           605           2558           398           1733           800           707           935           1178           593           1217           1259           1340           530	hypothetical protein           hypothetical protein           CAAX amino terminal protease family protein           trigger factor tig           hypothetical protein           DegT/DnrJ/EryC1/StrS family aminotransferase           flavin reductase domain-containing protein           transcription antitermination factor NusB           radical SAM domain-containing protein           DNA-binding protein           YkuD domain-containing protein           GGDEF/EAL domain-containing protein           GNAT family acetyltransferase           dihydroorotate dehydrogenase electron transfer subunit           HTH domain-containing protein           glycosyl transferase           exodeoxyribonuclease VII large subunit XseA           hypothetical protein           bifunctional phosphoritosyl-AMP cyclohydrolase/phosphoritosyl-ATP pyrophosphatase           protein HisIE           6-phosphofructokinase PfkA           Matt efflux family protein           hypothetical protein
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84           84           84           84           84           84           85           85           85           85           85           85           85           85           85           85           85           85           85           85           85           85           86           86           86           86           86           86           86           86           86           86           86           86           86           86           86           86           86	75092 68354 76960 61835 64917 70548 76905 68744 77681 91222 62918 74063 65258 65715 56288 71050 711792 69186 69946 79571 91645 63646 76607 657336 57108	68728           77688           62812           64946           65636           71687           77522           69148           79561           91500           63523           76621           65656           67448           57088           71757           72277           70364           70539           80788           92904           64986           77137	374           728           977           1508           719           1139           617           404           1880           278           605           2558           398           1733           800           707           935           1178           593           1217           1259           1340           530           566           1313	hypothetical protein           hypothetical protein           CAAX amino terminal protease family protein           trigger factor tig           hypothetical protein           DegT/DnrJ/EryC1/StrS family aminotransferase           flavin reductase domain-containing protein           transcription antitermination factor NusB           radical SAM domain-containing protein           DNA-binding protein           YkuD domain-containing protein           GGDEF/EAL domain-containing protein           GNAT family acetyltransferase           dihydroorotate dehydrogenase electron transfer subunit           HTH domain-containing protein           glycosyl transferase           exodeoxyribonuclease VII large subunit XseA           hypothetical protein           bifunctional phosphoritosyl-AMP cyclohydrolase/phosphoritosyl-ATP pyrophosphatase           protein HisIE           6-phosphofructokinase PfkA           Matt efflux family protein           hypothetical protein
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88         78399         78827         428         translation ini           88         70345         70578         233         exodeoxyribonucle           88         7042         72759         1337         cobalt ABC transpor           88         71422         72759         1337         cobalt ABC transpor           88         94128         94334         206         hypo           88         66994         67632         638         hypo           88         66994         67632         638         hypo           88         80279         80779         500         shikin           88         67067         68095         1028         Lacl family tr           88         71039         71659         620         peptidyl-t           88         73173         74801         1628         hypo           89         80913         83864         2951         carbohyd           89         75454         76512         1058         glycc           89         78897         79097         200         ribosoma           89         70578         71504         926         geranylgeranyl py           89 </th <th>rolase family 30 Gh30A itiation factor IF-3 infC ease VII small subunit XseB ter ATP-binding protein CbiO thetical protein mate kinase Aro ranscriptional regulator iRNA hydrolase pth thetical protein poside hydrolase ul protein L35 rpmI rorophosphate synthase IspA thetical protein dehydrogenase HisD</th>	rolase family 30 Gh30A itiation factor IF-3 infC ease VII small subunit XseB ter ATP-binding protein CbiO thetical protein mate kinase Aro ranscriptional regulator iRNA hydrolase pth thetical protein poside hydrolase ul protein L35 rpmI rorophosphate synthase IspA thetical protein dehydrogenase HisD
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88         80279         80779         500         Shikin           88         67067         68095         1028         Lacl family tr           88         67067         68095         1028         Lacl family tr           88         71039         71659         620         peptidyl-t           88         73173         74801         1628         hypo           89         80913         83864         2951         carbohydr           89         75454         76512         1058         glycc           89         78897         79097         200         ribosoma           89         70578         71504         926         geranylgeranyl py           89         72809         73339         530         hypo           89         81564         82853         1289         histidinol c           89         67611         68195         584         hypo           89         71764         72051         287         Spo V           89         59343         60551         1208         D-alanine-F	nate kinase Aro ranscriptional regulator IRNA hydrolase pth thetical protein rate binding protein oside hydrolase 11 protein L35 rpml rorophosphate synthase IspA thetical protein dehydrogenase HisD
88         67067         68095         1028         LacI family tr           88         71039         71659         620         peptidyl-t           88         71373         74801         1628         hypo           89         80913         83864         2951         carbohyd           89         75454         76512         1058         glycc           89         75897         79097         200         ribosona           89         70578         71504         926         geranylgeranyl py           89         72809         73339         530         hypo           89         81564         82853         1289         histidinol c           89         67611         68195         584         hypo           89         71764         72051         287         SpoV(           89         59343         60551         1208         D-alanine-F	ranscriptional regulator IRNA hydrolase pth thetical protein protein protein oside hydrolase ul protein L35 rpmI ryrophosphate synthase IspA thetical protein dehydrogenase HisD
88         71039         71659         620         peptidyl-t           88         73173         74801         1628         hypo           89         80913         83864         2951         carbohydr           89         7454         76512         1058         glycc           89         78897         79097         200         ribosoma           89         70578         71504         926         geranylgeranyl py           89         72809         73339         530         hypo           89         81564         82853         1289         histidinol c           89         67611         68195         584         hypo           89         71764         72051         287         SpoV(           89         59343         60551         1208         D-alanine-F	IRNA hydrolase pth thetical protein rate binding protein oside hydrolase ul protein L35 rpmI rrophosphate synthase IspA thetical protein dehydrogenase HisD
88         73173         74801         1628         hypo           89         80913         83864         2951         carbohyd           89         75454         76512         1058         glyco           89         78897         79097         200         ribosoma           89         70578         71504         926         geranylgeranyl py           89         72809         73339         530         hiptoinol           89         81564         82853         1289         histidinol           89         67611         68195         584         hypo           89         71764         72051         287         SpoV           89         59343         60551         1208         D-alanine-F	thetical protein rate binding protein sside hydrolase Il protein L35 rpmI rrophosphate synthase IspA thetical protein dehydrogenase HisD
89         80913         83864         2951         carbohydr           89         75454         76512         1058         glyca           89         75454         76512         1058         glyca           89         78897         79097         200         ribosoma           89         70578         71504         926         geranylgeranyl py           89         72809         73339         530         hypo           89         81564         82853         1289         histidinol c           89         67611         68195         584         hypo           89         71764         72051         287         Spo V           89         59343         60551         1208         D-alanine-F	rate binding protein oside hydrolase Il protein L35 rpmI yrophosphate synthase IspA thetical protein dehydrogenase HisD
89         75454         76512         1058         glycc           89         78897         79097         200         ribosoma           89         70578         71504         926         geranylgeranyl py           89         72809         73339         530         hppo           89         81564         82853         1289         histidinol c           89         67611         68195         584         hppo           89         71764         72051         287         Spo V           89         59343         60551         1208         D-alanine-F	oside hydrolase 11 protein L35 rpmI yrophosphate synthase IspA thetical protein dehydrogenase HisD
89         78897         79097         200         ribosoma           89         70578         71504         926         geranylgeranyl py           89         72809         73339         530         httpp           89         81564         82853         1289         histidinol c           89         67611         68195         584         httpp           89         71764         72051         287         SpoV(           89         59343         60551         1208         D-alanine-E	ıl protein L35 rpmI yrophosphate synthase IspA thetical protein dehydrogenase HisD
89         70578         71504         926         geranylgeranyl py           89         72809         73339         530         hypo           89         81564         82853         1289         histidinol c           89         67611         68195         584         hypo           89         71764         72051         287         SpoV           89         59343         60551         1208         D-alanine-D	vrophosphate synthase IspA thetical protein dehydrogenase HisD
89         72809         73339         530         hypo           89         81564         82853         1289         histidinol c           89         67611         68195         584         hypo           89         71764         72051         287         SpoV(           89         59343         60551         1208         D-alanine-E	thetical protein dehydrogenase HisD
89         81564         82853         1289         histidinol of           89         67611         68195         584         hypo           89         71764         72051         287         Spo VO           89         59343         60551         1208         D-alanine-E	dehydrogenase HisD
89         67611         68195         584         hypo           89         71764         72051         287         SpoVG           89         59343         60551         1208         D-alanine-E	
89         71764         72051         287         SpoV(           89         59343         60551         1208         D-alanine-E	thetical protein
89 59343 60551 1208 D-alanine-E	G family protein
	D-alanine ligase DdlA
89 74777 75895 1118 NAD-depender	nt epimerase/dehydratase
	oside hydrolase
	anotransferase Mal77A
	al protein L20 rplT
	synthesis protein CobW
	ribosyltransferase HisG
90 94376 95443 1067 hypot	thetical protein
90 68188 68703 515 hypot	thetical protein
	ase family oxidoreductase
	stidine dipeptidase pepD
	5-phosphate synthase Dxs
	g alcohol dehydrogenase
	ribosyltransferase HisG
	' family protein
	drogenase/shikimate kinase
	inase PfkB family protein
	ate adenylyltransferase glgD
	nyl pentapeptide synthase MurF
	ate glucose phosphotransferase
	ranscriptional regulator
	TlyA family protein transcriptional regulator
	unsferase regulatory subunit HisZ
	ptidase M24 family
	thetical protein
	phate isomerase Tpi
	ranscriptional regulator
	ate adenylyltransferase glgC
	fold family hydrolase
92 77849 78736 887 EAL doma	in-containing protein
92 77430 79034 1604 polysaccharia	de biosynthesis protein
93 63055 64629 1574 endo-1,4-b	eta-glucanase Cel9A
93 76260 77165 905 ABC transport	ter ATP-binding protein
	tion protein U RecU
	ransporter ATP-binding protein
	lycerate kinase Pgk
	thetical protein
	ter, ATP-binding protein
	erase GT26 family protein
	actosidase Aga36A
A	douridylate synthase
	ransporter ATP-binding protein
	hosphate dehydrogenase Gap
· · · · · · · · · · · · · · · · · · ·	thetical protein
	ramatealanine ligase murC re hydratase AcnA
	ase family oxidoreductase
	AD kinase PpnK
	thetical protein
	thetical protein
51	ABC transporter permease
1 K	psphate phosphatase His
K K	RNA synthetase GlnS
	ome protein DnaD
1	TP-binding/permease protein
	thetical protein
51	sterase family 12 Est12A
· · · ·	thetical protein
	e repressor ArgR
	insporter permease
	thetical protein
	ABC transporter permease
96 91297 92034 737 GGDEF dom	nain-containing protein

1	1			1
96	74463	77177	2714	GGDEF/EAL domain-containing protein
96	77740	78723	983	DNA replication protein DnaC
96	82310	83686	1376	hypothetical protein
96	82163	83125	962	radical SAM domain-containing protein
97	75664	77355	1691	DNA repair protein RecN
97	86840	87502	662	HAD-superfamily hydrolase
97	101285	102925	1640	ABC transporter ATP-binding protein
97	74335	75867	1532	peptide/nickel ABC transporter substrate-binding protein
97	77212	78663	1451	IMP dehydrogenase GuaB
97	78723	79937	1214	ribose-phosphate diphosphokinase prs
97	67046	68560	1514	hypothetical protein
97	83520	84209	689	hypothetical protein
98	77360	78007	647	hypothetical protein
98	80273	81169	896	ABC transporter permease
98	87506	88234	728	RNA pseudouridylate synthase
98	76035	76547	512	NrdR family transcriptional regulator
98	92009	92995	986	
98				transglutaminase domain-containing protein
	80016	80672	656	HAD superfamily hydrolase
99	85524	86393	869	sugar ABC transporter permease
99	81198	82715	1517	RND family transporter
99	88257	89306	1049	N-acetylmuramoyl-L-alanine amidase
99	103010	103882	872	phosphoribosylaminoimidazole-succinocarboxamide synthase PurC
99	93014	94066	1052	type II secretion system protein F Gsp
99	78684	79196	512	hypothetical protein
99	68563	69084	521	CMP/dCMP deaminase zinc-binding domain-containing protein
99	83877	84629	752	two component system response regulator
100	78007	80466	2459	ATP-dependent DNA helicase PcrA
100	82715	83989	1274	ABC transporter permease
100	89363	90061	698	A A
				hypothetical protein
100	76723	77970	1247	cell division protein FtsZ
100	94076	94420	344	hypothetical protein
100	79508	80305	797	hypothetical protein
100	80653	81435	782	phosphoglycerate mutase family protein
100	69178	69588	410	Rrf2 family transcriptional regulator
100	84638	86365	1727	two component system histidine kinase
101	80549	80815	266	hypothetical protein
101	83993	86476	2483	ABC transporter substrate-binding protein
101	90080	90565	485	pantetheine-phosphate adenylyltransferase CoaD
101	103951	105981	2030	methyl-accepting chemotaxis protein McpA
101	94430	94918	488	
				hypothetical protein
101	80358	81677	1319	aspartate kinase
101	81450	81743	293	hypothetical protein
101	69821	70912	1091	hypothetical protein
101	84310	85860	1550	hypothetical protein
102	81769	84873	3104	beta-galactosidase Bga2A
102	86393	87490	1097	sugar ABC transporter permease
102	80828	82240	1412	23S rRNA methyltransferase
102	86596	87081	485	mechanosensitive ion channel protein MscL family
102	90562	91119	557	hypothetical protein
102	106239	108278	2039	methyl-accepting chemotaxis protein McpA
102	78081	78782	701	cell division protein FtsQ
102	81703	82923	1220	homoserine dehydrogenase
102	70999	72108	1109	ABC transporter ATP-binding protein
102	86368	87411	1043	iron ABC transporter substrate-binding protein
103	82625	82843	218	hypothetical protein
103	87153	88607	1454	cobyric acid synthase CobQ
103	91116	93353	2237	DNA topoisomerase IV subunit A ParC
103	108707	109309	602	phosphoserine phosphatase/homoserine phosphotransferase bifunctional protein ThrH
103	78901	80043	1142	cell division protein FtsW
103	95089	95457	368	hypothetical protein
103	82948	83412	464	ACT domain-containing protein
103	84877	87438	2561	hypothetical protein
103	72307	73098	791	hypothetical protein
103	87415	87759	344	hypothetical protein
104	87568	88944	1376	sugar ABC transporter substrate-binding protein
104	88612	89691	1079	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase TrmU
104	93375	95297	1922	DNA topoisomerase IV subunit B ParE
104	80065	95297 81441	1922	
				UDP-N-acetylmuramoylalanine-D-glutamate ligase MurD
104	83551	84057	506	HTH domain-containing protein
104	73123	73527	404	GNAT family acetyltransferase
104	87919	88287	368	hypothetical protein
	85872	87404	1532	hypothetical protein
104		90282	1013	LacI family transcriptional regulator
105	89269			hypothetical protein
	89269 82904	83293	389	nypotitettetti proteini
105			389 1025	LacI family transcriptional regulator
105 105	82904 89932	83293 90957		LacI family transcriptional regulator
105 105 105 105	82904 89932 95333	83293 90957 96202	1025 869	LacI family transcriptional regulator degV family protein
105 105 105 105 105 105	82904 89932 95333 109321	83293 90957 96202 110712	1025 869 1391	LacI family transcriptional regulator degV family protein tryptophan synthase beta subunit TrpB
105 105 105 105 105 105 105	82904 89932 95333 109321 81473	83293 90957 96202 110712 82438	1025 869 1391 965	LacI family transcriptional regulator degV family protein tryptophan synthase beta subunit TrpB phospho-N-acetylmuramoyl-pentapeptide-transferase MraY
105 105 105 105 105 105 105 105	82904 89932 95333 109321 81473 95992	83293 90957 96202 110712 82438 96354	1025 869 1391 965 362	LacI family transcriptional regulator degV family protein tryptophan synthase beta subunit TrpB phospho-N-acetylmuramoyl-pentapeptide-transferase MraY response regulator domain-containing protein
105 105 105 105 105 105 105 105	82904 89932 95333 109321 81473 95992 87491	83293 90957 96202 110712 82438 96354 87970	1025 869 1391 965 362 479	LacI family transcriptional regulator degV family protein tryptophan synthase beta subunit TrpB phospho-N-acetylmuramoyl-pentapeptide-transferase MraY response regulator domain-containing protein hypothetical protein
105           105           105           105           105           105           105           105           105           105           105           105           105           105	82904 89932 95333 109321 81473 95992 87491 73604	83293 90957 96202 110712 82438 96354 87970 74557	1025 869 1391 965 362 479 953	LacI family transcriptional regulator degV family protein tryptophan synthase beta subunit TrpB phospho-N-acetylmuramoyl-pentapeptide-transferase MraY response regulator domain-containing protein hypothetical protein alpha/beta fold family hydrolase
105 105 105 105 105 105 105 105	82904 89932 95333 109321 81473 95992 87491	83293 90957 96202 110712 82438 96354 87970	1025 869 1391 965 362 479	LacI family transcriptional regulator degV family protein tryptophan synthase beta subunit TrpB phospho-N-acetylmuramoyl-pentapeptide-transferase MraY response regulator domain-containing protein hypothetical protein

106	84309	86333	2024	glycoside hydrolase family 31 Gh31C
106	90480	91454	974	hypothetical protein
106	83829	83996	167	hypothetical protein
106	90963	92381	1418	glucuronate isomerase UxaC
106	96273	98342	2069	ATP-dependent DNA helicase RecG
106	110768	111631	863	PHP domain-containing protein
106	82457	84715	2258	cell division protein FtsI
106	96445	97068	623	hypothetical protein
106	87973	89154	1181	cell wall hydrolase
106	90059	90436	377	hypothetical protein
106	88850	89980	1130	hypothetical protein
107	91552	93213	1661	sucrose phosphorylase Suc13P
107	84044 84763	84334 85203	290 440	hypothetical protein
107	97101	97412	311	cell division protein FtsL hypothetical protein
107	86691	88250	1559	sugar ABC transporter substrate-binding protein
107	89167	89649	482	deoxycytidylate deaminase
107	74645	76681	2036	methionyl-tRNA synthetase MetG
107	90552	91721	1169	hypothetical protein
107	90076	91161	1085	hypothetical protein
108	84544	85566	1022	hypothetical protein
108	92570	94072	1502	altronate hydrolase UxaA
108	98411	100180	1769	dihydroxyacetone kinase family protein
108	111757	112725	968	hypothetical protein
108	85236	86171	935	S-adenosyl-methyltransferase MraW
108	97705	98112	407	hypothetical protein
108	88341	89285	944	sugar ABC transporter permease
108	76708	77598	890	methionine aminopeptidase Map
108	91854	92789	935	HAMP/SpoIIE domain-containing protein
108	91163	91804	641	hypothetical protein
109	85579	88236	2657	McrBC restriction endonuclease system protein McrB
109	94243	95091	848	xylose isomerase domain-containing protein
109	100217	100579	362 440	hypothetical protein
109	86181 98144	86621 98860	716	MraZ protein
109	89314	98860	809	endonuclease V sugar ABC transporter permease
109	89674	90303	629	uracil phosphoribosyltransferase upp
109	77633	79165	1532	5'-nucleotidase domain-containing protein
109	91829	93358	1532	polysaccharide biosynthesis protein
110	88249	89556	1307	McrBC restriction endonuclease system protein McrC
110	100788	100973	185	ribosomal protein L28 RpmB
110	112730	114235	1505	hypothetical protein
110	90240	91262	1022	LacI family transcriptional regulator
110	90320	90748	428	ribose 5-phosphate isomerase RpiB
110	79170	79994	824	phosphonate ABC transporter permease protein PhnE
110	92786	93430	644	SpoIIE domain-containing protein
110	93366	94400	1034	acyltransferase
111	89596	90342	746	hypothetical protein
111	95177	95950	773	hypothetical protein
111	101028	101444	416	hypothetical protein
111	90788	91846	1058	Sua5/YciO/YrdC/YwlC family protein
111	79997	80818	821	phosphonate ABC transporter permease protein PhnE
112	91851 90476	93554 91747	1703 1271	chitinase Chi18A ATP-dependent metallopeptidase HflB
112	95990	98113	2123	hypothetical protein
112	114270	115088	818	HAD superfamily hydrolase
112	98853	99302	449	hypothetical protein
112	80824	81597	773	phosphonate ABC transporter ATP-binding protein phnC
112	93645	93812	167	hypothetical protein
113	91649	94093	2444	cellobiose phosphorylase Cbp94A
113	91821	92396	575	hypothetical protein
113	98167	99537	1370	hypothetical protein
113	101446	102213	767	RNA polymerase sigma factor sigma-70 family protein
113	115090	115344	254	hypothetical protein
113	94256	95056	800	MecA family protein
113	81747	82856	1109	phosphonate ABC transporter substrate-binding protein
113	93879	94586	707	purine nucleoside phosphorylase DeoD
113	94402	96297	1895	hypothetical protein
114	93926	95839	1913	hypothetical protein
114	92412 99518	93119	707 1196	hypothetical protein
114	102226	100714 103104	878	acetate kinase AckA hypothetical protein
114	115360	115944	584	septum formation protein Maf
114	99452	100450	998	septum formation protein Man
114	99432	95001	779	metallopeptidase M23 family protein
114	94222	95470	866	hypothetical protein
114	96281	97669	1388	hypothetical protein
115	96107	97171	1064	hypothetical protein
115	93217	93960	743	hypothetical protein
115	100886	101746	860	AraC family transcriptional regulator
115	103122	105857	2735	two component system histidine kinase/response regulator hybrid protein
115	115962	118112	2150	polyphosphate kinase Ppk
115	100468	101157	689	hypothetical protein

