Caracterização molecular de linhagens clínicas de *Providencia rettgeri* transportando os genes *bla*$_{NDM}$ e *bla*$_{TEM}$

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São Luís-MA

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Defesa apresentada ao programa de Pós-Graduação Meio Ambiente como parte dos requisitos para obtenção do Título de Mestre em Meio Ambiente

Orientador Prof[a] Dra. Andrea de Souza Monteiro.

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2017

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“O que não tem remédio, remediado está! ”

Andrea Monteiro

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Resumo

Providencia rettgeri é um bacilo Gram-negativo amplamente distribuído no meio ambiente e atualmente é considerado um patógeno emergente, associado a infecções nosocomiais. O objetivo deste estudo foi analisar o perfil de susceptibilidade antimicrobiana de linhagens de *P. rettgeri* isoladas de amostras clínicas e realizar uma caracterização genômica das linhagens *P. rettgeri* PR01 e *P. rettgeri* PR02. Neste estudo foram isoladas oito (08) linhagens de *P. rettgeri* a partir de amostras clinicas de pacientes atendidos em unidades de terapia intensiva. A presença do gene *bla*$_{NDM}$ foi determinada pela reação de PCR. Além disso, as concentrações mínimas inibitórias (CIM) dos antimicrobianos foram determinadas usando o sistema automatizado VITEK-02. Os genomas das linhagens PR01 e PR02, caracterizadas como transportadora dos genes bla$_{NDM-1}$ e bla$_{TEM}$ foram sequenciados utilizando a plataforma Illumina - MiSeq. Após o sequenciamento, as sequências de DNA genômico pré-montadas foram anotadas usando o software Prokka. Uma análise complementar do genoma foi realizada utilizando a tecnologia de subsistema de anotação rápida (RAST). Todas as oito (08) linhagens de *P. rettgeri*, as 08 estavam albergando o gene *bla*$_{NDM}$ e apresentaram resistência ao meropenem. Os valores de CIM, realizados pelo teste de crescimento em placa variaram de 8-128 µg/mL para o antimicrobiano meropenem. Uma caracterização genômica parcial para as linhagens *P*. *rettgeri* PR01 e *P*. *rettgeri* PR02 utilizando o RAST indicou uma ampla gama de genes relacionados a bombas de efluxo de drogas antimicrobianas. Os sistemas genéticos foram caracterizados, como a extrusão de múltiplas drogas (MATE), a divisão de família (RND), e a grande superfamília do facilitador (MFS). Nestas analises foram detectados em média 91 genes que estavam relacionados ao subsistema de virulência, doença e defesa. A análise genômica parcial de *P. rettgeri* PR01 e *P. rettgeri* PR02 confirmou a presença do gene *bla*$_{NDM-1}$ e outros genes para a resistência à β-lactâmicos, como *bla*$_{TEM}$. Além disso, foram identificados vários sistemas genéticos para a produção e liberação de sideróforos, que estão associados à absorção de ferro, e outros genes, como para receptores e transportadores do anel heme e de hemina. Cerca de 43 genes foram identificados e expressaram proteínas para absorção e metabolismo de ferro. A análise do genoma das linhagens PR01 e PR02 mostrou uma alta concentração de sequências de inserção, elementos móveis e pro-fagos, sugerindo que a espécie apresenta uma plasticidade genética considerável. Ademais, ainda foi verificado a presença de diversas ilhas genômicas, associadas a marcadores de persistência frente a ao estresse químico e nutricional, como o sistema-toxina e antitoxina, contendo os genes Pasl e Past. A diversidade de elementos genéticos em *P*. *rettgeri* relacionados aos mecanismos de resistência a antimicrobianos, pode levar a curto prazo uma ineficiência das terapias antimicrobianas no combate a infecções causadas por este micro-organismo, e sua rápida acessão como patógeno é resultado de sua plasticidade genética.

Palavras-chave: *Providencia rettgeri*, gene *bla*$_{NDM}$, gene *bla*$_{TEM}$ resistência antimicrobiana.

Abstract

Providencia rettgeri is a Gram-negative bacillus widely distributed in the environment and is currently considered an emerging pathogen, mainly associated with nosocomial infections. The objective of this study was to analyze the antimicrobial susceptibility profile of *P. rettgeri* strains isolated from clinical samples and to perform a genomic characterization of the *P. rettgeri* PR01 and *P. rettgeri* PR02 strains. In this study eight (08) strains of *P. rettgeri* were isolated from clinical samples of patients seen in intensive care units. The presence of the bla_{NDM} gene was determined by the PCR reaction. In addition, the minimum inhibitory concentrations (MIC) of antimicrobials were determined using the VITEK-02 automated system. The genomes of the PR01 and PR02 strains, characterized as carrier of the bla_{NDM-1} and bla_{TEM} genes were sequenced using the Illumina-MiSeq platform. After sequencing, the pre-assembled genomic DNA sequences were annotated using the Prokka software. A complementary genome analysis was performed using the Fast Annotation Subsystem technology (RAST). All eight (08) of *P. rettgeri* isolates, 08 (eight) were harboring the bla_{NDM} gene and showed resistance to meropenem. The MIC values, performed by the plaque growth test ranged from 8-128 µg/mL for the antimicrobial meropenem. A partial genomic characterization for the strains *P. rettgeri* PR01 and *P. rettgeri* PR02 using RAST serve indicated a wide range of genes related to efflux pumps of antimicrobial drugs, as genetic systems were characterized, such as multiple drug extrusion (MATE), the and the large family of the facilitator (MFS), in which a total of 91 genes were identified that were related to the virulence, disease and defense subsystem.The partial genomic analysis of *P. rettgeri* PR01 and *P. rettgeri* PR02 confirmed the presence of the bla_{NDM-1} gene and other genes for β-lactam resistance, such as bla_{TEM}. In addition, several genetic systems were identified for the production and release of siderophores, which are associated with iron absorption, and other genes, as well as for heme ring and hemine receptor and transporters. About 43 genes were identified and expressed proteins for uptake and metabolism of iron. Genome analysis of the PR01 and PR02 strains showed a high concentration of insertion sequences, motile elements and prophages, suggesting that the species presents a considerable genetic plasticity. It was also verified the presence of several genomic islands, associated to persistence markers in relation to chemical and nutritional stress, such as the toxin and antitoxin system, containing the Pasl and Past genes. The diversity of genetic elements in *P. rettgeri* related to mechanisms of antimicrobial resistance can lead in the short term to an inefficiency of antimicrobial therapies in the fight against infections caused by this microorganism and its rise rapid as pathogen is a result of genetic plasticity.

Key words: *Providencia rettgeri*, bla_{NDM} gene, bla_{TEM} gene, antimicrobial resistance

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LISTA DE ABREVIATURAS

AcrB- Proteína de resistência à Acriflavina.

CIM- Concentração inibitória mínima.

CmeA- Sistema de efluxo RND, proteína de fusão de membrana CmeA.

CmeB- Sistema de efluxo RND, transportador de membrana interna.

FhuA - Receptor de membrana externa hidroxamato férrico fhuA.

FhuB - Transportador de hidroxamato férrico ABC FhuB componente permease.

FhuC - transportador de hidroxamato férrico ABC, Proteína de ligação de ATP.

FhuD - Transportador de hidroxamato férrico ABC, substrato periplasmático de alimentos de proteína de ligação.

KPC- *Klebsiella pneumoniae* carbapenemase.

MacA- proteína de efluxo específicos de macrólideos.

MacB- Exportação de Macrolídeos pelo ATP/ Proteína Permease MacB.

MATE_family_MDR_Pum - Proteína de extrusão antimicrobiana (Na(+) /antiporter drogas), Bombas de Efluxo Resistentes a Múltiplas drogas da família MATE.

MFS- Importante transportador de múltiplas drogas, superfamília (MFS).

PCR- Reação em cadeia da polimerase.

RAST- Anotações rápidas usando tecnologia de subsistemas.

RND - Proteína de fusão da membrana de bombas de efluxo a multidrogas

ShlA/*ShlB*- Genes de hemolisina de *Serratia marcescens.*

TolC - O tipo I de secreção de proteínas da membrana externa

Sumário

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Palavras-chave: Providencia rettgeri, blaNDM, blaTEM resistência antimicrobiana.

Artigo 1

2017

1. INTRODUÇÃO

As bactérias são micro-organismos que se caracterizam por apresentar constantes mudanças bioquímicas e fisiológicas devido a uma grande plasticidade do seu material genético (PILLAI et al., 2011). Esta plasticidade genética associada a evolução dinâmica do genoma proporciona uma resposta adaptativa celular rápida frente a pressão seletiva do meio circundante, ampliando de uma maneira significativa o repertório de espécies bacterianas que possuem amplos mecanismos para a resistência a antimicrobianos, além de um amplo espectro de fatores de virulência (PILLAI et al., 2011). Por sua vez, os efeitos das drogas antimicrobianas utilizadas para combater estes patógenos se tornam ineficazes, gerando a uma classe bacteriana conhecida como os *superbug*s (PILLAI et al., 2011).

A partir do surgimento dos "*superbugs*", foram criados dois novos conceitos com relação a características da resistência a drogas antimicrobianas. Estes conceitos se denominam como *Extensive Drug Resistance* (XDR), que se refere a isolados de bactérias que permanecem como suscetíveis a uma ou duas categorias de drogas antimicrobianas; e o termo *Pandrug Resistance* (PDR), que se refere a isolados bacterianos não sensíveis a todas as categorias de drogas antimicrobianas conhecidas (ARMBRUSTER et al., 2014).

A circulação de bactérias em ambientes nosocomiais com perfis de resistência a drogas antimicrobianas e que se enquadram tanto no padrão XDR quanto no padrão PDR tem causado uma apreessão na comunidade médica, uma vez que drogas de última escolha estão sendo ineficazes para o tratamento de pacientes com infecções graves (ARMBRUSTER. 2014).

Dentre as drogas antimicrobianas de última escolha, os carbapenêmicos são uma classe bem distinta de fármacos, principalmente introduzidos na antibioticoterapia de uso restrito em hospitais (OLAITAN. 2015).

Os carbapenêmicos são utilizados principalmente para o tratmento de infecções causadas por linhagens de bactérias da família Enterobacteriaceae multirresistentes a drogas e produtoras de β-lactamases de espectro extendido (ESBL, do inglês *Extended spectrum beta-lactamase*) (OLAITAN. 2015). Entretanto, o surgimento de resistência bacteriana aos carbapenêmicos tem sido cada vez mais

relatado entre as espécies de bactérias da família Enterobacteriaceae, sendo uma questão de grande preocupação na clínica médica (OLAITAN., 2015).

A resistência bacteriana aos carbapenêmicos e cefalosporinas de uso clínico observada em espécies de bactérias da família Enterobacteriaceae está relacionada principalmente com a expressão das enzimas serino-β-lactamases, das quais a uma das mais importantes, é a enzima *Klebsiella pneumoniae carbapenemase* (KPC) (CORDOVA., 2015) A enzima KPC foi detectada pela primeira vez no ano 2000 uma estirpe de *Klebsiella* na Carolina do Norte, nos Estados Unidos (CORDOVA 2015). Até o presente momento o gene blaKPC-2, e suas variantes foram detectado em todos os países, se tornando endêmico em praticamente todas as regiões (POIREL., 2010).

As enzimas do tipo KPC são classificadas no *grupo funcional 2f de Bush e* conferem resistência a todos os tipos de penicilinas, diversas cefalosporinas, monobactâmicos e carbapenêmicos (NORDMAM 2009). As enzimas carbapenemases do tipo KPC constituem um dos mecanismos de resistência a carbapenêmicos mais relevantes em espécies de bactérias da família Enterobacteriaceae. Sendo, que atualmente, os genes codificantes para enzimas KPC, são classificados em 21 variantes, todas estas variantes foram detectados em linhagens *K. pneumoniae* e é um dos mais distribuídos em todo o mundo (NAAS., 2008)..

Na América do Sul, a ocorrência do gene *bla*$_{KPC}$ em linhagens bacterianas obtidas de amostras clinicas é atualmente considerada endêmica, e sua distribuição ocorre em quase todas as regiões (ROSSI et al., 2012). Ademais, na América do Sul existe uma alta prevalência para o gene *bla*$_{KPC-2}$, em países como Colômbia, Argentina e Brasil, quando se analisa espécies de bactérias com perfil de resistência a multidrogas (MDR) obtidas de surtos hospitalares, sendo que as espécies mais frequentemente detectadas são *Klebsiella pneumoniae*, *Acinetobacter baumanni* e *Pseudomomas aureuginosa* (RIBEIRO., 2016). Entre as espécies transportadoras do gene *bla*$_{KPC}$ menos frequentes estão *Serratia marcescens* e *Enterobacter cloacae* (RIBEIRO., 2016).

Além da enzima KPC, várias espécies de bactérictas Gram-negativas

expressam metallo-β-lactamases (MβLs). As MβLs são enzimas que apresentam um largo espectro de atividade de hidrolise de antibióticos β–lactâmicos, como penicilinas, cefalosporinas (SAVARD. 2014), tendo a necessidade de cations divalentes (Zn++) como co-fatores enzimáticos, sendo inibidas pela ação de agentes quelantes ou por componentes derivados de tiois como o ácido tiolático ou ácido 2-mercaptopropiônico (2-MPA) (MENDES et al., 2006).

As MβLs estão classificadas no grupo funcional 3 de Busch e apresentam-se subdivididas em 3 subgrupos (A, B e C). Dentre os tipos de MβLs adquiridas, as de maior importância para a disseminação epidemiológica e relevância clínica são as enzimas IMP (imipenemase metallo-β-lactamase), VIM (Verona integron-borne metalo-β- lactamase), SPM (São Paulo metallo-ß-lactamase), e NDM (Nova Delhi metallo-β- lactamase) (MOOSAVIAN; RAHIMZADEH, 2015). Dentre as MβLs, a enzima NDM-1 constitui atualmente uma preocupação nos ambientes hospitalares devido à sua tendência à disseminação intercontinental (CUZON et al., 2013).

As MβLs conferem resistência a diferentes carbapenêmicos, como imipenem, meropenem e ertapenem, os quais se constituem em um suporte fundamental no tratamento de infecções bacterianas resistentes aos demais antibióticos de primeira escolha. As MßLs são enzimas produzidas intrinsecamente por algumas bactérias como *Bacillus cereus, Chryseobacterium meningosepticum* e *Stenotrophomonas maltophilia* (WOODFORD et al., 2005; CHEN et al., 20015). Entretanto, desde o início da década de 1990, genes que codificam MßLs têm sido descritos com grande frequência em bactérias isoladas de amostras clinicas e implicadas em infecções hospitalares, como *Acinetobacter* spp., *Pseudomonas* spp (CAMPOS. 2015).

A enzima NDM-1 e suas variantes são carbapenemases do tipo MßL capaz de inativar todos os antimicrobianos da classe dos β-lactamâmicos, sendo amplamente distribuída entre as bactérias Gram-negativas (FOMDA. 2014). O alelo do gene NDM possui atualmente 17 variantes distribuídas entre várias famílias de bactérias Gram-negativas, e são responsáveis por desencadear um maior nível de resistência bacteriana aos β-lactamâmicos (DORTET, 2014) Este padrão se deve a capacidade destas enzimas em inativar praticamente todos os antibióticos β-lactâmicos, pois a existência do gene confere um padrão de resistência a multidrogas (MDR) (DORTET., 2014). A enzima NDM codificada pelo gene *bla*$_{\text{NDM-1}}$, foi primeiramente detectada em

uma linhagem de *Klebsiella pneumoniiae isolada a partir de amostras clínicas de um paciente sueco que tinha sido anteriormente hospitalizado na Índia* em 2009 (YONG., 2009).

Até o momento no Brasil, foram identificadas três linhagens de bactérias de espécies distintas que transportam o gene *bla*$_{\text{NDM-1}}$. Todos esses isolados são pertencentes às espécies *Enterobacter hormaechei*, *Providencia rettgeri* e *Acinetobacter baumannii* (CARVALHO-ASSEF., 2013, CARVALHO., 2014). Todas as linhagens bacterianas foram isoladas na cidade de Londrina, no sul do Brasil. Em qualquer caso, o modo de aquisição de isolados portadores do gene *bla*$_{NDM-1}$ por pacientes nestes estudos não está claro.

P. rettgeri é uma espécie de bactéria patogênica considerada emergente, no mundo e algumas estirpes isoladas de algumas amostras clínicas tem apresentado o gene *bla*$_{\text{NDM-1}}$. Os primeiros relatos de isolados de *P. rettgeri* de origem clínica portadores do gene *bla*$_{\text{NDM-1}}$ ocorreram em 2008 em hospitais em Israel (ROLAIN., 2010). A partir de 2012, observa-se um aumento da detecção do gene *bla*$_{\text{NDM-1}}$ em *P. rettgeri* principalmente em linhagens isoladas de pacientes de hospitais do Nepal (TADA. 2013), e em 2013 na Colômbia foi notificada a presença do gene *bla*$_{\text{NDM-1}}$ em uma estirpe de *P. rettgeri* nomeada de RB151, isolada da amostra de urina de uma paciente de 53 anos (MARQUEZ-ORTRIZ. 2017). Com relação aos isolados de *P. rettgeri* de Israel, foi observado uma divergência filogenética entre as linhagens, demostrando que existe uma ampliação de clones não relacionados aos portadores do gene *bla*$_{\text{NDM-1}}$ (GEFEN 2013).

No Brasil recentemente foram detectadas linhagens de *P. rettgeri* portadoras do gene *bla*$_{\text{NDM-1}}$ em dois indivíduos no estado do Rio Grande do Sul, sendo um paciente colonizado e outro infectado. Sendo que a análise molecular foi conduzida pela Fundação Oswaldo Cruz (Fiocruz/RJ) (BRASIL, 2013). Considera-se então, que *a detecção de estipes bacterianas portadoras do gene NDM no Brasil são esporádicas até o momento. Diferentemente da presença do gene* bla$_{KPC}$*, que se tornou endêmica (*CARVALHO-ASSEF et al., 2013, RIBEIRO et al., 2016).

2. Gênero *Providencia*

O gênero *Providencia* é constituído de bactérias Gram-negativas pertencentes à família Enterobacteriaceae*. Sendo* bacilos residentes no solo, águas poluídas presentes em estações de tratamento de esgotos e em águas residuais (CLIFORD et al, 2012). As espécies que compõem o gênero *Providencia* podem ser isolados a partir de uma ampla gama de organismos vivos, sendo considerado para seres humanos microrganismos patógenos oportunistas (SHIMA et al., 2016). Dentre as espécies do gênero, *Providencia alcalifaciens* é responsável por causar infecções agudas no trato gastrointestinal e urinário, mais frequentemente em crianças e em pacientes com imunodeficiências ou que estejam sobre tratamento com imunossupressores após cirurgias (CHOI et al., 2017).

As primeiras espécies do gênero *Providencia* foram primeiramente descritas em 1920 por Ornstein, que as classificou como *Bacillus inconstans*. Em 1943-1946, Stuart isolou culturas bacterianas puras a partir de amostras de fezes de pacientes com infecções do trato gastrointestinal. Estes micro-organismos foram nomeados de "paracolon 29911". Em 1944, Gomes descreveu a espécie *Eberthella alcalifaciens*. Em 1952, Kauffmann e Edwards reclassificou este grupo como gênero *Providencia* a partir da observação das características bioquímicas especificas e sorológicas. Durante a década seguinte, a posição de bactérias do gênero *Providencia* na classificação taxonômica e suas relações com outros gêneros estreitamente relacionados como *Proteus e Morganella* foram revistas várias vezes culminando com a transferência de espécies de bactérias destes gêneros para gênero *Providencia* (O'HARA et al., 2000).

No ano de 1962, o gênero *Providencia* foi aceito como um gênero independente, e incluiu em conjunto com o gênero *Proteus*, à tribo Proteae; depois, o gênero *Morganella* foi anexado à tribo. Dois bio-grupos de *Providencia* foram descritos por Ewing e reconhecidas como as espécies *Providencia alcalifaciens* e *Providencia stuartii* (O'HARA et al., 1999).

As mais recentes mudanças na taxonomia em *Providencia* ocorreu após a introdução de hibridação DNA-DNA para a classificação de espécies bacterianas. Com base nas semelhanças no genoma, *Proteus rettgeri* foi reclassificado como *Providencia rettgeri* e *Providencia alcalifaciens (*FARMER et al., 1977)*,* o biogrupo 3 tornou-se uma espécie separada nomeada de *Providencia rustigianii (*HICKMAN-BRENNER et al., 1983). Em 1986, Muller, enquanto estudava bactérias isoladas de fezes dos pinguins, descreveram uma nova espécie, *Providencia heimbachae;* mais tarde, uma estirpe desta espécie foi também encontrada em um paciente com diarreia idiopática (O'HARA et al., 1999). Em 2006, uma nova espécie, *Providencia vermicola*, foi proposto para as estirpes que infectam formas juvenis de um nematóide entomopatogênico (SOMVANSHI et al., 2006). Já, em 2009, representantes de duas novas espécies, *Providencia sneebia* e *Providencia burhodogranariea*, foram isoladas de hemolinfa de moscas de fruta (JUNEJA et al., 2009). Em 2013, uma nova espécie denominada de *Providencia thailandensis,* foi descoberta após a obtenção de amostras de água em um sistema de tratamento de efluentes de uma fábrica de frutos do mar na província de Songkhla, na Tailândia (KHUNTHONGPAN et al., 2013). Deste modo, o número de espécies do gênero *Providencia* aumentaram para nove espécies reconhecidas pela taxonomia clássica.

O gênero *Providencia* é formado por bacilos Gram-negativos produtores de urease e pertencentes a família *Enterobacteriaceae.* Algumas espécies do gênero *c*ontribuem para uma serie de infecções humanas, destacando, entre elas as espécies *Providencia stuartti* e *Providencia rettgeri* (PILLAI. 2011). A espécie *P. rettgeri* pode ser encontrada em diversos ambientes como água, solo e ainda habitando tecidos de plantas (PILLAI. 2011). *P. rettgeri* também faz parte da microbiota normal do intestino de humanos. Frequentemente tem sido relatado a associação de *P. rettgeri* com infecções das vias urinarias, e em alguns casos estas infecções estão associadas a quadros de gastroenterite e bacteremia (OLAITAN. 2015).

P. rettgeri é considerada uma bactéria patogênica emergente que pode apresentar uma elevada taxa de resistência a agentes antimicrobianos comumente empregados na clínica médica (OLAITAN 2015). *P. rettgeri* apresenta resistência intrínseca aos antibióticos polimixinas B e E, que são drogas antimicrobianas de

última escolha para o tratamento de infecções causadas por bactérias resistentes a antibióticos β-lactâmicos (OLAITAN. 2015), essa resistência no ambiente hospitalar vem se tornando um evento de grande preocupação, principalmente pois tais genes relacionados a resistência se encontram em plasmídeos moveis.

Dentre as espécies clinicas do gênero *Providencia*, a espécie *P. rettgeri* tem emergido nas duas últimas décadas como bactéria patogênica nosocomial, que frequentemente causa infecções do trato urinário em pacientes hospitalizados e recentemente foi relacionada a disseminação de genes de resistência por transferência plasmidial (LAHLAOUI.2014).

P. rettgeri é uma bactéria com motilidade, capaz de crescer em agar MacConkey, e catalisar a dissociação da ureia em amônia e dióxido de carbono, além de desaminar a fenilalanina e de produzir gás a partir da fermentação de glicose. No entanto, a maioria das linhagens são não fermentadoras de lactose, *uma característica importante utilizada para classificar micro-organismos no* gênero *Providencia (*FARMER et al., 1977).

Os primeiros membros da espécie *P. rettgeri* foram isolados por Leo F. Rettger do *Sheffield Laboratory* da Universidade de Yale. Esses isolamentos bacterianos foram realizados como parte de uma investigação epidemiológica sobre uma epidemia de cólera de aves em 1904 (O'HARA et al., 2000). Entretanto, os micro-organismos *não foram caracterizados até o ano de 1918 quando Phillip Hadley realizou uma avaliação superficial do gênero e propôs o nome de Bacterium rettgeri* para se referir a uma nova estirpe produtoras de uréase (O'HARA et al., 2000). Em 1943, Rustigian e Stuart recomendaram a inclusão de *Bacterium rettgeri* no gênero *Proteus, sendo denominada de Proteus rettgeri*, com base em características bioquímicas comuns (STUART. 1945).

A primeira descrição de uma infecção humana provocada por *P. rettgeri* foi publicado em 1951 (Goldfarb E Bakey, 1951). Este relatório, de Goldfarb e De Bakey, descreve um caso de empiema (pleurite purulenta) associada a *P. rettgeri*. Entretando, as primeiras descrições de linhagens de *P. rettgeri* resistentes a drogas antimicrobianas só foram relatadas já em 1971 (TRAUB. et al., 1971), e a notificação de surtos hospitalares relacionados à *P. rettgeri* resistente a antibióticos em 1974,

com a identificação da espécie entre os pacientes de uma enfermaria cirúrgica (TRAUB.1974).

O segundo grande surto de *P. rettgeri* foi relacionada a infecções do trato urinário relatada por Edwards e colaboradores, em 1974 (EDWARDS et al., 1974). Mesmo com a *P. rettgeri* implicada na etiologia em infecções do trato gastrointestinal em 1986, diarreia em um viajante em 2004, e em casos de infecção ocular em 2006 (YOH et al., 2005; KOREISHI et al., 2006).

Com relação à susceptibilidade antimicrobiana, *P. rettgeri* é uma bactéria tipicamente resistente à gentamicina, a colistina e a tobramicina, mas susceptível à amicacina. Estirpes de *P. rettgeri*, produtoras de enzimas beta-lactamase de espectro estendido (ESBL) foram relatadas com muita frequência na Europa Oriental (MARCHANDIN et al., 1999). A detecção de estirpes de *P. rettgeri* portadoras da enzima NDM-1 foram relatados na América do Sul a partir de 2013 (CARVALHO-ASSEF et al., 2013)

O primeiro relato de uma estirpe de *P. rettgeri transportando o gene bla$_{NDM}$ foi notificado a partir de 2013 em Porto Alegre/RS, região Sul do Brasil. Esta estirpe foi obtida de uma amostra de ferida do dedo de paciente diabético com doença vascular periférica* (CARVALHO-ASSEF et al., 2013). O segundo relato de uma linhagem *P. rettgeri* NDM-positiva também foi obtida de um paciente hipertenso de 55 anos internado em um hospital público com cuidado terciário (Hospital Heliópolis) na cidade de São Paulo, para sofrer amputação do 4º dedo devido à complicação da osteomielite (CARMO. 2015).

3. Carreamento do gene *bla*$_{NDM}$

Alguns plasmídeos carreadores do gene *bla*$_{NDM}$ e de suas variantes genéticas têm sido extensivamente caracterizados em espécies da família *Enterobacteriaceae (YONG 2009).* O histórico de descrições para o carreamento do gene *bla*$_{NDM}$ mostra uma ampla variação no contexto genético para o gene *bla$_{NDM}$* que estão alocados em plasmídeos *(YONG 2009).* Os genes das variantes da enzima NDM são translocados por vários tipos de plasmídeos em espécies de *Enterobacteriaceae*, como *Inc* (WAILAN 2014), IncF (HISHINUMA 2013), *Inc*L/M (HO 2011), *Inc*H (VILLA 2012), IncN (SCHULTZ 2017), e IncX (WANG 2014). Entretanto, observa-se que existe uma

variação sobre os mecanismos de replicação nestes plasmídeos e também uma elevada diversidade de sequências de inserção nestes segmentos genéticos. Para os plasmídeos encontrados nas espécies de *Enterobacteriaceae* que carreiam o gene *bla*$_{NDM}$, existe duas características predominantes. Em primeiro lugar, o gene *bla*$_{NDM}$ é frequentemente associado ao transposon Tn125 de 10.099 pb, este possui dois elementos flanqueadores denominados de *ISAba125*, que são sequências de inserção (PARTRIDGE. 2012).

A estrutura do transposon Tn125 contendo o gene *bla*$_{NDM}$ em *Enterobacteriaceae* é frequentemente truncada em vários comprimentos (SCHULTZ. 2017). Em segundo lugar, a sequência flanqueando a estrutura Tn125 envolve vários mecanismos de aquisição de genes, incluindo diferentes elementos de transposição, como integrons de classe 1, sequências de inserção flanqueadoras (IS), elementos de transposição de repetição inversa em miniatura (MITEs) (WAILAN 2016). Estas características do ambiente genético do gene *bla*$_{NDM}$ têm contribuído para os diferentes contextos genéticos do gene *bla*$_{NDM}$ relatados até o presente momento, mesmo considerando o mesmo tipo de plasmídeo transportador (WAILAN. 2015).

O transporte do gene *bla*$_{NDM}$ por plasmídeos em *P. rettgeri* foi recentemente caracterizado em algumas linhagens bacterianas de origem clínica. Contudo, ainda existem poucos estudos que enfocam o contexto genético de genes de metalo-β-lctamases em *P. rettgeri*. Em um estudo utilizando como modelo a linhagem H1736 foi possível verificar a existência de 5 plasmídeos simultaneamente na bactéria, sendo que o plasmídeo transportador do gene *bla*$_{NDM}$ apresentava um tamanho de 48.5-kb e foi relacionado ao plasmídeo pPrY2001 (*GenBank* número de acesso: KF295828.1) (OLAITAN. 2015). Por sua vez, outra linhagem de origem clinica denominada de *P. rettgeri* RB151 isolada de amostra clínica de um paciente da Colômbia em 2013, teve o seu genoma sequenciado e caracterizado recentemente, nesta linhagem o transporte do gene *bla*$_{NDM}$ foi relacionado com o plasmídeo pRB151 com tamanho de 1.08 Kb (MARQUEZ ORTIS 2017). Além disso, estes estudos evidenciaram a presença de outros elementos genéticos móveis, como genes de bacteriófagos associados ao genoma de linhagens de *P. rettgeri.* Estes genes associados às sequências de inserção estão ligados a uma extensa transferência de genes por eventos de transferências horizontais. Estas inserções no genoma de *P. rettgeri* tem contribuído para as alterações genéticas e a evolução da patogenicidade desta espécie bacteriana (OLAITAN 2015).

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Artigo 2

2017

Introdução

O gênero *Providencia* faz parte da família Enterobacteriaceae e alberga bacilos Gram-negativos móveis produtores de urease. Atualmente o gênero *Providencia* é composto por nove espécies nomeadas*: P. alcalifaciens, P. stuartii, P. rettgeri, P. rustigianii, P. heimbachae, P. vermicola, P. sneebia, P. burhodogranariea, e P. thailandensis* (Shima et al., 2016)*.* Algumas espécies do gênero *c*ontribuem para uma série de infeções humanas, destacando-se, entre as espécies *Providencia stuartti* e *Providencia rettgeri* (Washington; Barnhill, 2015).

A espécie *P. rettgeri* pode ser encontrada em diversos ambientes como água, solo e ainda habitando tecidos de plantas*,* fazendo também parte da microbiota normal do trato gastrointestinal humano (Clifford et al.; 2012). *P. rettgeri* tem sido implicada em infecções das vias urinarias, e em alguns casos estas infecções estão associadas a quadros de gastroenterite e bacteremia (Yoh et al., 2005; Tada et al., 2014)***.*** *P. rettgeri* é considerada uma bactéria patogênica emergente e que pode apresentar uma elevada taxa de resistência a agentes antimicrobianos comumente empregados na clínica médica (Tshisevhe et al., 2017). *P. rettgeri* apresenta resistência intrínseca aos antibióticos polimixina B e E (colistina), que são drogas antimicrobianas de última escolha para o tratamento de infecções causadas por bactérias resistentes a antibióticos β-lactâmicos, como carbapenêmicos (Olaitan et al., 2016).

P. rettgeri é uma espécie bacteriana que tem sido descrita nos últimos anos como um micro-organismo importante para a disseminação do gene *New Delphi Metallo-β-lactamase* (comumente chamada de bla_{NDM}) na América do Sul (Carvalho-Assef et al, 2013; Marquez-Ortiz, 2017). As enzimas classificadas como NDM, são caracterizadas como carbapenemases, que atualmente possuem 16 variantes detectáveis em bactérias Gram-negativas. Tais enzimas são capazes de inativar alguns dos antibióticos da classe dos β-lactâmicos (Khan; Maryam; Zarrilli, 2017), sendo que as NDM´s são amplamente distribuídas entre as bactérias Gram-negativas, e são responsáveis por desencadear um maior nível de resistência bacteriana aos antimicrobianos (Khan; Maryam; Zarrilli, 2017).

A enzima NDM-1, que é codificada pelo gene *bla*$_{NDM-1}$, foi primeiramente detectada em linhagens de *Escherichia coli* e *Klebsiella pneumoniae* isoladas a partir de amostras clínicas de um paciente sueco, cujo o histórico médico demonstrava sua hospitalização na Índia no ano de 2009 (Pillai; Mcgeer; Low, 2011). A disseminação do gene *bla*$_{NDM-1}$ e suas variantes apresenta um desafio para profissionais de saúde sobre como lidar com pacientes infectados (Olaitan et al., 2016).

A alta mobilidade do gene *bla*$_{NDM}$ está relacionada com os mecanismos de transferência horizontal de genes (THG), que ocorre principalmente por via plasmidial (eventos de conjugação), atrelado ao encontro das bactérias no ambiente (Rolain; Parola; Cornaglia, 2010). Estes genes de resistência são facilmente mobilizados devido a sua localização no material genético móvel (MGEs), como o trasnposon Tn125 contendo 10092pb, também encontrado na espécie *Acinetobacter baumannii* (Poirel et al., 2012). Germinalmente estes encontros contribuem bastante para a sobrevivência bacteriana (Jackson et al., 2011). O gene *bla*$_{NDM-1}$ já foi detectado nos plasmídeos pMR0211 em *P. stuartii* (Gann et al., 2012), e nos plasmídeos M15628 e pPrY2001 portados por *P. rettgeri* (Mataseje, 2014). Entretanto, o gene *bla*$_{NDM-1}$ em algumas linhagens bacterianas pode estar integrado ao cromossomo bacteriano, como evidenciado em linhagens de *P. rettgeri* (Gefen-Halevi et al., 2013).

Após sua descrição em 2009, o gene *bla*$_{NDM-1}$ foi identificado em bactérias isoladas de amostras clínicas de pacientes de hospitais do Reino Unido, Índia e outras regiões do globo, principalmente em isolados de *E. coli e K. pneumoniae* (PillaI; McGeer, Low, 2011). No Brasil, em 2013 foram detectadas linhagens bacterianas portadoras do gene *bla*$_{NDM-1}$ em amostras clínicas de dois pacientes de um hospital do estado do Rio Grande do Sul, estirpe: CCBH11880 com número de acesso no *GenBank*: GCA000805715.1 (Carvalho-Assef et al., 2013). A segunda detecção do gene *bla*$_{NDM-1}$ em espécies de bactérias circulantes em pacientes no Brasil foi reportada no estado de São Paulo. Nesta descrição um paciente estava colonizado e outro infectado por *P. rettgeri* (Carmo-Junior et al., 2015).

Este trabalho teve como objetivo a caracterização dos genes e mecanismos moleculares envolvidos na disseminação de resistência à carbapenêmicos e outras drogas antimicrobianas em isolados clínicos de *Providencia rettgeri.* Bem como caracterizar os genes relacionados a virulência em duas linhagens de *P. rettgeri* denominadas de PR01 e PR02 a partir de sequenciamento parcial do genoma.

Material e Métodos

Obtenção e identificação dos isolados bacterianos

Neste estudo foram avaliadas 8 (oito) linhagens de *Providencia rettgeri*, obtidas de hemoculturas e amostras de urina de pacientes atendidos em hospitais do estado do Maranhão. Estes micro-organismos foram fornecidos pelo serviço de rotina do Laboratório de Análises Clinica Cedro, localizado na cidade de São Luis-MA.

A identificação da espécie bacteriana foi obtida pelo sistema MALDI-TOF MS (*Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry)* utilizando o sistema Biotyper (Bruker, Billerica, MA*).* A célula das bactérias foram cultivadas em placas de meio ágar TSB (Himedia, India), durante 24 h, a 37 °C. Para o teste, uma amostra da colônia foi transferida com auxílio de uma alça bacteriológica calibrada de 1 µL para uma lamina metálica de modo a apresentar uma fina camada sobre a placa de detecção, e seguida, foram adicionados a amostra 1 µL de uma solução de matriz (ácido α-ciano-4-hidroxicinâmico). As amostras foram submetidas à incidência de um feixe de laser para extração dos peptídeos ribossomais energizados. Finalmente, os espectros de massa adquiridos para cada linhagem bacteriana foram comparados com os espectros de massa conhecida contidas no software para classificação (Versão 3.1, Library 1.0).

O perfil de suscetibilidade a drogas antimicrobianas das linhagens bacterianas foi determinado com os cartões AST Nº 105 para o sistema automatizado VITEK 2 (BioMerieux SA, Marcy-l'Etoile, França). Utilizando os antibióticos, amicacina, ampicilina, ampicilina/sulbactam, cefepima, ceftazidima, ceftriaxona, cefuroxima, cefuroxima axetil, ciprofloxacina, ertapenem, gentamicina, imipenem, meropenem, piperacilina/tazobactam. As análises de suscetibilidade foram feitas de acordo com as recomendações do fabricante e de acordo com as normas do *Clinical Laboratory Standards Institute* (CLSI ,2016). As bactérias foram estocadas em caldo BHI

acrescido de 20% de glicerol e armazenadas em criotubos à temperatura de -80 ºC.

Identificação molecular dos genes *bla*$_{KPC}$, *bla*$_{NDM-1}$, *bla*$_{TEM}$, *bla*$_{SHV}$ e *bla*$_{AMPC}$

Extração do DNA e PCR

Para a amplificação dos fragmentos dos genes alvos relacionados às enzimas β-lactamases, foram utilizadas culturas bacterianas obtidas a partir de um crescimento bacteriano a 37ºC por até 18 horas em meio líquido BHI (Difco, Detroit, MI, USA). Após a incubação, 500 µL da cultura foi centrifugada a 10.000 rpm por 20 minutos para obtenção do pellet para extração de DNA utilizando kit "Wizard® Genomic DNA Purification" (Promega Corporation, Madison, WI USA), seguindo-se o protocolo original do fabricante. O DNA genômico foi quantificado em Nanodrop™ 1000 a 260 e 280 nm e utilizado para as reações de amplificação de fragmentos de genes relacionados a resistência aos β-lactâmicos. As reações de PCR foram realizadas utilizando-se um par de específico de iniciadores (*primers*) em um volume final de reação de 25 µL, contendo 12,5 µL de uma solução de GoTaq® Green Master Mix (Promega, Madison, WI, USA). As sequências dos iniciadores específicos que foram utilizados estão neste estudo estão listadas na Tabela 1.

Sequenciamento genômico

As reações de amplificação foram conduzidas de acordo com métodos padronizados pelos seguintes autores: Cunningham et al. (2013), Liu et al. (2012), Khalilzadegan et al., (2015) e Dallenne et al. (2010). Os produtos de PCR foram separados em gel de agarose na concentração de 1,5% e visualizados sob exposição a luz ultravioleta. Para o sequenciamento do gene *bla*$_{NDM}$, os fragmentos obtidos foram submetidos a reações de sequenciamento usando o kit DYEnamic *ET Terminator Cycle Sequencing* (GE Healthcare Life Sciences, Buckinghamshire, UK), de acordo com as instruções do fabricante. Os fragmentos foram analisados no sistema de sequenciamento automático Genetic *Analyze* ABI PRISM® 3100 (Applied Biosystems, USA).

A qualidade dos eletroferogramas das sequências obtidas durante o processo de sequenciamento foi analisada com o software ChromasPro (http://www.technelysium.com.au/chromas.html). Para o alinhamento, pelo menos três sequências consenso de cada fragmento sequenciado do tipo NDM foram

escolhidas a partir do banco de dados para alinhamentos usando MEGA 6.0 (Tamura et al., 2013). As semelhanças entre as sequências de nucleotídeos obtidas foram verificadas usando BLASTn disponível em https://blast.ncbi.nlm.nih.gov/Blast.cgi.

Para identificar as variantes do gene *bla*$_{NDM}$, todas as sequências foram traduzidas em aminoácidos usando o software ExPASy [ferramenta de tradução (http://web.expasy.org/translate/)]. A tradução correta foi escolhida com base nos dados disponíveis no *GenBank*. As sequências de aminoácidos foram comparadas com as sequências da proteína NDM obtidas pelo *GenBank* usando BLASTx. Os valores de similaridade para as sequências de aminoácidos variaram de 99 a 100%, indicando uma região altamente conservada.

Caracterização dos Grupos de Incompatibilidade dos Plasmídeos

A determinação dos grupos de incompatibilidade dos plasmídeos foi realizada de acordo com o método descrito por Carattoli et al. (2005). Utilizando 8 reações de amplificações por cadeia da polimerase de ácidos nucléicos (5 multiplex-PCR e 3 simplex-PCR). Para esta reações são testados os tipos de plasmídeos mais representativos da família Enterobacteriaceae, tais como: FIA, FIB, FIC, HI1, HI2, I1-Iγ, L/M, N, P, W, T, A/C, K, B/O, X, Y, F e FIIA. As reações de PCR foram preparadas em um volume final de reação de 25 µL, contendo 12,5 µL de uma solução de GoTaq® Green Master Mix (Promega, Madison, WI, USA), e 100 ng de de DNA molde por reação. O programa do termociclador, à exceção do que se utilizou para a reação simplex-F (cuja diferença é a temperatura de anelamento de 52 ºC), consistiu num passo inicial de 5 minutos a 94 ºC seguido de 30 ciclos de 1 minuto à 94 ºC, 30 segundos à 60 ºC e 1 min. a 72 ºC e um período de elongação final de 10 min.

Reação em Cadeia da Polimerase Multiplex-para detecção de integrons de Classe 1, 2 e 3

A caracterização dos integrons foi realizada tendo como alvos as sequencias intI1, intI2 intI3. Estas foram amplificadas pelo método de reação de PCR-Multiplex utilizando os iniciadores descritos por Goldstein et al (2001). As reações de PCR foram realizadas utilizando-se um par específico de iniciadores (*primers*) em um volume final de reação de 25 µL, contendo 12,5 µL de uma solução de GoTaq® Green Master Mix (Promega, Madison, WI, USA contendo 12,5 µL de uma solução de DNA Polimerase Martex-mix (Promega), 25 pmol de cada iniciador e 1 µL de molde de DNA (100 ng de DNA/reação). As condições de PCR foram utilizadas como descrito por Khoramrooz et al. (2016). Os produtos amplificados, 280 pb para a classe íntegron 1, 233 pb para a classe integron 2 e 600 pb para a classe *integron* 3 foram separados por eletroforese em gel de agarose a 1% contendo 0,5 µg/mL de brometo de etídio. O gel foi então fotografado sob exposição de iluminação UV.

Sequenciamento do genoma e anotações

O genoma das linhagens PR01 e PR02 portadoras dos genes *bla*$_{NDM}$ foram submetidos ao processo de montagem de dados obtidos pelo MiSeq, como auxílio do pipeline A5 (http://www.ncbi.nlm.nih.gov/pubmed/23028432). Este utiliza uma abordagem de sequenciamento *de novo* para genomas procariotos A5 (*Andrew And Aaron's Awesome Assembly pipeline*). O *pipeline* e os programas associados são de códigos abertos distribuídos sob licença GPLv3, executado em ambiente Linux, e está instalado no servidor local para análise bioinformática de Neoprospecta (Configuração: 03 servidores Linux, Core i7, 64 GB RAM, 2 TB HD).

Os genes sequenciados foram previstos utilizando como inferência de proteínas constante no BLAST (http://www.ncbi.nlm.nih.gov/). A partir dessa análise, foi identificado sequências relacionadas em outras espécies de bactérias de interesse constantes no banco de dados RAST (*Rapid Annotation using Subsystem Technology*), que é uma importante ferramenta de bioinformática para a previsão de genes putativos (acessível em http://rast.nmpdr.org).

Construção da arvore filogenética

As sequências de *Providencia rettgeri* PR01 e PR02 foram submetidas a analise ao software RNAmmer presente em: http://www.cbs.dtu.dk/services/RNAmmer (Lagesen et al., 2007) para identificação do gene ribossomal 16S. As analises foram realizadas com o *algoritmo BLAST,* utilizando-se pelo menos uma sequência do gene 16S rDNA. Algumas sequências do gene 16S rDNA de espécies do gênero *Providencia* foram utilizadas para a elaboração das relações filogenéticas. Para a determinação da raiz da Árvore (*outgroup*) foi utilizada a sequência parcial do gene 16S rDNA (RNA ribossomal) de *Serratia plymuthica* K-7 (NR_037111). As sequências obtidas das espécies bacterianas foram então alinhadas no software MEGA 7.0 (Kumar; Stecher; Tamura, 2016). Para a construção da arvore filogenética foi utilizado o método de máxima verossimilhança (*Maximum likelihood)* aplicando o algoritmo *MUSCLE (Multiple Sequence Comparison by Log-Expectation*) (Edgar; Drive; ValleY, 2004).Os valores de *bootstrap* menores que 70% foram ocultos na formação da figura da arvore filogenética.