115         0101         9217         453         hyperbolic protein           115         0101         9207         500         Protein Annual Science Science           115         9752         9400         100         Protein Annual Science           116         9752         9400         100         Protein Annual Science           116         9752         9400         Base Science         Protein Annual Science           116         9752         9400         Base Science         Protein           116         9752         9400         Base Science         Protein           116         9752         9400         Base Science         Protein           116         9701         511         Base Science         Base Science         Base Science           117         10519         1037         458         Base Science         Base Science         Base Science           117         10519         10537         458         Base Science         Base Science         Base Science           117         10519         10507         960         Base Science         Base					
115         8780         8770         666         Trichos-phaphas, Septimar Re           115         9777         9816         488         byskelici primi           116         9777         9816         488         byskelici primi           116         10272         10834         1490         byskelici primi           116         10276         10834         4590         Philosympolici primi           116         8077         8468         941         maakrabe, soluti R Ri           116         8077         8468         941         maakrabe, soluti R Ri           117         10978         9551         152         byskelici primi           117         10979         9551         168         biskerse apprimi           117         10974         10977         448         biskerse apprimi           117         10974         10977         449         biskerse apprimi           117         10974         10971         1098         biskerse apprimi           118         1077         4568         110         charase apprimi           118         1077         10868         111         charase apprimi           118         9778 <t< td=""><td></td><td></td><td></td><td></td><td></td></t<>					
115         9572         9688         130         urry-RKA quitaxe for           115         10762         9180         488         bygetade special constraints for a constraint for a constra					
113         9702         98100         448         Important press           116         10783         10501         1118         according to the second press           116         10703         10703         10704         10704           116         8707         45045         966         Ph2NMARE EQA           116         8707         85080         9710         123         PhysRet IA           116         8700         9631         1355         PhysRet IA         PhysRet IA           117         10705         10705         10704         PhysRet IA         PhysRet IA           117         10705         10715         PhysRet IA         PhysRet IA         PhysRet IA           117         10705         10714         10704         10717         PhysRet IA	115	83051	83707	656	ribulose-phosphate 3-epimerase Rpe
116         1078         10981         118         actify syste marker Ed2.           116         10750         10550         1550         1570         1570           116         10750         10550         1570         1570         1570           116         9980         9780         1570         1570         1570           117         1070         1071         148         1570         1570           117         1070         1075         1074         1570         1570           117         10750         10754         10754         1570         1570           117         10754         10754         10754         1570         1570           117         10754         10754         10754         1570         1570           118         10754         10757         270         1570         1570           118         10754         10757         270         1570         1570           118         10757         10780         1078         1570         1570           118         10757         2700         1070         1570         1570           118         10570         2700	115	95529	96830	1301	seryl-tRNA synthetase SerS
116         10781         10201         1118         acopi systemers Etcl.           116         01076         10055         4150         FrickScofffe Hump protein           116         01076         10055         4150         FrickScofffe Hump protein           116         9580         97601         523         Epidemical protein           117         10056         61071         438         Epidemical protein           117         10056         61071         438         Biodeneric superfamily formin           117         10056         61071         438         Biodeneric superfamily formin           117         101560         10176         10176         10176         10176           117         101850         101660         1326         Epidemical protein           117         101850         101660         1326         Epidemical protein           118         10170         10171         10171         10171         10171           118         10170         10180         10160         Epidemical protein           118         10170         10180         1010         Epidemical protein           118         101970         10180         Edidmical protein <td>115</td> <td>97672</td> <td>98160</td> <td>488</td> <td>hypothetical protein</td>	115	97672	98160	488	hypothetical protein
116         9962         9448         996         Ippoteining presis           116         9075         11555         4550         PicKSQUIP lendy presis           116         9084         9023         100         forstatu           116         9080         901         113         instructioner situates         This           117         9090         9913         1133         Ippoteining press           117         11095         11037         488         Minocore sequences         Minocore sequences           117         11095         11037         11085         1109         11037         1109         1107         1109	116	101783	102901	1118	
116         10270         105823         1700         FackSpatile makey protein           116         5307         8664         941         markeolae ubwell Tu           116         6307         8664         941         markeolae ubwell Tu           117         10599         1051         105         10599           117         10599         10523         2272         105074         1050           117         10598         10523         2272         105074         1050           117         10598         10523         2272         105074         10507           117         10580         10640         250         10507         10508         1050           118         10509         10564         110         00509         1050         10509           118         10507         10564         112         ADP-obsciglpsophistic lastic growth         118           118         10507         10564         112         ADP-obsciglpsophistic lastic growth           118         10507         10564         1000         Topkeokic growth         119           118         10507         10508         11418         Obscie growth         119 <td< td=""><td>116</td><td>93962</td><td>94948</td><td>986</td><td></td></td<>	116	93962	94948	986	
116         9908         9233         170         Interval           116         8680         9740         521         Hyperbinding presis           116         98080         9740         521         Hyperbinding presis           117         101099         101577         558         Hyperbinding presis           117         101099         101577         158         Hoho Wanneonstamp presis           117         110556         10580         10166         258         Hyperbinding presis           117         110564         10166         258         Hyperbinding presis         Presidential presis           117         11680         10166         258         Hyperbinding presis         Presidential presis           118         101580         10166         258         Hyperbinding presis         Presidential presis           118         101590         10166         258         APP Complex presis         APP					
1146         3370         8464         941         translotion provide a provide provid					
11/16         9960         97601         221         byodistical presis           11/6         98100         99515         1358         byodistical presis           11/7         10590         10537         438         Biodistical presis           11/7         10590         10537         438         Biodistical presis           11/7         10590         10536         10566         123           11/7         14600         8549         237         Biodistical presis           11/7         14600         8549         830         transkolos abuela ATL           11/8         97545         9856         116         Chromos particinal presis           11/8         97515         9850         116         Chromos particinal presis           11/8         9750         12909         128         Chromos particinal presis           11/8         9701         12909         124         Chromos particinal presis           11/8         9701         779         Chromos particinal presis         400           11/8         9701         779         Chromos particinal presis         400           11/9         97051         1280         120         120         120					
116         94015         94015         135         hypotocial presin           117         105920         103377         458         theorems usperfunity proxin           117         10395         103588         222         TIB CVPF domits containing presin           117         1181         10548         10559         10559           117         1181         10544         1057         concord/op/datata PA           117         9415         96564         432         ADBr-toxylphoightmata PA           118         01550         10585         1148         chronorsense particoming presin         118           118         01550         10585         1148         chronorsense particoming presin         118           118         01570         10580         1148         chronorsense particoming presin         1050           118         9571         9560         1050         10640         107         chronorsen particoming presin           118         9573         9583         158         hypotocial presin         107         chronorsen particoming presin         108           119         9660         9758         158         Laf family mancripholid presin         118         1080         1070 </td <td></td> <td></td> <td></td> <td></td> <td></td>					
117         9907         9561         572         hypotocla procis           117         10376         458         100-constrare-upperform/point         100-constrare-upperform/point           117         10384         1577         exceptylop/points-constraint procis           117         10384         1657         exceptylop/points-constraint procis           117         16840         1567         hypotocla procis           118         10564         168         hypotocla procis           118         10556         10564         116         ritro-constraint constraint					
117         10979         10372         448         thesestere septiming protein           117         11871         119644         1657         excepting hopshate Pys           117         11814         116460         1526         hyperheting protein           117         11848         116460         1526         hyperheting protein           118         116540         1168         1168         1168           118         11075         115860         1168         excepting hyperheting protein         127 Ref           118         110772         115860         1168         chorison tensory probants dividual Pach           118         110772         115860         1168         chorison tensory probants dividual Pach           118         110772         115864         206         hyperheting protein         117           118         96051         9797         241         TrapeLine protein         118         118           118         96051         9798         128         hyperheting protein         118           119         100554         1010         faty ackipophicing protein         118         hyperheting protein           119         100554         10104         11017					
117         10028         1072         110 CVP densi containing poten           117         11857         11857         11857         11857           117         10586         10616         350         Layoltchical protein           117         4069         8509         Lower and the state of the					hypothetical protein
117         1193         11994         1247         Comprehensional Pyter           117         8466         8549         850         transcension submit A Ta           118         9753         9056         812         chorencome particining provide her           118         9754         9056         812         ADF-chorency hybrid by the	117	102919	103377	458	thioesterase superfamily protein
171         10340         106166         326         hypohesical proxin           171         9445         96317         802         chromosome parisoning provin FAT           171         9445         9656         802         ADR-Chooglychoghothychocho           178         10580         1168         chromosome parisoning provin FAT         Regat           178         10580         1168         chromosome parisoning provin FAT         Regat           178         10570         10580         1168         chromosome parisoning provin FAT           178         10570         10580         1168         chromosome parisoning provin Path           178         95930         95930         105930         10504         10504           178         95930         95930         10504         1077         chromosome parisoning provin Path           179         95600         95958         1298         hypohetal cymera         107           179         10587         1197         1044         hypohetal cymera         107           179         10587         1197         1044         hypohetal cymera         107           179         10549         1054         105         107         1056 <td>117</td> <td>105956</td> <td>108328</td> <td>2372</td> <td>HD-GYP domain-containing protein</td>	117	105956	108328	2372	HD-GYP domain-containing protein
117         4460         5599         830         transition of the princip protein park           118         9734         5956         812         ADP-thosylghyolybloke failing protein           118         10589         11068         114         chronoun particining protein           118         10590         106863         114         chronoun particining protein           118         10670         106469         200         hyochronic protein           118         10670         106469         200         hyochronic protein           118         98311         99100         779         chronoun particining protein           119         99352         9990         Lact faulty turnorization regulator         hyochronic protein           119         106601         10737         response regulator domin containing protein         hyochronic protein           119         106857         10100         fary solution protein         hyochronic protein           119         106867         10103         fary solution protein         hyochronic protein           119         10652         10104         hyochronic protein         hyochronic protein           119         10652         10105         hyochronic protein         hyochronic	117	118137	119684	1547	exopolyphosphatase Ppx
117         9413         9407         9405         demonse partitioning protein protein           118         105569         103885         116         mboxal protein         12 RpuB           118         119702         120805         1148         christowic motics/epipediane ddyntrates PIKA           118         119702         120805         1148         christowic motics/epipediane ddyntrates PIKA           118         5603         39707         2341         TripR4 late protein ddyntrates PIKA           118         99703         100040         121         replace ddyntrates PIKA           118         99707         241         TripR4 late protein ddyntrates PIKA           119         99737         98535         989         Lat family transer spread and D           119         19857         10487         1010         faty acid/phonoligid ynthesis protein and D           119         108358         104067         133         Psynthesia protein and D           119         108585         104067         133         Psynthesia protein 3 pill           119         10954         10105         123         methormachese GdB           119         100554         236         replacod donana sete transet and and doddod donana protein clypl	117	105840	106166	326	hypothetical protein
118         9754         9966         812         ADP-showlighted by location in the production i	117	84669	85499	830	transketolase subunit A Tkt
118         9754         9966         812         ADP-showlighted by location in the production i	117	97415	98317	902	chromosome partitioning protein ParB
118         10569         1148         encount protein L32 (gard)           118         119702         106469         290         hypothetial protein           118         19505         29575         284         TypK Lie protein VeCY vcD           118         95935         395975         284         TypK Lie protein VeCY vcD           118         95935         39597         284         TypK Lie protein VeCY vcD           118         95935         39505         49604         44604           118         95835         39505         49604         44604           119         95857         9585         LaC fully Units protein PrA           110         105357         10467         1010         Enty adopted protein PrA           110         105357         10467         1010         Enty adopted protein PrA           119         96544         10667         383         hypothetical protein PrA           119         90554         9644         200         cold Adopted protein PrA           119         90554         10105         1472         MBOAT fully adopted protein PrA           119         90554         10105         1472         MBOAT fully adopted protein Adopted protein PrA     <					A 01
118         11902         12085         148         choicean managerephane delythmar Pack           118         19607         2961         TipsHile protein YeC YeO D           118         99303         100466         1343         TipsHile protein YeC YeO D           118         87303         86400         4955         L-mbines-Sphosphat-4-ginesmax AnD           118         87317         98825         989         Lacl family transcriptional regulars           119         018353         10110         furty sci0/probabilied synthesis protein PKA           119         108353         104167         1010         furty sci0/probabilied synthesis protein PKA           119         108353         104110         Tipsthesia protein PKA         1010           119         106354         101010         furty sci0/probabilied synthesis protein PKA           119         106354         104057         333         10         10904661         1000           119         99391         101035         433         10         1000466         10005         10005           119         99393         100135         236         mershylanes fund         100         100105         100105         100105         100105         100105 <t< td=""><td></td><td></td><td></td><td>-</td><td></td></t<>				-	
118         106179         106469         290         TypeIblic protocol protocol           118         95993         100546         1343         reglication: DNA bicleac funds           118         95703         100546         1343         reglication: DNA bicleac funds           118         95731         95825         089         Lat fund y uncerprised regulator           119         9660         97853         10967         Lat fund y uncerprised regulator           119         106567         10100         futy science regulator         futy science regulator           119         105857         101667         10100         futy science regulator         futy science regulator           119         106537         10107         futy science regulator         futy science regulator         futy science regulator           119         106537         10107         futy science regulator         futy science regulator         futy science regulator           119         99593         101050         1472         MBOAT fundy science regulator         futy science regulator           119         99533         101056         2309         glycogen holydon plase GBP           120         109542         101556         2309         glycogen holydon plase GBP </td <td></td> <td></td> <td></td> <td></td> <td>* *</td>					* *
118         9903         9979         284         TrgR-Kac pools 'a CV ScD           118         89703         100646         1343         replactive Sprinter AuD           118         89703         98910         Carbon-S-phosphat - Sprinter AuD           119         97873         98826         989         Lat family transcriptional regulator           119         97837         98826         1982         haraccipated regulator           119         103537         104857         10487         1000         faty sci4/phospholipid synthesis protein           119         108538         109111         773         regenore regulator downais-containing protein           119         108533         119177         1044         hypothesical protein           119         0.0553         101056         1377         Lathokanas AuB           119         0.0553         101056         2369         glycogen phosphosphose           110         96957         101256         2369         glycogen phosphosphose           120         10974         11338         4214         rwo component ystem hakitis kinase/rsporen englator hybrid protein           120         100759         10354         2484         100056         10494					
118         9930         10064         1343         epicative DNA holicosa dnaB           118         9831         99110         779         chrubox-5-phoptatspinzrae AnD           119         99660         97958         1298         that family uncerpitotal regulator           119         99660         97958         1298         thypotherial protein           119         108857         10101         faty act/bypotheptid yubrics i protein PKX           119         108858         109111         773         response regulator domain containing protein           119         106844         108867         383         hypotherical protein           119         106848         108867         383         hypotherical protein           119         00650         101056         446         rebornal protein 2 Pdf           119         99525         101056         2260         abypotherical protein           120         09857         10156         226         abypotherical protein           120         09957         10156         226         abypotherical protein           120         00714         1338         4514         two componer system hesitata timato regulato hybrid protein           120         100					
118         8540         0951         1thuse-S-phophat -4gramma AuD           119         9733         98826         980         Lacf Lamly transcriptional grotin PaA           119         9763         1298         hypothetical precin           119         100857         104857         1010         fury achiphophipity synthesis           119         100853         12937         1044         hypothetical precin           119         12033         121937         1044         hypothetical precin           119         100853         121937         1044         hypothetical precin           119         100854         101066         response regulator domain-containing protein           119         96254         96354         200         cold sbc.4 domain precine CpD           119         99373         101056         472         MBOAT funity segment action           120         104920         10526         236         acyl carter precin           120         10614         10739         3315         phosphorbical precin           120         10614         10734         335         phosphorbical precin           120         10610         10318         208         phosphorbical precin </td <td></td> <td></td> <td></td> <td></td> <td>* *</td>					* *
118         99313         99110         779         chonous partitioning provide Park           119         97837         9885         1298         Depotencial provide           119         108837         10101         Ent Barly increasing provide         Park           119         108838         109111         773         response regulator domain-containing provide           119         106844         108857         381         hypothetical provide           119         106444         108857         381         hypothetical provide           119         106450         101056         446         relaxonal domain provide CpD           119         90554         96454         200         cold shock domain provide CpD           119         90853         101055         422         MBOAT Enang/seqUandShows           119         99333         101055         422         MBOAT Enang/seqUandShows         methylytransferas CiBB           120         101124         11338         4214         two component system histidiae Linase-response regulator hybrid protein           120         101124         11338         4214         two component system histidiae Linase-response HIA           120         100124         11338         4214 <td></td> <td></td> <td></td> <td></td> <td>*</td>					*
119         9937         99826         999         Lacl family mascription regulator           119         100587         104867         1010         fury acidybopholipd synthesis protein Pix           119         100383         12917         1004         hypothexial protein           119         100383         121977         1004         hypothexial protein           119         106544         1006667         383         hypothexial protein           119         90534         99454         200         odd bock domain protein CspD           119         90539         101056         446         rebuokase AraB           119         99539         101055         777         methybranefraze GaB           120         109531         101256         236         acyl carrier protein           120         109470         10156         236         acyl carrier protein           120         109141         107349         335         hypothexicit protein           120         109124         10734         355         hypothexicit protein           120         101026         10749         355         hypothexicit protein           120         101026         10749         1448         <					
119         99660         97958         1298         bypothskin protein           119         100357         1000         Taty ack/polopidy synbssis protein PbX           119         100358         109111         773         response regulator domain containing protein           119         100453         121917         1004         hypothckial protein           119         100550         121917         1004         hypothckial protein           119         90554         2001         ood shock domain protein         hypothckial protein           119         90553         101096         466         rebornal protein         hypothckial protein           119         90551         101005         1472         MBOAT famaly acytrasticase GlaB           120         90957         101266         2269         gbycogen phosphorysterogen regulator hytein protein           120         100124         11338         4214         two component system histiller kinas-reponse regulator hytein protein           120         100124         11338         4214         two component system histiller kinas-reponse regulator hytein protein           120         100126         10338         4214         two component system histiller kinas-reponse regulator hytein protein           120 </td <td></td> <td></td> <td></td> <td></td> <td></td>					
119         108387         109807         1010         farty science provides growth and second and provides and second and seco	119	97837	98826	989	LacI family transcriptional regulator
119         10838         10911         773         response regulator formin containing protein           119         106454         100667         383         hypothesial protein           119         10650         101076         466         relevant           119         90254         200         cold shock domain protein CoPD           119         90505         101076         466         relevant           119         99379         100136         737         methybrankerse GuB           119         99379         101266         2269         glycogen phosphorybranker GuB           120         100734         11338         4214         two component ystem histilter kinas-reportser regulator hybrid protein           120         100714         11338         4214         two component ystem histilter kinas-reportser regulator hybrid protein           120         100714         10338         4214         two component ystem histilter kinas-reportser regulator hybrid protein           120         100714         10338         4214         two component ystem histilter kinas-reportsen regulator hybrid protein           120         100754         10318         2081         DHI domain-containing protein           120         100754         10351	119	96660	97958	1298	hypothetical protein
119         10338         109111         773         response regulator domin. containing protein           119         100644         100867         383         bypothexial protein           119         10050         101096         446         response           119         90254         200         cold abck. domain protein CopD           119         90503         101096         446         rebornal protein CopD           119         99573         101036         737         methybrandfraze GaB           119         99573         101056         226         asyltrase GaB           120         100724         11338         4214         two component ystem histiline kinas-toreaxing protein           120         100724         11338         4214         two component ystem histiline kinas-toreaxing protein           120         100724         11338         4214         two component ystem histiline kinas-toreaxing protein           120         100724         11338         4214         two component ystem histiline kinas-toreaxing protein           120         100105         10318         2081         BiB	119	103857	104867	1010	fatty acid/phospholipid synthesis protein PlsX
119         120033         12107         1004         Payobising proxim           119         106541         106667         338         Dayobising proxim           119         100551         96544         200         cold shock domain proxim (CqD           119         10055         110106         446         rebosonal proxim (CqD           119         96512         88017         1595         L-rebokismes AraB           119         99533         110105         1472         MBOAT family septimask and           110         99533         110105         1472         MBOAT family septimask and           120         109524         11333         4214         tree comporent system histifue kinas: response regulare hybrid protein           120         109134         11733         325         phypohenical protein           120         109104         107349         335         phypohenical protein           120         101010         163181         2081         DHH domain comparent system histifue kinas: response regulare hybrid protein           120         101025         163053         1448         hypohenical protein           121         102751         163054         713         aphypohenical protein	119	108338	109111	773	
119         106484         106867         338         Payobasis           119         10050         101096         446         ribosoma protein CypD           119         10050         101096         446         ribosoma protein CypD           119         99399         100136         777         methybrane GaB           119         99937         101366         239         glycogen phosphorylace GlgP           120         19977         101366         239         glycogen phosphorylace GlgP           120         199720         101566         236         glycogen phosphorylace GlgP           120         199724         11338         4214         two component system initiatina kinascirespoore regulator hybrid protein           120         199744         107249         333         Dipotentoxylforminin-Scanabar ribotak isomerespone regulator hybrid protein           120         101010         103181         2081         Diff domain protein         Diff domain protein           120         100126         102042         1916         (fRN Aurdin's S-arboxymethylaminochylamothyl	119	120933			
119         9054         9054         200         cold shock domain protein CpD           119         10056         101096         446         ribosomal protein L PpH           119         9852         18017         1555         L-ribokama Adl           119         9953         101056         1472         MBOAT family acyltransferase           120         99877         101266         2309         gly carpt potoin           120         106120         101266         236         acyl cariste protein           120         106124         11338         4214         two component system histidine kinasse response regulator hybrid protein           120         106614         107249         335         phosphorboxyfirmmine-5-aninoinifacton carboxamide ribotale isomerase HisA           120         106624         97377         773         phosphorboxyfirmmine-5-aninoinifacton carboxamide ribotale isomerase HisA           120         101005         10243         1448         RN undite S-carboxymethylaminomethyl motification carboxamide ribotale protein           121         101025         10242         1916         (REN variation activation					* * *
119         100:50         1100         446         riboscal program           119         9692         100136         777         methytransferase GidB           119         99939         100136         777         methytransferase GidB           119         99939         100136         2379         methytransferase GidB           120         19857         101356         2369         glycogen phosphylas GidP           120         109124         11333         4214         two component system histlike kinase/response regulator hybrid protein           120         109124         11333         4214         two component system histlike kinase/response regulator hybrid protein           120         109124         10333         4214         two component system histlike kinase/response regulator hybrid protein           120         100105         10318         2081         Diff domini-constanting protein           120         101026         10242         1916         (RN arkine S-carboxymethylinminics)           121         10253         1448         phypothetical protein           121         10254         105451         249           121         10253         10455         3575           121         107551					
119         8422         88017         1595         L-irbubkanse AnB           119         99533         101005         1472         MBOAT markerase           120         99697         101266         2309         glycogen phosphorylase GigP           120         109720         105156         236         acyl carrie protein           120         109714         113338         4214         two component system histiline Kanacice-poner ignular hybrid protein           120         100714         113338         4214         two component system histiline Kanacice-poner ignular hybrid protein           120         100714         101338         4214         two component system histiline Kanacice-poner ignular hybrid protein           120         100714         101318         2081         10141         Difficion carging forein           120         101005         102453         1448         Nayotheraxerphaniomethybraser ignus         10161           121         101005         102453         1448         Nayotheraxerphanybraserse PyrB         101           121         10105         102453         1448         Nayotheraxer protein         101           121         10279         129315         956         aspartate caranybransferase PyrB         101 </td <td></td> <td></td> <td></td> <td></td> <td>A A</td>					A A
19         99999         100136         177         methylyransframe Gall           119         99897         101266         2309         glycogen phosphorylase GigP           120         104920         105156         230         acj Jarrie pnotein           120         1069124         11338         4214         two component system histiline kinasciresponse regulator hybrid protein           120         106914         107249         133         hosphorboxytem histiline kinasciresponse regulator hybrid protein           120         106012         107249         133         hosphorboxytem histiline consamile protein           120         10100         103181         2081         DHH domains containing protein           120         101012         102412         1916         tRNA undine 5-carboxynethylaminonethyl modification enzyme GidA           121         101024         102412         1916         tRNA undine 5-carboxynethylaminonethyl modification enzyme GidA           121         10224         105947         713         riboxetace BufB           121         10272         107551         299         hybrothecial protein           121         10294         90103         839         &-asognamine DNA glycoxylace Ogg           121         102944					
19         99333         101006         1472         MBAT           120         99957         101266         239         glycogen phosphorplase GigP           120         109124         113338         4214         two component system histiliae knawlersponse regulator hybrid protein           120         100914         107338         4214         two component system histiliae knawlersponse regulator hybrid protein           120         100914         107338         4214         two component system histiliae knawlersponse regulator hybrid protein           120         100106         103181         2081         DHI domain-containing protein           120         100106         10242         1916         tRNA urdine 5-arthoxymethytamionethytin modification carym GidA           120         100106         102433         1448         tRNA urdine 5-arthoxymethytamionethytin modification carym GidA           121         107252         107551         299         hypothochical protein           121         07440         98195         753         dihydrodipicolinate reductase DapB           121         10752         107551         129         Nypothetical protein           122         107646         10242         RNA modification protein           122         105928 </td <td></td> <td></td> <td></td> <td></td> <td></td>					
120         98957         101266         2309         glecare proping           120         1009124         11333         4214         two component system histing kinas/regionar regulator hybrid protein           120         1009124         11333         4214         two component system histing kinas/regionar regulator hybrid protein           120         1009124         11333         4214         two component system histing kinas/regionar regulator hybrid protein           120         96624         97397         773         phosphoribosylforminino-5-aminoimidacole carboxamide ribotide isomerase His.A           120         101010         103181         2081         DHI domain-containing protein           120         100126         102042         1916         tRN uridine S-carboxymethylaminomethyl modification enzyme GidA           121         101025         102537         1448         hypothetical protein           121         102524         105547         735         dihydyothylase Giga           121         107521         107551         299         hypothetical protein           121         107240         98195         755         dihydyothylase Ogg           121         107250         103993         1724         HTM domain-containing protein           1					
120         109/20         105156         236         acyl carrier protein           120         10914         11338         4214         two component system histikhe kinascrepasse regulator hybrid protein           120         106914         107349         335         phosphoribosylforminino-5 aminoimidazok carboxanide ribotide isomerase HisA           120         101100         103181         2081         DHH domain-containing protein           120         100125         102422         1916         UKN avidine 5-carboxymethylamiforation enzyme GidA           120         100105         102423         1448         hybrohetical protein           121         100252         10757         713         riboxeclease PyrB           121         102523         107571         299         hybrohetical protein           121         102725         107571         299         hybrohetical protein           121         102725         107591         299         hybrohetical protein           121         102724         98195         755         dihydrohydrohetical protein           121         10264         10434         14421         thNA modification CFPare TrmE           122         10269         10399         1724         hybrohetical pr					
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120         109914         107249         335         1         1         1         1           120         96624         97397         773         phosphoribosylformimino-5 aminoimidazole carboxanide ribotide isomerase HisA           120         101100         103181         2081         DHfI domain-containing protein           120         100126         102424         1916         ttRN ardine 5-aminoimidazole carboxmichyl andification enzyme GidA           120         100105         102433         1448         ttRN ardine 5-ampontelyl andification enzyme GidA           121         105234         105947         713         ribonclease III Re           121         107252         107551         299         hypothetical protein           121         107252         107551         299         hypothetical protein           121         107264         90103         839         8-acogunine DNA bylycosylace Ogg           121         102694         103993         1724         Bylycosylace Ogg           122         102298         90014         212         HTH domain-containing protein           122         10280         90014         212         HTH domain-containing protein           122         102804         3557	120	104920	105156	236	acyl carrier protein
120         96624         97397         773         phosphoriboxyfforminino 2-minominizava exhoxamile ribotide isomerase HisA           120         10100         103181         2081         DHH domain-containing protein           120         88004         89116         1112         Graft Ramity transcriptional regulator           120         100126         102042         1916         transcriptional regulator           120         100126         102042         1916         transcriptional regulator           121         105234         105937         1448         Number Second Se	120	109124	113338	4214	two component system histidine kinase/response regulator hybrid protein
120         96624         97397         773         phosphorboxyforminno-saminoimidazole carboxamide ribotide isomerase HisA           120         101010         101311         2081         DHH domais-containing protein           120         88004         89116         1112         GmR family transcriptional regulator           120         101026         10242         1916         tRNA uridine 5-carboxymethylamitomethyl modification enzyme GidA           121         10534         105947         713         ribonuclease III Re           121         10752         107551         299         hypothetical protein           121         107252         107551         299         hypothetical protein           121         107252         107551         299         hypothetical protein           121         107264         90103         839         8-oxogaanine DNA glycosylase Ogg           121         102644         103465         1421         RND modifical protein           122         102645         103455         357         chromosone segregation protein Sne           122         110351         115486         2135         HD-QTP domain-containing protein           122         107616         109055         1439         hypothetical					
120         101100         103181         2081         DH H domain-containing protein           120         88004         89116         1112         GmR family transcriptional regulator           120         100126         102453         1448         Insponse           121         105234         105947         713         ribouckase II Rac           121         105234         105947         713         ribouckase II Rac           121         105234         105947         73         ribouckase II Rac           121         107252         107551         299         hypothetical protein           121         107252         107551         299         hypothetical protein           121         107244         050103         839         8-oxoganine DNA glycoylase Ogg           122         102269         103993         1724         hypothetical protein           122         102509         109393         1724         hypothetical protein           122         105928         109485         3557         chromsome segregation protein Smc           122         105928         109485         3557         chromsome segregation protein Smc           122         105937         104262 <t< td=""><td>120</td><td>106914</td><td>107249</td><td>335</td><td>hypothetical protein</td></t<>	120	106914	107249	335	hypothetical protein
120         88044         89116         1112         GntR family transcriptional regulator           120         100126         10242         1916         ttRNA tridine 5-carboxymethylaminomethyl modification enzyme GidA           120         101005         102433         1448         hypothetical protein           121         10534         105947         713         ribonucless III Rac           121         10722         107551         299         hypothetical protein           121         97440         98195         755         dihydnodipicolinate reductase DapB           121         97440         98195         755         dihydnodipicolinate reductase DapB           121         10252         103365         1421         tRNA modification GTPase TrmE           122         10269         103993         1724         hypothetical protein           122         10351         115486         2135         chromssome segregation protein Smc           122         103531         115486         2135         HD -GYP domin-containing protein           122         107616         109055         1439         hypothetical protein           122         90100         90558         458         restriction endonuclease family protein </td <td></td> <td></td> <td></td> <td></td> <td></td>					
120         100126         102042         1916         rRNA urdime 5-carboxymethylamicomethyl modification enzyme GidA           120         101005         102453         1448         hypothetical protein           121         102534         105947         713         ribonucless III Re           121         107525         107551         299         hypothetical protein           121         107252         107551         299         hypothetical protein           121         97440         98195         755         dihydydodjkooljane Obg           121         107244         103465         1421         reductas DagB           122         107269         103993         1724         hypothetical protein           122         10828         199014         212         HTH domain-containing protein non           122         19831         115486         2135         ehronsome segregation protein Smc           122         105928         109485         3557         chronsome segregation protein Smc           122         10357         104436         aspartate carbanoyltransferase regulatory subunit Pyr1           122         10357         104562         725         single stranded muckica acib dinding protein	120	96624	97397	773	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA
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121         105234         105947         713         ribonuclease III Ruc           121         121979         12295         956         asparate carbumyltransferase PyB           121         107252         107551         299         hypothetical protein           121         97440         98195         755         dihydrodipicolinate reductase DapB           121         97440         103465         1421         (RNA modification GTPase TrmE           122         102269         103993         1724         Hypothetical protein           122         98802         99014         212         HTH domain-containing protein           122         105928         109485         3557         chronnsome segregation protein Sme           122         11351         115486         2135         HD-GYP domain-containing protein           122         103928         1094485         3557         chronnsome segregation protein Sme           122         11351         115486         2135         HD-GYP domain-containing protein           122         10355         1439         hypothetical protein         123           123         104144         106004         1856         GGDEVicate domain-containing protein           123	120 120 120	96624 101100 88004	97397 103181 89116	773 2081 1112	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GntR family transcriptional regulator
121         121979         12235         956         aspartate carbanoyltransferase PyrB           121         107252         107551         299         hypothetical protein           121         107240         98195         755         didydrolipoilnate reductase DapB           121         89244         90103         839         B-oxogunine DNA glycosylase Ogg           121         102044         103465         1421         tRNA modification GTPase TrmE           122         102269         103993         1724         hypothetical protein           122         102280         109485         3557         chromos segregation protein Smc           122         103281         115486         2135         HD-GYP domain-containing protein           122         107616         109055         1439         hypothetical protein           122         98197         99087         890         dihydrodipicolinate synthase dapA           122         90100         90558         458         restriction endonuclease family protein           123         10448         106004         1856         GGDEF/cache durai-containing protein           123         19449         1970         1109         hypothetical protein <td< td=""><td>120 120 120 120</td><td>96624 101100 88004 100126</td><td>97397 103181 89116 102042</td><td>773 2081 1112 1916</td><td>phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GntR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA</td></td<>	120 120 120 120	96624 101100 88004 100126	97397 103181 89116 102042	773 2081 1112 1916	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GntR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA
121         107252         107551         299         hypothetical protein           121         97440         98195         755         dihydrodipicolinate reductase DapB           121         89264         90103         839         8-oxoguanie DNA glycosylase Ogg           121         102044         103465         1421         tRNA modification GTPase TrmE           122         102269         103993         1724         hypothetical protein           122         98802         99014         212         HTH domain - containing protein           122         103351         115486         2135         HD-CPV domain- containing protein           122         112310         115486         2135         HD-CPV domain- containing protein           122         10351         115486         2135         HD-CPV domain- containing protein           122         107616         109055         1439         hypothetical protein           122         90100         90558         458         restriction endonuclease family protein           123         104148         106004         1886         GGDEF/cache domain- containing protein           123         104262         725         single stranded macleia acid binding protein	120 120 120 120 120 120	96624 101100 88004 100126 101005	97397 103181 89116 102042 102453	773 2081 1112 1916 1448	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GntR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein
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121         89264         90103         839         8-oxogunine DNA glycosylase Ogg           121         102044         103465         1421         (RNA modification GTPase TrmE           122         102269         103993         1724         hypothetical protein           122         102269         103993         1724         hypothetical protein           122         103528         109485         3557         chromsome segregation protein Smc           122         113351         115486         2135         HD-GYP domain-containing protein           122         107616         109055         1439         hypothetical protein           122         98197         99087         890         dihydrodipicolinate synthase dapA           122         90100         90558         458         restriction endonuclease family protein           123         104148         106004         1856         GGDEF/cache domain-containing protein           123         104148         10400         S-adenosylmethionine:RNA ribosyltransferase-isomerase QueA           123         104148         10400         S-adenosylmethionine:RNA ribosyltransferase-isomerase QueA           123         99450         1304         membrane insertion protein           123	120 120 120 120 120 120 121 121	96624 101100 88004 100126 101005 105234 121979	97397 103181 89116 102042 102453 105947 122935	773 2081 1112 1916 1448 713 956	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein Gruft family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein ribonuclease III Rnc aspartate carbamoyltransferase PyrB
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122         103269         103993         1724         hypothetical protein           122         98802         99014         212         HTH domain-containing protein           122         105928         109485         3557         chromosome segregation protein Smc           122         113351         115486         2135         HD-GYP domain-containing protein           122         122663         123406         443         aspartate carbamoyltransferase regulatory subunit PyrI           122         107616         109055         1439         hypothetical protein           122         98197         99087         890         dihydrodipicolinate synthase dapA           122         90100         90558         458         restriction endonuclease family protein           123         104148         106004         1856         GGDEF/coche domain-containing protein           123         104148         106004         1856         GGDEF/coche domain-containing           123         102462         1030         S-adenosylmethionine:RNA ribosyltransferase-isomerase QueA           123         99439         100713         1274         hypothetical protein           123         102462         103991         1529         hypothetical protein	120 120 120 120 120 120 121 121 121 121	96624 101100 88004 100126 101005 105234 121979 107252 97440	97397 103181 89116 102042 102453 105947 122935 107551 98195	773 2081 1112 1916 1448 713 956 299 755	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GntR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein ribonuclease III Rnc aspartate carbamoyltransferase PyrB hypothetical protein dihydrodipicolinate reductase DapB
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122         105928         109485         3557         chromosome segregation protein Smc           122         113351         115486         2135         HD-GYP domain-containing protein           122         122963         123406         443         aspartate carbamoyltransferase regulatory subunit PyrI           122         107616         109055         1439         hypothetical protein           122         98197         99087         890         dihydrodipicolinate synthase dapA           122         90100         90558         458         restriction endonuclease family protein           122         103537         104262         725         single stranded nucleic acid binding protein           123         104148         106004         1856         GGDEF/cache domain-containing protein           123         123484         124524         1040         S-adenosylmethionine: "IRN ribosyltransferase-isomerase QueA           123         99049         100713         1274         hypothetical protein           123         104286         105590         1304         membrane insertion protein           123         104286         105590         1304         membrane insertion protein           124         109428         110414         92	120 120 120 120 120 121 121 121 121 121	96624 101100 88004 100126 101005 105234 121979 107252 97440 89264 102044	97397 103181 89116 102042 102453 105947 122935 107551 98195 90103	773 2081 1112 1916 1448 713 956 299 755 839	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GntR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein ribonuclease III Rnc aspartate carbamoyltransferase PyrB hypothetical protein dihydrodipicolinate reductase DapB 8-oxoguanine DNA glycosylase Ogg
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122         123406         443         aspartate carbamoyltransferase regulatory subunit Pyrl           122         107616         109055         1439         hypothetical protein           122         98197         99087         890         dihydrodipicolinate synthase dapA           122         98197         99087         890         dihydrodipicolinate synthase dapA           122         98197         99088         458         restriction endonuclease family protein           123         104148         106004         1856         GGDEF/cache domain-containing protein           123         19908         99445         437         hypothetical protein           123         192484         1040         S-adenosylmethionic:tRNA ribosyltransferase-isomerase QueA           123         192484         1040         S-adenosylmethionic:tRNA ribosyltransferase-isomerase QueA           123         192484         1040         S-adenosylmethionic:tRNA ribosyltransferase-isomerase QueA           123         10426         105590         1304         membrane insertion protein           123         10426         10599         1529         hypothetical protein           124         109425         110414         929         signal recognition particle-docking protein	120 120 120 120 120 121 121 121 121 121	96624 101100 88004 100126 101005 105234 121979 107252 97440 89264 102044 102269	97397 103181 89116 102042 102453 105947 122935 107551 98195 90103 103465 103993	773 2081 1112 1916 1448 713 956 299 755 839 1421 1724	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GntR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein ribonuclease III Rnc aspartate carbamoyltransferase PyrB hypothetical protein dihydrodipicolinate reductase DapB 8-oxoguanine DNA glycosylase Ogg tRNA modification GTPase TrmE hypothetical protein
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122         107616         109055         1439         hypothetical protein           122         98197         99087         890         dihydrodipicolinate synthase dapA           122         90100         90558         458         restriction endonuclease family protein           122         100337         104262         725         single stranded nucleica cid binding protein           123         104148         106004         1856         GGDEF/cache domain-containing protein           123         199008         99445         437         hypothetical protein           123         194184         126004         1856         GGDEF/cache domain-containing protein           123         19439         100713         1274         hypothetical protein           123         99439         100713         1274         hypothetical protein           123         90661         91770         1109         hypothetical protein           123         104286         105590         1304         membrane insertion protein           124         109485         110414         929         signal recognition particle-docking protein FtsY           124         109485         110414         929         hypothetical protein	120           120           120           120           120           121           121           121           121           121           121           121           121           121           121           121           121           121           121           122           122           122           122	96624 101100 88004 100126 101005 105234 121979 107252 97440 89264 89264 102044 102269 98802 105928	97397 103181 89116 102042 102453 1055947 122935 107551 98195 90103 103465 103993 99014 109485	773 2081 1112 1916 1448 713 956 299 755 839 1421 1724 212 3557	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GruR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein ribonuclease III Rnc aspartate carbamoyltransferase PyrB hypothetical protein dihydrodipicolinate reductase DapB 8-oxoguanine DNA glycosylase Ogg tRNA modification GTPase TrmE hypothetical protein HTH domain-containing protein chromosome segregation protein Smc
122         98197         99087         890         dihydrodipicolinate synthase dapA           122         90100         90558         458         restriction endonuclease family protein           122         103537         104262         725         single stranded nucleia cid binding protein           123         104148         106004         1886         GGDEF/cache domain-containing protein           123         99008         99445         437         hypothetical protein           123         123484         124524         1040         S-adenosylmethionine:tRNA ribosyltransferase-isomerase QueA           123         99661         91770         1109         hypothetical protein           123         104286         105590         1304         membrane insertion protein           123         104262         103991         1529         hypothetical protein           124         104285         110414         929         signal recognition particle-docking protein FtsY           124         109485         110414         929         signal recognition particle-docking protein           124         109124         109135         251         hypothetical protein           124         109128         102182         1454         pep	120           120           120           120           120           121           121           121           121           121           121           121           121           121           121           121           121           121           121           121           122           122           122           122           122	96624 101100 88004 100126 101005 105234 121979 107252 97440 89264 89264 102044 102269 98802 105928 113351	97397 103181 89116 102042 102453 105947 122935 107551 98195 90103 103465 103993 99014 109485 115486	773 2081 1112 1916 1448 713 956 299 755 839 1421 1724 212 3557 2135	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GntR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein ribonuclease III Rnc aspartate carbamoyltransferase PyrB hypothetical protein dihydrodipicolinate reductase DapB 8-oxoguanine DNA glycosylase Ogg tRNA modification GTPase TrmE hypothetical protein HTH domain-containing protein chromosome segregation protein Smc HD-GYP domain-containing protein
122         90100         90558         458         restriction endonuclease family protein           122         103537         104262         725         single stranded nucleic acid binding protein           123         104148         106004         1856         GGDEF/cack edomain-containing protein           123         104148         106004         1856         GGDEF/cack edomain-containing protein           123         123484         124524         1040         S-adenosylmethionine:tRNA ribosyltransferase-isomerase QueA           123         99439         100713         1274         hypothetical protein           123         90661         91770         1109         hypothetical protein           123         104286         105590         1304         membrane insertion protein           123         104286         105590         1304         membrane insertion protein           124         109485         110414         929         signal recognition particle-docking protein FtsY           124         109472         102028         1499         peptidase M18 family protein           124         109728         102182         1454         peptidase U62 family protein           124         100728         102182         1454	120           120           120           120           120           121           121           121           121           121           121           121           121           121           121           121           121           121           121           121           121           122           122           122           122           122	96624 101100 88004 100126 101005 105234 121979 107252 97440 89264 102044 102269 98802 105928 113351 122963	97397 103181 89116 102042 102453 105947 122935 107551 98195 90103 103465 103993 99014 109485 115486 123406	773 2081 1112 1916 1448 713 956 299 755 839 1421 1724 212 3557 2135 443	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GntR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein ribonuclease III Rnc aspartate carbamoyltransferase PyrB hypothetical protein dihydrodipicolinate reductase DapB 8-oxoguanine DNA glycosylase Ogg tRNA modification GTPase TrmE hypothetical protein HTH domain-containing protein chromosome segregation protein Smc HD-GYP domain-containing protein aspartate carbamoyltransferase regulatory subunit PyrI
122         103537         104262         725         single stranded nucleic acid binding protein           123         104148         106004         1856         GGDEF/cache domain-containing protein           123         99008         99445         437         hypothetical protein           123         123484         124524         1040         S-adenosylmethionine:tRNA ribosyltransferase-isomerase QueA           123         99439         100713         1274         hypothetical protein           123         99436         105590         1304         membrane insertion protein           123         104262         103991         1529         hypothetical protein           124         109485         110414         929         signal recognition particle-docking protein ftsY           124         109485         102182         1454         peptidase U62 family protein           124         109124         109375         251         hypothetical protein           124         10928         102182         1454         peptidase U62 family protein           125         106087         106692         605         TetR family transcriptional regulator           125         106087         106692         605         TetR family transcri	120           120           120           120           121           121           121           121           121           121           121           121           121           121           121           121           122           122           122           122           122           122           122           122           122	96624 101100 88004 100126 101005 105234 121979 107252 97440 89264 102044 102269 98802 105928 113351 122963 107616	97397 103181 89116 102042 1022453 105947 122935 107551 98195 90103 103465 103993 99014 109485 115486 123406 109055	773 2081 1112 1916 1448 713 956 299 755 839 1421 1724 212 3557 2135 443 1439	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GrtR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein ribonuclease III Rnc aspartate carbamoyltransferase PyrB hypothetical protein dihydrodipicolinate reductase DapB 8-oxoguanine DNA glycosylase Ogg tRNA modification GTPase TrmE hypothetical protein HTH domain-containing protein chromosome segregation protein Smc HD-GYP domain-containing protein aspartate carbamoyltransferase regulatory subunit PyrI hypothetical protein
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124         109485         110414         929         signal recognition particle-docking protein FtsY           124         124529         126028         1499         peptidase M18 family protein           124         109124         109375         251         hypothetical protein           124         100728         102182         1454         peptidase U62 family protein           124         100728         106078         2867         hypothetical protein           125         106087         106692         605         TetR family transcriptional regulator           125         99662         99826         164         hypothetical protein           125         110433         111659         1226         threonine dehydratase IIvA           125         115714         119961         4247         CoA-substrate-specific enzyme activase           125         126711         128594         2423         phenylalanyl-tRNA synthetase beta subunit PheT           125         10269         104201         1832         GTP-binding protein           125         102369         104201         1832         GTP-binding protein           125         106125         107024         899         sugar ABC transporter permease	120           120           120           120           121           121           121           121           121           121           121           121           121           121           122           122           122           122           122           122           122           122           122           122           123           123           123           123	96624 101100 88004 100126 101005 105234 121979 107252 97440 89264 102044 102269 98802 105928 113351 122963 107616 98197 90100 103537 104148 99008 1233484 99439 900661	97397 103181 89116 102042 102453 105947 122935 107551 98195 90103 103465 103993 99014 109485 115486 123406 109055 99087 90558 104262 106004 99445 124524 100713 91770	773           2081           1112           1916           1448           713           956           299           755           839           1421           1724           212           3557           2135           443           1439           890           458           725           1856           437           1040           1274           1109	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GrtR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein ribonuclease III Rnc aspartate carbamoyltransferase PyrB hypothetical protein dihydrodipicolinate reductase DapB 8-oxoguanine DNA glycosylase Ogg tRNA modification GTPase TrmE hypothetical protein HTH domain-containing protein chromosome segregation protein Smc HD-GYP domain-containing protein aspartate carbamoyltransferase egulatory subuit PyrI hypothetical protein dihydrodipicolinate synthase dapA restriction endonuclease family protein single stranded nucleic acid binding protein GGDEF/cache domain-containing protein s-adenosylmethionine:RNA ribosyltransferase-isomerase QueA hypothetical protein
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124         109124         109375         251         hypothetical protein           124         100728         102182         1454         peptidase U62 family protein           124         103211         106078         2867         hypothetical protein           125         106087         106692         605         TetR family transcriptional regulator           125         99662         99826         164         hypothetical protein           125         110433         111659         1226         threonine dehydratase IlvA           125         110433         111659         1226         threonine dehydratase IlvA           125         115714         119961         4247         CoA-substrate-specific enzyme activase           125         126711         128594         2423         phenylalanyl-tRNA synthetase beta subunit PheT           125         109683         110180         497         hypothetical protein           125         102369         104201         1832         GTP-binding protein TypA           125         102152         107024         899         sugar ABC transporter permease	120           120           120           120           121           121           121           121           121           121           121           121           121           121           122           122           122           122           122           122           122           122           122           122           123           123           123           123	96624 101100 88004 100126 101005 105234 121979 107252 97440 89264 102269 98802 105928 113351 122963 107616 98197 90100 103537 104148 99008 123484 99008	97397 103181 89116 102042 102453 1055947 122935 107551 98195 90103 103465 103993 99014 109485 115486 123406 109055 99087 99058 104262 106004 99445 124524 100713 991770 105590	773           2081           1112           1916           1448           713           956           299           755           839           1421           1724           212           3557           2135           443           1439           890           458           725           1856           437           1040           1274           1109           1304	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GruR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein ribonuclease III Rnc aspartate carbamoyltransferase PyrB hypothetical protein dihydrodipicolinate reductase DapB 8-oxoguanine DNA glycosylase Ogg tRNA modification GTPase TrmE hypothetical protein HTH domain-containing protein chromosome segregation protein Smc HD-GYP domain-containing protein aspartate carbamoyltransferase regulatory subunit PyrI hypothetical protein dihydrodipicolinate synthase dapA restriction endonuclease family protein single stranded nucleic acid binding protein GGDEF/cache domain-containing protein bypothetical protein hypothetical protein dihydrodipicolinate synthase dapA restriction endonuclease family protein single stranded nucleic acid binding protein bypothetical protein Mypothetical protein bypothetical protein bypothetical protein bypothetical protein bypothetical protein bypothetical protein bypothetical protein hypothetical protein hypothetical protein hypothetical protein
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124         100728         102182         1454         peptidase U62 family protein           124         103211         106078         2867         hypothetical protein           125         106087         106692         605         TetR family transcriptional regulator           125         99662         99826         164         hypothetical protein           125         110433         111659         1226         threonine dehydratase IlvA           125         115714         119961         4247         CoA-substrate-specific enzyme activase           125         126711         128594         2423         phenylalanyl-tRNA synthetase beta subunit PheT           125         109683         110180         497         hypothetical protein           125         102369         104201         1832         GTP-binding protein TypA           125         106125         107024         899         sugar ABC transporter permease	120           120           120           120           121           121           121           121           121           121           121           121           121           121           121           122           122           122           122           122           122           122           122           122           122           123           123           123           123           123           123           123           123           123           123           123           123           123           123           123           124	96624 101100 88004 100126 105234 121979 107252 97440 89264 102044 102269 98802 105928 105928 105928 107616 98197 90100 103537 104148 99008 123484 99439 90661 104286 102462 109485	97397 103181 89116 102042 102453 105947 122935 107551 98195 90103 103465 103993 99014 109485 115486 123406 109055 99087 90558 104262 106004 99445 124524 100713 91770 105550 103991 110414	773 2081 1112 1916 1448 713 956 299 755 839 1421 1724 212 3557 2135 443 1439 890 458 725 1856 437 1040 1274 1109 1304 1529 929	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein GrtR family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein ribonuclease III Rnc aspartate carbamoyltransferase PyrB hypothetical protein dihydrodipicolinate reductase DapB 8-oxoguanine DNA glycosylase Ogg tRNA modification GTPase TrmE hypothetical protein HTH domain-containing protein chromosome segregation protein Smc HD-GYP domain-containing protein aspartate carbamoyltransferase regulatory subunit PyrI hypothetical protein dihydrodipicolinate synthase dapA restriction endonuclease family protein Single stranded nucleic acid binding protein hypothetical protein
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125         106087         106692         605         TetR family transcriptional regulator           125         99662         99826         164         hypothetical protein           125         110433         111659         1226         threonine dehydratase IIvA           125         115714         119961         4247         CoA-substrate-specific enzyme activase           125         126171         128594         2423         phenylalanyl-tRNA synthetase beta subunit PheT           125         126683         110180         497         hypothetical protein           125         102369         104201         1832         GTP-binding protein TypA           125         106125         107024         899         sugar ABC transporter permease	120           120           120           120           121           121           121           121           121           121           121           121           121           121           121           121           121           122           122           122           122           122           122           122           122           123           123           123           123           123           123           123           123           123           124           124	96624 101100 88004 100126 105234 121979 107252 97440 89264 102269 98802 105928 113351 122963 107616 98197 90100 103537 104148 99008 123484 99439 900661 104286 102462 109485 124529 109124	97397 103181 89116 102042 102453 105947 122935 107551 98195 90103 103465 103993 99014 109485 115486 123406 109055 99087 90055 104262 106004 99445 124524 100713 91770 105590 103991 110414 126028 109375	773           2081           1112           1916           1448           713           956           299           755           839           1421           1724           212           3557           2135           443           1439           890           458           725           1856           437           1040           1274           1109           1304           1529           929           1499           251	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA DHH domain-containing protein Gruft family transcriptional regulator tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA hypothetical protein ribonuclease III Rnc aspartate carbamoyltransferase PyrB hypothetical protein dihydrodipicolinate reductase DapB 8-oxoguanine DNA glycosylase Ogg tRNA modification GTPase TrmE hypothetical protein HTH domain-containing protein chromosome segregation protein Smc HD-GYP domain-containing protein aspartate carbamoyltransferase regulatory subunit PyrI hypothetical protein dihydrodipicolinate synthase dapA restriction endonuclease family protein Single stranded nucleic acid binding protein GGDEF/cache domain-containing protein single stranded nucleic acid binding protein hypothetical protein hypothetical protein hypothetical protein GGDEF/cache domain-containing protein single stranded nucleic acid binding protein hypothetical protein hypothetical protein hypothetical protein single stranded nucleic acid binding protein single stranded nucleic acid binding protein GGDEF/cache domain-containing protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
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128         1246         12271         965         bosomeric ductoplanaticsa MatA           128         11060         111868         501         transcriptional cguidor. AuC fumly           128         10000         111869         1017         transcriptional cguidor. AuC fumly           128         02564         30400         1076         sphatchist press         Hea alwant Daw           128         100531         107446         515         bypothetical protein         bypothetical protein           129         10464         102593         947         bypothetical protein         bypothetical protein           129         11866         11848         815         AacK fumly mercinional regulator         bypothetical protein           129         11892         11892         11893         11648         Nato component yotes hinding traine           129         11894         12526         388         bypothetical protein         bypothetical protein           120         11894         1253         1263         1189         bypothetical protein           120         11895         11997         138         bypothetical protein         bypothetical protein           120         11897         12377         713         Regu	127	105250	106473	1223	hypothetical protein
128         11180         11189         933         Hypothesial protein           128         116400         11189         1019         menorphonal equipute Art. Fundy           128         10852         10731         1199         DRA polymerse III that subant DaN           128         108531         107344         515         hypothesial protein           129         101646         16293         947         hypothesial protein           129         101646         14481         845         Art. Campy transcriptional regular           129         11182         112200         398         hypothesial protein           129         111842         112200         398         hypothesial protein           129         111842         11220         398         hypothesial protein           129         111842         11220         398         hypothesial protein           129         111844         11220         215         Ste-specific combinese TDA inverses hypothesial protein           130         11237         112277         771         RNA protein/davidue subats           130         11237         112277         470         hypothesial protein           130         11237         112277 </td <td>128</td> <td>100968</td> <td>101321</td> <td>353</td> <td>hypothetical protein</td>	128	100968	101321	353	hypothetical protein
118         11040         1119         transport           128         19294         99400         1076         DNA phymera III best subset Daw           128         106531         107046         515         Dypoptreal III best subset Daw           128         101634         10233         947         Dypoptreal III best subset Daw           129         11444         845         Ant/C Emily transcriptional regulator           129         112344         12300         NAD-dependent DAN lapset LyA           129         11244         9000         NAD-dependent DAN lapset LyA           129         11294         12344         24304         9000           129         11044         9573         1697         Ste-specific combinase DAA increase IIA and the starse in the s	128	121406	122371	965	homoserine O-succinyltransferase MetA
128         19600         10701         10701         DNA polymers in the subabil DnN           128         10552         107011         1090         DNA polymers in the subabil DnN           129         11363         107014         515         Hypothesial protein           129         11363         11481         845         AntC family transcriptional regulator           129         11363         11234         12344         State in the subability of the s	128	111365	111868	503	hypothetical protein
128         10959         109704         1199         DDA phytherase III best shown Don's           128         100531         102046         1515         hypotherial protein           129         113646         10233         947         hypotherial protein           129         113646         10233         947         hypotherial protein           129         113867         114481         845         Andre Emprecipion           129         113842         102406         1364         MATE efftus family protein           129         118942         109406         1364         MATE efftus family protein           129         119145         11432         2573         Respecific recombinase DNA interace Protein           130         11858         114432         2573         Respecific recombinase DNA interace Protein           130         112370         11277         470         hypotherical protein         130           130         112453         112370         11277         470         hypotherical protein           130         112454         112370         11277         470         hypotherical protein           130         112454         112370         11277         470         hypotherical	128	110040	111059	1019	transcriptional regulator AraC family
128         100146         515         pypothetical protein           129         11346         102303         947         NaD-dypothetial protein           129         113560         114481         845         AndC family transcriptional regulator           129         112834         2000         NaD-dypothetial protein           129         11892         11280         388         Protocolar DNA ligaes LgA           129         11892         11280         18888         Iveo composent system Middle Knose           129         198942         109406         1364         Watter State S					acyltransferase
129         101466         10229         1947         Psycholoxia protein           129         112366         11481         845         AAC family immerptional regulator           129         112394         12494         2000         NAD-dependen DA piges LipA           129         111892         119406         1364         MATE efflox family protein           129         111184         119205         1888         Investment system hist-line kinase           129         111118         119205         1879         Site-specific recombinase DA Anomin protein VacA           130         112497         119452         273         Regeline FIC           130         112407         11277         470         hypothesial protein           130         112407         11277         470         hypothesial protein           130         112808         11331         203         ribisomal protein Sile TipK           130         19997         111104         1103         DNA replexiton and repute TipK           131         114558         11351         12544         1350         hypothesial protein           131         114562         114912         350         hypothesial protein           131 <t< td=""><td></td><td></td><td></td><td></td><td>A *</td></t<>					A *
129         11866         114481         845         Arc. Camiy transcriptional regulator           129         11292         11290         398         ND-d-speeden DNA ligos LipA           129         111892         11220         398         North second DNA ligos LipA           129         11118         11220         108012         NAT         Second DNA ligos LipA           129         11118         11220         109040         215         Second DNA ligos LipA           130         11489         114412         2573         Regetin FilC           130         112307         1237         Regetin FilC           130         112307         1247         Aro         Protecical protein           130         112307         11432         203         reloaved protein           130         110515         110971         482         metallophosphorestrese           130         110531         110931         203         reloaved notestrese           130         100531         110494         503         hypothecical protein           131         110355         719         hypothecical protein           131         110452         1250         hypothecical protein					
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130         11189         114432         2373         Bage           130         112407         125170         713         RN pseudom/plue symbac           130         11005         110097         452         metallophospheserase           130         110165         110097         452         metallophospheserase           130         110068         11331         263         ribosomal protein S18 rpaR           130         109957         111040         103         DNA replocheserase           130         109957         111040         103         DNA replochesical protein           131         102537         115603         1025         hypothetical protein           131         102537         114578         116019         878         hypothetical protein           131         1125241         12619         878         hypothetical protein         1131           131         112593         1949         DNA symphosphaze submit B GyrB         1131         11019         114183         1141473         1141473         1141473         114141         1141473         114141         1141473         1141473         114141         1141473         114141         1141411         1141473         114141 </td <td></td> <td></td> <td></td> <td></td> <td></td>					
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132         126175         127185         1010         hydrogenase expression/formation protein HypE           132         1113373         113987         614         hypothetical protein           132         111366         112607         971         N-acetylnarmov/L-alanine amidase           132         113349         113804         455         single-stranded DNA binding protein ssb           132         97566         97778         212         hypothetical protein           133         11631         117037         1406         aldehyde dehydrogenase GT2 family protein           133         103791         104399         608         hypothetical protein           133         112648         113802         1154         RNA methylase family protein           133         112648         113802         1154         RNA methylase family protein           133         113012         115570         2558         DNA gyrase suburit A GyrA           133         100076         110314         1238         nucleotid sugar dehydrogenase           134         117071         118186         1115         N-acetylglucosamine-6-phosphate dacetylase NagA           134         116362         10487         245         ribosomal protein <td>131</td> <td>107591</td> <td>107920</td> <td>329</td> <td>hypothetical protein</td>	131	107591	107920	329	hypothetical protein
132         113373         113987         614         hypothetical protein           132         111636         112607         971         N-acetylmuramoyl-Lalanine amidase           132         113349         113804         455         single-stranded DNA binding protein ssb           132         197566         97778         212         hypothetical protein           132         108031         109029         998         glycosyl transferase GT2 family protein           133         103791         104399         608         hypothetical protein           133         103791         104399         608         hypothetical protein           133         103791         104399         608         hypothetical protein           133         1127199         128245         1046         hydrogenase expression/formation protein HypD           133         113824         11411         287         ribosomal protein 56 rpsF           133         113824         11411         287         ribosomal protein 56 rpsF           133         11314         1288         mucleotide sugar dehydrogenase         1133           134         117071         118186         1115         N-acetylglucosmine-6-phosphate deacetylase NagA				1370	
132         111636         112607         971         N-acetylmuramoyl-L-alanine amidase           132         113349         113804         455         single-stranded DNA binding protein ssb           132         97566         97778         212         hypothetical protein           132         108031         109029         998         glycosyl transferase GT 2 family protein           133         115631         117037         1406         aldehyde dehydrogenase family protein           133         103791         104399         608         hypothetical protein           133         1127199         128245         1046         hydrogenase expression/formation protein HypD           133         112648         113802         1154         RNA methylase family protein           133         112799         128245         1046         hydrogenase expression/formation protein HypD           133         113824         11411         287         ribosomal protein S of psF           133         113012         115570         2558         DNA gyrase subunit A GyrA           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         110632         104878         353 <t< td=""><td></td><td></td><td></td><td></td><td></td></t<>					
132         113804         455         single-stranded DNA binding protein ssb           132         97566         97778         212         hypothetical protein           132         108031         109029         998         glycosyl transferase GT2 family protein           133         115631         117037         1406         aldehyde delydrogenase family protein           133         103791         104399         608         hypothetical protein           133         102791         128245         1046         hydrogenase expression/formation protein HypD           133         112648         113802         1154         RNA methylase family protein           133         112648         113802         1154         RNA methylase family protein           133         112648         114111         287         ribosomal protein S6 rpsF           133         113012         115570         2558         DNA gyrase submit A GyrA           133         109076         110314         1238         nucleotide suga dehydrogenase           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         104525         104878         353         hypothetical protein					
132         97566         97778         212         hypothetical protein           132         108031         109029         998         glycosyl transferase GT2 family protein           133         115631         117037         1406         aldehyde dehydrogenase family protein           133         103791         104399         608         hypothetical protein           133         103791         104399         608         hypothetical protein           133         103791         104399         608         hypothetical protein           133         112648         113802         1154         RNA methylase family protein           133         112648         113802         1154         RNA methylase family protein           133         112648         113802         1154         RNA methylase family protein           133         113012         115570         2558         DNA gyrase submit A GyrA           134         110071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         1107071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         110452         104878         353         hypothetical protein <tr< td=""><td></td><td></td><td></td><td></td><td></td></tr<>					
132         108031         109029         998         glycosyl transferase GT2 family protein           133         115631         117037         1406         aldehyde dehydrogenase family protein           133         103791         104399         608         hypothetical protein           133         103791         104399         608         hypothetical protein           133         103791         104399         608         hypothetical protein           133         1128245         1046         hypothetical protein         model           133         113824         11411         287         ribosomal protein Sf rpsF           133         113824         11411         287         ribosomal protein         GyrA           133         113012         115570         2558         DNA gyrase subunit A GyrA         133           133         109076         110314         1238         nucleotid sugar dehydrogenase         134           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         104525         104878         353         hypothetical protein           134         116607         245         ribosomal protein S16 RpsP					
133         115631         117037         1406         aldehyde dehydrogenase family protein           133         103791         104399         608         hypothetical protein           133         127199         128245         1046         hydrogenase expression/formation protein HypD           133         112648         113802         1154         RNA methylase family protein           133         112648         114111         287         ribosomal protein S rpsF           133         97796         98242         446         hypothetical protein           133         113012         115570         2558         DNA gyrase suburit A GyrA           133         109076         110314         1238         nucleotide sugar dehydrogenase           134         117071         118186         1115         N-accetylglucosamine-6-phosphate deacetylase NagA           134         114071         118186         1115         N-accetylglucosamine-6-phosphate deacetylase NagA           134         116362         104607         245         ribosomal protein S16 RpsP           134         1128245         128463         218         hypothetical protein           134         113987         117571         3584         hypothetical protein					
133         103791         104399         608         hypothetical protein           133         127199         128245         1046         hydrogenase expression/formation protein HypD           133         112648         113802         1154         RNA methylase family protein           133         113824         11411         287         ribosomal protein 56 rpsF           133         97796         98242         446         hypothetical protein           133         113012         115570         2558         DNA gyrase subunit A GyrA           133         109076         110314         1238         mucleotide sugar dehydrogenase           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         116362         104878         353         hypothetical protein           134         116362         116607         245         ribosomal protein S16 RpsP           134         1128245         128463         218         hypothetical protein           134         113987         117571         3584         hypothetical protein					
133         127199         128245         1046         hydrogenase expression/formation protein HypD           133         112648         113802         1154         RNA methylase family protein           133         113824         114111         287         ribosomal protein S6 rpsF           133         97796         98242         446         hypothetical protein           133         97796         98242         446         hypothetical protein           133         113012         115570         2558         DNA gyrase subunit A GyrA           133         109076         110314         1238         nucleotide sugar dehydrogenase           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         104525         104878         353         hypothetical protein           134         104525         104878         353         hypothetical protein           134         104525         104878         353         hypothetical protein           134         116362         116607         245         ribosomal protein S16 RpsP           134         1128245         128463         218         hypothetical protein           134         11					
133         112648         113802         1154         RNA methylase family protein           133         113824         114111         287         ribosomal protein S6 rpsF           133         97796         98242         446         hypothetical protein           133         113012         115570         2558         DNA gyrase subunit A GyrA           133         109076         110314         1238         nucleotide sugar dehydrogenase           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         1104525         104878         353         hypothetical protein           134         116362         116607         245         ribosomal protein S16 RpsP           134         112845         128463         218         hypothetical protein           134         114997         117571         3584         hypothetical pro					
133         113824         114111         287         ribosomal protein S6 psF           133         97796         98242         446         hypothetical protein           133         113012         115570         2558         DNA gyrase subunit A GyrA           133         109076         110314         1238         nucleotide sugar dehydrogenase           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         1104525         104878         353         hypothetical protein           134         116362         116607         245         ribosomal protein S16 RpsP           134         1128245         128463         218         hydrogenase assembly chaperone HypC           134         113987         117571         3584         hydrogenase regulator domain-containing protein           134         114010         115149         1139         HD-GYP/response regulator domain-containing protein           134         114394         115152         758         SIR2 family protein           134         114394         115152         758         SIR2 famil					
133         97796         98242         446         hypothetical protein           133         113012         115570         2558         DNA gyrase subunit A GyrA           133         109076         110314         1238         nucleotide sugar dehydrogenase           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         11052         104878         353         hypothetical protein           134         116362         116607         245         ribosomal protein S16 RpsP           134         11387         117571         3584         hypothetical protein           134         114987         117571         3584         SIR2 family protein           134         11494         115152         758         SIR2 family protein           134         114394         115152         758         SIR2 family protein           134         114394         115152         758         extradiol ring-cleavage dioxygenase class III protein </td <td></td> <td></td> <td></td> <td></td> <td>· · · · ·</td>					· · · · ·
133         113012         115570         2558         DNA gyrase subunit A GyrA           133         109076         110314         1238         nucleotide sugar dehydrogenase           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         116362         104607         245         ribosomal protein S16 RpsP           134         116362         116607         245         ribosomal protein S16 RpsP           134         1128245         128463         218         hydrogenase assembly chaperone HypC           134         113987         117571         3584         hypothetical protein           134         114394         115152         758         SIR2 family protein           134         114394         115152         758         SIR2 family protein           134         114394         115152         758         SIR2 family protein           134         114394         11517         770         hypothetical protein					
133         109076         110314         1238         nucleotide sugar dehydrogenase           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         104525         104878         353         hypothetical protein           134         116362         116607         245         ribosomal protein SIG RpsP           134         128245         128463         218         hydrogenase assembly chaperone HypC           134         1128245         128463         218         hydrogenase regulator domain-containing protein           134         113987         117571         3584         hypothetical protein           134         114010         115149         1139         HD-GYP/response regulator domain-containing protein           134         114394         115152         758         SIR2 family protein           134         114394         115172         758         SIR2 family protein           134         110367         111137         770					
134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         1104525         104878         353         hypothetical protein           134         116562         116607         245         ribosomal protein S16 RpsP           134         128245         128463         218         hydrogenase assembly chaperone HypC           134         113987         117571         3584         hydrogenase assembly chaperone HypC           134         114394         11512         758         SIR2 family protein           134         114394         11517         70         hypothetical protein           134         11067         11117         770         hypothetical protein           135         118276         119661         1385         extradiol ring-cleavage dioxygenase class III protein subunit B      <					
134         117071         118186         1115         N-acetylglucosamine-6-phosphate deacetylase NagA           134         104525         104878         353         hypothetical protein           134         116362         116607         245         ribosomal protein S16 RpsP           134         128245         128463         218         hydrogenase assembly chaperone HypC           134         113987         117571         3584         hypothetical protein           134         114394         11512         758         SIR2 family protein           134         11437         770         hypothetical protein         hypothetical protein           135         118276         119661         1385         extradiol ring-cleavage dioxygenase class III protein subunit B           135         104882         105172         290         hypothetical protein           135					
134         104525         104878         353         hypothetical protein           134         116362         116607         245         ribosomal protein S16 RpsP           134         128245         128463         218         hydrogenase assembly chaperone HypC           134         113987         117571         3584         hypothetical protein           134         113987         117571         3584         hypothetical protein           134         114010         115149         1139         HD-GYP/response regulator domain-containing protein           134         114394         115152         758         SIR2 family protein           134         114394         115152         758         SIR2 family protein           134         114394         115152         758         SIR2 family protein           134         114394         11517         770         hypothetical protein           134         110367         111137         770         hypothetical protein           135         118276         119661         1385         extradiol ring-cleavage dioxygenase class III protein subunit B           135         104882         105172         290         hypothetical protein           135					
134         128245         128463         218         hydrogenase assembly chaperone HypC           134         113987         117571         3584         hypothetical protein           134         114010         115149         1139         HD-GYP/response regulator domain-containing protein           134         114394         115152         758         SIR2 family protein           134         114394         115152         758         SIR2 family protein           134         114394         115152         758         SIR2 family protein           134         114394         115172         758         SIR2 family protein           134         114394         115172         758         SIR2 family protein           134         115578         117011         1433         GGDEF domain-containing protein           134         110367         111137         770         hypothetical protein           135         118276         119661         1385         extradiol ring-cleavage dioxygenase class III protein subunit B           135         104882         105172         290         hypothetical protein           135         116652         116879         227         RNA binding protein           135	134	104525	104878	353	
134         113987         117571         3584         hypothetical protein           134         114010         115149         1139         HD-GYP/response regulator domain-containing protein           134         114394         115152         758         SIR2 family protein           134         114394         115152         758         SIR2 family protein           134         98414         98743         329         hypothetical protein           134         115578         117011         1433         GGDEF domain-containing protein           134         110367         111137         770         hypothetical protein           135         118276         119661         1385         extradiol ring-cleavage dioxygenase class III protein subunit B           135         104882         105172         290         hypothetical protein           135         116652         116879         227         RNA binding protein           135         128465         130744         2279         hydrogenase maturation protein HypF	134	116362	116607	245	ribosomal protein S16 RpsP
134         114010         115149         1139         HD-GYP/response regulator domain-containing protein           134         114394         115152         758         SIR2 family protein           134         98414         98743         329         hypothetical protein           134         115578         117011         1433         GGDEF domain-containing protein           134         110567         111177         770         hypothetical protein           135         118276         119661         1385         extradiol ring-cleavage dioxygenase class III protein subunit B           135         104882         105172         290         hypothetical protein           135         116652         116879         227         RNA binding protein           135         128465         130744         2279         hydrogenase maturation protein HypF	134	128245	128463	218	hydrogenase assembly chaperone HypC
134         114394         115152         758         SIR2 family protein           134         98414         98743         329         hypothetical protein           134         115578         117011         1433         GGDEF domain-containing protein           134         110567         111137         770         hypothetical protein           135         118276         119661         1385         extradiol ring-cleavage dioxygenase class III protein subunit B           135         104882         105172         290         hypothetical protein           135         116552         116879         227         RNA binding protein           135         128465         130744         2279         hydrogenase maturation protein HypF					
134         98414         98743         329         hypothetical protein           134         115578         117011         1433         GGDEF domain-containing protein           134         110567         111137         770         hypothetical protein           135         118276         119661         1385         extradiol ring-cleavage dioxygenase class III protein subunit B           135         104882         105172         290         hypothetical protein           135         116652         116879         227         RNA binding protein           135         128465         130744         2279         hydrogenase maturation protein HypF					
134         115578         117011         1433         GGDEF domain-containing protein           134         110367         111137         770         hypothetical protein           135         118276         119661         1385         extradiol ring-cleavage dioxygenase class III protein subunit B           135         104882         105172         290         hypothetical protein           135         116652         116879         227         RNA binding protein           135         128465         130744         2279         hydrogenase maturation protein HypF					
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135         118276         119661         1385         extradiol ring-cleavage dioxygenase class III protein subunit B           135         104882         105172         290         hypothetical protein           135         116652         116879         227         RNA binding protein           135         128465         130744         2279         hydrogenase maturation protein HypF					
135         104882         105172         290         hypothetical protein           135         116652         116879         227         RNA binding protein           135         128465         130744         2279         hydrogenase maturation protein HypF					
135         116652         116879         227         RNA binding protein           135         128465         130744         2279         hydrogenase maturation protein HypF					
135 128465 130744 2279 hydrogenase maturation protein HypF					
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155 117/90 1179/5 185 hypothetical protein					
	135	117790	117975	185	hypothetical protein