Analise de ilhas genômicas e ilhas de patogenicidade

Os genomas das linhagens *P. rettgeri* PR01 e *P. rettgeri* PR02 foram analisados com relação a presença de ilhas genômicas, ilhas de patogenicidade (PAIs) e de resistência a antibióticos (RIs). Para estas análises, os genomas *draft* foram trabalhados utilizando *in house scripts* para a concatenação dos *contigs/scaffolds.* Para estas analises primeiramente foi uma busca por genomas de bactérias do mesmo gênero ou mais próximo possível aos genomas das linhagens *P. rettgeri* PR01 e *P. rettgeri* PR02. Nesta busca chegou-se a espécie *Providencia alcalifaciens* DSM 30120*.* As analises foram realizadas tendo *P. rettgeri* PR01 (query) e um genoma de referência, neste caso *P. alcalifaciens* (subject) para predição das ilhas genômicas. Depois de preditas as ilhas, uma figura no BRIG foi gerada, utilizando, *P. rettgeri* PR01 como referência. Nesta mesma figura, foram adicionadas as coordenadas das ilhas preditas anteriormente. Adicionalmente, foram plotados mais dois anéis correspondentes aos *contigs* do genoma de *P. rettgeri* PR01, onde, os *contigs* pares foram marcados em azul e os ímpares, em verde. Uma curadoria manual foi feita em cima dos dados gerados pelo software GIPSy. Assim, foram

identificadas PAIs (ilhas de patogenicidade), GEIs (ilhas genômicas) e ilhas mistas (MSIs) utilizando o software GIPSy. Paralelamente as ilhas genômicas de *P. rettgeri* PR01 e *P. rettgeri* PR02 foram preditas utilizando o *software* IslandViewer 4 (Bertelli et al., 2017) associado aos programas IslandPick, SIGI-HMM, e IslandPath-DIMOB.

Resultados

Determinação do perfil de suscetibilidade a agentes antimicrobianos

Neste estudo foi observado que as 08 (oito) linhagens de *P. rettgeri* designadas como PR01, PR02, PR12, PR13, PR18, PR20, PR21 e PR27 apresentaram resistência a múltiplas drogas antimicrobianas de diferentes classes (Tabela 2), amicacina e gentamicina (aminoglicosideos), resistência com CIM ≥ 16 µg/mL, cefalosporinas com CIM ≥ 8 µg/mL e carbapenemicos com CIM ≥ 4 µg/mL. Onde a PR27 foi o único isolado que apresentou um padro de sensibilidade para todos os antibióticos testados, incluindo os β-lactâmicos.

Detecção de genes relacionados a enzimas β - lactamases

Os genes $bla_{TEM,}$ $bla_{AmpC\ e}$ bla_{NDM} foram identificados nas linhagens de *P. rettgeri*. Entretanto para os genes bla_{shv} e bla_{KPC} os resultados foram negativos em todas as linhagens de *P. rettgeri*, como observado na tabela 3.

Identificação e caracterização dos grupos de incompatibilidade e integrons

Todas as linhagens de *Providencia rettgeri* apresentaram integrons de classe 1 e 2, assim como o grupo de incompatibilidade plasmidial FIIA como visto na tabela 3. Na caracterização dos grupos de incompatibilidade plasmidial, foi observado que todos os isolados de *P. rettgeri* eram portadores do *replicon* FIIA juntamente com integrons de classe 1 e 2 (Tabela 3).

Analises filogenéticas de *P. rettgeri* PR01 e *P. rettgeri* PR02

As relações evolutivas entre os isolados *P. rettgeri* PR01 e *P. rettgeri* PR02 foram determinadas pelo método da máxima verossimilhança, os resultados indicaram que as linhagens mais próximas aos isolados foram *P. rettgeri* DSM4542 *P. rettgeri* NCTC11801 (89% de *bootstrap*), estirpes já identificadas e protocoladas no genbank, apresentando uma similaridade genética com a estirpe RB151 como visto na figura 2.

Caracterização genômicas das linhagens PR01 e PR02

Os dados gerais da anotação dos genomas parciais das linhagens PR01 e PR02 estão representados na Tabela 04. A identificação das sequências genicas codificantes ou CDS (do inglês, *coding sequence*) presentes nas linhagens foi de 4425 e 4477 para as linhagens PR01 e PR02, respectivamente. Nas análises realizadas pelo RAST foram observados vários genes associados a diferentes categorias de sub-sistemas (Figuras 3,4). Contudo, neste estudo destacamos as proteínas associados a bombas de efluxo para antibióticos e biocidas, proteínas para captura de ferro, proteínas associadas a motilidade e elementos associados aos mecanismos de transferência gênica. Estes elementos foram comparados pelo BLASTn e por fim suas identidades foram então indicadas no suplemento I. Em adição, verificou-se a presença de genes associados a mobilidade do genoma tais como aqueles relacionados a proteína de mobilidades e bacteriófagos. Por fim, as análises dos genes e proteínas relacionadas também foram direcionadas ao sub-sistema relacionado ao metabolismo e captura de ferro.

Caracterização do perfil de resitência e virulência das linhagens *P. rettgeri* PR01 e *P. rettgeri* PR02

Bombas de efluxo de drogas e biocidas

Para uma análise mais especifica sobre as características genéticas das linhagens de *P. rettgeri* PR01 e PR02, estas foram caracterizadas no nível genômico após o sequenciamento de nova geração, utilizando o sistema Illumina- Miseq. Nestas análises foram identificadas 16 (dezesseis) tipos de bombas de efluxo para drogas antimicrobianas e biocidas para a PR01 e PR02 (Figuras 5 e 6).

Entre as 16 (dezesseis) bombas de efluxo presentes nas estirpes PR01 e PR02 foram identificadas a MacA (*Macrolide-specific efflux protein MacA*), MacB (*Macrolide export ATP-binding/permease protein Mac*, TolC *(RND efflux system, outer membrane lipoprotein CmeC*), AcrB (*RND multidrug efflux transporter, Acriflavin resistance protein*), MATE_Family_MDR_Pump (Multi antimicrobial extrusion protein (Na(+) / drug antiporter, MATE family of MDR efflux pumps).

Caracterização do sistema de captação de ferro

As linhagens PR01 e PR02, apresentaram 6 categorias de genes relacionados a captação e metabolismo de ferro, tendo dois grupos majoritários representados nas categorias de caputra de Heme e Hemia com 22 regiões genicas relacionadas seguido de transporte de Hemina com 14 regiões. Como visto na figura 7, possuindo genes associados as proteínas IutA, e FhuC com a localização no BLASTn de gi|490378242|WP_004257840.1 com 99% de identidade para o IutA, e dois genes para o FhuC com as respectivas localizações gi|490382157|WP_004261670.1 e gi|757595221|WP_042843418.1 ambos com 100% de identidade. Apresentando uma vasta gama de sistemas de siderophoros do tipo aerobactina e para transporte de ferro (TonB) apresentados no suplemento I.

As linhagens PR01 e PR02, possuem genes associados as proteínas iutA, e FhuC com a localização no BLASTn de gi|490378242|WP_004257840.1 com 99% de identidade para o iutA, e dois genes para o FhuC com as respectivas localizações gi|490382157|WP_004261670.1 e gi|757595221|WP_042843418.1 ambos com 100% de identidade.

Caracterização Ilhas genômicas

Nas análises de ilhas genômicas realizadas pelo programa IslandViewer 4 foi observado 22 ilhas genômicas nos genomas das linhagens PR01 e PR02 como visto nas figuras 11 e 12 com uma grande diversidade de genes relacionados a virulência bacteriana, resistência a drogas antimicrobianas e a mercúrio, sistema toxina-antitoxina, regulação genica, entre outros no suplemento II. A maior ilha genômica identificada na linhagem PR01 apresentou 114.821 pb (>10 Kb) e albergando os genes para resistência a aminoglicosídeos e β-lactâmicos. Nesta ilha genômica se encontram o gene *bla*$_{TEM}$ e *bla*$_{NDM}$, além de um gene para resolvase associada ao transposon Tn3.

Paralelamente, a análise pelo programa BRIG comparou 6 ilhas de patogenicidade com 6 estirpes, sendo 2 P.*rettgeri* e 4 P. *stuartii, com um* identidade *de 100%* como mostrado na figura 10.

Analise do mobiloma bacteriano

Sequências de inserção

Nas análises realizadas no genoma da linhagem *P. rettgeri* PR01 utilizando o *Software* ISsaga (*Insertion Sequence semi-automatic genome annotation* foram detectadas 12 (doze) tipos de sequências putativas de inserção, como visto na figuras 13 e 14, com um total de 54 elementos, sendo que a maior porcentagem para os elementos de inserção foram para IS3 com 19,64% para PR01 e 19,23% para PR02 seguido de IS5 com 12,5% para PR01 e 13,46 para PR02. Cerca de 8,93% das sequências de inserção em PR01 e 11,54 % em PR02 não foram identificadas pela base de dados, sendo denominadas de ISNCY (do inglês, IS *not classified yet*, IS não classificadas).

Também foram identificadas que cerca de 10,71% e 13,46% dos elementos de inserção em PR01 e PR02, respectivamente, pertencem ao transposon Tn3. O *transposon* Tn3 foi caracterizado com uma variação de média de 2.306 a 3.282 pb apresentando uma identidade de 99% (2892/2896) com a sequência albergada no plasmídeo pNDM15-1091 transportado por *P rettgeri* linhagem N15-01091 (*GenBank,* código: CP012903.1).

Sequencias de DNA associadas à bacteriofágos

Nas análises de sequências de CDs de bacteriófagos realizadas pelo programa PHSAST, foram observadas 6 regiões relacionados a estes elementos. Das sequências encontradas cinco estavam incompletas apresentando o tamanho de 2.4 Kb até 30 Kb, sendo relacionados a sequências encontradas nas bactérias da família Enterobacteriaceae (como por exemplo *Salmonella* spp), além de gram-positivos como *Staphylococcus* spp. A única sequência de bacteriófago intacta encontrada, foi referente ao fago (PHAGE_Salmon_RE_2010_NC_019488), uma sequência de 33.7 Kb (posição no genoma: 4233321-4267110). Esta sequência apresenta 49 CDs e a maioria destas sequências se encontram derivadas de um bacteriófago de *Salmonella* spp. (código no *GenBank* NC019488).

Elementos transponíveis

Nas análises realizadas pelo RAST, foram observados vários genes associados a elementos transponíveis ou transposons. Estes elementos tiveram suas

identidades comparadas pelo algoritmo BLASTn. As linhagens PR01 e PR02 albergam dois tipos de transposons, estes elementos são responsáveis pela transposição de proteínas, sendo eles Tn7 e Tn21, como pode ser visto no suplemento I.

Nas análises de elementos transponíveis foi possível verificar que sequências associadas ao Tn7 estão presentes em ambas as linhagens PR01 e PR02 (Suplemento I). Estas sequencias foram relacionadas com os fragmentos de 882 e 1026 pb, e estão localizados no transposon Tn7. Contudo a linhagem PR02 contém apenas uma sequência associada ao Tn21, indicado pela sequência 372 pb, já o PR01, possui três sequencias do Tn21 relacionados aos fragmentos de 372, 252 e 240 pb com suas respectivas localizações e % de identidade no BLASTn de gi|519733601|EPP24804.1 e 98% de ID, gi|1119200185|WP_072209121.1 com 100% de ID gi|1119200185|WP_072209121.1 com 99% de ID.

Discussão

Todos os isolados bacterianos foram resistentes à carbapenêmicos, como ertapenem, meropenem e imipenem. Uma característica particular destes isolados bacterianos é que eles são originários de dois hospitais localizados a uma distância 250 km. Uma vez que os carbapenêmicos estão entre as melhores opções para tratamento de infecções por de micro-organismos Gram-negativos resistentes a múltiplos drogas antimicrobianas (Johnson, Woodford, 2017; Zafer et al, 2014), evidencia-se assim uma situação preocupante para a saúde pública, onde esses micro-organismos são uma fonte comum de infecções adquiridas em hospitais (Rolain; Parola; Cornaglia, 2010). O perfil MDR é advindo de genes relacionados a bombas de efluxo, ou genes mais específicos, como aqueles codificantes para enzimas β-lactamases, como por exemplo o gene *bla*$_{NDM}$ e o gene *bla*$_{KPC}$. Estes genes são comumente encontrados em espécies de bactérias da família Enterobacteriaceae (Wu; Feng; Carattoli, 2015).

Os genes *bla*$_{TEM}$ *e bla*$_{AmpC}$ são responsáveis pela expressão de uma cefalosporinase do tipo ESBL, de uma AmpC β-lactamase, e uma metallo-β-lactamase, respectivamente. A resistência aos antibióticos amicacina, gentamicina, ampicilina, sulbactam, cefepima, ceftazidima, cetriaxona, cefuroxma, ciprofloxacina, piperacilina e tazobactam se dá pela correlação de vários mecanismos de defesa,

que os MDR`s possuem, como bombas de efluxos, e enzimas especificas (Li; PlésiaT, 2015).

O gene *bla*$_{TEM}$ expressa uma cefalosporinase do tipo ESLB, frequentemente detectado em *Escherichia coli e Klebsiella spp.* sendo todos micro-organismos Gram negativos (Oduro-Mensah et al., 2016). A presença do gene *bla*$_{TEM}$ *em P. rettgeri*, indica que há troca de material genético via transferência de elementos transponíveis moveis de maneira horizontal. Uma característica dos genes de resistência é sua associação com uma região *Cassette* dos *integrons*, região a qual está localizada entre dois sítios de recombinação (attl e attC), sítios de recombinação inicial e de finalização respectivamente, desta maneira os genes moveis podem fazer parte integral da molécula de DNA (Deng et al., 2015).

O gene *bla*$_{NDM}$ tem apresentado uma relevância clinica nos últimos anos, uma vez que este gene é responsável pela produção da enzima carbapenemase, uma metallo-β-lactamase dependente de zinco, que atua na hidrolise dos antibióticos carbapenêmicos (Galdiero et al., 2012). As carbapenemases são usualmente capazes de hidrolisar não só carbapenêmicos, mas também todos os antibióticos β-lactâmicos, como cefalosporinas, penicilinas e monobactâmicos (Lorenzoni et al., 2016).

Neste estudo foram identificados integrons de classe I e II nas linhagens de *P. rettgeri* de todas as amostras clinicas obtidas, pelo aspecto da resistência apresentada possivelmente os marcadores de resistência a β-lactâmicos estão presentes entre os sítios de recombinações dos integrons, que são comumente genes de resistência a fármacos ou genes de patogenicidades (Rajpara et al., 2015). Tais genes podem estar alocados no cromossomo uma vez que a presença dos integrons de classe I em conjunto com transposons da família Tn3 possibilitam tal inserção genica (Deng et al., 2015; Jackson et al., 2017; Rajpara et al., 2015).

O grupo de incompatibilidade FIIA detectado nas linhagens *P. rettgeri* confere um padrão único com relação a barreiras de transconjugação entre estas estirpes. O replicon FIIA (*replicon typing*) é denominado IncF ou plasmídeo conjugativo IncF é o de referência para o desenho dos iniciadores (*primers*) (Carattoli et al., 2005). Este grupo de incompatilibilidade foi identificado primeiramente em *Salmonella enterica*

(Typhimurium). O *replicon* FIIA também já foi identificado em um plasmídeo recuperado de uma linhagem de *Salmonella enterica* serovar Kentucky, isolada a partir de amostras de fezes de galinha (Fricke et al., 2009). O grupo de incompatibilidade FIIA foi relacionado com fatores de virulência, e resistência a estreptomicina e tetraciclina nestas linhagens de *Salmonella enterica* (Fricke et al., 2009). Contudo, existem poucos relatos sobre a presença do grupo de incompatibilidade FIIA em outras espécies de bactérias da família Enterobacteriaceae.

Ademais, acredita-se que a presença do *replicon* FIIA seja rara em outras espécies de bactérias Gram-negativas, contudo sua aquisição por outras espécies, como *P. rettgeri* possa ser possível, principalmente se estas espécies se relacionarem em ambientes como o trato gastrointestinal de animais como as aves ou hospedeiros humanos. Recentemente, o *replicon* FIIA foi identificado em linhagens de *Enterobacter* spp. de origem clínica (Logan et al., 2016). Estas linhagens bacterianas eram portadoras dos genes *bla*$_{\text{ACT/MIR,}}$ que conferem resistência a oxiimino-β-lactâmicos e outros antibióticos β-lactâmicos (Logan et al., 2016). Verifica-se então, que existe a possibilidade do *replicon* FIIA não ser restrito a *Salmonella* spp. como anteriormente havia se proposto, podendo circular em bactérias de outros gêneros, entretanto com menor frequência de transmissão.

As linhagens PR01 e PR02 apresentaram uma grande semelhança genética com a estirpe de *P. rettgeri* RB151 que é um patógeno transportador do gene *bla*$_{\text{NDM-1,}}$ sendo relacionada com (89% de *bootstrap*), que transporta o gene *metallo*-β-*lactamase* (Castro-Cardozo et al., 2017). A linhagem RB151 foi isolada no ano 2013, a partir uma amostra de urina de uma paciente do sexo feminino de 58 anos idade. Esta paciente foi diagnosticada com infecção do trato urinário e estava sendo atendida no serviço de emergência de um hospital na cidade de Bucaramanga, Colômbia (Saavedra-Rojas et al., 2015). O interessante é que o gene *bla*$_{\text{NDM-1}}$ presente na linhagem RB151, está albergado em um plasmídeo denominado de pRB151-NDM (Marquez-Ortiz et al., 2017), o que talvez não ocorra com as linhagens PR01 e PR02. Foi observado em uma primeira analise após um sequenciamento parcial, que o plasmídeo de PR01 (pPR01 9,8 Kb) não apresentou o gene *bla*$_{\text{NDM}}$, somente albergava gene *bla*$_{\text{TEM}}$ localizado no suplemento II. Este plasmídeo

apresentou 99% de Identidade com o plasmídeo pCR14_2 transportado por *Klebsiella pneumoniae* linhagem CR14 (ID no gene Bank: CP015394.1). O gene *bla*$_{NDM-1}$ estar integrado ao cromossomo da linhagem *P. rettgeri* PR01, como tem sido relatado anteriormente para outras espécies, já que ensaios de conjugação falharam em demonstrar a transferência horizontal entre linhagens clinicas *Escherichia coli* (NDM positivas) e a linhagem receptora permissiva *E. coli* J53 (Shaheen et al., 2013).

Analises dos subsistemas de *P. rettgeri* PR01 e *P. rettgeri* PR02

Em *P. rettgeri* PR01 e *P. rettgeri* PR02, possivelmente os sistemas MATE, TolC, MacAB, AcrB RND estão relacionadas de maneira direta a resistência a drogas antimicrobianas, tais como fluoroquinolonas (ciprofloxacina, norfloxacina, norfloxacina), rifampicina, e antibióticos macrolídeos (ritromicina, azitromicina e claritromicina), além da resistência bacteriana à cobalto e zinco, esta evidencia foi correlacionada com o padrão de resistência no teste de CIM. Uma vez que as linhagens foram resistentes a maioria dos antimicrobianos testados.

Nos genomas dos isolados PR01 e PR02 também foi possível detectar a presença de 04 (quatro) genes para β-lactamases, a quais estão relacionadas com a resistência a penicilinas ID BLASTn gi|926465406|ALD19783.1 com 100% de identidade, cefalosporinas de 1ª e 2ª geração, ID BLASTn gi|490383288|WP_004262799.1 com 99% de identidade e gi|446804399|WP_000881655.1 com 100% de identidade, de 3ª e 4ª geração ID BLASTn gi|1002048020|AMM70781.1 com 100% de identidade.

As proteínas de aquisição de ferro nos isolados PR01 e PR02 foram iutA (receptor de aerobactina), FhuB (ferrichrome permease) e FhuC (proteína de ligação a ATP), que são caracterizadas como receptores associados a captação de ferro (Cabrera et al., 2001). Também, são elementos responsáveis pelo rompimento da parede celular microbiana, consequentemente os queladores de ferro como as enterobactinas ficam liberados no espaço extracelular (West et al., 1987).

O gene FhuC já foi identificado anteriormente em algumas especies de Enterobacteriaceae, como *Edwardsiella ictaluri (*Abdelhamed et al., 2016*)* e *Yersinia enterocolitica* biovar 1 (Kanaujia; Bajaj; VIrdi, 2015). Em *E. ictaluri*, a proteína FhuC contribue para a aquisição de hidroxamate férrico *(*Abdelhamed et al., 2016*)*. A

detecção de uma grande diversidade de genes em *P. rettgeri* que são responsáveis pela produção de inúmeros elementos, como sideróforos e proteínas de membrana e transporte que contribuem para a captação e transporte de ferro, indicam que estes produtos possam ser relevantes na virulência e a rápida multiplicação desta espécie bacteriana.

Ilhas genômicas

A grande diversidade de genes adquiridos por transferência horizontal em *P. rettgeri* PR01 e *P. rettgeri* PR02, indicam uma alta resiliência da espécie com relação a sobrevivência a ambientes com condições adversas e estressantes, como por exemplo, na presença de agentes oxidantes, biocidas, além de ambientes com limitações de nutrientes.

O sistema toxina-antitoxina representado por diferentes sequências genicas no suplemento II em *P. rettgeri* PR01 e *P. rettgeri* PR02 encontrados nas ilhas genômicas podem contribuir para a formação de biofilmes em superfícies abióticas e colonização de tecidos do hospedeiro, como as vias urinárias, além da geração de células persistentes em condições inóspitas, como observado para células que sobrevivem na presença de drogas antimicrobianas (Page; Peti, 2016; Wang; Wood, 2011). Estas suposições foram levantadas, levando-se em consideração que o sistema toxina-antitoxina é um fator importante em *Escherichia coli* uropatogênica para a colonização nicho-específica (vias urinárias), resistência ao estresse provocado por ciprofloxacina, além da resistência a oxidação por nitrito de sódio e por outros intermediários reativos do nitrogênio (Norton; Mulvey, 2012).

Analise das sequencias de inserção e transposons no mobiloma bacteriano

Entre as sequencias de inserções observadas, a presença do Tn3 em ambas as linhagens PR01 e PR02 é referente a uma transposase de 1.845 pb. O transposon Tn3 tem sido relacionado a presença do gene *bla*$_{\text{TEM-1D}}$ (uma beta-lactamase class A) em algumas espécies de bactérias da família Enterobacteriaceae (Sandner-Miranda et al., 2016). As linhagens *P. rettgeri* PR01 e *P. rettgeri* PR02, caracterizadas neste estudo transportam o gene *bla*$_{\text{TEM}}$, e provavelmente existe uma boa correlação ente a presença do transposon Tn3 e a disseminação deste gene.

A contribuição das sequências de inserção para a plasticidade genética em *Providencia* spp. ainda não foi estudada profundamente, entretanto pode-se estipular que sua contribuição possa ser muito similar a observada para outras espécies de bactérias da família Enterobacteriaceae. Em *E. coli* O157 (um sorotipo enterro-hemorrágico), por exemplo, foi sugerido que os elementos IS possivelmente tenham um papel na inativação e imobilização de fagos e plasmídeos recebidos pelas linhagens bacterianas (Ooka et al., 2009).

Nas análises de CDs realizadas a presença de sequências de bacteriófagos nos genomas bacterianos, principalmente em enterobactérias, pode ser resultado da aquisição do material genético por transferência horizontal em nichos mais específicos como o trato gastrointestinal de hospedeiros animais (Huddleston, 2014). Esta suposição se baseia na evidencia sobre a existência de uma maior disponibilidade de material genético viral no lume intestinal após a sua liberação durante o ciclo lítico das bactérias neste nicho (Waller et al., 2014). Evidências experimentais utilizando PCR quantitativo para DNA de bacteriófagos presente em fezes humanas, indicam que estes elementos transportam uma grande quantidade de genes de resistência, como por exemplo genes para β-lactamases *bla*$_{\text{TEM}}$ e *bla*$_{\text{CTX-M-1}}$ (Modi et al., 2014) . Estas observações podem corroborar para dimensionar o impacto dos genomas de bacteriófagos na circulação e veiculação de genes de resistência a antibióticos pela população bacteriana (Modi et al., 2014). Por fim, acredita-se que os bacteriófagos associados aos eventos de transdução possam aumentar o aporte de mecanismos no resistoma da população bacteriana no trato gastrointestinal principalmente entre as Enterobacteriaceae, assim ter um grande impacto na evolução de patógenos emergentes, como a espécie *P. rettgeri*.