125	115181	116362	1181	thiology Thi A
135	117059	110502	713	thiolase ThIA exodeoxyribonuclease III (xth) xth
135	119781	120641	860	radical SAM domain-containing protein
136	116972	117682	710	tRNA (guanine-N1)-methyltransferase TrmD
136	130744	131247	503	ech hydrogenase subunit F EchF
136	117991	118992	1001	hypothetical protein
136	116498	117244	746	cobalt ABC transporter ATP-binding protein CbiO
136	115271	116983	1712	sugar ABC transporter substrate-binding protein
136	99351	100436	1085	NUDIX domain-containing protein
136	117831	118757	926	alpha/beta fold family hydrolase
136	111145	112626	1481	polysaccharide biosynthesis protein
137	118914	120428	1514	alpha-L-arabinofuranosidase Arf51B
137	117686	118198	512	16S rRNA processing protein RimM
137	131273	132277	1004	ech hydrogenase subunit E EchE
137	119009	119467	458	hypothetical protein
137	117241 117116	118014 118045	773 929	cobalt ABC transporter permease CbiQ
137	112705	114585	1880	sugar ABC transporter permease asparagine synthase glutamine-hydrolyzing AsnB
137	120967	122502	1535	alpha-amylase Amy13G
138	118289	119065	776	uridine phosphorylase Udp
138	132368	132700	332	ech hydrogenase subunit D EchD
138	119521	119871	350	hypothetical protein
138	118030	119034	1004	cobalamin biosynthesis protein CbiM
138	118059	119063	1004	sugar ABC transporter permease
138	100674	101408	734	metallo-beta-lactamase family protein
138	120479	121006	527	GNAT family acetyltransferase
138	114599	115783	1184	glycosyl transferase GT4 family protein
139	106108	106668	560	TetR family transcriptional regulator
139	132700	133383	683	ech hydrogenase subunit C EchC
139	119864	120931	1067	hypothetical protein
139	119201	120286	1085	methylthioribose-1-phosphate isomerase MtnA
139	119257	120255	998	AraC family transcriptional regulator
139	101412	102086	674	HAD superfamily hydrolase
139	121019	121786	767	phosphorylase Pnp/Udp family protein
140	123167	124276	1109	arabinogalactan endo-1,4-beta-galactosidase Agn53B
140	120387	121436	1049	unsaturated rhamnogalacturonyl hydrolase Gh105A
140	119114 133407	120304 134276	1190 869	Bmp family protein
140	133407	120490	194	ech hydrogenase subunit B EchB
140	115785	116987	1202	hypothetical protein glycosyl transferase GT4 family protein
140	121467	123635	2168	lacto-N-biose phosphorylase
141	124533	125035	707	IMP cyclohydrolase purO
141	106803	108296	1493	radical SAM domain-containing protein
141	120458	121999	1541	ABC transporter ATP-binding protein
141	120955	121464	509	hypothetical protein
141	120581	121630	1049	electron transfer flavoprotein alpha subunit EtfA
141	102095	103408	1313	hypothetical protein
141	116984	117916	932	glycosyl transferase
142	125273	126451	1178	5-aminoimidazole-4-carboxamide ribonucleotide transformylase
142	108364	108606	242	hypothetical protein
142	134276	136123	1847	ech hydrogenase subunit A EchA
142	121486	122499	1013	hypothetical protein
142	121659	122450	791	electron transfer flavoprotein beta subunit EtfB
142	103601	105097	1496	23S rRNA methyltransferase
142	122110	123486	1376	MatE efflux family protein
142 143	117919 122134	119385 123141	1466 1007	ABC transporter permease
143	136255	123141	302	ABC transporter permease hypothetical protein
143				nyponeticu protein
	123007	123462	455	hypothetical protein
143	123007 122487	123462 123662	455 1175	hypothetical protein butvrvl-CoA dehydrogenase Bcd
143 143	123007 122487 123706	123462 123662 124614	455 1175 908	hypothetical protein butyryl-CoA dehydrogenase Bcd S1 RNA binding domain-containing protein
	122487	123662	1175	butyryl-CoA dehydrogenase Bcd
143	122487 123706	123662 124614	1175 908	butyryl-CoA dehydrogenase Bcd S1 RNA binding domain-containing protein
143 143	122487 123706 123523	123662 124614 124641	1175 908 1118	butyryl-CoA dehydrogenase Bcd S1 RNA binding domain-containing protein citrate transporter family protein
143 143 144	122487 123706 123523 127041	123662 124614 124641 127604	1175 908 1118 563	butyryl-CoA dehydrogenase Bcd S1 RNA binding domain-containing protein citrate transporter family protein hypothetical protein
143 143 144 144	122487 123706 123523 127041 108944	123662 124614 124641 127604 109510	1175 908 1118 563 566	butyryl-CoA dehydrogenase Bcd S1 RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD
143 143 144 144 144	122487 123706 123523 127041 108944 136686 123481 124637	123662 124614 124641 127604 109510 137129	1175 908 1118 563 566 443	butyryl-CoA dehydrogenase Bcd S1 RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator
143 143 144 144 144 144 144 144 144	122487 123706 123523 127041 108944 136686 123481 124637 105113	123662 124614 124641 127604 109510 137129 124269 125635 105607	1175 908 1118 563 566 443 788 998 494	butyryl-CoA dehydrogenase Bcd SI RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein hypothetical protein rRNA methylase SpoU family protein
143 143 144 144 144 144 144 144 144 144	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675	123662 124614 124641 127604 109510 137129 124269 125635 105607 125394	1175 908 1118 563 566 443 788 998 494 719	butyryl-CoA dehydrogenase Bcd S1 RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein hypothetical protein rRNA methylase SpoU family protein 5/3'-nucleotidase
143 143 144 144 144 144 144 144 144 144	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389	123662 124614 127604 109510 137129 124269 125635 105607 125394 120273	1175 908 1118 563 566 443 788 998 494 719 884	butyryl-CoA dehydrogenase Bcd S1 RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein hypothetical protein rRNA methylase SpoU family protein 5%'-nucleotidase glycosyl transferase
143           143           144	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389 127635	123662 124614 124641 127604 109510 137129 124269 125635 105607 125394 120273 128180	1175 908 1118 563 566 443 788 998 494 719 884 545	butyryl-CoA dehydrogenase Bcd SI RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein hypothetical protein rRNA methylase SpoU family protein 5//3'-nucleotidase glycosyl transferase hypothetical protein
143 143 144 144 144 144 144 144 144 144	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389 127635 109552	123662 124614 124641 127604 109510 137129 124269 125635 105607 125394 120273 128180 110502	1175 908 1118 563 566 443 788 998 494 719 884 545 950	butyryl-CoA dehydrogenase Bcd SI RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein rRNA methylase SpoU family protein 5'/3'-nucleotidase glycosyl transferase hypothetical protein hypothetical protein
143 143 144 144 144 144 144 144 144 144	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389 127635 109552 123252	123662 124614 124641 109510 137129 124269 125635 105607 125394 120273 128180 110502 124082	1175 908 1118 563 566 443 788 998 494 719 884 545 545 950 830	butyryl-CoA dehydrogenase Bcd SI RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein rRNA methylase SpoU family protein 5/3-nucleotidase glycosyl transferase hypothetical protein hypothetical protein ABC transporter permease
143           143           144           144           144           144           144           144           144           144           144           144           144           144           144           144           144           144           145           145           145           145           145	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389 127635 109552 123252 137219	123662 124614 124641 127604 109510 137129 124269 125635 105607 125394 120273 128180 110502 124082 137497	1175           908           1118           563           566           443           788           998           494           719           884           545           950           830           278	butyryl-CoA dehydrogenase Bcd SI RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein rRNA methylase SpoU family protein 5/3'-nucleotidase glycosyl transferase hypothetical protein hypothetical protein ABC transporter permease septum site-determining protein MinE
143           143           144           144           144           144           144           144           144           144           144           144           144           144           144           144           144           144           145           145           145           145           145           145           145	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389 127635 109552 103552 133252 137219 124347	123662 124614 124641 127604 109510 137129 124269 125635 105607 125394 120273 128180 110502 124082 137497 124853	1175 908 1118 563 566 443 788 998 494 719 884 545 950 830 278 506	butyryl-CoA dehydrogenase Bcd S1 RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein frRNA methylase SpoU family protein 5/3'-nucleotidase glycosyl transferase hypothetical protein hypothetical protein ABC transporter permease septum site-determining protein MinE hypothetical protein
143           143           144           144           144           144           144           144           144           144           144           144           144           144           144           144           144           145           145           145           145           145           145           145           145	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389 127635 109552 123252 137219 124347 123674	123662 124614 124641 127604 109510 137129 124269 125635 105607 125394 120273 128180 110502 124082 137497 124853 124549	1175 908 1118 563 566 443 788 998 494 719 884 545 950 830 278 506 875	butyryl-CoA dehydrogenase Bcd SI RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein hypothetical protein rRNA methylase SpoU family protein 57/3'-nucleotidase glycosyl transferase hypothetical protein ABC transporter permease septum site-determining protein MinE hypothetical protein 3-hydroxybutyryl-CoA dehydrogenase Hbd
143           143           144           144           144           144           144           144           144           144           144           144           144           144           144           144           145           145           145           145           145           145           145           145           145           145	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389 127635 109552 123252 137219 124347 123674 105634	123662 124614 124641 127604 109510 137129 124269 125635 105607 125394 120273 128180 110502 124082 137497 124853 124549 107070	1175           908           1118           563           566           443           788           998           494           719           884           545           950           830           278           506           875           1436	butyryl-CoA dehydrogenase Bcd SI RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein rRNA methylase SpoU family protein 5//3'-nucleotidase glycosyl transferase hypothetical protein ABC transporter permease septum site-determining protein MinE hypothetical protein 3-hydroxpbutryl-CoA dehydrogenase Hbd two component system histidine kinase
143           143           144           144           144           144           144           144           144           144           144           144           144           144           144           144           145           145           145           145           145           145           145           145           145           145           145           145           145           145           145	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389 127635 109552 123252 137219 124347 123674 105634	123662 124614 124641 127604 109510 137129 124269 125635 105607 125394 120273 128180 110502 124082 137497 124853 124549 107070 126588	1175           908           1118           563           566           443           788           998           494           719           884           545           950           830           278           506           875           1436           1025	butyryl-CoA dehydrogenase Bcd SI RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein rRNA methylase SpoU family protein 5%'-nucleotidase glycosyl transferase hypothetical protein hypothetical protein ABC transporter permease septum site-determining protein MinE hypothetical protein 3-hydroxybutryl-CoA dehydrogenase Hbd two component system histidime kinase hypothetical protein
143           143           144           144           144           144           144           144           144           144           144           144           144           144           144           144           144           145           145           145           145           145           145           145           145           145           145           145           145           145           145           145           145           145	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389 127635 109552 123252 137219 124347 123674 105634 125563 120335	123662 124614 127604 109510 137129 124269 125635 105607 125394 120273 128180 110502 124082 137497 124853 124549 107070 126588 121855	1175           908           1118           563           566           443           788           998           494           719           884           545           950           830           278           506           875           1436           1025           1520	butyryl-CoA dehydrogenase Bcd SI RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein rRNA methylase SpoU family protein 5/3-nucleotidase glycosyl transferase hypothetical protein hypothetical protein ABC transporter permease septum site-determining protein MinE hypothetical protein 3-hydroxybutyryl-CoA dehydrogenase Hbd two component system histidine kinase hypothetical protein MBOAT family acyltransferase
143           143           144           144           144           144           144           144           144           144           144           144           144           144           144           144           144           144           145           145           145           145           145           145           145           145           145           145           145           145           145           145           145           145           145           145           146	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389 127635 109552 123252 137219 124347 123674 105634 125563 120335 128299	123662 124614 124641 127604 109510 137129 124269 125635 105607 125394 120273 128180 110502 124082 137497 124853 124553 126588 121855 129333	1175           908           1118           563           566           443           788           998           494           719           884           545           950           830           278           506           875           1436           1025           1520           1034	butyryl-CoA dehydrogenase Bcd S1 RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein rRNA methylase SpoU family protein 5/3'-nucleotidase glycosyl transferase hypothetical protein hypothetical protein ABC transporter permease septum site-determining protein MinE hypothetical protein 3-hydroxybutyryl-CoA dehydrogenase Hbd two component system histidine kinase hypothetical protein MBOAT family acyltransferase GntR family transcriptional regulator
143           143           144           144           144           144           144           144           144           144           144           144           144           144           144           144           144           145           145           145           145           145           145           145           145           145           145           145           145           145           145           145           145           145	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389 127635 109552 123252 137219 124347 123674 105634 125563 120335 128299 124088	123662 124614 127604 109510 137129 124269 125635 105607 125394 120273 128180 110502 124082 137497 124853 124549 107070 126588 121855	1175           908           1118           563           566           443           788           998           494           719           884           545           950           830           278           506           875           1436           1025           1520	butyryl-CoA dehydrogenase Bcd SI RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein hypothetical protein rRNA methylase SpoU family protein 5%3'-nucleotidase glycosyl transferase hypothetical protein ABC transporter permease septum site-determining protein MinE hypothetical protein 3-hydroxybutyryl-CoA dehydrogenase Hbd two component system histidine kinase hypothetical protein MBOAT family acyltransferase GnR family transcriptional regulator cytidine deaminase Cdd
$\begin{array}{r} 143\\ 143\\ 144\\ 144\\ 144\\ 144\\ 144\\ 144\\$	122487 123706 123523 127041 108944 136686 123481 124637 105113 124675 119389 127635 109552 123252 137219 124347 123674 105634 125563 120335 128299	123662 124614 124641 127604 109510 137129 124269 125635 105607 125394 120273 128180 110502 124082 137497 124853 124539 107070 126588 121855 129333 124510	1175           908           1118           563           566           443           788           998           494           719           884           545           950           830           278           506           875           1436           1025           1520           1034           422	butyryl-CoA dehydrogenase Bcd S1 RNA binding domain-containing protein citrate transporter family protein hypothetical protein acyl carrier protein phosphodiesterase AcpD MarR family transcriptional regulator hypothetical protein rRNA methylase SpoU family protein 5/3'-nucleotidase glycosyl transferase hypothetical protein hypothetical protein ABC transporter permease septum site-determining protein MinE hypothetical protein 3-hydroxybutyryl-CoA dehydrogenase Hbd two component system histidine kinase hypothetical protein MBOAT family acyltransferase GntR family transcriptional regulator