Nas análises de elementos transponíveis o transposon Tn21 detectado nas estirpes PR01 e PR02, está relacionado de maneira direta a resistência antibióticos, como os aminoglcosídeos, que pode ser observado na tabela 2, tal característica advém da presença do gene *2''-aminoglycoside nucleotidyl-transferase* ANT(2'') (Schmidt; Nucken; Henschke, 1988). O Tn21 també é relacionado ao gene *ampC*, que também se mostrou positivo nas estirpes conferindo resistência a penicilinas e cefalosporinas de 1ª e 2ª nas linhagens de *K. pneumoniae*, denominadas de LCT-KP214 e LCT-KP289 (Guo et al., 2014).

A transponase do Tn7 identificada nas estirpes é heteromérica, e se distingue das demais pela complexidade de sua transposição de inserção do sitio alvo, att Tn7, por requerer quatro proteínas, Tn7, TnsABC + D e dois DNA de substrato (Young et al., 2013). A presença de sequências no DNA em *P. rettgeri* PR01 e *P. rettgeri* PR02, relacionadas ao transposon Tn7 indica uma alta versatilidade destas linhagens na disseminação de genes de resistência a antibióticos para este micro-organismo. O *transposon* Tn7 é um elemento móvel particularmente sofisticado, e se desenvolveu em alguns micro-organismos Gram negativos, como *E. coli* e *Acidithiobacillus ferrooxidans*, que apresentam estilos de vida completamente diferentes (Oppon et al., 1998; Peters, Craig, 2001). O transposon Tn7 apresenta mecanismos alternativos para promover sua propagação entre a população bacteriana. Este elemento móvel pode-se mover para sítios de baixa frequência de inserção, como outros elementos moveis transponíveis, na medida em que transpõe para muitos sítios, sem a existência de uma sequência especifica no DNA receptor. Ainda, este elemento pode se mover de preferência para a uma sequência de inserção para o Tn7 em determinados *replicons*, preferencialmente em plasmídeos conjugativos. Esta última contribui de maneira significativa para a dispersão do Tn7 entre as populações bacterianas, acarretando assim na aquisição de genes associados à resistência a antibióticos por muitas espécies de bactérias (Peters, Craig, 2001).

Este estudo evidenciou várias características moleculares analisadas após o sequenciamento parcial do genoma de dois isolados de *Providencia rettgeri* (PR01 e PR02). Estas características que estão relacionados a capacidade destas linhagens em suportar a presença de vários antibióticos, principalmente da classe dos β-lactâmicos de uso clínico como cefalosporinas e carbapenêmicos. A presença de uma

grande diversidade de bombas de efluxo, além de enzimas inativadoras de aminoglicosídeos, β-lactamases que são expressas a partir do gene *bla*$_{NDM}$ e *bla*$_{TEM}$ estão contribuindo para a rápida disseminação e acessão de *Providencia rettgeri* em ambientes nosocomiais brasileiros, aqui em primeira instancia detectados em isolados de hospitais Maranhenses. Verificou-se também que as linhagens de *P. rettgeri* podem se adaptar a ambientes com caraterísticas diversas, principalmente no tocante a capitação de ferro e sistemas de auto-regulação, como o sistema toxina e anti-toxina. Em adição, as análises parciais do genoma indicaram ainda que esta espécie possui um genoma altamente dinâmico, composto por um mobiloma caracterizado por vários segmentos gênicos relacionados a proteínas de mobilidade e genes de bacteriófagos. Por fim, a disseminação destes elementos genéticos pode contribuir para transmissão de genes associados à virulência e resistência bacteriana a biocidas e drogas antibióticas entre outras especies de bactéria da família Enterobacteriaceae.

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Legendas de Tabelas

Legendas de Figuras

Tabela 1 Genes relacionados à enzimas -lactamases utilizados como alvo para a Reação em Cadeia da Polimerase

Gene alvo	Iniciadores para os genes de β-lactamase	Fragmento	Temperatura de anelamento °C	Referências
bla$_{KPC-2}$	F- TGTCACTGTATCGCCGTC R- TCAGTGCTCTACAGAAAACC	1011 pb	65	(Cunningham et al., 2013)
bla$_{NDM-1}$	F- CAGCACACTTCCTATCTC R- CCGCAACCATCCCCTCTT	984 pb	56	(Liu et al., 2012)
bla$_{TEM}$	F-GAGTATTCAACATTTCCGTGTC R-TAATCAGTGAGGCACCTATCTC	800 pb	56	(Khalilzadegan et al., 2015)
bla$_{SHV}$	F-AGCCGCTTGAGCAAATTAAAC R-ATCCCGCAGATAAATCACCAC	713 pb	56	(Dallenne et al.,et al., 2010)

Tabela 2 Perfil de suscetibilidade das linhagens de *Providencia rettgeri* a diferentes antibióticos

	Linhagens de *Providencia rettgeri*							
Antibiotico(S)	P(R)01	P(R)02	P12	P13	P18	P20	P21	P27
Amicacina	16 (S)	16 (S)	16 (S)	≥64 (R)	16 (S)	8 (S)	16 (S)	≤4 (S)
Ampicilina	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥16 (S)
Sulbactam	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	ND
Cefepima	≥64 (R)	16 (S)	≥64 (R)	4 (S)	≥64 (R)	≤1 (S)	≤1 (S)	8 (S)
Ceftazidima	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≤0.5 (S)
Ceftriaxona	8 (S)	16 (S)	≥64 (R)	≥64 (R)	16 (S)	2 (S)	≥64 (R)	8 (S)
Cefuroxima	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	ND
Ciprofloxacina	≥4 (R)	1 (S)	≥4 (R)	≥4 (R)	1 (S)	≤0.25 (S)	≥4 (R)	>2 (S)
Ertapepenem	4 (R)	4 (R)	≥8 (R)	≥8 (R)	≥16 (R)	≥8 (R)	4 (R)	≤0.25 (S)
Gentamicina	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	1 (S)	>8 (S)
Imipenem	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≤1 (S)
Meropenem	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	8 (S)	≤0.25 (S)
Pieracilina/Tazobactam	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≤4/4 (R)

Tabela 3 Caracterização molecular dos mecanismos de resistência em linhagens de *Providencia rettgeri*

Marcadores de Resistencias	Linhagens de *Providencia rettgeri*							
	p3	p11	p12	p13	p18	p20	p21	p27
*bla*NDM	P	P	P	P	P	P	NC	NC
*bla*SHV	N	N	N	N	N	N	N	N
*bla*KPC	N	N	N	N	N	N	N	N
*bla*TEM	P	P	P	P	P	P	P	P
*bla*AMPC	P	P	P	P	P	P	P	P
Plasmídeos	FIIA5	FIIA5	FIIA5	FIIA5	FIIA5	FIIA5	FIIA5	FIIA5
Integrons	Classe 1 e 2	Classe 1 e 2	Classe 1 e 2	Classe 1 e 2	Classe 1 e 2	Classe 1 e 2	Classe 1 e 2	Classe 1 e 2

Tabela 4 Características da montagem do genoma das linhagens *Providencia rettgeri* PR01 e PR02 indicadas pelo RAST

Características	Linhagens	
	PR01	PR02
Tamanho	4.734,158	4.665,741
Conteúdo de GC	41.2	41.5
N50*	27355	102640
L50*	51	13
Número de sub-sistemas	367	510
Número de se sequências codificantes	4425	4477
Número de RNase	88	89

Figura 1- Detecção do gene blaNDM em linhagens de *Providencia rettgeri*, fragmento de 984 pb

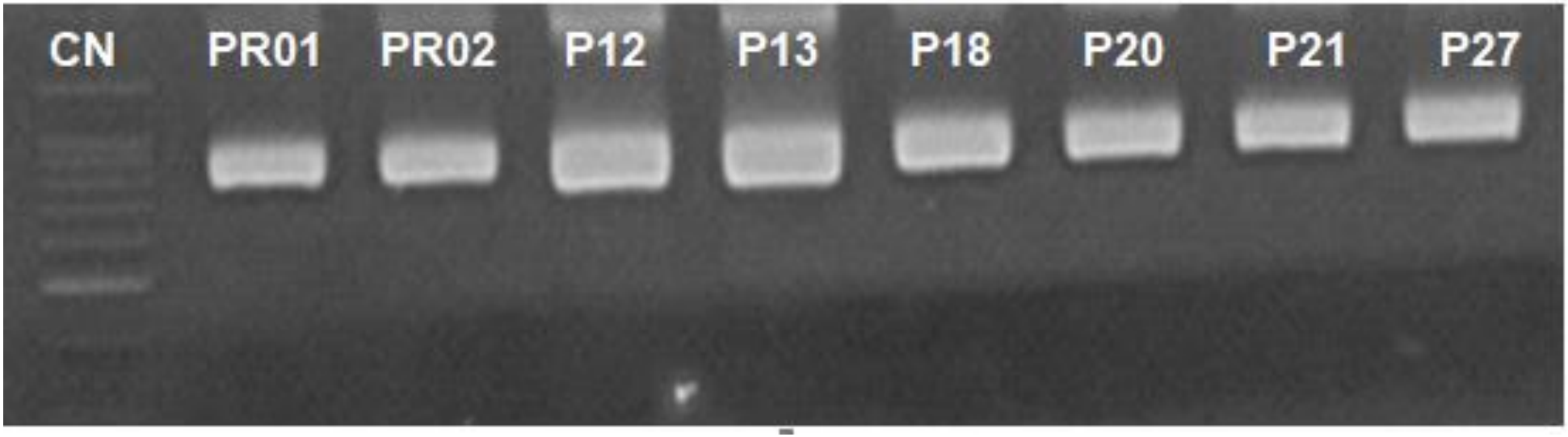


Figura 2-Analises de filogenia molecular das linhagens *Providencia rettgeri* PR01 e *Providencia rettgeri* PR02, pelo método de máxima verossimilhança. A porcentagem em que os taxa associados agrupados na árvore são mostrados ao lado dos ramos.

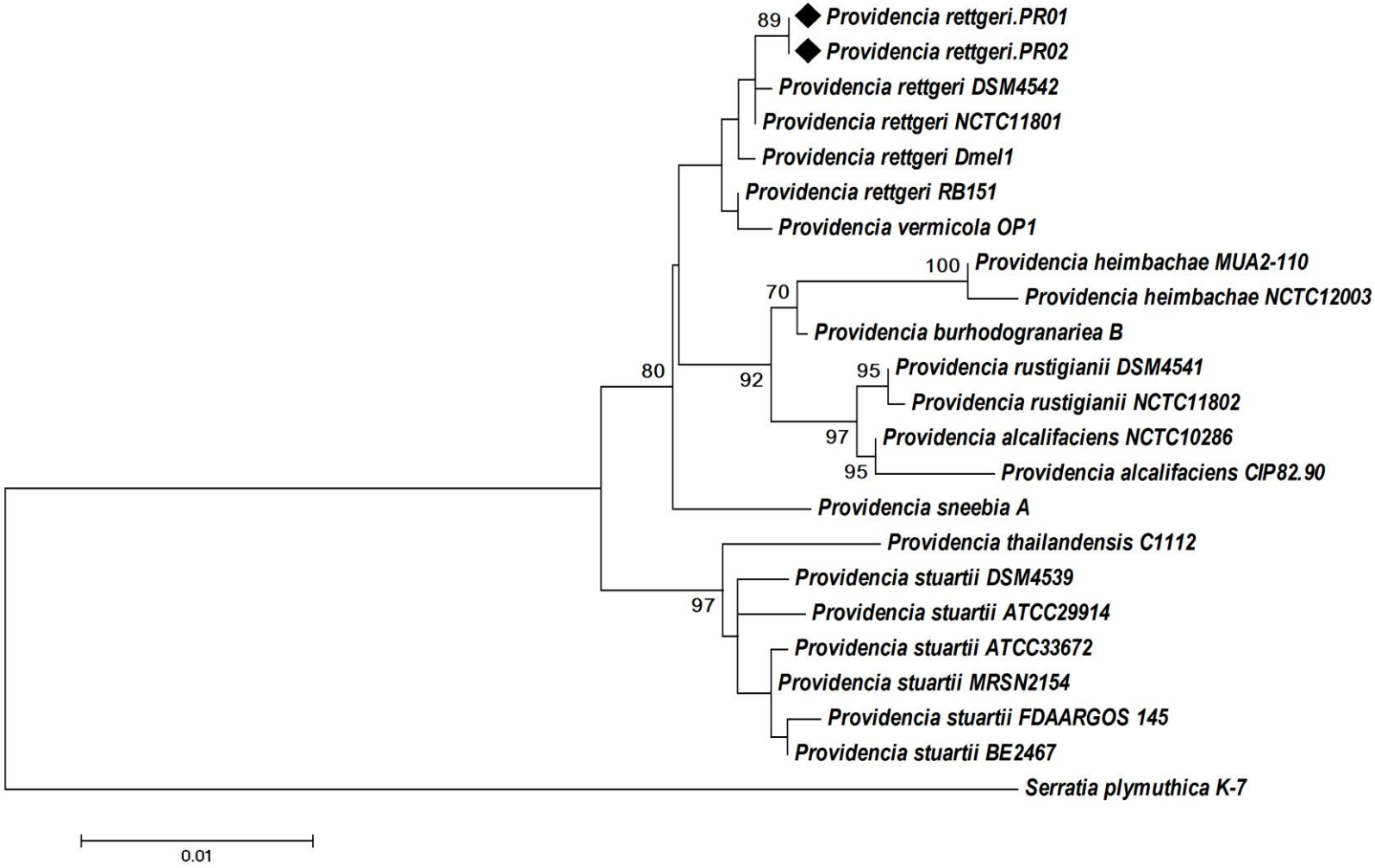


Figura 3-Perfil genético da linhagem *Providencia rettgeri* PR01

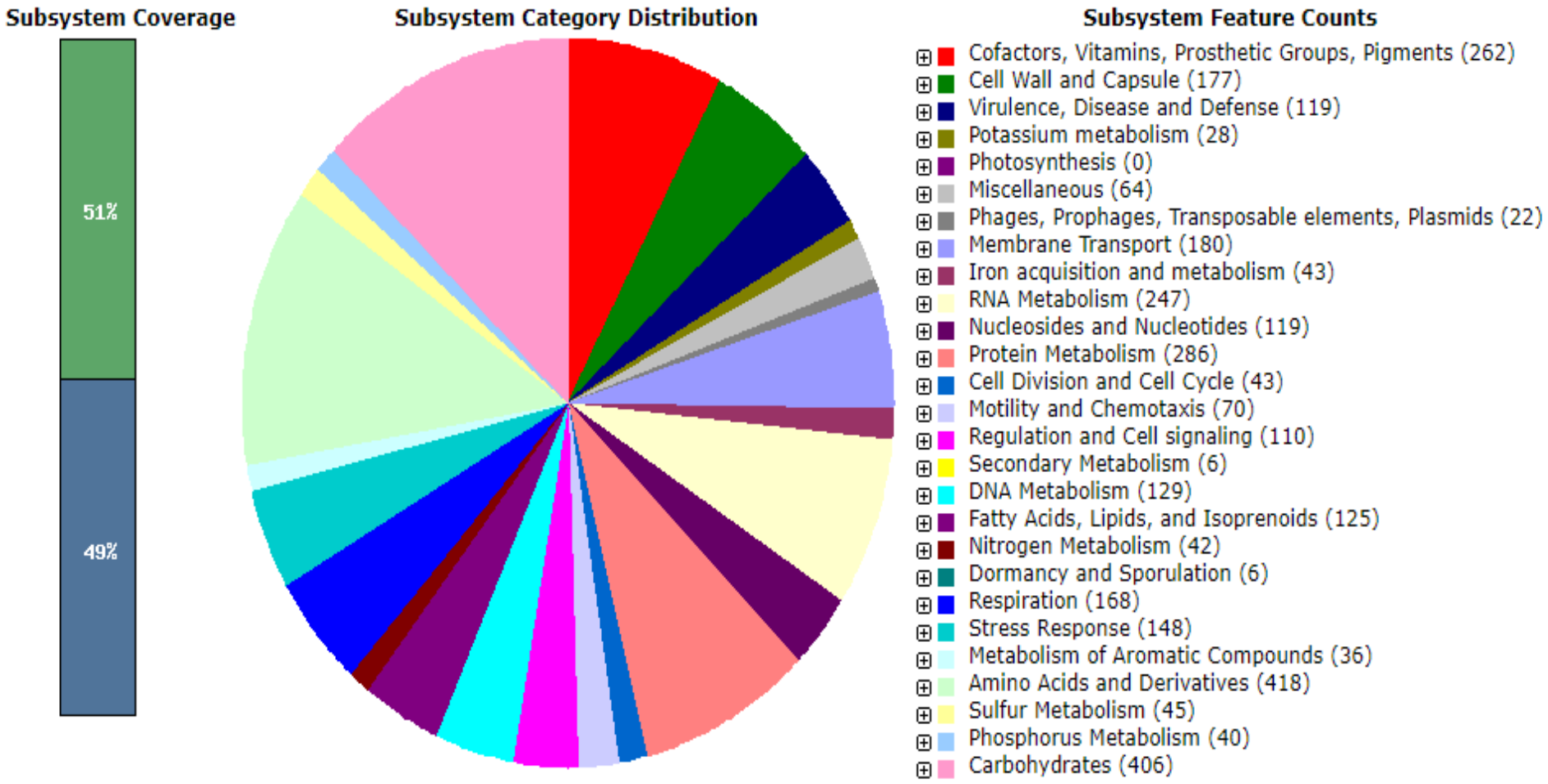


Figura 4-Perfil genético da linhagem *Providencia rettgeri* PR02

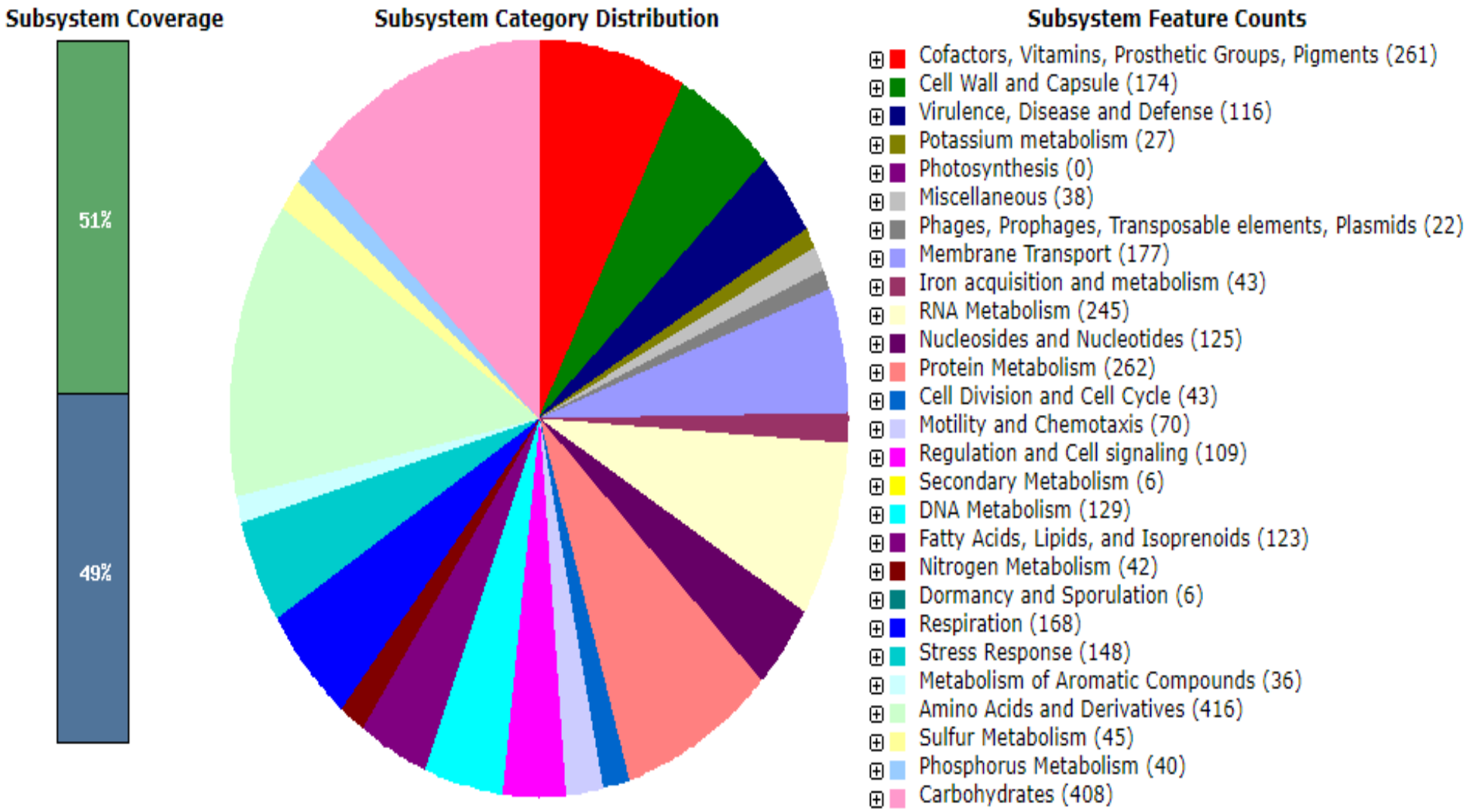


Figura 5-Perfil genético do subsistema de virulência e defesa da Providencia rettgeri PR02

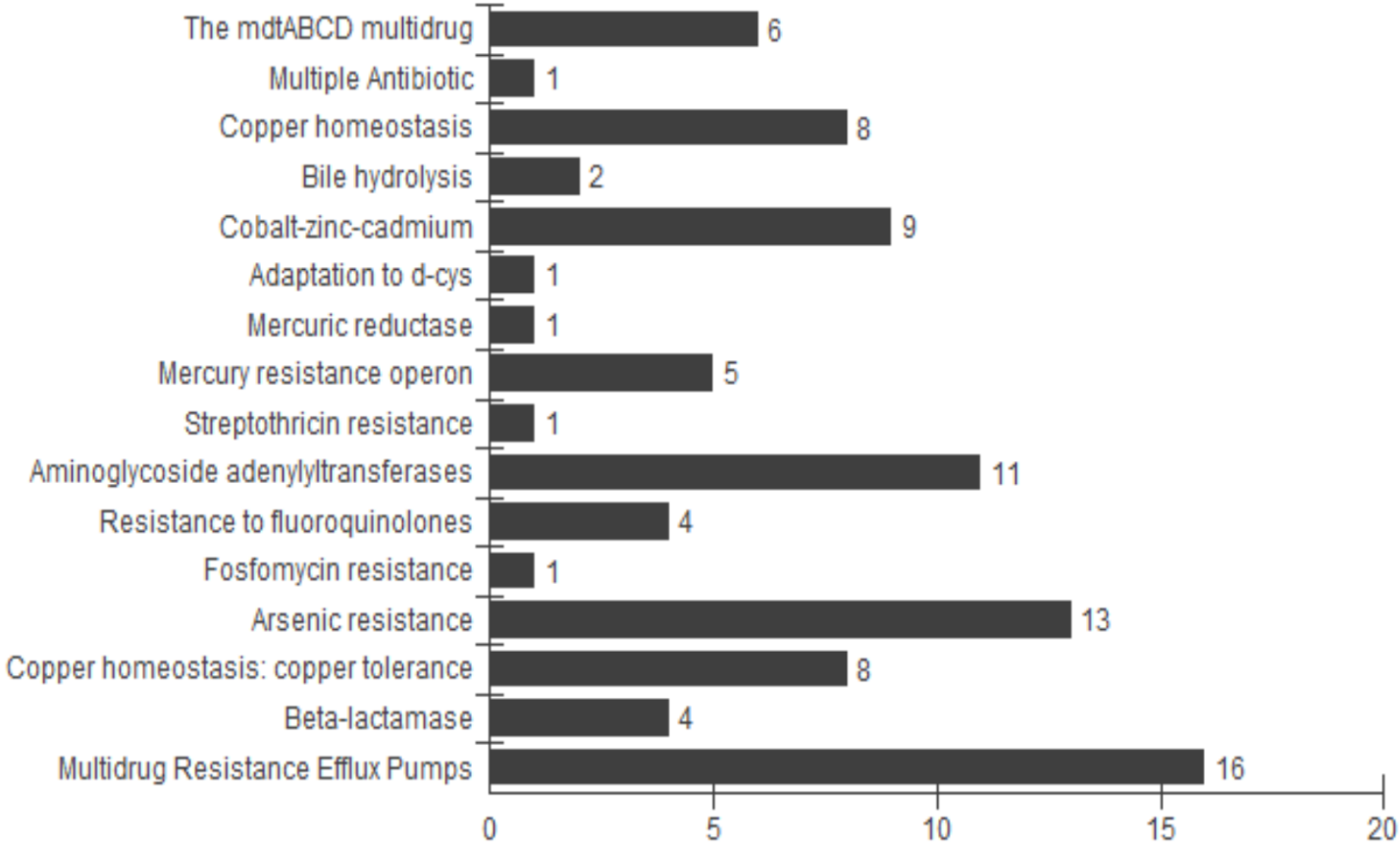


Figura 6-Perfil genético do subsistema de virulência e defesa da Providencia rettgeri PR02

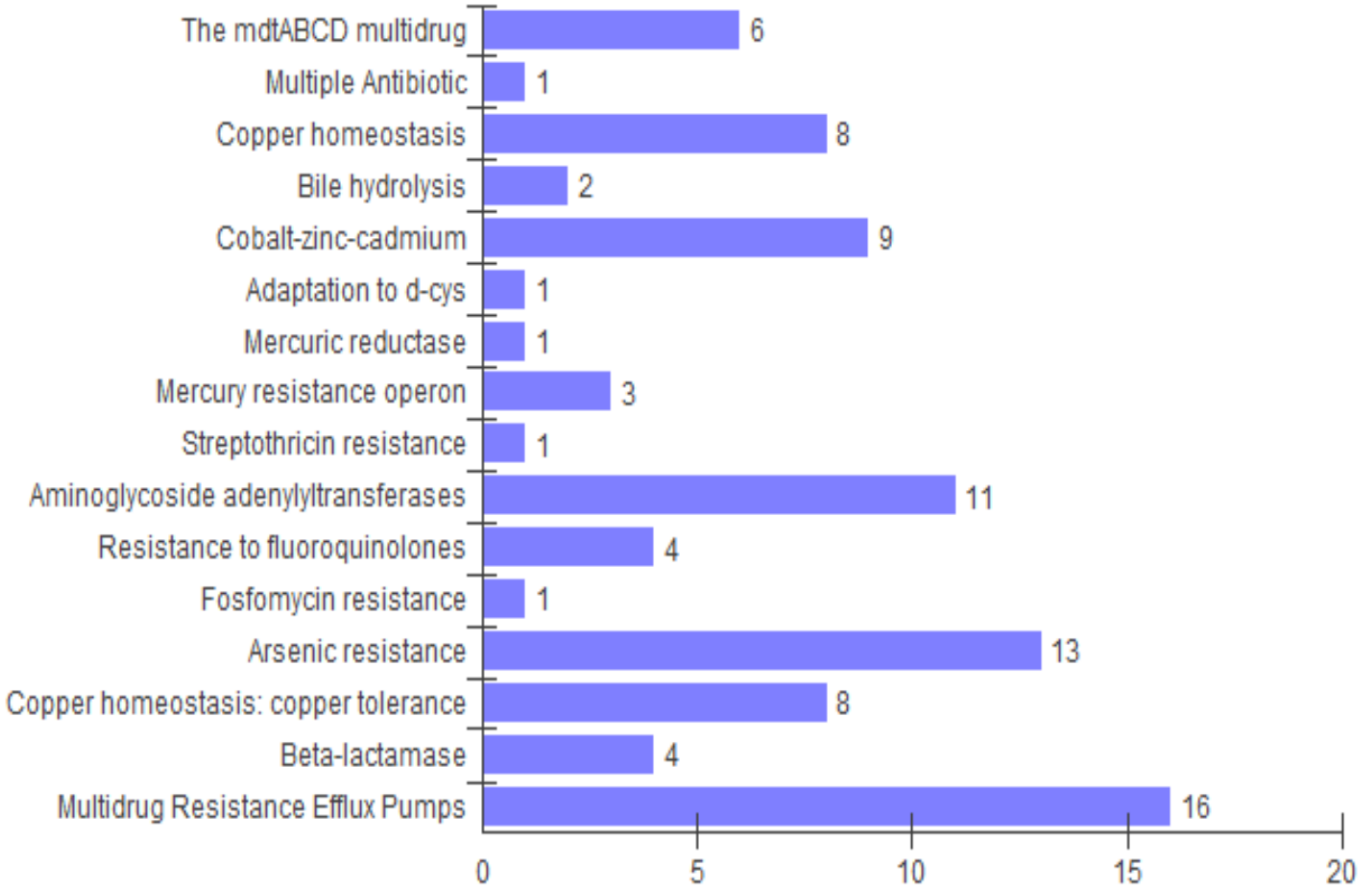


Figura 7-Perfil genético do subsistema de metabolismo e aquisição de ferro das linhagens de Providencia rettgeri PR01 e PR02

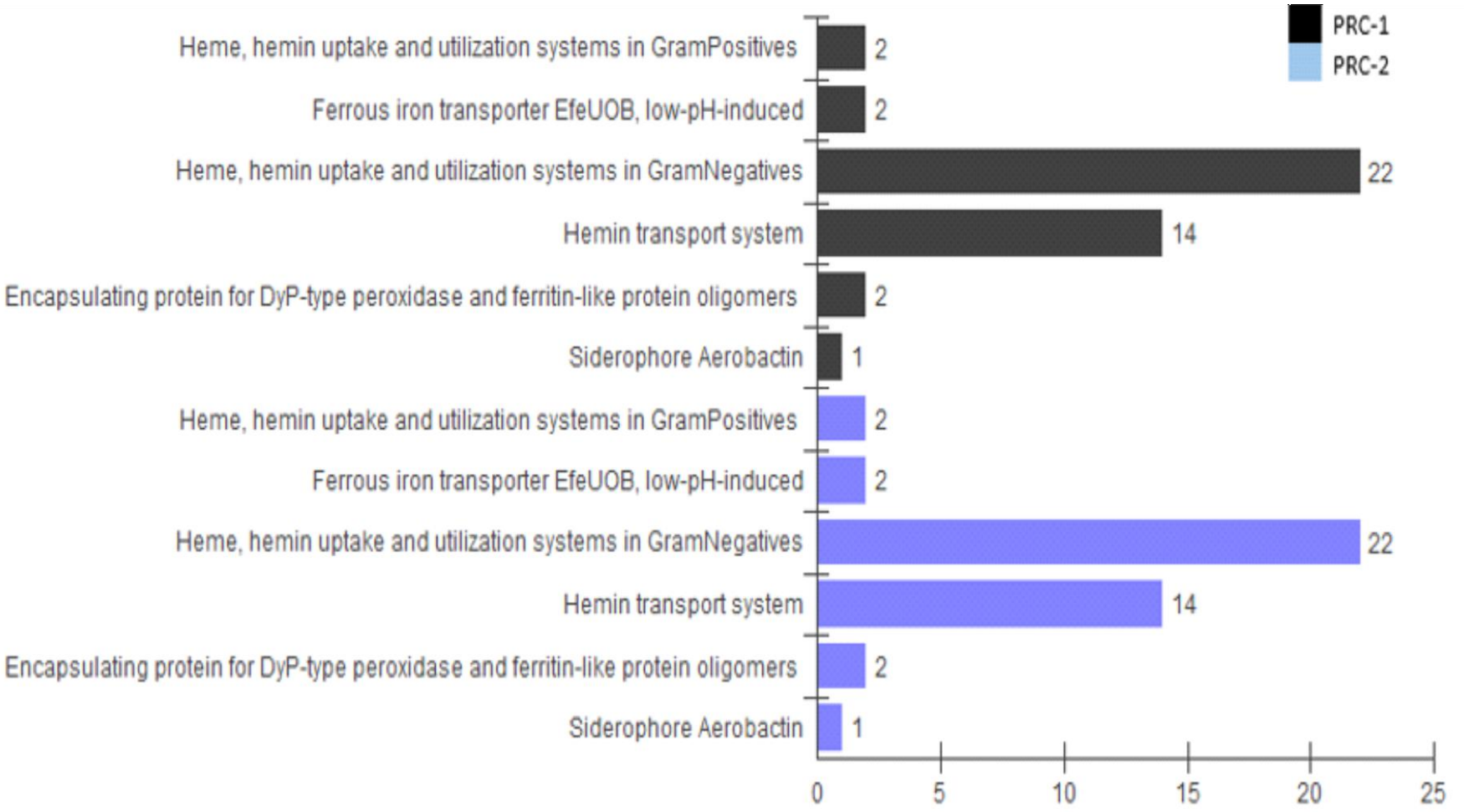


Figura 8-Perfil genético do subsistema apresentando fagos, pro-fagos, elementos móveis transponíveis e plasmídeos das linhagens de Providencia rettgeri PR01 e PR02

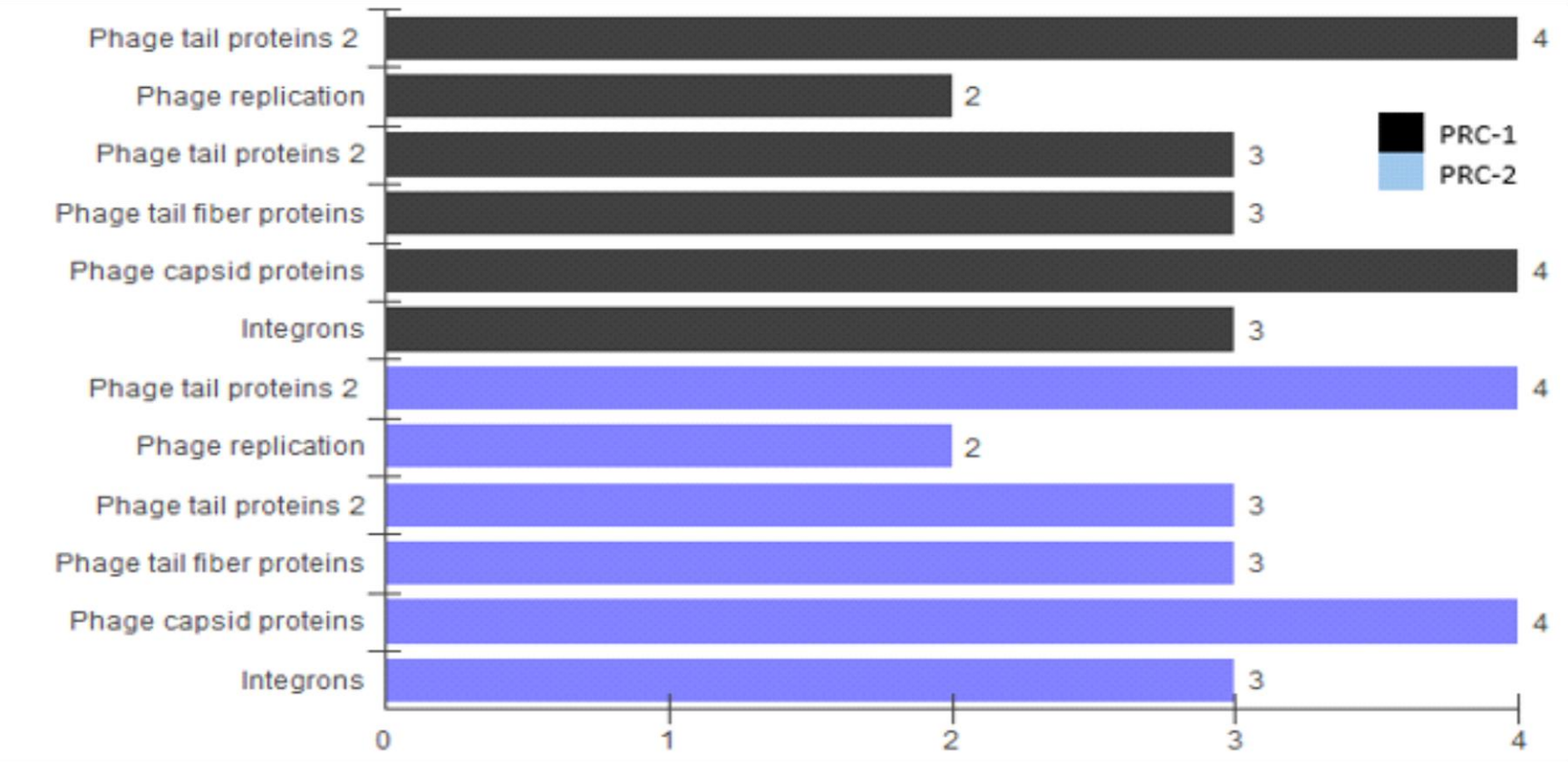


Figura 9-Perfil genético do subsistema de mobilidade e quimiotaxia das linhagens de Providencia rettgeri PR01 e PR02

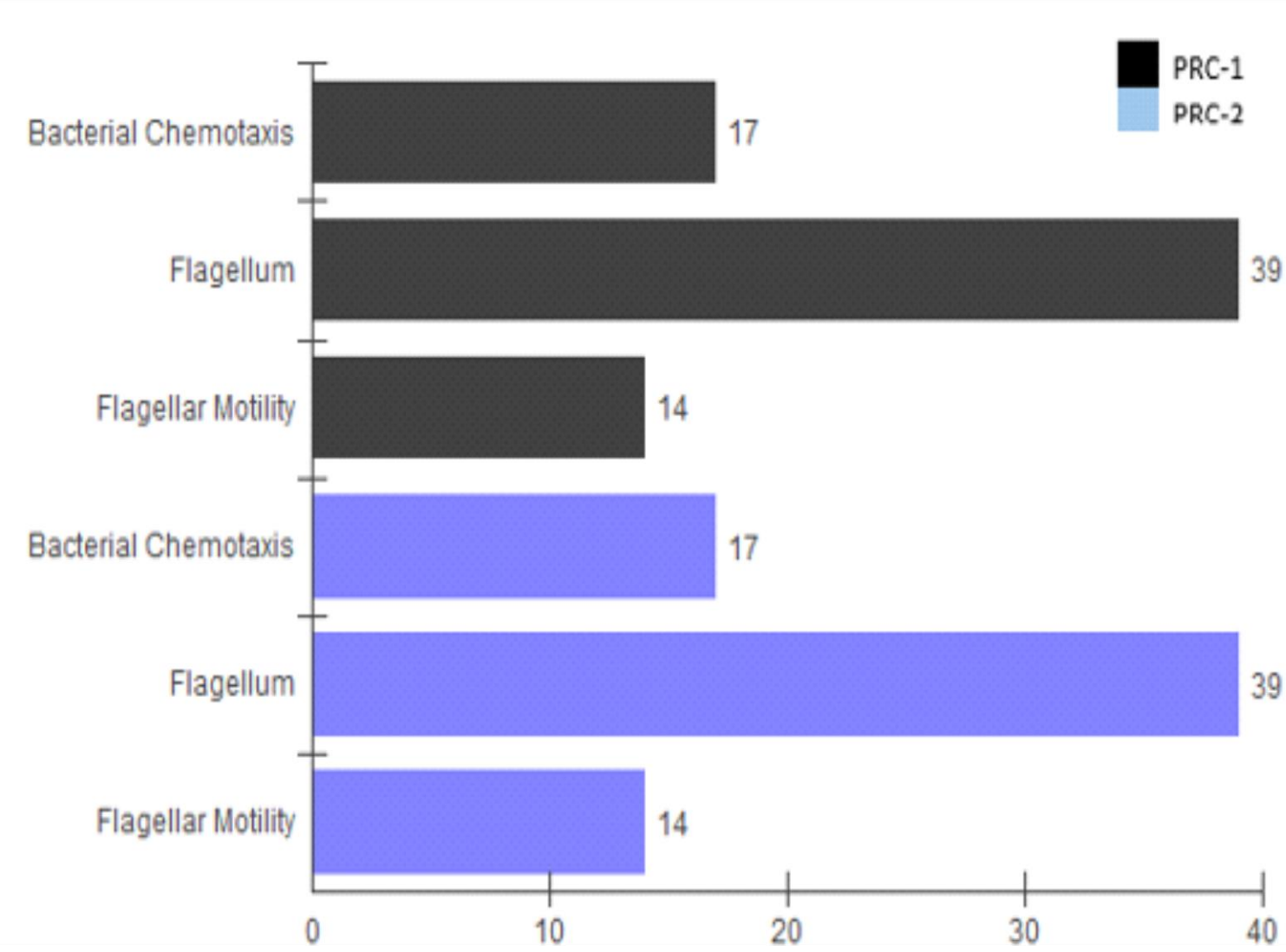


Figura 10- Predição de ilhas genômicas, ilhas de patogenicidade (PAIs) e de resistência a antibióticos (RIs) em *P. rettgeri PR01 e P. rettgeri* PR02