146	12(500	107492	004	how whether how we do
146	126599 129411	127483 129734	884 323	hypothetical protein
147	129411 110667	111137	470	hypothetical protein hypothetical protein
147	124614	124964	350	** *
				ribosomal protein L19 RplS
147	138305 125136	139066 125639	761 503	septum site-determining protein MinC
147	125130	125039	1205	hypothetical protein
147	125382	127685	425	thiolase ThIA hypothetical protein
147	127200	107772	701	
147	127526	128227	701	two component system response regulator
147	127320	122614	734	hypothetical protein
147	121880	132018	2132	hypothetical protein GGDEF/EAL domain-containing protein
148	139226	140179	953	
148	139220	127490	530	translation elongation factor Ts Tsf
148	120900	122990	389	ribosomal subunit interface protein
148	111463	122990	656	hypothetical protein
149	125035	125631	596	PAP2 family protein
149	123035	140990	734	signal peptidase I LepB
149				ribosomal protein S2 RpsB
149	126028 107789	126315	287 2399	hypothetical protein
		110188		MutS2 family protein
149	128250	128855	605	hypothetical protein
149	123028	123267	239	hypothetical protein
150	132116	135592	3476	ATP-dependent nuclease subunit B addB
150	112126	112746	620	hypothetical protein
150	125696	126523	827	GTP-binding protein
150	126455	129091	2636	hypothetical protein
150	128879	129532	653	hypothetical protein
150	123270	124823	1553	hydrolase HAD superfamily
151	127828	129336	1508	alpha-L-arabinofuranosidase Arf51A
151	135622	139311	3689	ATP-dependent nuclease subunit A addA
151	112767	113396	629	GNAT family acetyltransferase
151	126556	127089	533	signal peptidase I LepB
151	141310	142065	755	hypothetical protein
151	110348	111712	1364	serine protease HtrA family protein
151	129569	131080	1511	MBOAT family acyltransferase
151	125070	126137	1067	hypothetical protein
152	139298	139999	701	proton-coupled thiamine transporter YuaJ
152	113456	114334	878	GNAT family acetyltransferase
152	142081	143079	998	hypothetical protein
152	129351	130286	935	sugar ABC transporter permease
152	111741	112685	944	HD domain-containing protein
152	126436	127572	1136	glycosyl transferase GT4 family protein
153	140235	141575	1340	GTP-binding protein HflX
153	114453	115865	1412	MatE efflux family protein
153	127089	127850	761	ribonuclease HII RnhB
153	129381	131411	2030	ABC transporter ATP-binding/permease
153	112738	113895	1157	aspartate/tyrosine/aromatic aminotransferase
153	131090	132184	1094	hypothetical protein
153	127573	128538	965	glycosyl transferase GT2 family protein
154	141628	142638	1010	aspartateammonia ligase asnA
154	115923	116903	980	aminoglycoside phosphotransferase
154	127892	129511	1619	hypothetical protein
154	143152	143541	389	hypothetical protein
154	131413	133095	1682	ABC transporter ATP-binding/permease
154	130273	131196	923	sugar ABC transporter permease
154	113892	114380	488	AsnC family transcriptional regulator
154	132250	132498	248	hypothetical protein
155	142663	142953	290	hypothetical protein
155	129526	129810	284	FlhB domain-containing protein
155	143584	145161	1577	hypothetical protein
155	133180	133650	470	MarR family transcriptional regulator
155	131267	132925	1658	sugar ABC transporter substrate-binding protein
155	114420	115394	974	thiamine-monophosphate kinase ThiL
155	132523	133605	1082	undecaprenyldiphospho- muramoylpentapeptide beta-N-acetylglucosaminyltransferase
				MurG
155	128576	130150	1574	hypothetical protein
156	117256	118746	1490	hypothetical protein
156	145195	145968	773	flagellar biosynthesis sigma factor FliA
156	115434	116993	1559	VanW-like family protein
156	133668	134147	479	S-ribosylhomocysteinase LuxS
156	130176	131204	1028	hypothetical protein
157	143059	145512	2453	Rad3-related DNA helicase
157	118730	119503	773	hypothetical protein
157	130218	131090	872	hypothetical protein
157	145995	146330	335	hypothetical protein
157	133118	134146	1028	LacI family transcriptional regulator
157	134156	135022	866	HTH/SIS domain-containing protein
157	131201	132475	1274	polysaccharide ABC transporter ATP-binding/permease
158	146032	147603	1571	GGDEF/TPR repeat domain-containing protein
158	131154	131876	722	two component system response regulator
158	146327	146812	485	chemotaxis protein CheD
158	135165	135596	431	hypothetical protein
159	148000	150672	2672	valyl-tRNA synthetase valS

150	131990	12/225	2245	two component system histiding kinese
159	131990	134335 147459	2345 632	two component system histidine kinase
159	133817	134584	767	chemotaxis protein CheC family protein
159	117117	117719	602	tryptophan synthase alpha subunit TrpA
				hypothetical protein
159 159	135612	136190	578 851	rubrerythrin Rbr1
	132518	133369		polysaccharide ABC transporter permease
160	119595 134402	120935	1340	MFS transporter
160		135601	1199	ribose-phosphate pyrophosphokinase PrsA
160	147474	147968	494	chemotaxis protein CheW family protein
160	134577	135767	1190	tryptophan synthase beta subunit TrpB
160	134399	135676	1277	MFS transporter
161	120961	122034	1073	HTH domain-containing protein
161	135737	137101	1364	Fe-S oxidoreductase
161	135808	136440	632	phosphoribosylanthranilate isomerase TrpF
161	136326	137021	695	MTA/SAH nucleosidase
161	133429	134568	1139	hypothetical protein
162	150978	152363	1385	tetrahydrofolate biosynthesis FolC
162	137105	138433	1328	GTP-binding protein
162	148005	150116	2111	chemotaxis histidine kinase CheA
162	136444	137229	785	indole-3-glycerol phosphate synthase TrpC
162	117777	119282	1505	galactose-1-phosphate uridylyltransferase GalT
162	134578	136023	1445	MBOAT family acyltransferase
163	152380	152544	164	hypothetical protein
163	122399	123403	1004	ribosome small subunit-dependent GTPase A RsgA
163	138438	139139	701	hypothetical protein
163	150256	151326	1070	chemotaxis-specific methylesterase CheB
163	137226	138266	1040	anthranilate phosphoribosyltransferase trpD
163	135928	136512	584	sugar-phosphate isomerase LacAB/RpiB family
163	119337	120536	1199	galactokinase GalK
163	137018	139270	2252	hypothetical protein
163	13/018	137293	1097	hypothetical protein
165	123462	124016	554	HAD superfamily hydrolase
164	123462	140175	1022	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase GpsA
	159133	152051	722	
164				flagellar protein
164	136531	136689	158	hypothetical protein
164	120695	121858	1163	toxic anion resistance family protein
164	139338	140918	1580	glucose-6-phosphate isomerase Gpi
165	141083	142021	938	xylosidase/arabinofuranosidase Xsa43G
165	152547	153965	1418	TPR domain-containing protein
165	124074	124514	440	LytTR domain-containing protein
165	152087	153019	932	flagellar biosynthesis protein FlhG
165	138819	141635	2816	NADPH-dependent glutamate synthase GltA
165	136857	137021	164	hypothetical protein
165	137478	137705	227	hypothetical protein
166	154161	155357	1196	MBOAT family acyltransferase
166	124516	124980	464	hypothetical protein
166	153044	154303	1259	flagellar biosynthesis protein FlhF
166	141706	142842	1136	hypothetical protein
166	137154	138032	878	acetyltransferase GNAT family
166	121902	123128	1226	hypothetical protein
167	155459	156313	854	GDSL-family lipase/acylhydrolase
167	125077	125775	698	ABC transporter ATP-binding protein
167	142852	143472	620	chemotaxis protein CheC family protein
167	138084	139421	1337	NLPC/P60 domain-containing protein
167	123298	124203	905	AraC family transcriptional regulator
167	142110	143621	1511	two component system histidine kinase
167	138008	139519	1511	BCCT family transporter
168	124195	126669	2474	glycogen phosphorylase GlgP
168	156331	156576	245	hypothetical protein
168	125853	126569	716	ABC transporter permease
168	154305	156362	2057	flagellar biosynthesis protein FlhA
168	143751	144497	746	DeoR family transcriptional regulator
168	143662	144333	671	two component system response regulator
168	139521	140243	722	cholinephosphate cytidylyltransferase
169	156601	156978	377	endoribonuclease L-PSP
169	126718	127119	401	hypothetical protein
169	156403	157557	1154	flagellar biosynthetic protein FlhB
169	130403	142083	1134	choline kinase
170	140230	142085	1049	
170			785	TPR domain-containing protein
	157532	158317		flagellar biosynthetic protein FliR
170	144512	145417	905	1-phosphofructokinase pfkB
170	139526	140464	938	thioredoxin-disulfide reductase trxB
170	144449	145138	689	RNA pseudouridylate synthase
171	158061	158858	797	hypothetical protein
171	127242	128309	1067	sugar ABC transporter substrate-binding protein
171	158327	158599	272	flagellar biosynthetic protein FliQ
171	142080	143000	920	hypothetical protein
172	158865	160778	1913	hypothetical protein
172	128425	129780	1355	two component system histidine kinase
172	158611	159546	935	flagellar biosynthetic protein FliP
172	145433	147523	2090	PTS system IIABC fructose-specific family protein
172	140562	141338	776	hydrolase HAD superfamily
172	145156	146628	1472	hypothetical protein

International future of by the second seco	172	143020	144246	1226	glycosyl transferase
193         1956         1936         English prime Ref.           193         1435         1455         122         3 acaught prime Ref.           193         1435         1455         1455         1455           193         1403         1455         1455         1455           194         1400         1455         1456         1456           194         1598         1413         123         1466           194         1598         1413         123         1466           194         1598         1413         123         1466           194         1598         1413         123         1466           197         1461         1344         1598         1413           197         1461         1344         1598         1413           197         1462         131         1498         1497           198         14451         161         1598         141           198         14451         161         1598         141           198         1452         161         1598         141           198         14531         161         1598         161					
11.13         14.1430         14.030         12.03         13.03         14.030         12.03           11.3         14.035         14.036         14.036         14.035					
119         14338         14300         172         beamsplus/subjecture/perture present publics of point           113         14455         14455         1442         hypothesial present           113         14455         14455         1442         hypothesial present           114         14590         14556         1412         hypothesial present           114         14590         14555         1756         Hypothesial present           115         14517         14525         153         hypothesial present           115         14525         14537         153         hypothesial present           116         14527         153         hypothesial present         hypothesial present           116         14537         15458         16459         hypothesial present           117         14545         14547         1434         genes present hypothesial present           116         14547         14548         14550         1434         genes present hypothesial present           117         14548         14550         1434         feature         hypothesial present           117         14545         14350         1434         feature         hypothesial present					
1973         14603         1475         1475         1475           1974         1475         1475         1475         1475           1974         1475         1475         1579         1579           1974         1579         1579         1579         1579           1975         16766         16802         1579         1579         1579           1975         14217         14243         1580         1590         1590         1590           1975         14217         14253         1573         1579         1590					
1713         1422         15297         1532         1550           174         15297         15332         1550         two component system recovers explained           174         15780         16454         178         transfer and system recovers explained           173         16780         16454         178         type system recovers explained           175         16470         16454         178         type system recovers explained system recovers explained           175         164717         164881         1384         two component system recovers explained           176         16469         16477         548         CKAT limits accelerate recovers explained           176         16491         16497         548         CKAT limits accelerate recovers explained           176         16492         16117         CKAT limits accelerate recovers explained         176           176         16498         17625         1611         Two component system recovers explained           177         16498         17625         1611         Two component system recovers explained           177         16498         1722         1734         16498         1775           178         164991         1797         15798					
174         1.599         1.512         1.596         rev composed system reprise regulator           174         1.6980         1.6113         1.235         RagBar motor works predict PIX           175         1.6406         1.6406         1.6406         1.6407           175         1.6417         1.4417         1.4417         1.4417         1.4417           175         1.44217         1.4418         1.53         reverse support system leading system           176         1.6417         1.4441         1.73         reverse support system leading system           176         1.6422         1.6444         1.73         reverse support system leading system           176         1.6417         1.6418         1.73         reverse support system system system system           176         1.6429         1.6413         6.74         reverse support system system system system           176         1.6459         1.6411         1.74         reverse support system system system system system system           177         1.6525         1.071         reverse support system system system system         reverse support system system system system system system system           177         1.6537         1.6548         1.575         1.6744         reversupport system system system s	-				
1944         1950         1953         1923         ftgglan zow study synch by your hyperballing press           113         14580         14580         14500         16000         16001         16001           115         16002         16002         16001         16001         16001         16001           115         16002         16001         1500         16001         16001         16001           115         16102         16101         16001<					
114         14760         1976         1778         1975         1976         1976           175         18966         18977         123         Bayesholical presis           175         18407         14221         131         reputer regular domain coating presis           175         11470         14221         131         reputer regular domain coating presis           176         18409         18409         18417         18418           176         18418         18355         1943         Style ARC many cost with group of the style and the sty					
1975         1976         198022         1977         1175         198022         1977         1185         Topolocial presis           1975         147707         14818         134         recover. regular dominic-corning presis           1975         11431         124323         1353         recover. regular dominic-corning presis           1976         11432         124324         1243         presis           1976         11433         12433         1313         1313           1976         14313         1313         1313         1313         1313           1976         14329         1413         844         Regular more works presis         Ref           1976         14359         1413         844         Regular more works presis         Ref           1976         14359         14135         641         recover works presis         Ref					
195         14403         14233         135         repose regular densissaming proton           195         147107         142831         136         repose regular densissaming proton           195         147177         142831         142832         142832         142832           195         142832         142842         142842         142842         142842           196         16197         17081         041         1997         1997           1976         149741         18082         911         bypothetial provin         1997           1976         149781         149431         844         bypothetial provin         1997           1976         149783         149783         14973         14973         14973         14973           1976         149783         14974         14974         149					
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135         14432         14436         1121         provest manuses GT4 family present           176         15143         15245         1033         xylow ARC transports solutus bading present           176         161137         162681         644         flighter more roke for present present           176         161137         162681         644         flighter more roke for present present present           176         164931         16303         6103         hypothcial present splats           177         16253         16326         701         rowen present splats         hypothcial present splats           177         15262         13314         1172         hypothcial present splats         hypothcial present splats           178         16253         16324         1344         Global contexplats         hypothcial present splats           178         16253         16328         1432         cylose ABC transport and hypothcial present           179         16453         16454         1427         hypothcial present           179         16453         1642         hypothcial present           179         16454         1677         hypothcial present           179         16454         1677         hypothcial pre					
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H82         H3781         H41048         2267         oligopeptide ABC transporter substrate-binding protein OppA           H82         164427         164600         173         flagellar protein FIbD           H82         145251         146582         1331         amino acid carrier protein FIbD           H83         169549         169980         431         peptide methonino salid carrier protein AGCS family           H83         161757         147516         740         SAM-depender methyltransporter permease OpB           H83         151500         151793         293         hypothetical protein           H83         15500         151793         293         hypothetical protein           H84         152602         153768         1166         hypothetical protein           H84         170056         17213         2075         methyl-acceptitic chenotasis protein MepA           H84         165172         165906         734         To oligopeptide ABC transporter Permease OpC           H84         165079         155365         1286         bacterial SH3 domain containing protein           H84         165075         145541         1766         oligopeptide ABC transporter ATP-binding protein OppD           H85         165925         3260 <td></td> <td></td> <td></td> <td></td> <td>·</td>					·
182         164427         164600         173         flagellar protein FIbD           182         145251         146582         1331         amino acid carrie protein AGCS family           183         169449         169980         431         peptide methionine sulfoxide reductase MsrA           183         141176         142759         1583         Olgopeptide ABC transporter permease OppB           183         155077         15052         1115         GFO/DEH/MOCA family oxidoreductase           183         15500         151793         293         hypothetical protein           183         15500         151793         293         hypothetical protein           184         10056         172131         2075         methyl-accepting chemotaxis protein McpA           184         142752         143762         977         oligopeptide ABC transporter permease OppC           184         145517         165365         1286         bacterial SH3 dumain-containing protein           185         17230         175278         2948         beta-glucosidase Bgl3D           185         165654         157267         683         hypothetical protein           185         165654         157267         683         hypothetical protein					
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183         141176         142759         1583         oligopeptide ABC transporter permass OppB           183         146776         147516         740         SAM dependent methyltransferase           183         146776         147516         740         SAM dependent methyltransferase           183         15500         151793         293         hypothetical protein           184         170056         172131         2075         methyl-accepting chemotasis protein McpA           184         142785         143762         977         Oligopeptide ABC transporter permass OppC           184         165079         156365         1286         bacterial SH3 domain-containing protein           184         165079         156365         1286         bacterial SH3 domain-containing protein           185         17230         175278         2948         beta-glucosidase Bg13D           185         165965         169225         3260         flagellar hook protein FlgE           185         165964         157267         683         hypothetical protein           186         14534         146835         1301         oligopeptide ABC transporter ATP-binding protein OppF           186         147960         144840         flagellar hook capping	-				
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189         158959         159201         242         hypothetical protein           189         150748         151398         650         hypothetical protein           189         155274         156482         1208         hypothetical protein           190         179276         180787         1511         DHH domain-containing protein           190         147829         148080         251         hypothetical protein           190         172150         173088         938         hypothetical protein           190         159215         159454         239         hypothetical protein					
189         150748         151398         650         hypothetical protein           189         155274         156482         1208         hypothetical protein           190         179276         180787         1511         DHH domain-containing protein           190         147829         148080         251         hypothetical protein           190         172150         173088         938         hypothetical protein           190         159215         159454         239         hypothetical protein					
189         155274         156482         1208         hypothetical protein           190         179276         180787         1511         DHH domain-containing protein           190         147829         148080         251         hypothetical protein           190         172150         173088         938         hypothetical protein           190         159215         159454         239         hypothetical protein					
190         179276         180787         1511         DHH domain-containing protein           190         147829         148080         251         hypothetical protein           190         172150         173088         938         hypothetical protein           190         159215         159454         239         hypothetical protein					
190         147829         148080         251         hypothetical protein           190         172150         173088         938         hypothetical protein           190         159215         159454         239         hypothetical protein					
190         172150         173088         938         hypothetical protein           190         159215         159454         239         hypothetical protein					
190 159215 159454 239 hypothetical protein					
170 15555 154514 /01 FeS assembly AlPase SufC					
	190	153553	154314	/01	res assembly ATPase SufU