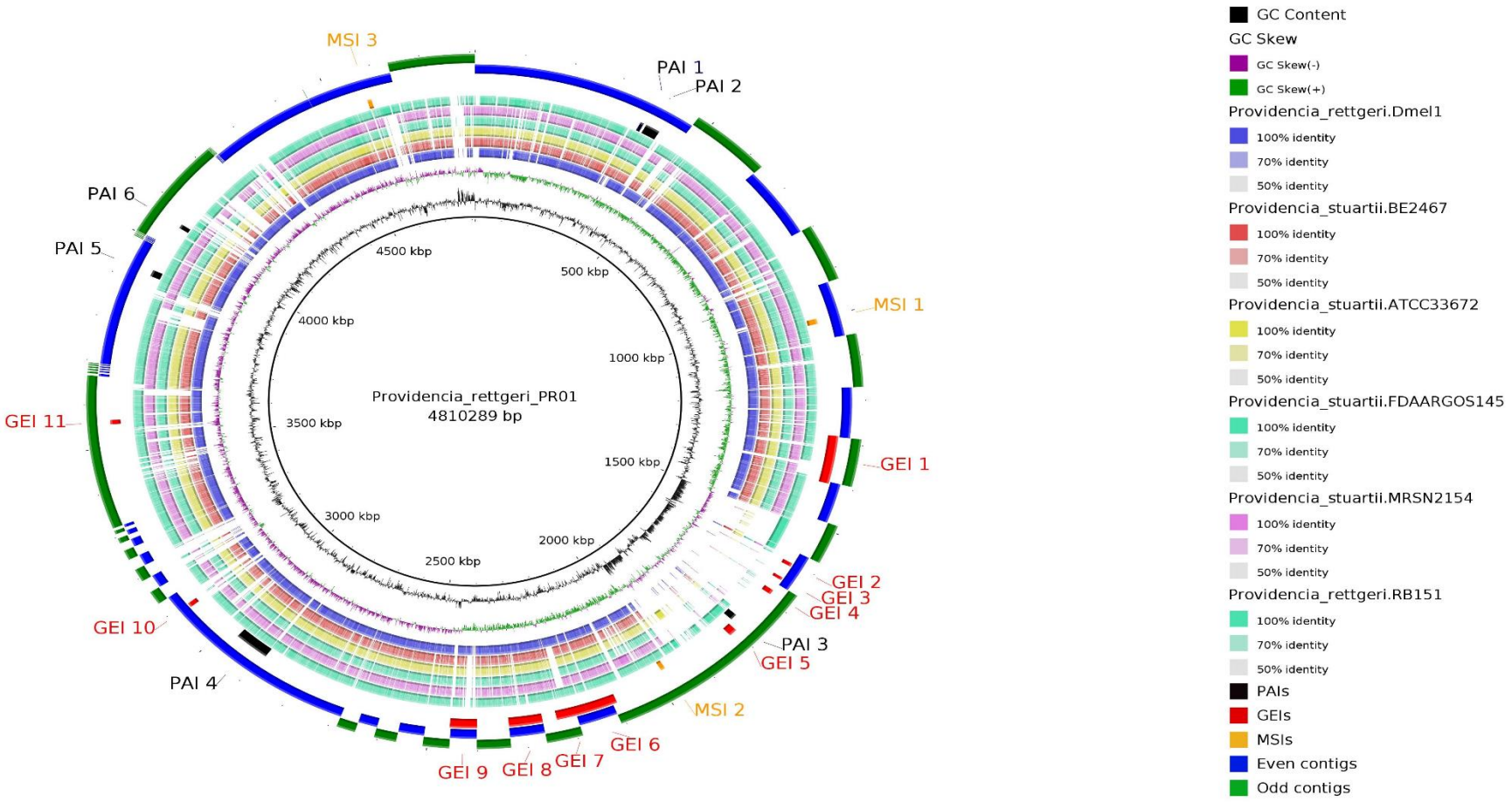


Figura 11- Ilha Genômica PR01

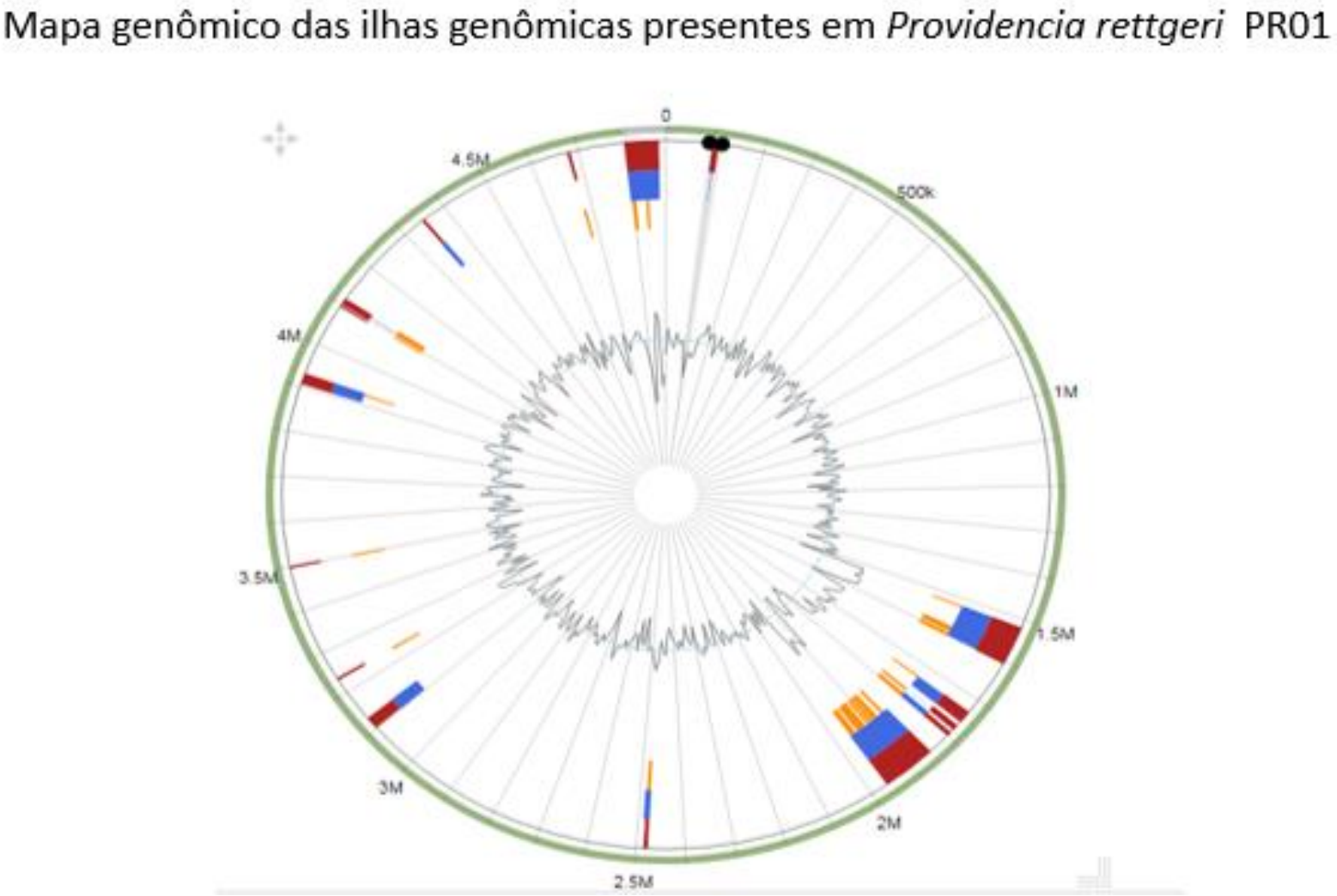


Figura 12- Ilha genômica PR02

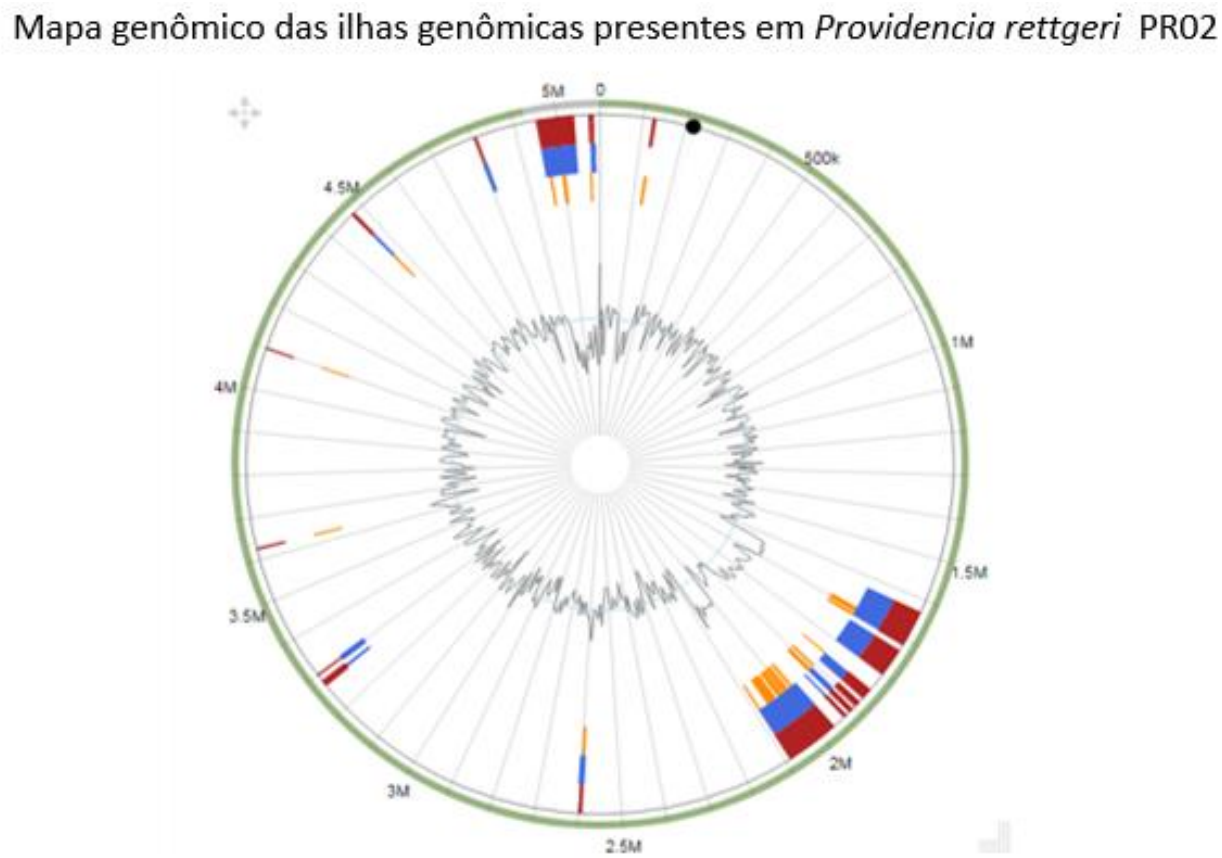
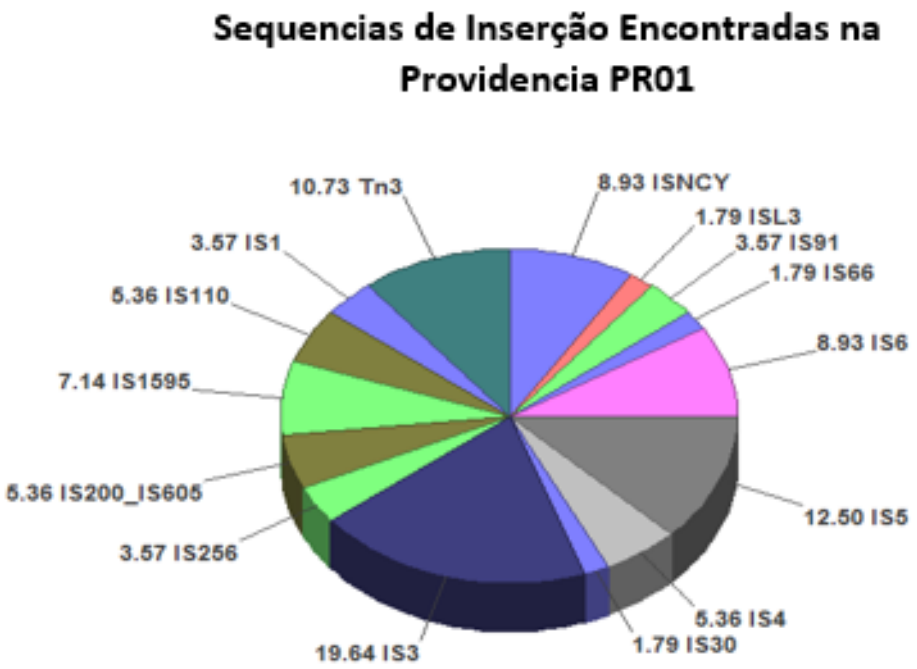
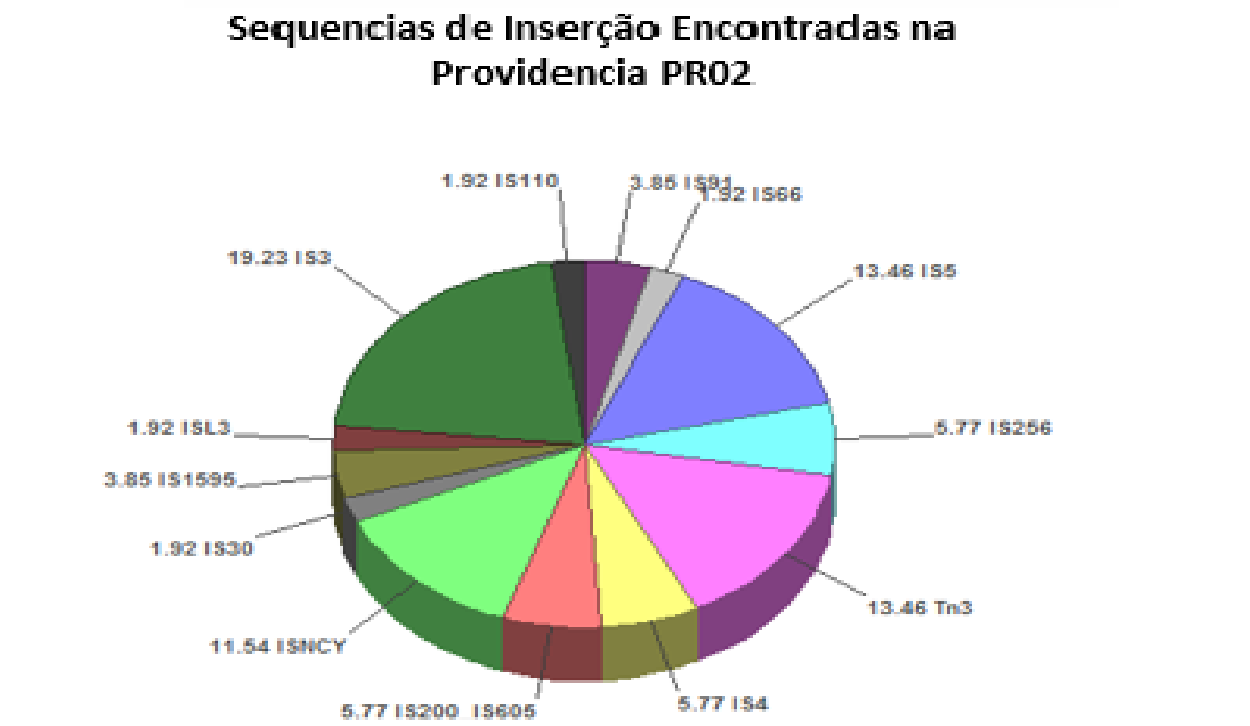


Figura 13- Sequência de Inserção PR01



Tn3	10.73%	IS110	5.36%	IS200_IS605	5.36%	IS3	19.64%	IS4	5.36%	IS6	8.93%
IS91	3.57%	IS1	3.57%	IS1595	7.14%	IS256	3.57%	IS30	1.79%	IS5	12.50%
IS66	1.79%	ISL3	1.79%	ISNCY	8.93%						

Figura 14-Sequência de Inserção PR02



IS110 1,92%	IS1595 3,85%	IS200_IS605 5,77%	IS256 5,77%	IS66 1,92%
IS3 19,23%	IS30 1,92%	IS4 5,77%	IS5 13,46%	IS91 3,85%
ISL3 1,92%	ISNCY 11,54%	Tn3 13,46%		

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Suplemento I

Sub-sistemas PR01

Virulence, Disease and Defense

Sigla	Gene	Tamanho	Aminoácidos	Identidade	Sequenciamento	E. value
			Tolerance to colicin E2			
CbrC-like	Colicin E2 tolerance protein CbrC-like protein	588bp	196aa	99%	gi|490381407|WP_004260923.1	8.00E-151
CreA	Conserved uncharacterized protein CreA	477bp	159aa	100%	gi|491044024|WP_004905686.1	2.00E-108
			Colicin V and Bacteriocin Production Cluster			
R1	tRNA pseudouridine synthase A (EC 4.2.1.70)	816bp	272aa	100%	gi|490377681|WP_004257279.1	0.0
DedA	DedA protein	687bp	229aa	99%	gi|490377686|WP_004257284.1	5E-159
R3	Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)	972bp	324aa	99%	gi|490377689|WP_004257287.1	0.0
R4	Dihydrofolate synthase (EC 6.3.2.12), Folylpolyglutamate synthase (EC 6.3.2.17)	1287bp	429aa	99%	gi|490377692|WP_004257290.1	0.0
R5	Dihydrofolate synthase (EC 6.3.2.12), Folylpolyglutamate synthase (EC 6.3.2.17)	1287bp	429aa	99%	gi|490377692|WP_004257290.1	0.0
DedD	DedD protein	642bp	214aa	100%	gi|739086890|WP_036957975.1	3E-147
*toxin	Colicin V production protein	504bp	168aa	100%	gi|490377706|WP_004257304.1	3E-115
PurF	Amidophosphoribosyltransferase (EC 2.4.2.14)	1518bp	506aa	100%	gi|490377709|WP_004257307.1	0.0
			Mediator of hyperadherence YidE in Enterobacteria and its conserved region			
YidE	Mediator of hyperadherence YidE	1659bp	553aa	99%	gi|490383146|WP_004262657.1	0.0
YidR	Uncharacterized protein YidR	1317bp	439aa	99%	gi|291312036|EFE52489.1	0.0
YidQ	Outer membrane lipoprotein YidQ	243bp	81aa	98%	gi|291312035|EFE52488.1	6.00E-51
			Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins)			
Rv0682	SSU ribosomal protein S12p (S23e)	375bp	125aa	100%	gi|490386408|WP_004265905.1	1E-84
Rv0683	SSU ribosomal protein S7p (S5e)	471bp	157aa	100%	gi|490382975|WP_004262486.1	4E-105
Rv0684	Translation elongation factor G	2127bp	709aa	100%	gi|490382972|WP_004262483.1	0.0

Rv0685	Translation elongation factor Tu	405bp	135aa	100%	gi|414098736|EKT60381.1	6E-92
Rv0685	Translation elongation factor Tu	138bp	46aa	98%	gi|391630004|EIS69838.1	2E-23
Rv0685	Translation elongation factor Tu	891bp	297aa	99%	gi|1042401681|OBY35966.1	0.0
Mycobacterium virulence operon involved in DNA transcription						
Rv0667	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	4029bp	1343aa	100%	gi|490384883|WP_004264386.1	0.0
Rv0668	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	4224bp	1408aa	100%	gi|1042401688|OBY35973.1	0.0
Mycobacterium virulence operon possibly involved in quinolinate biosynthesis						
Rv1594	Quinolinate synthetase (EC 2.5.1.72)	1041bp	347aa	99%	gi|490377169|WP_004256768.1	0.0
Rv1595	L-aspartate oxidase (EC 1.4.3.16)	1596bp	532aa	99%	gi|739087991|WP_036959065.1	0.0
Rv1596	Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)	903bp	301aa	99%	gi|490382479|WP_004261992.1	0.0
Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins)						
Rv1641	Translation initiation factor 3	432bp	144aa	100%	gi|291311981|EFE52434.1	1E-95
Rv1641	Translation initiation factor 3	432bp	144aa	99%	gi|291311982|EFE52435.1	1E-94
Rv1642	LSU ribosomal protein L35p	198bp	66aa	100%	gi|490384195|WP_004263702.1	4E-40
Rv1643	LSU ribosomal protein L20p	357bp	119aa	100%	gi|490384208|WP_004263714.1	2E-75
Beta-lactamase						
BL	Beta-lactamase (EC 3.5.2.6)	861bp	287aa	100%	gi|1002048020|AMM70781.1	0.0
BL	Beta-lactamase (EC 3.5.2.6)	876bp	292aa	100%	gi|446804399|WP_000881655.1	0.0
BL	Beta-lactamase (EC 3.5.2.6)	1143bp	381aa	94%	gi|490383288|WP_004262799.1	0.0
bl	Beta-lactamase	813bp	271aa	100%	gi|926465406|ALD19783.1	0.0
Multiple Antibiotic Resistance MAR locus						
MarC	Multiple antibiotic resistance protein MarC	705bp	235aa	100%	gi|490384158|WP_004263665.1	2E-161
The mdtABCD multidrug resistance cluster						
BaeS	Sensory histidine kinase BaeS	1293bp	431aa	99%	gi|490373912|WP_004253515.1	0.0
BaeR	Response regulator BaeR	708bp	236aa	100%	gi|490373910|WP_004253513.1	8E-167

MdtA	Probable RND efflux membrane fusion protein	1245bp	415aa	99%	gi|490373920|WP_004253523.1	0.0
MdtA	Probable RND efflux membrane fusion protein	1152bp	384aa	99%	gi|489146363|WP_003056109.1	0.0
MdtB	Multidrug transporter MdtB	3102bp	1034aa	99%	gi|490373917|WP_004253520.1	0.0
MdtC	Multidrug transporter MdtC	3123bp	1041aa	99%	gi|490373914|WP_004253517.1	0.0
		Multidrug Resistance Efflux Pumps				
CmeB	RND efflux system, inner membrane transporter CmeB	3159bp	1053aa	100%	gi|490380917|WP_004260435.1	0.0
*TolC	RND efflux system, outer membrane lipoprotein CmeC	1419bp	473aa	99%	gi|414097180|EKT58835.1	0.0
*TolC	RND efflux system, outer membrane lipoprotein CmeC	1389bp	463aa	100%	gi|739086918|WP_036958003.1	0.0
*TolC	RND efflux system, outer membrane lipoprotein CmeC	1395bp	465aa	93%	gi|491044003|WP_004905665.1	0.0
*Reg	Transcription repressor of multidrug efflux pump acrAB operon, TetR (AcrR) family	651bp	217aa	99%	gi|490380911|WP_004260429.1	1E-150
*MATE_family_MDR_Pump	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	306bp	102aa	96%	gi|384481908|AFH95703.1	2E-39
*MATE_family_MDR_Pump	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	1029bp	343aa	99%	gi|491048771|WP_004910423.1	0.0
MFS	Multidrug-efflux transporter, major facilitator superfamily (MFS) (TC 2.A.1)	1227bp	409aa	99%	gi|490376269|WP_004255869.1	0.0
MacA	Macrolide-specific efflux protein MacA	1107bp	369aa	99%	gi|490376798|WP_004256397.1	0.0
MacA	Macrolide-specific efflux protein MacA	1182bp	394aa	100%	gi|414097178|EKT58833.1	0.0
MacB	Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-)	1944bp	648aa	99%	gi|490376796|WP_004256395.1	0.0
MacB	Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-)	1974bp	658aa	100%	gi|491046017|WP_004907673.1	0.0
MtrF	Multidrug efflux pump component MtrF	1572bp	524aa	99%	gi|490379478|WP_004258999.1	0.0
RND	Membrane fusion protein of RND family multidrug efflux pump	1188bp	396aa	100%	gi|490380914|WP_004260432.1	0.0

AcrB	RND multidrug efflux transporter, Acriflavin resistance protein	1095bp	365aa	77%	gi|739105285|WP_036975758.1	0.0
AcrB	RND multidrug efflux transporter, Acriflavin resistance protein	3105bp	1035aa	100%	gi|490381616|WP_004261131.1	0.0
		Bile hydrolysis				
bsh	Choloylglycine hydrolase (EC 3.5.1.24)	1080bp	360aa	100%	gi|490382593|WP_004262105.1	0.0
DamX	DamX, an inner membrane protein involved in bile resistance	906bp	302aa	99%	gi|490383694|WP_004263203.1	0.0
		Fosfomycin resistance				
FosA	Fosfomycin resistance protein FosA	414bp	138aa	100%	gi|490384164|WP_004263671.1	3E-98
		Copper homeostasis				
*CIA	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5), Copper-translocating P-type ATPase (EC 3.6.3.4)	2925bp	975aa	98%	gi|739087196|WP_036958281.1	0.0
*CIA	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5), Copper-translocating P-type ATPase (EC 3.6.3.4)	2400bp	800aa	99%	gi|1042403368|OBY37647.1	0.0
BCO	Blue copper oxidase CueO precursor	1617bp	539aa	99%	gi|490381034|WP_004260551.1	0.0
*HL	Cytochrome c heme lyase subunit CcmF	1932bp	644aa	99%	gi|491051693|WP_004913344.1	0.0
*HL	Cytochrome c heme lyase subunit CcmL, Cytochrome c heme lyase subunit CcmH	1071bp	357aa	99%	gi|490382689|WP_004262201.1	0.0
CRD	Copper resistance protein D	897bp	299aa	99%	gi|490374296|WP_004253898.1	0.0
CopG	CopG protein	423bp	141aa	98%	gi|491043999|WP_004905661.1	2E-97
copCp	Copper resistance protein C precursor	387bp	129aa	100%	gi|490374293|WP_004253895.1	7E-86
		Streptothricin resistance				
SatA	Streptothricin acetyltransferase, Streptomyces lavendulae type	525bp	175aa	100%	gi|446626810|WP_000704156.1	1E-125
		Adaptation to d-cysteine				
DcyD	D-cysteine desulfhydrase (EC 4.4.1.15)	990bp	330aa	99%	gi|490374828|WP_004254429.1	0.0