100	15(502	157190	(90	how the start is a source in
190	156502 159637	157182 161877	680 2240	hypothetical protein Polysaccharide lyase Pl11A
191	139637	148319	149	· ·
191	148170	151857	326	hypothetical protein
				hypothetical protein
191 192	154329 148547	155747 150013	1418 1466	FeS assembly protein SufB
192	148347	173549	458	methyl-accepting chemotaxis protein McpH
192	173091	173349	317	flagellar export protein FliJ hypothetical protein
192	151895	156929	1169	
192	153760	150929	743	FeS assembly protein SufD hypothetical protein
192	161896	162630	734	carbohydrate esterase family 12 Est12B
193	180833	182850	3134	hypothetical protein
193	150247	152316	2069	
193	173553	174911	1358	methyl-accepting chemotaxis protein McpG flagellar protein export ATPase FliI
193	173333	152948	701	· · · ·
193	152247	152948	1220	hypothetical protein cysteine desulfurase SufS
193	174924	175778	854	flagellar assembly protein FliH
194	162635	165220	2585	
194	152962			hypothetical protein
194	152962	153300 158602	338 443	hypothetical protein
194	158103		1253	FeS assembly protein SufE
		159356		hypothetical protein
195 195	184125	184760 153464	635	endonuclease III nth
	152397		1067	glucose-1-phosphate adenylyltransferase GlgD
195	175798	176847	1049	flagellar motor switch protein FliG
195	165292	166872	1580	sugar ABC transporter permease
195	153455	154081	626	HAD superfamily hydrolase
195	159078 159422	159854 160540	776	TatD family hydrolase
195			1118	hypothetical protein
196	153512	154654	1142	glucose-1-phosphate adenylyltransferase GlgC
196	176860	178479	1619	flagellar M-ring protein FliF
196 196	154140 159855	155444 160715	1304	hypothetical protein
			860	dimethyladenosine transferase KsgA
196	160694	161500	806	hypothetical protein
197	184854	185087	233	hypothetical protein
197	154762	155679	917	hypothetical protein
197	178511	178855	344	flagellar hook-basal body complex protein FliE
197	166939	167853	914	sugar ABC transporter permease
197	155489	156787	1298	peptidase M18 family protein
198	185491	185754	263	hypothetical protein
198	155779	157005	1226	HDOD domain-containing protein
198	167871	168791	920	sugar ABC transporter permease
198	161481	162629	1148	acyltransferase
199	185959	186855	896	hypothetical protein
199	157016	157711	695	4-phosphopantetheinyl transferase
199	178879	179328	449	flagellar basal-body rod protein FlgC
199	168957	171212	2255	AraC family transcriptional regulator
199	156888 160775	158156	1268	Na+/H+ antiporter
199		163630	2855	hypothetical protein
199	162677	163204	527	hypothetical protein
200	157736	158767	1031	hypothetical protein
200	179344	179736	392	flagellar basal-body rod protein FlgB
200	163208	164581	1373	hypothetical protein
201	163662	165653	1991	1,4-alpha-glucan branching enzyme GlgB
201	187489	189918	2429	leucyl-tRNA synthetase leuS
201	158883	159437	554	phosphoglycerate mutase family protein
201	179944	180723	779	GTP-sensing transcriptional pleiotropic repressor CodY
201	171407	171841	434	3-dehydroquinate dehydratase type II aro
202	190339	194061	3722	hypothetical protein
202	180859	182973	2114	DNA topoisomerase I TopA
202	158452	158730	278	ribonuclease inhibitor
202	165744	168866	3122	hypothetical protein
202	164843	165277	434	hypothetical protein
203	194076	194885	809	serine/threonine protein phosphatase
203	183106	185973	2867	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
203	171857	172519	662	hypothetical protein
203	158730	159863	1133	hypothetical protein
203	168899	170062	1163	flagellin FliC
203	165291	165848	557	hypothetical protein
204	194982	196580	1598	serine/threonine protein kinase
204	159616	161400	1784	hypothetical protein
204	172542	175808	3266	carbamoyl-phosphate synthase large subunit carB
204	159872	160336	464	hypothetical protein
204	170081	170557	476	flagellar protein FliS
205	196598	197017	419	hypothetical protein
205	186002	186346	344	hydrogenase nickel insertion protein HypA
205	175808	177019	1211	carbamoyl-phosphate synthase small subunit carA
205	166281	166925	644	flavin reductase domain-containing protein
206	161481	162419	938	hypothetical protein
206	186467	187135	668	hydrogenase accessory protein HypB
206	177046	180852	3806	phosphoribosylformylglycinamidine synthase Pur
206	171077	172	-170905	ATPase
206	167091	167690	599	hypothetical protein
207	197070	198449	1379	GGDEF domain-containing protein

207	162464	1/2/02	219	how the start is a second size
207 207	162464 187135	162682 188256	218 1121	hypothetical protein hypothetical protein
207	18/133	188236	596	
207	160482	167819	7337	TetR family transcriptional regulator
				cell surface protein
207 208	172068 198433	173312 200076	1244 1643	Flp pilus assembly protein ATPase TadA GGDEF/EAL/PAS domain-containing protein
208	198433	189845	1415	
208	188430	189843	467	oxygen-independent coproporphyrinogen III oxidase HemN
208		168088	215	hypothetical protein
208	167873 173422	174015	593	hypothetical protein
208	167806	169398	1592	Flp pilus assembly protein TadB
208	200076	200813	737	hypothetical protein
209	162809	164995	2186	hypothetical protein
209	182809	190527	662	hypothetical protein
209	174141	175487	1346	metallo-beta-lactamase family protein
209	1/4141 169438	175487	965	Flp pilus assembly protein TadC
209	164997	165902	905	glycosyl transferase GT2 family protein
210			2297	xylosidase/arabinofuranosidase Xsa43I
	183363	185660		mannose 6-phospahe isomerase/glycoside hydrolase family 1 protein
210 210	201032 168294	201280 170198	248 1904	hypothetical protein
				thiamine pyrophosphate enzyme
210	175545	175763	218	hypothetical protein
210	170458 201434	170865	407	WxcM-like protein
211		201631	197	hypothetical protein
211	165930	167591	1661	hypothetical protein
211	185683	186828	1145	hypothetical protein
211	175819	177186	1367	hypothetical protein
212	186838	187860	1022	glycoside hydrolase
212	201662	202324	662	hypothetical protein
212	167810	168337	527	hypothetical protein
212	190527	192806	2279	RelA/SpoT family protein
212	170205	170984 189046	779	glucose-1-phosphate cytidylyltransferase RfbF
213	187877		1169	glycoside hydrolase
213	202558	203181	623	hypothetical protein
213	168430	168714	284	hypothetical protein
213	192813	193337	524	adenine phosphoribosyl transferase Apt
213	171027	172178	1151	hypothetical protein
213	170958	172301	1343	glycosyl transferase GT4 family protein
214	189260	190273	1013	LacI family transcriptional regulator
214	177183	178076	893	hypothetical protein
214	172349	173149	800	glycosyl transferase GT4 family protein
215	190305	192497	2192	alpha-galactosidase Aga
215	203327	204097	770	NCAIR mutase-related protein
215	172175	173125	950	xylose isomerase domain-containing protein
215	178090	178521	431	hypothetical protein
215	173580	175196	1616	hypothetical protein
216	204157	204897	740	hypothetical protein
216	168763	169728	965	hypothetical protein
216	192596	193522	926	hypothetical protein
216	173122	174447	1325	hypothetical protein
216	178559	178963	404	hypothetical protein
217	204894	205472	578	ABC transporter ATP-binding protein
217	193599	194507	908	LysR family transcriptional regulator
217	174488	176863	2375	hypothetical protein
217	178963	180273	1310	FHA domain-containing protein
217	175649	176782	1133	glycosyl transferase GT4 family protein
218	180312	181322	1010	hypothetical protein
218	176806	177825	1019	hypothetical protein
219	205491	206960	1469	iron-only hydrogenase
219	170125	171267	1142	GGDEF domain-containing protein
219	194565	196280	1715	methyl-accepting chemotaxis protein Mcp
219	176937	178763	1826	hypothetical protein
219	181335	181997	662	membrane-associated peptidase rhomboid family
220	171407	172393	986	sugar ABC transporter substrate-binding protein
220	196522	197817	1295	adenylosuccinate synthetase pur
220	178883	179518	635	HTH domain-containing protein
220	181997	182407	410	HIT domain-containing protein
220	177838	179250	1412	MBOAT family acyltransferase
221	207378	209984	2606	two component system histidine kinase/response regulator hybrid protein
221	179818	180018	200	hypothetical protein
221	182463	183260	797	fumarate hydratase alpha subunit FumA
222	210014	210784	770	response regulator domain-containing protein
222	172395	173864	1469	two component system histidine kinase
222	179264	180079	815	hypothetical protein
223	210801	211727	926	orotidine 5'-phosphate decarboxylase pyrF
223	173845	175101	1256	two component system response regulator
223	183272	183829	557	fumarate hydratase beta subunit FumB
223	180287	180445	158	rubredoxin Rub
224	211743	212423	680	orotate phosphoribosyltransferase pyrE
224	198166	198663	497	hypothetical protein
224	180083	180946	863	hypothetical protein
224	184369	184617	248	hypothetical protein
225	212450	212602	152	hypothetical protein
225	175241	176224	983	sugar ABC transporter substrate-binding protein

225	181128	182438	1310	aluggari transferres CT2 femily protein
223	212602	212967	365	glycosyl transferase GT2 family protein hypothetical protein
226	176311	177810	1499	sugar ABC transporter ATP-binding protein
226	198806	199735	929	hypothetical protein
226	181066	182361	1295	NAD-dependent epimerase/dehydratase
227	199863	201458	1595	glycoside hydrolase
227	212979	215060	2081	peptidase M29 family protein
227	177810	178880	1070	sugar ABC transporter permease
227	182438	183781	1343	hypothetical protein
227	183082	183618	536	hypothetical protein
228	215136	215636	500	phosphoribosylaminoimidazole carboxylase PurE
228	178877 201490	179902 202380	1025 890	sugar ABC transporter permease HAD superfamily hydrolase
228	182380	183606	1226	glycosyl transferase GT4 family protein
229	215698	216729	1031	phosphoribosylformylglycinamidine cyclo-ligase purM
229	179923	180372	449	chemotaxis protein CheW family protein
229	202593	203510	917	ArsR family transcriptional regulator
229	184096	184950	854	hypothetical protein
229	183667	184755	1088	NAD dependent epimerase/dehydratase
230	216729	217373	644	phosphoribosylglycinamide formyltransferase purN
230	180365	180811	446	chemotaxis protein CheW family protein
230	203601	206300	2699	translation elongation factor EF-G-like protein
230	184947	186251	1304	hypothetical protein
231	217394	218677	1283	phosphoribosylamineglycine ligase purD
231	181197	181676	479	hypothetical protein
231 231	186273 184801	187418 186183	1145 1382	glycosyl transferase GT2 family protein
231	218674	220185	1582	exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase bacterial SH3 domain-containing protein
232	181694	183706	2012	methyl-accepting chemotaxis protein McpA
232	187512	188630	1118	hypothetical protein
233	220323	221615	1292	hypothetical protein
233	183914	184819	905	LysR family transcriptional regulator
233	206391	208163	1772	methyl-accepting chemotaxis protein Mcp
233	188748	189938	1190	glycosyl transferase
233	186183	187352	1169	UDP-N-acetylglucosamine 2-epimerase
234	208158	209402	1244	6-phosphofructokinase PfkA
234	189972	191072	1100	glycosyl transferase
234	187365	188564	1199	DegT/DnrJ/EryC1/StrS family aminotransferase
235	184865	186025	1160 875	hypothetical protein
235	209513 191096	210388 191431	335	GDSL-family lipase/acylhydrolase hypothetical protein
235	221794	222531	737	hypothetical protein
236	210477	211802	1325	two component system histidine kinase
237	211954	213741	1787	ABC transporter ATP-binding/permease
237	191440	193314	1874	carbamoyl transferase
237	189009	190241	1232	hypothetical protein
238	222644	223021	377	GntR family transcriptional regulator
238	186173	187483	1310	hypothetical protein
238	213758	215539	1781	ABC transporter ATP-binding/permease
238	193311	195113	1802	hypothetical protein
239	223039	225651	2612	ATP-dependent Clp protease ATP-binding subunit ClpC
239	195242	196288	1046	SAM-dependent methyltransferase
239	225741	226151	410	hypothetical protein hypothetical protein
240	187549	188334	785	hypothetical protein
240	215734	217422	1688	GGDEF domain-containing protein
240	196325	197383	1058	SAM-dependent methyltransferase
241	217832	218101	269	hypothetical protein
241	197528	198562	1034	hypothetical protein
241	191691	191885	194	hypothetical protein
242	226258	227634	1376	DNA repair protein RadA
242	188509	189216	707	hypothetical protein
242	218200	219141	941	hypothetical protein
242	198794	200362	1568	hypothetical protein
243	189304	189801 201525	497	hypothetical protein
243 243	200377 192731	201525 193399	1148 668	CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase 1-acyl-sn-glycerol-3-phosphate acyltransferase PlsC
243	227827	230277	2450	1-acyi-sn-giyceroi-s-phosphate acyitransierase Pisc RND family transporter
244 244	219668	220552	884	hypothetical protein
244	201630	202388	758	glycerophosphoryl diester phosphodiesterase
244	193532	194566	1034	5'-3' exonuclease C-terminal domain-containing protein
245	190024	190515	491	hypothetical protein
	220743	221162	419	hypothetical protein
245		203410	989	glycerol-3-phosphate cytidyltransferase
245 245	202421		2551	GGDEF/EAL domain-containing protein
245 246	190853	193414	2561	÷.
245 246 246	190853 221167	193414 221490	323	hypothetical protein
245 246 246 246	190853 221167 203439	193414 221490 204791	323 1352	hypothetical protein glycerol-3-phosphate cytidylyltransferase tagD
245 246 246 246 246 247	190853           221167           203439           221564	193414 221490 204791 222199	323 1352 635	hypothetical protein glycerol-3-phosphate cytidylyltransferase tagD hypothetical protein
245 246 246 246 246 247 247	190853           221167           203439           221564           204814	193414 221490 204791 222199 205791	323 1352 635 977	hypothetical protein glycerol-3-phosphate cytidylyltransferase tagD hypothetical protein hypothetical protein
245 246 246 246 247 247 247 247	190853           221167           203439           221564           204814           194699	193414 221490 204791 222199 205791 195481	323 1352 635 977 782	hypothetical protein glycerol-3-phosphate cytidylyltransferase tagD hypothetical protein hypothetical protein mechanosensitive ion channel protein MscS family
245 246 246 247 247 247 247 247 248	190853 221167 203439 221564 204814 194699 230297	193414 221490 204791 222199 205791 195481 233965	323 1352 635 977 782 3668	hypothetical protein glycerol-3-phosphate cytidylyltransferase tagD hypothetical protein hypothetical protein mechanosensitive ion channel protein MscS family GLUG domain-containing protein
245 246 246 247 247 247 247	190853           221167           203439           221564           204814           194699	193414 221490 204791 222199 205791 195481	323 1352 635 977 782	hypothetical protein glycerol-3-phosphate cytidylyltransferase tagD hypothetical protein hypothetical protein mechanosensitive ion channel protein MscS family

248	205802	207508	1706	LicD family protein
248	234051	235922	1871	hypothetical protein
249	194333	194875	542	hypothetical protein
249	222764	223912	1148	malate dehydrogenase Mdh
249	207522	209237	1715	LicD family protein
249	195514	196782	1268	hypothetical protein
250	236154	236990	836	hypothetical protein
250	194877	195365	488	flavodoxin family protein
250	223946	225745	1799	hypothetical protein
250	209256	209975	719	nucleotidyl transferase
251	237259	237951	692	transglutaminase domain-containing protein
251	195389	196006	617	Hypothetical protein
251	225765	227096	1331	recombination factor protein Rar
251	209978	210304	326	hypothetical protein
252	237964	238359	395	hypothetical protein
252 252	196024 227178	196281 228035	257 857	hypothetical protein
252	210301	211029	728	radical SAM domain-containing protein nucleotidyl transferase
252	197262	198314	1052	hypothetical protein
252	238626	239504	878	sugar ABC transporter substrate-binding protein
253	196283	196843	560	hypothetical protein
253	211026	211658	632	beta-phosphoglucomutase family hydrolase
253	198466	199011	545	thymidine kinase Tdk
255	197241	198068	827	hypothetical protein
254	228167	229609	1442	MatE efflux family protein
254	211648	212298	650	hypothetical protein
254	199288	199746	458	molecular chaperone Hsp20
255	239501	241072	1571	hypothetical protein
255	198072	198428	356	hypothetical protein
255	212397	213344	947	hypothetical protein
255	199853	200059	206	hypothetical protein
256	241398	242756	1358	hypothetical protein
256	198443	198997	554	hypothetical protein
256	229606	230556	950	hypothetical protein
256	213339	214346	1007	glycosyl transferase GT2 family protein
256	200076	201383	1307	glutamine synthetase, type I, glnA
257	242791	243861	1070	hypothetical protein
257	201539	201967	428	ANTAR domain-containing protein
258 258	243983	244750	767	hypothetical protein
258	199500 214351	200837 215451	1337 1100	hypothetical protein
258	202034	203167	1133	hypothetical protein beta-lactamase family protein
259	244747	245550	803	hypothetical protein
259	200855	201634	779	hypothetical protein
259	230580	231698	1118	hypothetical protein
259	215517	216686	1169	hypothetical protein
259	203216	204493	1277	OAH/OAS sulfhydrylase
260	245558	245917	359	hypothetical protein
260	201822	202403	581	phosphotyrosine protein phosphatase
260	231785	232450	665	sugar fermentation stimulation protein Sfs
260	216688	217527	839	glycosyl transferase GT2 family
260	204527	205888	1361	hypothetical protein
261	245988	246176	188	hypothetical protein
261	202621	203469	848	degV family protein
261	217539	218489	950	glycosyl transferase GT8 family
262	246226	247362	1136	hypothetical protein
262	203571	203945	374	desulfoferrodoxin Dfx
262	233015	233842	827	hypothetical protein
262 262	218491 206059	219087 207045	596 986	hypothetical protein diaminopimelate dehydrogenase
262	200039	247508	167	hypothetical protein
263	203946	204254	308	hypothetical protein
263	233829	234626	797	hypothetical protein
263	219059	220168	1109	glycosyl transferase group 1
263	207085	208323	1238	EAL domain-containing protein
264	247649	248422	773	hypothetical protein
264	204271	205311	1040	UmuC-like DNA repair protein
264	234664	234984	320	rhodanese domain-containing protein
264	220289	221260	971	glycosyl transferase GT2 family protein
264	208623	209555	932	hypothetical protein
265	248862	249509	647	hypothetical protein
265	205291	205602	311	hypothetical protein
265	221269	221643	374	hypothetical protein
265	209593	210258	665	hypothetical protein
266	250196	251011	815	CAAX amino terminal protease family protein
266	205631	207226	1595	hypothetical protein
266	234997	236454	1457	hypothetical protein
266	221645	223105	1460	hypothetical protein
266	210595	211395	800	hypothetical protein
267	250996	251580	584	hypothetical protein
267 267	207461 236441	207907 237316	446 875	hypothetical protein glycosyl transferase GT2 family
267	236441 211388	23/316 211618	230	hypothetical protein
207	211500	211010	230	nypotietien protein