Mercuric reductase						
MIR	Mercuric ion reductase (EC 1.16.1.1)	1686bp	562aa	100%	gi|446131441|WP_000209296.1	0.0
Resistance to fluoroquinolones						
parC	Topoisomerase IV subunit A (EC 5.99.1.-)	2256bp	752aa	99%	gi|490378099|WP_004257697.1	0.0
parE	Topoisomerase IV subunit B (EC 5.99.1.-)	1896bp	632aa	99%	gi|490378103|WP_004257701.1	0.0
gyrA	DNA gyrase subunit A (EC 5.99.1.3)	2616bp	872aa	99%	gi|491050539|WP_004912190.1	0.0
gyrB	DNA gyrase subunit B (EC 5.99.1.3)	2415bp	805aa	99%	gi|491044587|WP_004906247.1	0.0
Cobalt-zinc-cadmium resistance						
*CzcD	Cobalt-zinc-cadmium resistance protein	930bp	310aa	100%	gi|490382252|WP_004261765.1	0.0
*CzcA?	Cobalt-zinc-cadmium resistance protein CzcA, Cation efflux system protein CusA	3078bp	1026aa	99%	gi|491044000|WP_004905662.1	0.0
*CusB/CzsB	Probable Co/Zn/Cd efflux system membrane fusion protein	1095bp	365aa	62%	gi|1093685069|WP_070928012.1	6E-144
*CusB/CzsB	Probable Co/Zn/Cd efflux system membrane fusion protein	1110bp	370aa	99%	gi|490381614|WP_004261129.1	0.0
*CusB/CzsB	Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family	1269bp	423aa	99%	gi|491044001|WP_004905663.1	0.0
*CusA	Cobalt-zinc-cadmium resistance protein CzcA, Cation efflux system protein CusA	3078bp	1026aa	99%	gi|491044000|WP_004905662.1	0.0
*CzrR	DNA-binding heavy metal response regulator	684bp	228aa	97%	gi|491044004|WP_004905666.1	1E-153
cusF	Cation efflux system protein CusF precursor	342bp	114aa	97%	gi|491044002|WP_004905664.1	4E-74
*TR	Transcriptional regulator, MerR family	423bp	141aa	99%	gi|490374914|WP_004254515.1	2E-92
Mercury resistance operon						
MerR	Mercuric resistance operon regulatory protein	456bp	152aa	100%	gi|447089372|WP_001166628.1	4E-103
MerT	Mercuric transport protein, MerT	366bp	122aa	100%	gi|447217400|WP_001294656.1	8E-84
MerC	Mercuric transport protein, MerC	426bp	142aa	100%	gi|446445141|WP_000522996.1	3E-98
MerA	Mercuric ion reductase (EC 1.16.1.1)	1686bp	562aa	100%	gi|446131441|WP_000209296.1	0.0

MerD	Mercuric resistance operon coregulator	246bp	82aa	99%	gi|585339711|WP_024221342.1	2E-47
			Copper homeostasis: copper tolerance			
ScsB	Membrane protein, suppressor for copper-sensitivity ScsB	2073bp	691aa	99%	gi|490377422|WP_004257021.1	0.0
ScsC	Secreted protein, suppressor for copper-sensitivity ScsC	732bp	244aa	99%	gi|490377417|WP_004257016.1	7E-169
ScsD	Membrane protein, suppressor for copper-sensitivity ScsD	501bp	167aa	100%	gi|491047306|WP_004908960.1	5E-115
CutF	Copper homeostasis protein CutF precursor, Lipoprotein NlpE involeved in surface adhesion	657bp	219aa	99%	gi|490377815|WP_004257413.1	3E-156
CutE	Apolipoprotein N-acyltransferase (EC 2.3.1.-), Copper homeostasis protein CutE	1530bp	510aa	99%	gi|490377396|WP_004256995.1	0.0
CorC	Magnesium and cobalt efflux protein CorC	1287bp	429aa	99%	gi|1042400154|OBY34443.1	0.0
CorC	Magnesium and cobalt efflux protein CorC	909bp	303aa	99%	gi|291314305|EFE54758.1	0.0
CorC	Magnesium and cobalt efflux protein CorC	1368bp	456aa	100%	gi|491044300|WP_004905961.1	0.0
			Aminoglycoside adenylyltransferases			
AadA1	Streptomycin 3"-O-adenylyltransferase (EC 2.7.7.47), Spectinomycin 9-O-adenylyltransferase	159bp	53aa	100%	gi|487942357|WP_002015823.1	3E-31
AadA1	Streptomycin 3"-O-adenylyltransferase (EC 2.7.7.47), Spectinomycin 9-O-adenylyltransferase	1014bp	338aa	100%	gi|678222195|AIM49564.1	0.0
AadA1	Streptomycin 3"-O-adenylyltransferase (EC 2.7.7.47), Spectinomycin 9-O-adenylyltransferase	792bp	264aa	100%	gi|501453940|WP_012477385.1	0.0
AadA1	Streptomycin 3"-O-adenylyltransferase (EC 2.7.7.47), Spectinomycin 9-O-adenylyltransferase	150bp	50aa	100%	gi|486167809|WP_001531151.1	5E-29
AadA1	Streptomycin 3"-O-adenylyltransferase (EC 2.7.7.47), Spectinomycin 9-O-adenylyltransferase	789bp	263aa	100%	gi|447129059|WP_001206315.1	0.0
AadA2	Spectinomycin 9-O-adenylyltransferase	765bp	255aa	99%	gi|490381153|WP_004260670.1	2E-178

AadA2	Spectinomycin 9-O-adenylyltransferase	159bp	53aa	100%	gi|487942357|WP_002015823.1	3E-31
AadA2	Spectinomycin 9-O-adenylyltransferase	1014bp	338aa	100%	gi|678222195|AIM49564.1	0.0
AadA2	Spectinomycin 9-O-adenylyltransferase	792bp	264aa	100%	gi|501453940|WP_012477385.1	0.0
AadA2	Spectinomycin 9-O-adenylyltransferase	150bp	50aa	100%	gi|486167809|WP_001531151.1	5E-29
AadA2	Spectinomycin 9-O-adenylyltransferase	789bp	263aa	100%	gi|447129059|WP_001206315.1	0.0
			Arsenic resistance			
arsR	Arsenical resistance operon repressor	336bp	112aa	100%	gi|757599390|WP_042847035.1	4E-73
arsR	Arsenical resistance operon repressor	336bp	112aa	99%	gi|739097345|WP_036968128.1	6E-72
arsR	Arsenical resistance operon repressor	189bp	63aa	92%	gi|1116088436|WP_072144547.1	2E-33
arsD	Arsenical resistance operon trans-acting repressor ArsD	366bp	122aa	100%	gi|757599389|WP_042847034.1	2E-85
arsD	Arsenical resistance operon trans-acting repressor ArsD	366bp	122aa	99%	gi|739097347|WP_036968130.1	2E-84
arsA	Arsenical pump-driving ATPase (EC 3.6.3.16)	1752bp	584aa	99%	gi|827610366|KLO01850.1	0.0
arsA	Arsenical pump-driving ATPase (EC 3.6.3.16)	1572bp	584aa	99%	gi|739097348|WP_036968131.1	0.0
arsB	Arsenic efflux pump protein	1290bp	430aa	98%	gi|490357905|WP_004237678.1	0.0
arsB	Arsenic efflux pump protein	1290bp	430aa	99%	gi|739104700|WP_036975217.1	0.0
arsB	Arsenic efflux pump protein	1362bp	454aa	98%	gi|739104700|WP_036975217.1	0.0
arsC	Arsenate reductase (EC 1.20.4.1)	357bp	119aa	99%	gi|490373943|WP_004253545.1	1E-78
arsC	Arsenate reductase (EC 1.20.4.1)	417bp	139aa	91%	gi|749308148|WP_040132278.1	8E-88
arsC	Arsenate reductase (EC 1.20.4.1)	441bp	147aa	100%	gi|739097354|WP_036968137.1	2E-100

Iron acquisition and metabolism

Sigla	Gene	Tamanho	Aminoácidos	Identidade	Sequenciamento	E. value
			Siderophore Aerobactin			
iutA	Aerobactin siderophore receptor IutA TonB-dependent siderophore receptor	2202bp	734aa	99%	gi|490378242|WP_004257840.1	0.0
			Heme, hemin uptake and utilization systems in GramPositives			
*Heme_oxygenases	Hemin transport protein HmuS	1050bp	350aa	99%	gi|491051296|WP_004912947.1	0.0
*Heme_oxygenases	Hemin transport protein HmuS	1050bp	350aa	99%	gi|739087580|WP_036958663.1	0.0
			Ferrous iron transporter EfeUOB, low-pH-induced			
*EfeU	Ferrous iron transport permease EfeU	834bp	278aa	99%	gi|490381107|WP_004260624.1	0.0
EfeB	Ferrous iron transport peroxidase EfeB	1275bp	425aa	99%	gi|490381112|WP_004260629.1	0.0
			Encapsulating protein for DyP-type peroxidase and ferritin-like protein oligomers			
DyP	Predicted dye-decolorizing peroxidase (DyP), encapsulated subgroup	900bp	300aa	99%	gi|490385387|WP_004264885.1	0.0
Yfe	Predicted outer membrane lipoprotein YfeY	606bp	202aa	99%	gi|915327114|WP_050763802.1	4E-145
			Hemin transport system			
HBP	Periplasmic hemin-binding protein	822bp	274aa	99%	gi|491051298|WP_004912949.1	0.0
*Rec	TonB-dependent hemin , ferrichrome receptor	2019bp	673aa	91%	gi|739087359|WP_036958444.1	0.0
*Rec	TonB-dependent hemin , ferrichrome receptor	2145bp	715aa	99%	gi|490384250|WP_004263756.1	0.0
hmuS	Hemin transport protein HmuS	1050bp	350aa	99%	gi|491051296|WP_004912947.1	0.0
hmuS	Hemin transport protein HmuS	1050bp	350aa	99%	gi|739087580|WP_036958663.1	0.0
ATPb	ABC-type hemin transport system, ATPase component	789bp	263aa	98%	gi|1172252176|WP_080641516.1	0.0

ATPb	ABC-type hemin transport system, ATPase component	768bp	256aa	99%	gi|1042402961|OBY37241.1	2E-178
PP_7	Hemin ABC transporter, permease protein	1002bp	334aa	99%	gi|491051302|WP_004912953.1	0.0
PP_7	Hemin ABC transporter, permease protein	1017bp	339aa	100%	gi|1042402962|OBY37242.1	0.0
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	744bp	248aa	97%	gi|490382765|WP_004262277.1	1E-162
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	966bp	322aa	98%	gi|490378848|WP_004258445.1	0.0
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	720bp	240aa	99%	gi|739086610|WP_036957695.1	6E-173
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	783bp	261aa	99%	gi|739087479|WP_036958564.1	3E-179
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	756bp	252aa	97%	gi|490373999|WP_004253601.1	1E-165
	Heme, hemin uptake and utilization systems in GramNegatives					
HBP	Periplasmic hemin-binding protein	822bp	274aa	99%	gi|491051298|WP_004912949.1	0.0
fhuC	Ferrichrome transport ATP-binding protein FhuC (TC 3.A.1.14.3)	783bp	261aa	100%	gi|490382157|WP_004261670.1	0.0
fhuC	Ferrichrome transport ATP-binding protein FhuC (TC 3.A.1.14.3)	786bp	262aa	100%	gi|757595221|WP_042843418.1	8E-180
FCR	TonB-dependent hemin , ferrichrome receptor	2019bp	673aa	91%	gi|739087359|WP_036958444.1	0.0
FCR	TonB-dependent hemin , ferrichrome receptor	2145bp	715aa	99%	gi|490384250|WP_004263756.1	0.0
FR	Flavin reductase (EC 1.5.1.30)	624bp	208aa	99%	gi|739087413|WP_036958498.1	7E-143
ETFb	Electron transfer flavoprotein, beta subunit	756bp	252aa	99%	gi|490378882|WP_004258479.1	6E-168
ParA	Paraquat-inducible protein A	1227bp	409aa	99%	gi|1102614758|WP_071585858.1	0.0
ParA	Paraquat-inducible protein A	1227bp	409aa	99%	gi|739086601|WP_036957686.1	0.0
ParB	Paraquat-inducible protein B	1650bp	550aa	99%	gi|490376536|WP_004256135.	0.0

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ParB	Paraquat-inducible protein B	2340bp	780aa	99%	gi|490374304|WP_004253906.1	0.0
hmuS	Hemin transport protein HmuS	1050bp	350aa	99%	gi|491051296|WP_004912947.1	0.0
hmuS	Hemin transport protein HmuS	1050bp	350aa	99%	gi|739087580|WP_036958663.1	0.0
PP_7	Hemin ABC transporter, permease protein	1002bp	334aa	99%	gi|491051302|WP_004912953.1	0.0
PP_7	Hemin ABC transporter, permease protein	1017bp	339aa	100%	gi|1042402962|OBY37242.1	0.0
ATPb	ABC-type hemin transport system, ATPase component	789bp	263aa	98%	gi|1172252176|WP_080641516.1	0.0
ATPb	ABC-type hemin transport system, ATPase component	768bp	256aa	99%	gi|1042402961|OBY37241.1	2E-178
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	744bp	248aa	97%	gi|490382765|WP_004262277.1	1E-162
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	966bp	322aa	98%	gi|490378848|WP_004258445.1	0.0
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	720bp	240aa	99%	gi|739086610|WP_036957695.1	6E-173
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	783bp	261aa	99%	gi|739087479|WP_036958564.1	3E-179
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	756bp	252aa	97%	gi|490373999|WP_004253601.1	1E-165

Phages, Prophages

Sigla	Gene	Tamanho	Aminoácidos	Identidade	Sequenciamento	E. value
Transposable elements - CBSS-203122.12.peg.188						
R1	TniB NTP-binding protein	510bp	170aa	100%	gi|213054790|ACJ39692.1	2E-120
R8	MG(2+) CHELATASE FAMILY PROTEIN ComM-related protein	1527bp	509aa	99%	gi|491044471|WP_004906131.1	0.0
R9	MG(2+) CHELATASE FAMILY PROTEIN ComM-related protein	1527bp	509aa	99%	gi|491044471|WP_004906131.1	0.0
Phages, Prophages, Transposable elements, Plasmids - Integrons						
IntI2	Integron integrase IntI2	537bp	179aa	100%	gi|445994041|WP_000071896.1	8E-125
IntI2	Integron integrase IntI2	537bp	179aa	100%	gi|446419664|WP_000497519.1	9E-75
IntIPac	Integron integrase IntIPac	867bp	289aa	100%	gi|487966541|WP_002039642.1	0.0
Phages, Prophages - Phage tail proteins						
TP	Phage tail protein	444bp	148aa	100%	gi|1101502596|APC13989.1	2E-102
*Measure	Phage tail length tape-measure protein	2700bp	900aa	9800%	gi|873900395|WP_048606828.1	0.0
*Tube	Phage major tail tube protein	516bp	172aa	100%	gi|1101998870|WP_071548731.1	8E-120
*Sheath	Phage tail sheath monomer	1530bp	510aa	100%	gi|1101998871|WP_071548732.1	0.0
Phages, Prophages - Phage replication						
*Rep	Phage replication protein	2424bp	808aa	93%	gi|1101998888|WP_071548749.1	0.0
*dPol_3	DNA polymerase III alpha subunit (EC 2.7.7.7)	3483bp	1161aa	100%	gi|739086905|WP_036957990.1	0.0
Phages, Prophages - Phage tail proteins 2						
TMP1_1	Phage tape measure	447bp	149aa	99%	gi|873900393|WP_048606826.1	1E-99
TSM	Phage tail sheath monomer	1530bp	510aa	100%	gi|1101998871|WP_07154873	0.0

TMP	Phage tail length tape-measure protein	2700bp	900aa	98%	gi|873900395|WP_048606828.2 1	0.0
			Phages, Prophages Phage tail fiber proteins			
TFP	Phage tail fiber protein	1530bp	510aa	99%	gi|1101502589|APC13982.1	0.0
TFAP	Phage tail fiber assembly protein	645bp	215aa	100%	gi|1101502588|APC13981.1	2E-149
TFP2	Phage tail fibers	612bp	204aa	100%	gi|873900403|WP_048606836.1	2E-146
			Phages, Prophages Phage capsid proteins			
*Generic	Phage capsid and scaffold	444bp	148aa	100%	gi|739091104|WP_036962066.1	3.00E-108
MajCap	Phage major capsid protein	1095bp	365aa	99%	gi|1101998881|WP_071548742.1	0.0
*Scaffolding	Phage capsid scaffolding protein	828bp	276aa	99%	gi|1101998882|WP_071548743.1	0.0
HCSP	Phage head completion-stabilization protein	477bp	159aa	100%	gi|1101998879|WP_071548740.1	4.0E-108

Motility and Chemotaxis

Sigla	Gene	Tamanho	Aminoácidos	Identidade	Sequenciamento	E. value
			Bacterial Chemotaxis			
aer	Aerotaxis sensor receptor protein	1533bp	511aa	98%	gi|739086922|WP_036958007.1	0.0
tsr	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	1653bp	551aa	98%	gi|490373823|WP_004253426.1	0.0
tsr	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	1569bp	523aa	99%	gi|490376118|WP_004255718.1	0.0
tsr	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	1602bp	534aa	99%	gi|490376121|WP_004255721.1	0.0
tsr	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	1488bp	496aa	99%	gi|490378843|WP_004258440.1	0.0
*cheW-V	Positive regulator of CheA protein activity (CheW)	498bp	166aa	100%	gi|491048180|WP_004909833.1	3E-111
cheA	Signal transduction histidine kinase CheA (EC 2.7.3.-)	2058bp	686aa	99%	gi|739086771|WP_036957856.1	0.0
cheY	Chemotaxis regulator - transmits chemoreceptor signals to flagelllar motor components CheY	393bp	131aa	100%	gi|490376105|WP_004255705.1	7E-85
cheZ	Chemotaxis response - phosphatase CheZ	639bp	213aa	99%	gi|1042399717|OBY34011.1	8E-142
cheB	Chemotaxis response regulator protein-glutamate methylesterase CheB (EC 3.1.1.61)	1068bp	356aa	99%	gi|490376109|WP_004255709.1	0.0
fliG	Flagellar motor switch protein FliG	993bp	331aa	100%	gi|490376000|WP_004255600.1	0.0
fliM	Flagellar motor switch protein FliM	1008bp	336aa	99%	gi|490376019|WP_004255619.1	0.0
fliN	Flagellar motor switch protein FliN	417bp	139aa	100%	gi|490376021|WP_004255621.1	1E-90
malE	Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein MalE	1191bp	397aa	92%	gi|1057035456|WP_068445917.1	0.0
dppA	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	1608bp	536aa	100%	gi|490383128|WP_004262639.1	0.0
dppA	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	1560bp	520aa	99%	gi|739086975|WP_036958060.1	0.0
cheR	Chemotaxis protein methyltransferase CheR (EC 2.1.1.80)	837bp	279aa	100%	gi|490376113|WP_004255713.1	0.0

		Flagellum				
flgB	Flagellar basal-body rod protein FlgB	414bp	138aa	100%	gi|490376069|WP_004255669.1	2E-91
flgC	Flagellar basal-body rod protein FlgC	405bp	135aa	100%	gi|491048215|WP_004909868.1	3E-89
FlgD	Flagellar basal-body rod modification protein FlgD	858bp	286aa	99%	gi|490376064|WP_004255664.1	0.0
flgE	Flagellar hook protein FlgE	1221bp	407aa	96%	gi|873900357|WP_048606790.1	0.0
flgF	Flagellar basal-body rod protein FlgF	756bp	252aa	100%	gi|490376059|WP_004255659.1	2E-174
flgG	Flagellar basal-body rod protein FlgG	783bp	261aa	99%	gi|490376057|WP_004255657.1	0.0
FlgH	Flagellar L-ring protein FlgH	750bp	250aa	100%	gi|291314697|EFE55150.1	0.0
flgI	Flagellar P-ring protein FlgI	1104bp	368aa	100%	gi|490376051|WP_004255651.1	0.0
flgJ	Flagellar protein FlgJ [peptidoglycan hydrolase] (EC 3.2.1.-)	981bp	327aa	98%	gi|490376048|WP_004255648.1	0.0
flgK	Flagellar hook-associated protein FlgK	1644bp	548aa	99%	gi|739086767|WP_036957852.1	0.0
flgL	Flagellar hook-associated protein FlgL	936bp	312aa	98%	gi|491048236|WP_004909889.1	0.0
FlhA	Flagellar biosynthesis protein FlhA	2100bp	700aa	100%	gi|490376087|WP_004255687.1	0.0
fliE	Flagellar hook-basal body complex protein FliE	312bp	104aa	100%	gi|490375994|WP_004255594.1	4E-64
fliF	Flagellar M-ring protein FliF	1686bp	562aa	99%	gi|490375997|WP_004255597.1	0.0
fliG	Flagellar motor switch protein FliG	993bp	331aa	100%	gi|490376000|WP_004255600.1	0.0
fliH	Flagellar assembly protein FliH	729bp	243aa	99%	gi|490376003|WP_004255603.1	8E-177
FliI	Flagellum-specific ATP synthase FliI	1311bp	437aa	99%	gi|490376006|WP_004255606.1	0.0
fliK	Flagellar hook-length control protein FliK	1368bp	456aa	97%	gi|490376013|WP_004255613.1	0.0
fliJ	Flagellar protein FliJ	444bp	148aa	99%	gi|490376009|WP_004255609.1	3E-100
fliM	Flagellar motor switch protein FliM	1008bp	336aa	99%	gi|490376019|WP_004255619.1	0.0
fliN	Flagellar motor switch protein FliN	417bp	139aa	100%	gi|490376021|WP_004255621.1	1E-90
fliP	Flagellar biosynthesis protein FliP	744bp	248aa	99%	gi|739086765|WP_036957850.1	3E-167
fliQ	Flagellar biosynthesis protein FliQ	270bp	90aa	99%	gi|490376030|WP_004255630.1	2E-52
FliR	Flagellar biosynthesis protein FliR	780bp	260aa	99%	gi|490376033|WP_004255633.1	7E-180
*Flagellar-Regulation	RNA polymerase sigma factor RpoD	1854bp	618aa	100%	gi|1102614763|WP_071585863.1	0.0

*Flagellar-Regulation	Flagellar transcriptional activator FlhC	591bp	197aa	100%	gi|490376132|WP_004255732.1	1E-140
*Flagellar-Regulation	Flagellar biosynthesis protein FliZ	519bp	173aa	100%	gi|490376157|WP_004255757.1	4E-123
*Flagellar-Regulation	RNA polymerase sigma-54 factor RpoN	1446bp	482aa	99%	gi|490378708|WP_004258305.1	0.0
*Flagellar-Regulation	RNA polymerase sigma factor for flagellar operon	726bp	242aa	99%	gi|291314661|EFE55114.1	0.0
*Flagellin	Flagellar biosynthesis protein FliC	1170bp	390aa	87%	gi|1055836465|WP_067424616.1	0.0
fliD	Flagellar hook-associated protein FliD	1437bp	479aa	90%	gi|1057031755|WP_068442704.1	0.0
fliS	Flagellar biosynthesis protein FliS	399bp	133aa	100%	gi|491048316|WP_004909969.1	1E-86
fliT	Flagellar biosynthesis protein FliT	390bp	130aa	99%	gi|490375964|WP_004255564.1	2E-85
*fliO	Flagellar biosynthesis protein FliO	459bp	153aa	99%	gi|490376024|WP_004255624.1	7E-102
FlhB	Flagellar biosynthesis protein FlhB	1152bp	384aa	99%	gi|490376088|WP_004255688.1	0.0
MotA	Flagellar motor rotation protein MotA	954bp	318aa	99%	gi|291314724|EFE55177.1	0.0
MotB	Flagellar motor rotation protein MotB	918bp	306aa	99%	gi|490376126|WP_004255726.1	0.0
*flhD	Flagellar transcriptional activator FlhD	351bp	117aa	100%	gi|739086775|WP_036957860.1	3E-74
fliL	Flagellar biosynthesis protein FliL	480bp	160aa	99%	gi|490376015|WP_004255615.1	3E-107
		Flagellar motility				
FlhA	Flagellar biosynthesis protein FlhA	2100bp	700aa	100%	gi|490376087|WP_004255687.1	0.0
fliM	Flagellar motor switch protein FliM	1008bp	336aa	99%	gi|490376019|WP_004255619.1	0.0
fliN	Flagellar motor switch protein FliN	417bp	139aa	100%	gi|490376021|WP_004255621.1	1E-90
cheY	Chemotaxis regulator - transmits chemoreceptor signals to flagelllar motor components CheY	393bp	131aa	100%	gi|490376105|WP_004255705.1	7E-85
cheA	Signal transduction histidine kinase CheA (EC 2.7.3.-)	2058bp	686aa	99%	gi|739086771|WP_036957856.1	0.0
FlhB	Flagellar biosynthesis protein FlhB	1152bp	384aa	99%	gi|490376088|WP_004255688.1	0.0
FliI	Flagellum-specific ATP synthase FliI	1311bp	437aa	99%	gi|490376006|WP_004255606.1	0.0
FliR	Flagellar biosynthesis protein FliR	780bp	260aa	99%	gi|490376033|WP_004255633.1	7E-180