279	208261	200028	7/7	
268	208261	209028 238574	767	flagellin FliC hypothetical protein
268 268	237300 223117	225216	2099	
	223117 211710	213020	1310	hypothetical protein
268				hypothetical protein
269	251742 209517	252107	365 839	hypothetical protein
269		210356		oligopeptide ABC transporter permease protein OppB
269	238591	239502	911	hypothetical protein
269	225235	226284	1049	glycosyl transferase
269	213223	215286	2063	hypothetical protein
270	210374	211432	1058	oligopeptide ABC transporter permease protein OppC
270	239502	240380	878	glycosyl transferase GT2 family
270	226301	227260	959	conserved hypothetical
271	252120	253202	1082	hypothetical protein
271	211457	212461	1004	oligopeptide ABC transporter ATP-binding protein OppD
271	240430	241314	884	glycosyl transferase
271	227273	230125	2852	glycosyl transferase
271	215408	216256	848	hypothetical protein
272	253294	255357	2063	metalloendopeptidase M13 family
272	212461	213447	986	oligopeptide ABC transporter ATP-binding protein OppF
272	241293	242414	1121	glycosyl transferase GT4 family protein
272	230129	232144	2015	glycosyl transferase GT2 family protein
272	216299	216748	449	ribose 5-phosphate isomerase RpiB
273	255413	256258	845	hypothetical protein
273	232173	235379	3206	glycosyl transferase GT2 family protein
273	216779	217555	776	hypothetical protein
274	213552	215399	1847	oligopeptide ABC transporter substrate-binding protein OppA
274	242416	243351	935	radical SAM domain-containing protein
274	235386	236612	1226	hypothetical protein
274	217568	218227	659	hypothetical protein
275	256426	256986	560	hypothetical protein
275	215883	218963	3080	hypothetical protein
275	213883	218634	392	hypothetical protein
275	256983	257726	743	hypothetical protein
276	218978	220633	1655	sulfate permease SulP family
276	236774	237592	818	
				flagellin FliC
277	220668	221432	764	PHP domain-containing protein
277	244289	245077	788	HD domain-containing protein
277	237821	238639	818	flagellin FliC
277	218753	219190	437	hypothetical protein
278	257751	258587	836	hypothetical protein
278	221474	221977	503	hypothetical protein
278	245425	245790	365	hypothetical protein
278	219246	220106	860	hypothetical protein
279	258644	259489	845	hypothetical protein
279	245827	246456	629	hypothetical protein
279	238887	240059	1172	hypothetical protein
279	220118	220660	542	hypothetical protein
280	222155	222367	212	hypothetical protein
280	246491	247024	533	hypothetical protein
280	240071	240880	809	glycosyl transferase
280	220684	220980	296	anti-sigma factor antagonist
281	259488	261152	1664	GGDEF/EAL domain-containing protein
281	222546	223394	848	hypothetical protein
281	247105	248724	1619	D-mannonate oxidoreductase Uxu
281	240937	241416	479	hypothetical protein
282	261199	261753	554	hypothetical protein
282	248756	249832	1076	D-mannonate dehydratase Uxu
282	241440	241841	401	flagellar protein FliS
283	261956	263464	1508	ABC transporter ATP-binding protein
283	241883	243418	1535	flagellar hook-associated protein FliD
284	224575	224766	191	hypothetical protein
284	249979	250905	926	AraC family transcriptional regulator
284	243497	243970	473	flagellar protein FlaG
284	221162	223501	2339	ferrous iron transport protein FeoA/B
285	263630	264316	686	ABC transporter permease
285	224763	225332	569	hypothetical protein
285	250941	251417	476	methylglyoxal synthase mgs
285	244133	245320	1187	hypothetical protein
285	223630	223932	302	hypothetical protein
285	264331	265329	998	tRNA dihydrouridine synthase A dusA
286	251598	252317	719	hypothetical protein
280	265387	265743	356	hypothetical protein
287				
	225501	226112	611	hypothetical protein
287	245393	245608	215	global regulator family protein
288	226418	226576	158	hypothetical protein
288	252330	253328	998	hypothetical protein
288	245652	246110	458	flagellar assembly protein FliW
288	224084	225040	956	hypothetical protein
289	265819	266727	908	serine O-acetyltransferase cysE
289	226738	227028	290	hypothetical protein
289	253331	253666	335	PadR family transcriptional regulator
289	246207	248282	2075	flagellar hook-associated protein FlgL
290	253932	254561	629	hypothetical protein

200	249297	250224	10.47	finally hash and stated and in The IZ
290 291	248387 266965	250234 268293	1847 1328	flagellar hook-associated protein FlgK flagellar hook protein FlgE
291	200903	208293	1652	
291	254635	254853	218	hypothetical protein hypothetical protein
		226095		
291 292	225148 268881	226095	947 587	L-lactate dehydrogenase hypothetical protein
292 292	229945	231435	1490	anthranilate synthase component I TrpE
-	254971	256284	1313	erythromycin esterase
292	250250	251827	1577	flagellar hook-associated protein FlgK
293	269476	270057	581	signal peptidase I lepB
293	231453	232031	578	anthranilate synthase component II TrpG
293	256281	258284	2003	ABC transporter permease
293	252043	252570	527	FlgN family protein
293	226233	226952	719	4Fe-4S ferredoxin iron-sulfur binding domain- containing protein
294	232150	233541	1391	PhoH family protein
294	258274	259044	770	ABC transporter ATP-binding protein
294	252597	252884	287	negative regulator of flagellin synthesis FlgM
295	270070	274959	4889	LPxTG motif-containing cell surface protein
295	259180	260046	866	two component system histidine kinase
295	227050	227748	698	cNMP binding domain-containing protein
296	274984	276513	1529	LPxTG motif-containing cell surface protein
296	260096	260770	674	two component system response regulator
296	227767	228072	305	hypothetical protein
297	276653	27	-276626	sortase
297	234546	234758	212	hypothetical protein
297	260840	261631	791	GNAT family acetyltransferase
297	253691	256003	2312	hypothetical protein
298	234789	235010	221	hypothetical protein
298	261645	262139	494	SAM-dependent methyltransferase/GNAT family acetyltransferase
298	256000	256638	638	hypothetical protein
299	256655	257368	713	branched-chain amino acid ABC transporter ATP- binding protein LivF
299	228607	229320	713	hypothetical protein
300	235071	237359	2288	ferrous iron transport protein FeoA/B
300	262449	263453	1004	hypothetical protein
300	257397	258152	755	branched-chain amino acid ABC transporter ATP- binding protein LivG
301	277554	278669	1115	LPxTG motif-containing cell surface protein
				÷ .
301	258149	259189	1040	branched-chain amino acid ABC transporter permease LivM
302	263507	264829	1322	MATE efflux family protein
302	259220	259909	689	branched-chain amino acid ABC transporter permease LivH
302	229523	230284	761	hypothetical protein
303	278735	27	-278708	sortase
303	237875	238138	263	hypothetical protein
303	264876	266876	2000	hypothetical protein
303	260264	261451	1187	branched-chain amino acid ABC transporter substrate-binding protein LivJ
304	279601	280374	773	hypothetical protein
304	238151	238390	239	hypothetical protein
304	267015	268442	1427	hypothetical protein
304	261569	262123	554	hypothetical protein
304	230533	231303	770	histidinol phosphate phosphatase HisJ family
305	280390	281187	797	hypothetical protein
305	262202	262507	305	hypothetical protein
305	231410	234565	3155	hypothetical protein
306	238467	239405	938	RNA pseudouridylate synthase
306	268475	269095	620	methylated-DNA-protein-cysteine S- methyltransferase Ogt
306	234675	236780	2105	metalloendopeptidase M13 family
307	281252	281584	332	hypothetical protein
307	239464	240768	1304	UmuC-like DNA repair protein
307	269391	270143	752	hypothetical protein
308	281786	282829	1043	iron ABC transporter ATP-binding protein
308	270208	271143	935	hypothetical protein
308	262949	264241	1292	voltage gated chloride channel protein
309	271325	272068	743	hypothetical protein
309	264257	265204	947	sugar ABC transporter substrate-binding protein
309	237294	238901	1607	hypothetical protein
310	282844	283869	1025	iron ABC transporter permease protein
310	272049	272402	353	hypothetical protein
310	265257	267278	2021	methyl-accepting chemotaxis protein McpL
		284672	608	iron ABC transporter ATP-binding protein
311	284064		000	non rice transporter ritt official protein
311	284064 241162		779	CAAX amino terminal protease family protein
311	241162	241941	779 485	CAAX amino terminal protease family protein
311 311	241162 272399	241941 272884	485	hypothetical protein
311 311 311	241162 272399 238912	241941 272884 239505	485 593	hypothetical protein hypothetical protein
311 311 311 312	241162 272399 238912 285346	241941 272884 239505 285816	485 593 470	hypothetical protein hypothetical protein hypothetical protein
311 311 311 312 312 312	241162 272399 238912 285346 242185	241941 272884 239505 285816 242961	485 593 470 776	hypothetical protein hypothetical protein hypothetical protein sortase B family protein
311 311 311 312 312 312 312 312	241162 272399 238912 285346 242185 273200	241941 272884 239505 285816 242961 273748	485 593 470 776 548	hypothetical protein hypothetical protein hypothetical protein sortase B family protein hypothetical protein
311 311 311 312 312 312 312 312	241162 272399 238912 285346 242185 273200 267385	241941 272884 239505 285816 242961 273748 269052	485 593 470 776 548 1667	hypothetical protein hypothetical protein hypothetical protein sortase B family protein hypothetical protein spermidine synthase family protein
311 311 312 312 312 312 312 312 312 313	241162 272399 238912 285346 242185 273200 267385 285900	241941 272884 239505 285816 242961 273748 269052 286553	485 593 470 776 548 1667 653	hypothetical protein hypothetical protein hypothetical protein sortase B family protein hypothetical protein spermidjne synthase family protein HAD superfamily hydrolase
311 311 312 312 312 312 312 312 313 313	241162 272399 238912 285346 242185 273200 267385 285900 243127	241941 272884 239505 285816 242961 273748 269052 286553 243684	485 593 470 776 548 1667 653 557	hypothetical protein hypothetical protein hypothetical protein sortase B family protein hypothetical protein spermidine synthase family protein HAD superfamily hydrolase SCP domain-containing protein
311 311 311 312 312 312 312 312 313 313	241162 272399 238912 285346 242185 273200 267385 285900 243127 273749	241941 272884 239505 285816 242961 273748 269052 286553 243684 274120	485 593 470 776 548 1667 653 557 371	hypothetical protein hypothetical protein hypothetical protein sortase B family protein hypothetical protein spermidine synthase family protein HAD superfamily hydrolase SCP domain-containing protein hypothetical protein
311 311 312 312 312 312 312 313 313 313	241162 272399 238912 288346 242185 273200 267385 285900 243127 273749 269090	241941 272884 239505 285816 242961 273748 269052 286553 243684 274120 270085	485 593 470 776 548 1667 653 557 371 995	hypothetical protein hypothetical protein hypothetical protein sortase B family protein hypothetical protein spermidine synthase family protein HAD superfamily hydrolase SCP domain-containing protein hypothetical protein cobalamin biosynthesis protein CbiD
311 311 312 312 312 312 312 313 313 313	241162 272399 238912 285346 242185 267385 285900 243127 267385 285900 243127 269090 239617	241941 272884 239505 285816 242961 273748 269052 286553 243684 274120 270085 240345	485 593 470 776 548 1667 653 557 371 995 728	hypothetical protein hypothetical protein hypothetical protein sortase B family protein hypothetical protein spermidine synthase family protein HAD superfamily hydrolase SCP domain-containing protein hypothetical protein cobalamin biosynthesis protein CbiD hypothetical protein
311 311 312 312 312 312 312 313 313 313	241162 272399 238912 285346 242185 273200 267385 285900 243127 273749 269090 239617 286597	241941 272884 239505 285816 242961 273748 269052 286553 243684 274120 270085 240345 288258	485 593 470 776 548 1667 653 557 371 995 728 1661	hypothetical protein hypothetical protein hypothetical protein sortase B family protein hypothetical protein spermidine synthase family protein HAD superfamily hydrolase SCP domain-containing protein hypothetical protein cobalamin biosynthesis protein CbiD hypothetical protein sugar ABC transporter substrate-binding protein
311 311 312 312 312 312 313 313 313 313	241162 272399 238912 285346 242185 273200 267385 285900 243127 273749 269990 239617 286597 243764	241941 272884 239505 285816 242961 273748 269052 286553 243684 274120 270085 240345 240345 288258 243976	485 593 470 776 548 1667 653 557 371 995 728 1661 212	hypothetical protein hypothetical protein hypothetical protein sortase B family protein hypothetical protein spermidine synthase family protein HAD superfamily hydrolase SCP domain-containing protein hypothetical protein cobalamin biosynthesis protein CbiD hypothetical protein sugar ABC transporter substrate-binding protein hypothetical protein
311 311 312 312 312 312 312 313 313 313	241162 272399 238912 285346 242185 273200 267385 285900 243127 273749 269090 239617 286597	241941 272884 239505 285816 242961 273748 269052 286553 243684 274120 270085 240345 288258	485 593 470 776 548 1667 653 557 371 995 728 1661	hypothetical protein hypothetical protein hypothetical protein sortase B family protein hypothetical protein spermidine synthase family protein HAD superfamily hydrolase SCP domain-containing protein hypothetical protein cobalamin biosynthesis protein CbiD hypothetical protein sugar ABC transporter substrate-binding protein

315	288657	289100	443	hypothetical protein
315	243995	244336	341	hypothetical protein PilZ domain-containing protein
315	274721	275149	428	ribosomal protein L13 rpl
315	270095	270886	791	Cobalamin-5-phosphate synthase
315	240854	241258	404	NUDIX domain-containing protein
316	289133	289723	590	hypothetical protein
316	244444	245628	1184	nucleotide sugar dehydrogenase
316	275393	276169	776	tRNA pseudouridine synthase A tru
316	270883	271830	947	hypothetical protein
317	289762	290073	311	hypothetical protein
317	245634	246419	785	bifunctional biotinacetyl-CoA-carboxylase ligase/biotin operon
317	276191	276994	803	ABC transporter permease
317	241684	241902	218	hypothetical protein
318	277011 271832	277859 272653	848 821	ABC transporter ATP-binding protein
318	2/1832	243415	1514	>nicotinate (nicotinamide) nucleotide adenylyltransferase NadD< hypothetical protein
318	290999	243413	941	dGTP triphosphohydrolase Dgt
319	277877	278725	848	ABC transporter ATP-binding protein
319	272658	272996	338	>nicotinate (nicotinamide) nucleotide adenylyltransferase NadD<
319	243401	244957	1556	SpoIIE domain-containing protein
320	291944	293722	1778	DNA primase DnaG
320	246598	247161	563	hypothetical protein
321	278848	279726	878	hypothetical protein
322	293739	295463	1724	RNA polymerase sigma factor RpoD
322	279800	280375	575	ribosomal protein L17 rpl
322	273084	274163	1079	histidinol-phosphate aminotransferase HisC
323	295531	296262	731	hypothetical protein
323	280495	281451	956	DNA-directed RNA polymerase alpha subunit rpoA
323	274271	275194	923	lipoprotein NLPA family
323	244959	246731	1772	MatE efflux family protein
324	296272	297927	1655	phosphoribulokinase/uridine kinase family protein
324	248038	249459	1421	L-arabinose isomerase
324	281497	282090 276363	593 998	ribosomal protein S4 rpsD
324 324	275365 246872	276363	1001	ABC transporter ATP-binding protein
325	240872	298973	1043	hypothetical protein NAD-dependent epimerase/dehydratase
325	249496	250929	1433	rhamnulokinase RhaB
325	282250	282660	410	ribosomal protein S11 rpsK
325	276405	277025	620	ABC transporter permease
325	247903	248208	305	hypothetical protein
326	299020	299610	590	hypothetical protein
326	250954	251829	875	rhamnulose-1-phosphate aldolase RhaD
326	282762	283130	368	ribosomal protein S13 rpsM
326	277075	277860	785	SAM-dependent methyltransferase
326	248208	248735	527	NUDIX domain-containing protein
327	299712	300035	323	hypothetical protein
327	283323	283436	113	ribosomal protein L36 rpmJ
327	277891	278547	656	HAD superfamily hydrolase
327	248939	250087	1148	PP-loop family protein
328	300185	301720	1535	von Willebrand factor type A domain-containing protein
328	251965	252939	974 155	AraC family transcriptional regulator
328	278618	278773		Multimeric flavodoxin WrbA
329 329	301781 252953	302254 253840	473 887	RNA polymerase sigma factor sigma-70 family protein hypothetical protein
329	283635	284555	920	hypothetical protein
329	278895	280163	1268	MATE efflux family protein
329	250124	250720	596	radical SAM domain-containing protein
330	302370	302783	413	hypothetical protein
330	253925	255658	1733	GGDEF/EAL domain-containing protein
330	280298	281638	1340	hypothetical protein
331	255705	256040	335	hypothetical protein
331	284742	286121	1379	uracil-xanthine permease
331	282411	283217	806	hypothetical protein
331	250732	251259	527	hypothetical protein
332	303397	304284	887	5-keto 4-deoxyuronate isomerase KduI
332	286447	287307	860	aldo/keto reductase family oxidoreductase
332	283663	284421 252124	758 863	NAD synthetase nadE
332	251261 287374		725	pyridoxine kinase
333	28/3/4 304361	288099 305239	878	xylosidase/arabinofuranosidase Xsa 2-deoxy-D-gluconate 3-dehydrogenase kduD
333	305264	306226	962	2-debydro-3-deoxyphosphogluconate aldolase/4- hydroxy-2-oxoglutarate aldolase, eda
334	256154	257068	902	3-phosphoshikimate 1-carboxyvinyltransferase AroA
334	288285	289034	749	two component system response regulator
334	284453	285658	1205	nicotinate phosphoribosyltransferase pncB
334	252296	252883	587	hypothetical protein
335	306267	307292	1025	2-dehydro-3-deoxygluconokinase KdgK
335	289012	290613	1601	two component system histidine kinase
335	285672	286184	512	cytidyltransferase-related domain-containing protein
336	257497	258594	1097	prephenate dehydrogenase TyrA
336	290706	292376	1670	sugar ABC transporter substrate-binding protein
336	286199	2867	-283332	amidase
336	253222	253866	644	hypothetical protein
337	307615	308631	1016	GGDEF domain-containing protein

227	250025	2.001.5	2000	
337	258825 292381	260915 293250	2090 869	translation elongation factor EF-G-like protein
337	292381 286705	293250	728	sugar ABC transporter permease
				NUDIX domain-containing protein
338	260996	262939	1943	EAL domain-containing protein
338 338	293268 253868	294212	944 581	sugar ABC transporter permease
		254449		hypothetical protein HD-GYP domain-containing protein
339 339	308635	309900	1265 794	01
	288195	288989	947	lectron transport complex RnfB
339 340	254446 309991	255393 311040	1049	hypothetical protein
				LacI family transcriptional regulator
340	263124	264557	1433	pyruvate carboxyltransferase domain-containing protein
340	294401	296200	1799	methyl-accepting chemotaxis protein McpK
340	255582	256169	587	SAM-dependent methyltransferase
341	264574	265254	680	GntR family transcriptional regulator
341	289014	289601	587	electron transport complex RnfA
341	256172	256951	779	SAM-dependent methyltransferase
342	311275	312231	956	sugar ABC transporter permease
342	265282	266484	1202	isocitrate dehydrogenase Icd
342	296345	297361	1016	TRAP transporter solute receptor DctP family dct
342	256941	258035	1094	radical SAM domain-containing protein
343	312253	313176	923	sugar ABC transporter permease
343	266516	268492	1976	ABC transporter ATP-binding protein
343	297358	298146	788	two component system response regulator
343	289604	290383	779	electron transport complex RnfE
344	268627	269259	632	CAAX amino terminal protease family protein
344	290383	290991	608	electron transport complex rnfG
344	258351	259139	788	hypothetical protein
345	313420	314994	1574	sugar ABC transporter substrate-binding protein
345	269285	270664	1379	MFS transporter
345	298152	299507	1355	two component system histidine kinase
345	290994	291869	875	electron transport complex rnfD
345	259154	259633	479	RNA polymerase sigma factor sigma-70 family protein
346	315261	317129	1868	beta-galactosidase Bga35A
346	270788	271738	950	protease activity modulator HflK
346	299729	300151	422	hypothetical protein
346	291954	293270	1316	electron transport complex rnfC
346	259820	260383	563	hypothetical protein
347	317452	319323	1871	beta-galactosidase Bga2B
347	271748	272632	884	protease activity modulator HflC
347	300221	301366	1145	TRAP transporter DctM subunit dctM
347	260407	261495	1088	hypothetical protein
348	272862	274343	1481	transcription termination factor Rho
348	301516	302040	524	hypothetical protein
348	261626	262564	938	hypothetical protein
349	274391	275272	881	PilZ domain-containing protein
349	302079	303140	1061	TRAP transporter DctP subunit dctP
349	293492	294679	1187	hypothetical protein
349	262796	263290	494	hypothetical protein
350	275378	276073	695	
350	273378	295014	269	alanine racemase domain-containing protein hypothetical protein
				translation initiation factor IF-1 inf
351 351	303381 295152	303599 295889	218 737	
252	07/045	077707	001	MerR family transcriptional regulator
352	2/6845	277726	881	GGDEF domain-containing protein
352	303621	304379	758	methionine aminopeptidase, type I, map
352	295886	296791	905 893	hypothetical protein hypothetical protein
352	263533	264426		· · ·
353	296939	298090	1151 644	unsaturated glucuronyl hydrolase Ugl88B
353	304372	305016	1304	adenylate kinases adk
354	305106 277922	306410	-249872	preprotein translocase subunit Sec
355		28050		xylosidase
355	306425	306865	440	ribosomal protein L15 RplO
355	298115	299641	1526	polysaccharide biosynthesis protein
355	264596	265006	410	peptide deformylase def
356	280531	281802	1271	hypothetical protein
356	306989	307177	188	ribosomal protein L30 RpmD
356	265067	266299	1232	hypothetical protein
357	281808	282473	665	hypothetical protein
357	307194	307703	509	ribosomal protein S5 RpsE
358	307722	308090	368	ribosomal protein L18 RplR
358	299641	300570	929	glycosyl transferase GT11 family protein
358	266604	266936	332	hypothetical protein
359	308110	308649	539	ribosomal protein L6 RplF
359	300598	301740	1142	polysaccharide pyruvyl transferase
360	282557	283711	1154	hypothetical protein
360	308665	309066	401	ribosomal protein S8 RpsH
360	301767	302744	977	glycosyl transferase GT2 family protein
360	266933	267931	998	HNH endonuclease domain-containing protein
361	283846	285135	1289	alpha-L-fucosidase Fuc29A
361	309207	309377	170	ribosomal protein S14 RpsN
361	302729	304099	1370	hypothetical protein
361	267943	268806	863	hypothetical protein
362	309411	309905	494	ribosomal protein L5 RplE
362	268803	269891	1088	hypothetical protein

363         285449         286591         1142         hypothetical protein           363         309973         310302         329         ribosomal protein L24 rplX           363         304119         305297         1178         polysaccharide biosynthesis protein           364         310315         310683         368         ribosomal protein L14 rplN           364         305318         306274         956         glycosyl transferase GT17 family protein           364         270328         270729         401         hypothetical protein S17 rpsQ           365         310705         310959         254         305 ribosomal protein L27 family protein           366         310705         310959         254         305 ribosomal protein L27 family protein           366         306264         307298         1034         glycosyl transferase GT2 family protein           366         307313         308032         719         hypothetical protein         129 rpmC           366         307313         308032         719         hypothetical protein         16 rplP           367         311191         311622         431         ribosomal protein L16 rplP           367         308087         309124         1037	
363         304119         305297         1178         polysaccharide biosynthesis protein           364         310315         310683         368         ribosomal protein L14 rplN           364         305318         306274         956         glycosyl transferase GT17 family protein           364         305318         306274         956         glycosyl transferase GT17 family protein           364         270328         270729         401         hypothetical protein           365         310705         310959         254         30S ribosomal protein S17 rpsQ           365         306264         307298         1034         glycosyl transferase GT2 family protein           366         310992         311201         209         ribosomal protein L29 rpmC           366         307313         308032         719         hypothetical protein           366         270912         272651         1739         hypothetical protein           367         311191         311622         431         ribosomal protein L16 rplP           367         308087         309124         1037         glycosyl transferase GT11 family protein           367         272735         27588         -245147         helicase	
364         310315         310683         368         ribosomal protein L14 rplN           364         305318         306274         956         glycosyl transferase GT17 family protein           364         270328         270729         401         hypothetical protein           364         270328         270729         401         hypothetical protein           365         310705         310959         254         30S ribosomal protein S17 rpsQ           365         306264         307298         1034         glycosyl transferase GT2 family protein           366         307313         308032         719         hypothetical protein           366         270912         272651         1739         hypothetical protein           367         311191         311622         431         ribosomal protein L16 rplP           367         308087         309124         1037         glycosyl transferase GT11 family protein           367         272735         27588         -245147         helicase	
364         305318         306274         956         glycosyl transferase GT17 family protein           364         270328         270729         401         hypothetical protein           365         310705         310959         254         308 ribosomal protein S17 rpsQ           365         306264         307298         1034         glycosyl transferase GT2 family protein           366         310992         311201         209         ribosomal protein L29 rpmC           366         307313         308032         719         hypothetical protein           366         270912         272651         1739         hypothetical protein           367         311191         311622         431         ribosomal protein L16 rplP           367         308087         309124         1037         glycosyl transferase GT11 family protein           367         272735         27588         -245147         helicase	
364         270328         270729         401         hypothetical protein           365         310705         310959         254         30S ribosomal protein S17 rpsQ           365         306264         307298         1034         glycosyl transferase GT2 family protein           366         310992         311201         209         ribosomal protein L29 rpmC           366         307313         308032         719         hypothetical protein           366         270912         272651         1739         hypothetical protein           367         311191         311622         431         ribosomal protein L16 rpIP           367         308087         309124         1037         glycosyl transferase GT11 family protein           367         272735         27588         -245147         helicase	
365         310705         310959         254         305 ribosomal protein S17 rpsQ           365         306264         307298         1034         glycosyl transferase GT2 family protein           366         310992         311201         209         ribosomal protein L29 rpmC           366         307313         308032         719         hypothetical protein           366         270912         272651         1739         hypothetical protein           367         311191         311622         431         ribosomal protein L16 rplP           367         308087         309124         1037         glycosyl transferase GT11 family protein           367         272735         27588         -245147         helicase	
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367 272735 27588 -245147 helicase	
368 309138 310931 1793 ABC transporter ATP-binding/permease	
369         312319         312714         395         ribosomal protein L22 rplV	
369 310951 311823 872 glycosyl transferase GT11 family protein	
370 312745 313035 290 ribosomal protein S19 rpsS	
370 311858 313753 1895 asparagine synthase glutamine-hydrolyzing AsnB	
371 313047 313844 797 ribosomal protein L2 rplB	
371 313825 314913 1088 hypothetical protein	
372         313985         314284         299         ribosomal protein L23 RpIW	
373         314284         314907         623         ribosomal protein L4 RplD	
373 276609 276929 320 hypothetical protein	
374 314935 315618 683 ribosomal protein L3 rplC	
374 314930 316462 1532 MBOAT family acyltransferase	
375 315760 316071 311 ribosomal protein S10 rpsJ	
375 316494 317696 1202 glycosyl transferase GT4 family protein	
376 316589 317470 881 hypothetical protein	
376 277755 278639 884 hypothetical protein	
377 317687 319573 1886 asparagine synthase glutamine-hydrolyzing AsnB	
377 278670 280226 1556 hypothetical protein	
378 317538 318602 1064 hypothetical protein	
378         319642         320751         1109         glycosyl transferase GT4 family protein	
379 320758 321957 1199 glycosyl transferase GT4 family protein	
379         280486         280719         233         hypothetical protein	
380         280789         281520         731         feruloyl esterase Est1	
381         281563         282012         449         D-tyrosyl-tRNA(Tyr) deacylase dtd           382         323727         324461         734         polysaccharide deacetylase Est4E	
382 319536 320441 905 von Willebrand factor type A domain-containing protein	
382 282033 282848 815 nitroreductase family protein	
383 320495 321589 1094 von Willebrand factor type A domain-containing protein	
384         321589         321984         395         hypothetical protein	
384 324690 325664 974 NAD-dependent epimerase/dehydratase	
384         282951         283883         932         cobalamin biosynthesis protein CobW	
385         322052         322834         782         hypothetical protein	
385         325866         327209         1343         nucleotide sugar dehydrogenase	
385         283942         285009         1067         NADP-dependent alcohol dehydrogenase	
386         322964         323959         995         AAA family ATPase	
386         327279         328376         1097         glycosyl transferase GT4 family protein	
386         285232         286527         1295         MFS transporter	
387 323973 324836 863 5,10-methylenetetrahydrofolate reductase MetF	
387 328379 329374 995 hypothetical protein	
387 286517 287632 1115 HTH domain-containing protein	
388         324947         326461         1514         adenylosuccinate lyase purB	
388         329379         330005         626         bacterial sugar transferase	
389 326562 328007 1445 glutamine phosphoribosylpyrophosphate amidotransferase Pu	rF
389         330033         331304         1271         DegT/DnrJ/EryC1/StrS family aminotransferase	
389         287791         288069         278         hypothetical protein	
390 328127 329320 1193 hypothetical protein	
390         331307         333247         1940         polysaccharide biosynthesis protein	
390 288066 288488 422 hypothetical protein	
391 329343 330182 839 hypothetical protein	
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393 333263 335896 2633 hypothetical protein	
393 289232 289927 695 hypothetical protein	
394 331501 335094 3593 hypothetical protein	
394 335978 337603 1625 hypothetical protein	
394 289917 290219 302 hypothetical protein	
395 335209 336420 1211 ABC transporter permease	
395         337653         338597         944         glycosyl transferase GT2 family protein	
395         290491         290730         239         hypothetical protein	
396         336435         337646         1211         ABC transporter permease	
396         338613         339128         515         GNAT family acetyltransferase	
396         290746         291171         425         hypothetical protein	
390         250/40         251/1         425         hypometical protein           397         337662         339254         1592         RND family transporter	
397         291237         291629         392         Nypothetical protein	
397         291237         291029         392         hypometical protein           398         339283         339981         698         ABC transporter ATP-binding protein	
398         339141         340901         1760         hypothetical protein	

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425         363787         364893         1106         polysaccharide export protein           425         311371         311913         542         hypothetical protein           426         364911         366311         1400         exopolysaccharide biosynthesis polyrenyl glycosylphosphotransferase           426         311993         313015         1022         peptidase S15 milly protein           427         366330         367076         746         glycosyl transferase GT2 family protein           427         313012         313215         239         hypothetical protein           427         366330         367076         746         glycosyl transferase GT2 family protein           427         313012         313251         239         hypothetical protein           428         364108         364863         755         phosphomethylpyrimidine kinase thiD           428         313350         314222         872         LysR family transcriptional regulator           429         364946         365581         635         thamine-phosphate pyrophosphorylase thiE           429         314287         314883         596         SAM-dependent methyltransferase           430         315507         6620         hypothetical protein					
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426         364911         366311         1400         exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase           426         311993         313015         1022         peptidase S15 family protein           427         366730         364054         1304         thiamine biosynthesis protein ThiC           427         366330         367076         746         glycosyltransferase GT2 family protein           428         364108         364863         755         phosphomethylpyrimidine kinase thiD           428         313350         314222         872         LysR family transcriptional regulator           429         3664946         365581         635         thiamine-phosphate pyrophosphorylase thE           429         367076         3664957         881         glycosyl transferase GT2 family protein           429         3667076         367957         881         glycosyl transferase GT2 family protein           430         314887         315807         620         Myroyethylthiazole kinase thiM           431         366410         367075         665         thiazole transporter ThiW           431         315863         316840         977         hyroothetical protein           433         315963         316940					
426         311993         313015         1022         peptidase S15 family protein           427         362750         364054         1304         thiamine biosynthesis protein ThiC           427         366330         367076         746         glycosyl transferase GT2 family protein           427         313012         313251         239         hypothetical protein           428         364108         364863         755         phosphomethylpyrimidine kinase thiD           428         313350         314222         872         LysR family transcriptional regulator           429         364946         365581         635         thiamine-phosphate pyrophosphorylase thiE           429         367076         367957         881         glycosyl transferase GT2 family protein           429         367076         367957         881         glycosyl transferase GT2 family protein           429         314887         314883         596         SAM-dependent methyltransferase           430         365591         366409         818         hydroxyethylthiazole kinase thiM           431         316586         315867         281         hypothetical protein           433         315963         316940         977         hypothetical	-				
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427         313012         313251         239         hypothetical protein           428         364108         364863         755         phosphomethylpyrimidine kinase thiD           428         313350         314222         872         LysR family transcriptional regulator           429         364046         365581         635         thiamine-phosphate pyrophosphorylase thiE           429         367076         367957         881         glycosyl transferase GT2 family protein           429         314287         314883         596         SAM-dependent methyltransferase           430         365591         366409         818         hydroxyethylthiazole kinase thiM           430         314887         315507         620         hypothetical protein           431         366410         367075         665         thiazole transporter ThiW           431         315867         281         hypothetical protein           433         315963         316940         977         hypothetical protein           433         315963         316940         977         hypothetical protein           434         317598         318377         779         hypothetical protein           434         319203					
428         364108         364863         755         phosphomethylpyrimidine kinase thiD           428         313350         314222         872         LysR family transcriptional regulator           429         364946         365581         635         thiamine-phosphate pyrophosphorylase thiE           429         367957         881         glycosyl transferase GT2 family protein           429         367076         367957         881         glycosyl transferase GT2 family protein           429         314287         314883         596         SAM-dependent methylmasferase           430         365591         366409         818         hydroxyethylthiazole kinase thiM           430         314887         315507         620         hypothetical protein           431         366410         367075         665         thiazole transporter ThiW           433         315963         316940         977         hypothetical protein           433         315963         316940         977         hypothetical protein           433         315963         318377         779         hypothetical protein           434         317598         318377         779         hypothetical protein           436 <t< td=""><td></td><td></td><td></td><td></td><td></td></t<>					
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429         364946         365581         635         thiamine-phosphate pyrophosphorylase thiE           429         367076         367957         881         glycosyl transferase GT2 family protein           429         314287         314883         596         SAM-dependent methyltransferase           430         365591         366409         818         hydroxyethylthiazole kinase thiM           430         314887         315507         620         hypothetical protein           431         366410         367075         665         thiazole transporter ThiW           431         315586         315867         281         hypothetical protein           433         315963         316940         977         hypothetical protein           434         317598         318377         779         hypothetical protein           436         318619         319206         587         hypothetical protein           437         319203 <td< td=""><td></td><td></td><td></td><td></td><td></td></td<>					
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429         314287         314883         596         SAM-dependent methyltransferase           430         365591         366409         818         hydroxyethylthiazole kinase thiM           430         314887         315507         620         hypothetical protein           431         366410         367075         665         thiazole transporter ThiW           431         315586         315867         281         hypothetical protein           433         315963         316940         977         hypothetical protein           433         315963         316940         977         hypothetical protein           433         315963         316940         977         hypothetical protein           434         317598         318377         779         hypothetical protein           436         31819         319206         587         hypothetical protein           437         319203         319946         743         hypothetical protein           443         321177         719         hypothetical protein           443         321177         719         hypothetical protein           443         321177         322025         848         hypothetical protein <tr< td=""><td></td><td></td><td></td><td></td><td></td></tr<>					
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430         314887         315507         620         hypothetical protein           431         366410         367075         665         thiazole transporter ThiW           431         315586         315867         281         hypothetical protein           433         315963         316940         977         hypothetical protein           433         315963         316940         977         hypothetical protein           433         317598         318377         779         hypothetical protein           436         318619         319206         587         hypothetical protein           437         319203         319946         743         hypothetical protein           439         319959         320393         434         hypothetical protein           442         320438         321157         719         hypothetical protein           443         321177         322025         848         hypothetical protein           443         321177         322025         848         hypothetical protein           4445         322037         322624         587         hypothetical protein           4445         32367         323861         494         hypothetical pro					
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449 323869 324612 743 hypothetical protein					
450 324626 325507 881 hydrolase alpha/beta fold family					
	450	324626	325507	881	hydrolase alpha/beta fold family

451	005551	22/200	500	1 az 1
451 454	325561	326289 328019	728 1241	hypothetical protein
455	326778 328016	329002	986	hypothetical protein
455	328010	329002	779	hypothetical protein
				hypothetical protein
457	330032 330957	330955	923 899	hypothetical protein
459		331856		hypothetical protein
461	331850	332455	605	hypothetical protein
462	332472	333074	602	hypothetical protein
463	333113	333562	449	hypothetical protein
465	333621	334448	827	hypothetical protein
466	334467	335102	635	hypothetical protein
467	335108	335614	506	hypothetical protein
468	335629	336249	620	SAM-dependent methyltransferase
470	336253	336846	593	SAM-dependent methyltransferase
471	337007	337279	272	ferric uptake regulator family protein
472	337711	338667	956	succinylglutamate desuccinylase/aspartoacylase family protein
473	338686	339438	752	hypothetical protein
474	339447	340208	761	SAM-dependent methyltransferase
475	340247	340987	740	peptide/nickel ABC transporter ATP-binding protein
476	340989	341711	722	peptide/nickel ABC transporter ATP-binding protein
477	341715	342533	818	peptide/nickel ABC transporter permease
479	342533	343456	923	peptide/nickel ABC transporter permease
481	343449	345059	1610	peptide/nickel ABC transporter periplasmic protein
482	345186	345992	806	hypothetical protein
483	346122	347324	1202	MFS transporter
485	347417	347971	554	hypothetical protein
485	347995	348243	248	GNAT family acetyltransferase
480	347993	348243	140	GNAT family acetyltransferase
				· ·
488	348465	348908	443	MarR family transcriptional regulator
490	349270	350838	1568	lysyl-tRNA synthetase lysS
492	350958	351443	485	transcription elongation factor GreA/GreB
493	351588	352565	977	tRNA dihydrouridine synthase A DusA
494	352566	353048	482	hypothetical protein
496	353067	353882	815	Baf family transcriptional regulator
498	353895	354698	803	biotin-[acetyl-CoA-carboxylase] ligase birA
499	354700	355692	992	ornithine carbamoyltransferase argF
500	355818	356654	836	cell wall hydrolase
501	357076	357870	794	pyrroline-5-carboxylate reductase proC
502	357872	358675	803	rRNA methylase SpoU family protein
503	358795	359763	968	6-phosphofructokinase pfkA
504	359925	363464	3539	DNA polymerase III E DnaE
505	363741	364931	1190	S-adenosylmethionine synthetase MetK
506	365254	366723	1469	xylulokinase xylB
507	366792	367370	578	hypothetical protein
508	367367	369202	1835	hypothetical protein
509	369361	372033	2672	S1 RNA binding domain-containing protein
510	372115	372654	539	hypothetical protein
510	372664	373176	512	hypothetical protein
513	373202	373930	728	hypothetical protein
515	373202	375871	1925	glycoside hydrolase family 2 Gh2B
517	375951	377321	1323	
519	373931 377494		938	MatE efflux family protein carbamate kinase arcC
	250101	378432	1.500	
520	378486	380015	1529	ATP-dependent Clp protease ATP-binding subunit ClpX
521	380034	381455	1421	serine protease HtrA family protein
523	381707	381967	260	hypothetical protein
524	382054	382866	812	histidinol phosphate phosphatase HisJ family
526	382914	383930	1016	UDP-glucose 4-epimerase galE
527	384072	385343	1271	UTP-glucose-1-phosphate uridylyltransferase GalU
528	385422	387107	1685	lysozyme Lyc
530	387254	388732	1478	L-fucose isomerase related protein
531	388921	391044	2123	beta-xylosidase Xyl
533	391373	393085	1712	sugar ABC transporter substrate-binding protein
534	393150	394022	872	sugar ABC transporter permease
535	394038	394874	836	sugar ABC transporter permease
536	395023	397866	2843	alpha-glucuronidase Gh115
538	398069	398938	869	AraC family transcriptional regulator
540	398948	400936	1988	alpha-D-glucuronidase Agu67A
542	401017	401901	884	AraC family transcriptional regulator
544	401911	403791	1880	acetyl-xylan esterase
545	403871	405886	2015	beta-glucosidase Bgl3E
546	405906	407633	1727	hypothetical protein
547	407699	409177	1478	sugar ABC transporter substrate-binding protein
548	409246	410256	1010	sugar ABC transporter permease
549	410249	411157	908	sugar ABC transporter permease
551	411172	413538	2366	hypothetical protein
553	411172 413764	413338	659	hypothetical protein
553	413764 414428			
555		415954	1526	NHL repeat-containing protein
	415975	416850	875	sugar ABC transporter permease
556	416840	417778	938	sugar ABC transporter permease
558	417795	420710	2915	sugar ABC transporter substrate-binding protein
559	420728	422083	1355	endo-1,4-beta-xylanase Xyn
562	422448	423389	941	AraC family transcriptional regulator
564	423404	424852	1448	xylosidase/arabinofuranosidase Xsa43

566         425565         426333         788         hypothetical protein           567         426433         427686         1253         endo-1,4-beta-glucanase/xylanase Cel5           569         427707         430484         2777         xylosidase/arabinofuranosidase and esterase Xsa4           571         430842         431270         428         ATP synthase Fl epsilon subunit AtpC           572         431276         432670         1394         ATP synthase Fl painon subunit atpD           574         432848         433708         860         ATP synthase Fl apha subunit atpG           575         433726         435246         1520         ATP synthase Fl alpha subunit atpA           576         435269         435808         539         ATP synthase Fl abha subunit atpH           577         436969         436394         425         ATP synthase FO S subunit atpH           577         436852         436806         281         ATP synthase FO A subunit atpE           579         436858         437628         770         ATP synthase FO A subunit atpB           580         437639         438049         410         hypothetical protein           582         438073         438351         278         hypothetical protei	3
569         427707         430484         2777         xylosidase/arabinofuranosidase and esterase Xsa4           571         430842         431270         428         ATP synthase F1 epsilon subunit AtpC           572         431276         432670         1394         ATP synthase F1, beta subunit atpD           574         432848         433708         860         ATP synthase F1 apha subunit atpG           575         433726         435246         1520         ATP synthase F1 alpha subunit atpA           576         435269         435808         539         ATP synthase F1 delta subunit atpH           577         435969         436394         425         ATP synthase F0 B subunit atpF           578         436525         436806         281         ATP synthase F0 C subunit atpE           579         436858         437628         770         ATP synthase F0 A subunit atpB           580         437639         438049         410         hypothetical protein           582         438073         438351         278         hypothetical protein	3
571         430842         431270         428         ATP synthase F1 epsilon subunit AtpC           572         431276         432670         1394         ATP synthase F1, beta subunit atpD           574         432848         433708         860         ATP synthase F1 gamma subunit atpG           575         433726         435246         1520         ATP synthase F1 alpha subunit atpA           576         435269         435808         539         ATP synthase F1 delta subunit atpH           577         435969         436394         425         ATP synthase F0 B subunit atpF           578         436525         436806         281         ATP synthase F0 C subunit atpE           579         436858         437628         770         ATP synthase F0 A subunit atpB           580         437639         438049         410         hypothetical protein           582         438073         438351         278         hypothetical protein	9
572         431276         432670         1394         ATP synthase F1, beta subunit atpD           574         432848         433708         860         ATP synthase F1 gamma subunit atpG           575         433726         435246         1520         ATP synthase F1 alpha subunit atpA           576         435269         435808         539         ATP synthase F1 delta subunit atpH           577         435969         436394         425         ATP synthase F0 B subunit atpF           578         436525         436806         281         ATP synthase F0 C subunit atpE           579         436858         437628         770         ATP synthace F0 A subunit atpB           580         437639         438049         410         hypothetical protein           582         438073         438351         278         hypothetical protein	
574         432848         433708         860         ATP synthase F1 gamma subunit atpG           575         433726         435246         1520         ATP synthase F1 alpha subunit atpA           576         435269         435808         539         ATP synthase F1 delta subunit atpH           577         435969         436394         425         ATP synthase F0 B subunit atpF           578         436525         436806         281         ATP synthase F0 C subunit atpE           579         436858         437628         770         ATP synthase F0 A subunit atpB           580         437639         438049         410         hypothetical protein           582         438073         438351         278         hypothetical protein	
575         433726         435246         1520         ATP synthase F1 alpha subunit atpA           576         435269         435808         539         ATP synthase F1 delta subunit atpH           577         435969         436394         425         ATP synthase F0 B subunit atpF           578         436525         436806         281         ATP synthase F0 C subunit atpE           579         436858         437628         770         ATP synthase F0 A subunit atpB           580         437639         438049         410         hypothetical protein           582         438073         438351         278         hypothetical protein	
576         435269         435808         539         ATP synthase F1 delta subunit atpH           577         435969         436394         425         ATP synthase F0 B subunit atpF           578         436525         436806         281         ATP synthase F0 C subunit atpE           579         436858         437628         770         ATP synthase F0 A subunit atpB           580         437639         438049         410         hypothetical protein           582         438073         438351         278         hypothetical protein	
577         43596         436394         425         ATP synthase F0 B subunit atpF           578         436525         436806         281         ATP synthase F0 C subunit atpE           579         436858         437628         770         ATP synthase F0 A subunit atpB           580         437639         438049         410         hypothetical protein           582         438073         438351         278         hypothetical protein	
578         436525         436806         281         ATP synthase F0 C subunit atpE           579         436858         437628         770         ATP synthase F0 A subunit atpB           580         437639         438049         410         hypothetical protein           582         438073         438351         278         hypothetical protein	
579         436858         437628         770         ATP synthase F0 A subunit atpB           580         437639         438049         410         hypothetical protein           582         438073         438351         278         hypothetical protein	
580         437639         438049         410         hypothetical protein           582         438073         438351         278         hypothetical protein	
582         438073         438351         278         hypothetical protein	
583 438613 440643 2030 methyl-accepting chemotaxis protain MonC	
584         440875         442647         1772         aspartyl-tRNA synthetase aspS	
585         442800         443444         644         hypothetical protein	
586         443551         444006         455         LysM domain-containing protein	
587 444069 445055 986 hypothetical protein	
588 445170 446576 1406 PTS system N- acetylglucosamine-specific IIBC compose	ent NagE
589         446664         447164         500         PTS system N- acetylglucosamine-specific IIA compo	onent
591         447279         449027         1748         carbon starvation protein CstA	
592 449024 449596 572 hypothetical protein	
594 449937 451301 1364 magnesium transporter mgtE	
596 451345 45322 1877 oligopeptide ABC transporter substrate-binding prot	tein
597 453255 454607 1352 GGDEF domain-containing protein	
598 454811 456298 1487 glutamate synthase small subunit GltD	
599 456341 460858 4517 glutamate synthase large subunit GltB	
601 460889 462997 2108 glutamine synthetase type III GlnA	
602 463037 464563 1526 asparagine synthase glutamine-hydrolyzing AsnE	3
604 464647 466335 1688 amonium transporter ant	
605 466710 467873 1163 hypothetical protein	
607         467906         469072         1166         hypothetical protein	
608         469091         470821         1730         hypothetical protein	
609 470921 47021 1750 hypotectical protein	
610         471341         471700         359         hypothetical protein           612         471804         472580         776         hypothetical protein	
617         474911         477430         2519         adenosine deaminase add           618         477462         479100         777         adenosine deaminase add	-
618 477462 478199 737 amino acid ABC transporter ATP-binding protein	n
620 478186 478872 686 amino acid ABC transporter permease	
621 47883 479599 716 amino acid ABC transporter substrate-binding prote	ein
622 479823 482087 2264 pyruvate formate lyase Pfl	
623 482288 482992 734 pyruvate formate-lyase 1-activating enzyme pfl	
624 483010 483774 764 cNMP binding domain-containing protein	
625 483805 484365 560 NUDIX domain-containing protein	
626         484368         485522         1154         beta-lactamase family protein	
627         485545         487338         1793         Na/Pi-cotransporter II-related protein	
628         487448         488362         914         GNAT family acetyltransferase	
629 488649 48809 260 phosphocarrier HPr family protein	
630 488922 489845 923 hypothetical protein	
631 489861 490679 818 P-loop-containing ATPase	
632 490952 491749 797 UDP-N-acetylenolpyruvoylglucosamine reductase m	nurB
633 491889 492824 935 glucokinase Glk	
634         492849         493796         947         Hpr kinase/phosphatase HprK	
636 493852 495720 1868 excinuclease ABC subunit C uvr	
638         495785         497983         2198         ATP-dependent metallopeptidase Hfl	
639 498227 499837 1610 CTP synthase pyrG	
640 499912 500637 725 glucosamine-6-phosphate isomerase nag	
641 500634 501512 878 carbohydrate kinase ROK family protein	
642 501652 503232 1580 sugar ABC transporter substrate-binding protein	1
644 503422 504288 866 sugar ABC transporter permease	
645 504288 505289 1001 sugar ABC transporter permease	
646 505464 506471 1007 oligopeptide ABC transporter ATP-binding protein C	DppF
647 506458 507585 1127 oligopeptide ABC transporter ATP-binding protein C	
648 507563 508624 1061 oligopeptide ABC transporter permease OppC	
650 508681 509781 1100 oligopeptide ABC transporter permease OppB	
652 509874 511919 2045 oligopeptide ABC transporter substrate-binding protein	n OppA
653 512081 513235 1154 iron-containing alcohol dehydrogenase	
654 513250 514260 1010 myo-inositol 2-dehydrogenase	
655 514288 515124 836 Myo-inosose-2 dehydratase	
656 515217 515996 779 myo-inositol catabolism protein	
658 516025 517956 1931 myo-inositol catabolism protein	
660         518138         519154         1016         myo-inositol catabolism protein	
661         519201         520865         1664         hypothetical protein	
661         519201         520805         1004         hypothetical protein           662         520882         521808         926         carbohydrate kinase ROK family protein	
663         521825         522916         1091         unsaturated rhamogalacturonyl hydrolase Gh105	5
665         523099         523857         758         AraC family transcriptional regulator	~
670         526560         529721         3161         alpha-mannosidase Man38           671         520851         521218         1267         sugar transporter CPH family pretring	
671         529851         531218         1367         sugar transporter GPH family protein           672         531260         531005         656         hypothetical protein	
673 531269 531925 656 hypothetical protein	

675	531988	533601	1613	phosphoenolpyruvate carboxykinase Pck
676	533771	535099	1328	glycoside hydrolase family 27 Gh27
678	535102	535953	851	tetrapyrrole methylase family protein
679	535953	536696	743	SAM-dependent methyltransferase
680	536683	537621	938	PSP1 domain-containing protein
681	537618	538664	1046	DNA polymerase III delta subunit hol
682	538675	539115	440	hypothetical protein
683	539167	539760	593	guanylate kinase gmk
684	539769	541178	1409	pyruvate kinase pyk
685	541160	542593	1433	Orn/Lys/Arg decarboxylase
686	542586	543179	593	HD domain-containing protein

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