FlgD	Flagellar basal-body rod modification protein FlgD	858bp	286aa	99%	gi|490376064|WP_004255664.1	0.0
FlgH	Flagellar L-ring protein FlgH	750bp	250aa	100%	gi|291314697|EFE55150.1	0.0
MotA	Flagellar motor rotation protein MotA	954bp	318aa	99%	gi|291314724|EFE55177.1	0.0
MotB	Flagellar motor rotation protein MotB	918bp	306aa	99%	gi|490376126|WP_004255726.1	0.0
FliA	RNA polymerase sigma factor for flagellar operon	726bp	242aa	99%	gi|291314661|EFE55114.1	9E-167
RpoN	RNA polymerase sigma-54 factor RpoN	1446bp	482aa	99%	gi|490378708|WP_004258305.1	0.0

Sub-sistemas PR02

Virulence, Disease and Defense

Sigla	Gene	Tamanho	Aminoácidos	Identidade	Sequenciamento	E. value
	Tolerance to colicin E2					
CbrC-like	Colicin E2 tolerance protein CbrC-like protein	588bp	196aa	99%	gi|490381407|WP_004260923.1	8.00E-151
CreA	Conserved uncharacterized protein CreA	477bp	159aa	100%	gi|491044024|WP_004905686.1	2.00E-108
	Colicin V and Bacteriocin Production Cluster					
R1	tRNA pseudouridine synthase A (EC 4.2.1.70)	816bp	272aa	100%	gi|490377681|WP_004257279.1	0.0
DedA	DedA protein	687bp	229aa	99%	gi|490377686|WP_004257284.1	5E-159
R3	Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)	972bp	324aa	99%	gi|490377689|WP_004257287.1	0.0
R4	Dihydrofolate synthase (EC 6.3.2.12), Folylpolyglutamate synthase (EC 6.3.2.17)	1287bp	429aa	99%	gi|490377692|WP_004257290.1	0.0
R5	Dihydrofolate synthase (EC 6.3.2.12), Folylpolyglutamate synthase (EC 6.3.2.17)	1287bp	429aa	99%	gi|490377692|WP_004257290.1	0.0
DedD	DedD protein	642bp	214aa	100%	gi|739086890|WP_036957975.1	3E-147
*toxin	Colicin V production protein	504bp	168aa	100%	gi|490377706|WP_004257304.1	3E-115
PurF	Amidophosphoribosyltransferase (EC 2.4.2.14)	1518bp	506aa	100%	gi|490377709|WP_004257307.1	0.0
	Mediator of hyperadherence YidE in Enterobacteria and its conserved region					
YidE	Mediator of hyperadherence YidE	1659bp	553aa	99%	gi|490383146|WP_004262657.1	0.0
YidR	Uncharacterized protein YidR	1317bp	439aa	99%	gi|291312036|EFE52489.1	0.0
YidQ	Outer membrane lipoprotein YidQ	243bp	81aa	98%	gi|291312035|EFE52488.1	6.00E-51
	Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins)					
Rv0682	SSU ribosomal protein S12p (S23e)	375bp	125aa	100%	gi|490386408|WP_004265905.1	1E-84
Rv0683	SSU ribosomal protein S7p (S5e)	471bp	157aa	100%	gi|490382975|WP_004262486.1	4E-105

Rv0684	Translation elongation factor G	2127bp	709aa	100%	gi|490382972|WP_004262483.1	0.0
Rv0685	Translation elongation factor Tu	1185bp	395aa	99%	gi|490384870|WP_004264373.1	0.0
Rv0685	Translation elongation factor Tu	138bp	46aa	98%	gi|391630004|EIS69838.1	2E-23
	Mycobacterium virulence operon involved in DNA transcription					
Rv0667	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	4029bp	1343aa	100%	gi|490384883|WP_004264386.1	0.0
Rv0668	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	4224bp	1408aa	100%	gi|1042401688|OBY35973.1	0.0
	Mycobacterium virulence operon possibly involved in quinolinate biosynthesis					
Rv1594	Quinolinate synthetase (EC 2.5.1.72)	1041bp	347aa	99%	gi|490377169|WP_004256768.1	0.0
Rv1595	L-aspartate oxidase (EC 1.4.3.16)	1596bp	532aa	99%	gi|739087991|WP_036959065.1	0.0
Rv1596	Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)	903bp	301aa	99%	gi|490382479|WP_004261992.1	0.0
	Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins)					
Rv1641	Translation initiation factor 3	432bp	144aa	100%	gi|291311981|EFE52434.1	1E-95
Rv1641	Translation initiation factor 3	432bp	144aa	99%	gi|291311982|EFE52435.1	1E-94
Rv1642	LSU ribosomal protein L35p	198bp	66aa	100%	gi|490384195|WP_004263702.1	4E-40
Rv1643	LSU ribosomal protein L20p	357bp	119aa	100%	gi|490384208|WP_004263714.1	2E-75
	Beta-lactamase					
BL	Beta-lactamase (EC 3.5.2.6)	861bp	287aa	100%	gi|1002048020|AMM70781.1	0.0
BL	Beta-lactamase (EC 3.5.2.6)	876bp	292aa	100%	gi|446804399|WP_000881655.1	0.0
BL	Beta-lactamase (EC 3.5.2.6)	1143bp	381aa	94%	gi|490383288|WP_004262799.1	0.0
bl	Beta-lactamase	813bp	271aa	100%	gi|926465406|ALD19783.1	0.0
	Multiple Antibiotic Resistance MAR locus					
MarC	Multiple antibiotic resistance protein MarC	705bp	235aa	100%	gi|490384158|WP_004263665.1	2E-161
	The mdtABCD multidrug resistance cluster					
BaeS	Sensory histidine kinase BaeS	1293bp	431aa	99%	gi|490373912|WP_004253515.1	0.0
BaeR	Response regulator BaeR	708bp	236aa	100%	gi|490373910|WP_004253513.1	8E-167

MdtA	Probable RND efflux membrane fusion protein	1245bp	415aa	99%	gi|490373920|WP_004253523.1	0.0
MdtA	Probable RND efflux membrane fusion protein	1152bp	384aa	99%	gi|489146363|WP_003056109.1	0.0
MdtB	Multidrug transporter MdtB	3102bp	1034aa	99%	gi|490373917|WP_004253520.1	0.0
MdtC	Multidrug transporter MdtC	3123bp	1041aa	99%	gi|490373914|WP_004253517.1	0.0
		Multidrug Resistance Efflux Pumps				
CmeB	RND efflux system, inner membrane transporter CmeB	3159bp	1053aa	100%	gi|490380917|WP_004260435.1	0.0
*TolC	RND efflux system, outer membrane lipoprotein CmeC	1419bp	473aa	99%	gi|414097180|EKT58835.1	0.0
*TolC	RND efflux system, outer membrane lipoprotein CmeC	1389bp	463aa	100%	gi|739086918|WP_036958003.1	0.0
*TolC	RND efflux system, outer membrane lipoprotein CmeC	1395bp	465aa	93%	gi|491044003|WP_004905665.1	0.0
*Reg	Transcription repressor of multidrug efflux pump acrAB operon, TetR (AcrR) family	651bp	217aa	99%	gi|490380911|WP_004260429.1	1E-150
*MATE_family_MDR_Pump	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	306bp	102aa	96%	gi|384481908|AFH95703.1	2E-39
*MATE_family_MDR_Pump	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	1029bp	343aa	99%	gi|491048771|WP_004910423.1	0.0
MFS	Multidrug-efflux transporter, major facilitator superfamily (MFS) (TC 2.A.1)	1227bp	409aa	99%	gi|490376269|WP_004255869.1	0.0
MacA	Macrolide-specific efflux protein MacA	1107bp	369aa	99%	gi|490376798|WP_004256397.1	0.0
MacA	Macrolide-specific efflux protein MacA	1182bp	394aa	100%	gi|414097178|EKT58833.1	0.0
MacB	Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-)	1944bp	648aa	99%	gi|490376796|WP_004256395.1	0.0
MacB	Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-)	1974bp	658aa	100%	gi|491046017|WP_004907673.1	0.0
MtrF	Multidrug efflux pump component MtrF	1572bp	524aa	99%	gi|490379478|WP_004258999.1	0.0
RND	Membrane fusion protein of RND family multidrug efflux pump	1188bp	396aa	100%	gi|490380914|WP_004260432.1	0.0

AcrB	RND multidrug efflux transporter, Acriflavin resistance protein	1095bp	365aa	77%	gi|739105285|WP_036975758.1	0.0
AcrB	RND multidrug efflux transporter, Acriflavin resistance protein	3105bp	1035aa	100%	gi|490381616|WP_004261131.1	0.0
	Bile hydrolysis					
bsh	Choloylglycine hydrolase (EC 3.5.1.24)	1080bp	360aa	100%	gi|490382593|WP_004262105.1	0.0
DamX	DamX, an inner membrane protein involved in bile resistance	906bp	302aa	99%	gi|490383694|WP_004263203.1	0.0
	Fosfomycin resistance					
FosA	Fosfomycin resistance protein FosA	414bp	138aa	100%	gi|490384164|WP_004263671.1	3E-98
	Copper homeostasis					
*CIA	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5), Copper-translocating P-type ATPase (EC 3.6.3.4)	2925bp	975aa	98%	gi|739087196|WP_036958281.1	0.0
*CIA	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5), Copper-translocating P-type ATPase (EC 3.6.3.4)	2400bp	800aa	99%	gi|1042403368|OBY37647.1	0.0
BCO	Blue copper oxidase CueO precursor	1617bp	539aa	99%	gi|490381034|WP_004260551.1	0.0
*HL	Cytochrome c heme lyase subunit CcmF	1932bp	644aa	99%	gi|491051693|WP_004913344.1	0.0
*HL	Cytochrome c heme lyase subunit CcmL, Cytochrome c heme lyase subunit CcmH	1071bp	357aa	99%	gi|490382689|WP_004262201.1	0.0
CRD	Copper resistance protein D	897bp	299aa	99%	gi|490374296|WP_004253898.1	0.0
CopG	CopG protein	423bp	141aa	98%	gi|491043999|WP_004905661.1	2E-97
copCp	Copper resistance protein C precursor	387bp	129aa	100%	gi|490374293|WP_004253895.1	7E-86
	Streptothricin resistance					
SatA	Streptothricin acetyltransferase, Streptomyces lavendulae type	525bp	175aa	100%	gi|446626810|WP_000704156.1	1E-125
	Adaptation to d-cysteine					
DcyD	D-cysteine desulfhydrase (EC 4.4.1.15)	990bp	330aa	99%	gi|490374828|WP_004254429.1	0.0

		Mercuric reductase				
MIR	Mercuric ion reductase (EC 1.16.1.1)	1686bp	562aa	100%	gi|446131441|WP_000209296.1	0.0
		Resistance to fluoroquinolones				
parC	Topoisomerase IV subunit A (EC 5.99.1.-)	2256bp	752aa	99%	gi|490378099|WP_004257697.1	0.0
parE	Topoisomerase IV subunit B (EC 5.99.1.-)	1896bp	632aa	99%	gi|490378103|WP_004257701.1	0.0
gyrA	DNA gyrase subunit A (EC 5.99.1.3)	2616bp	872aa	99%	gi|491050539|WP_004912190.1	0.0
gyrB	DNA gyrase subunit B (EC 5.99.1.3)	2415bp	805aa	99%	gi|491044587|WP_004906247.1	0.0
		Cobalt-zinc-cadmium resistance				
*CzcD	Cobalt-zinc-cadmium resistance protein	930bp	310aa	100%	gi|490382252|WP_004261765.1	0.0
*CzcA?	Cobalt-zinc-cadmium resistance protein CzcA, Cation efflux system protein CusA	3078bp	1026aa	99%	gi|491044000|WP_004905662.1	0.0
*CusB/CzsB	Probable Co/Zn/Cd efflux system membrane fusion protein	1095bp	365aa	62%	gi|1093685069|WP_070928012.1	6E-144
*CusB/CzsB	Probable Co/Zn/Cd efflux system membrane fusion protein	1110bp	370aa	99%	gi|490381614|WP_004261129.1	0.0
*CusB/CzsB	Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family	1269bp	423aa	99%	gi|491044001|WP_004905663.1	0.0
*CusA	Cobalt-zinc-cadmium resistance protein CzcA, Cation efflux system protein CusA	3078bp	1026aa	99%	gi|491044000|WP_004905662.1	0.0
*CzrR	DNA-binding heavy metal response regulator	684bp	228aa	97%	gi|491044004|WP_004905666.1	1E-153
cusF	Cation efflux system protein CusF precursor	342bp	114aa	97%	gi|491044002|WP_004905664.1	4E-74
*TR	Transcriptional regulator, MerR family	423bp	141aa	99%	gi|490374914|WP_004254515.1	2E-92
		Mercury resistance operon				
MerC	Mercuric transport protein, MerC	426bp	142aa	100%	gi|446445141|WP_000522996.1	3E-98
MerA	Mercuric ion reductase (EC 1.16.1.1)	1686bp	562aa	100%	gi|446131441|WP_000209296.1	0.0
MerD	Mercuric resistance operon coregulator	246bp	82aa	99%	gi|585339711|WP_024221342.1	2E-47
		Copper homeostasis: copper tolerance				
ScsB	Membrane protein, suppressor for copper-sensitivity ScsB	2073bp	691aa	99%	gi|490377422|WP_004257021.1	0.0

ScsC	Secreted protein, suppressor for copper-sensitivity ScsC	732bp	244aa	99%	gi|490377417|WP_004257016.1	7E-169
ScsD	Membrane protein, suppressor for copper-sensitivity ScsD	501bp	167aa	100%	gi|491047306|WP_004908960.1	5E-115
CutF	Copper homeostasis protein CutF precursor, Lipoprotein NlpE involeved in surface adhesion	657bp	219aa	99%	gi|490377815|WP_004257413.1	3E-156
CutE	Apolipoprotein N-acyltransferase (EC 2.3.1.-), Copper homeostasis protein CutE	1530bp	510aa	99%	gi|490377396|WP_004256995.1	0.0
CorC	Magnesium and cobalt efflux protein CorC	1287bp	429aa	99%	gi|1042400154|OBY34443.1	0.0
CorC	Magnesium and cobalt efflux protein CorC	909bp	303aa	99%	gi|291314305|EFE54758.1	0.0
CorC	Magnesium and cobalt efflux protein CorC	1368bp	456aa	100%	gi|491044300|WP_004905961.1	0.0
	Aminoglycoside adenylyltransferases					
AadA1	Streptomycin 3''-O-adenylyltransferase (EC 2.7.7.47), Spectinomycin 9-O-adenylyltransferase	159bp	53aa	100%	gi|487942357|WP_002015823.1	3E-31
AadA1	Streptomycin 3''-O-adenylyltransferase (EC 2.7.7.47), Spectinomycin 9-O-adenylyltransferase	1014bp	338aa	100%	gi|678222195|AIM49564.1	0.0
AadA1	Streptomycin 3''-O-adenylyltransferase (EC 2.7.7.47), Spectinomycin 9-O-adenylyltransferase	792bp	264aa	100%	gi|501453940|WP_012477385.1	0.0
AadA1	Streptomycin 3''-O-adenylyltransferase (EC 2.7.7.47), Spectinomycin 9-O-adenylyltransferase	150bp	50aa	100%	gi|486167809|WP_001531151.1	5E-29
AadA1	Streptomycin 3''-O-adenylyltransferase (EC 2.7.7.47), Spectinomycin 9-O-adenylyltransferase	789bp	263aa	100%	gi|447129059|WP_001206315.1	0.0
AadA2	Spectinomycin 9-O-adenylyltransferase	765bp	255aa	99%	gi|490381153|WP_004260670.1	2E-178
AadA2	Spectinomycin 9-O-adenylyltransferase	159bp	53aa	100%	gi|487942357|WP_002015823.1	3E-31
AadA2	Spectinomycin 9-O-adenylyltransferase	1014bp	338aa	100%	gi|678222195|AIM49564.1	0.0
AadA2	Spectinomycin 9-O-adenylyltransferase	792bp	264aa	100%	gi|501453940|WP_012477385.1	0.0
AadA2	Spectinomycin 9-O-adenylyltransferase	150bp	50aa	100%	gi|486167809|WP_001531151.1	5E-29

AadA2	Spectinomycin 9-O-adenylyltransferase	789bp	263aa	100%	gi|447129059|WP_001206315.1	0.0
		Arsenic resistance				
arsR	Arsenical resistance operon repressor	336bp	112aa	100%	gi|757599390|WP_042847035.1	4E-73
arsR	Arsenical resistance operon repressor	336bp	112aa	99%	gi|739097345|WP_036968128.1	6E-72
arsR	Arsenical resistance operon repressor	189bp	63aa	92%	gi|1116088436|WP_072144547.1	2E-33
arsD	Arsenical resistance operon trans-acting repressor ArsD	366bp	122aa	100%	gi|757599389|WP_042847034.1	2E-85
arsD	Arsenical resistance operon trans-acting repressor ArsD	366bp	122aa	99%	gi|739097347|WP_036968130.1	2E-84
arsA	Arsenical pump-driving ATPase (EC 3.6.3.16)	1752bp	584aa	99%	gi|827610366|KLO01850.1	0.0
arsA	Arsenical pump-driving ATPase (EC 3.6.3.16)	1572bp	584aa	99%	gi|739097348|WP_036968131.1	0.0
arsB	Arsenic efflux pump protein	1290bp	430aa	98%	gi|490357905|WP_004237678.1	0.0
arsB	Arsenic efflux pump protein	1290bp	430aa	99%	gi|739104700|WP_036975217.1	0.0
arsB	Arsenic efflux pump protein	1362bp	454aa	98%	gi|739104700|WP_036975217.1	0.0
arsC	Arsenate reductase (EC 1.20.4.1)	357bp	119aa	99%	gi|490373943|WP_004253545.1	1E-78
arsC	Arsenate reductase (EC 1.20.4.1)	417bp	139aa	91%	gi|749308148|WP_040132278.1	8E-88
arsC	Arsenate reductase (EC 1.20.4.1)	441bp	147aa	100%	gi|739097354|WP_036968137.1	2E-100

Iron acquisition and metabolism

Sigla	Gene	Tamanho	Aminoácidos	Identidade	Sequenciamento	E. value
			Siderophore Aerobactin			
iutA	Aerobactin siderophore receptor IutA TonB-dependent siderophore receptor	2202bp	734aa	99%	gi|490378242|WP_004257840.1	0.0
			Heme, hemin uptake and utilization systems in GramPositives			
*Heme_oxygenases	Hemin transport protein HmuS	1050bp	350aa	99%	gi|491051296|WP_004912947.1	0.0
*Heme_oxygenases	Hemin transport protein HmuS	1050bp	350aa	99%	gi|739087580|WP_036958663.1	0.0
			Ferrous iron transporter EfeUOB, low-pH-induced			
*EfeU	Ferrous iron transport permease EfeU	834bp	278aa	99%	gi|490381107|WP_004260624.1	0.0
EfeB	Ferrous iron transport peroxidase EfeB	1275bp	425aa	99%	gi|490381112|WP_004260629.1	0.0
			Encapsulating protein for DyP-type peroxidase and ferritin-like protein oligomers			
DyP	Predicted dye-decolorizing peroxidase (DyP), encapsulated subgroup	900bp	300aa	99%	gi|490385387|WP_004264885.1	0.0
Yfe	Predicted outer membrane lipoprotein YfeY	606bp	202aa	99%	gi|915327114|WP_050763802.1	4E-145
			Hemin transport system			
HBP	Periplasmic hemin-binding protein	822bp	274aa	99%	gi|491051298|WP_004912949.1	0.0
*Rec	TonB-dependent hemin , ferrichrome receptor	2019bp	673aa	91%	gi|739087359|WP_036958444.1	0.0
*Rec	TonB-dependent hemin , ferrichrome receptor	2145bp	715aa	99%	gi|490384250|WP_004263756.1	0.0
hmuS	Hemin transport protein HmuS	1050bp	350aa	99%	gi|491051296|WP_004912947.1	0.0
hmuS	Hemin transport protein HmuS	1050bp	350aa	99%	gi|739087580|WP_036958663.1	0.0

ATPb	ABC-type hemin transport system, ATPase component	789bp	263aa	98%	gi|1172252176|WP_080641516.1	0.0
ATPb	ABC-type hemin transport system, ATPase component	768bp	256aa	99%	gi|1042402961|OBY37241.1	2E-178
PP_7	Hemin ABC transporter, permease protein	1002bp	334aa	99%	gi|491051302|WP_004912953.1	0.0
PP_7	Hemin ABC transporter, permease protein	1017bp	339aa	100%	gi|1042402962|OBY37242.1	0.0
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	744bp	248aa	97%	gi|490382765|WP_004262277.1	1E-162
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	966bp	322aa	98%	gi|490378848|WP_004258445.1	0.0
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	720bp	240aa	99%	gi|739086610|WP_036957695.1	6E-173
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	783bp	261aa	99%	gi|739087479|WP_036958564.1	3E-179
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	756bp	252aa	97%	gi|490373999|WP_004253601.1	1E-165
	Heme, hemin uptake and utilization systems in GramNegatives					
HBP	Periplasmic hemin-binding protein	822bp	274aa	99%	gi|491051298|WP_004912949.1	0.0
fhuC	Ferrichrome transport ATP-binding protein FhuC (TC 3.A.1.14.3)	783bp	261aa	100%	gi|490382157|WP_004261670.1	0.0
fhuC	Ferrichrome transport ATP-binding protein FhuC (TC 3.A.1.14.3)	786bp	262aa	100%	gi|757595221|WP_042843418.1	8E-180
FCR	TonB-dependent hemin , ferrichrome receptor	2019bp	673aa	91%	gi|739087359|WP_036958444.1	0.0
FCR	TonB-dependent hemin , ferrichrome receptor	2145bp	715aa	99%	gi|490384250|WP_004263756.1	0.0
FR	Flavin reductase (EC 1.5.1.30)	624bp	208aa	99%	gi|739087413|WP_036958498.1	7E-143
ETFb	Electron transfer flavoprotein, beta subunit	756bp	252aa	99%	gi|490378882|WP_004258479.1	6E-168
ParA	Paraquat-inducible protein A	1227bp	409aa	99%	gi|1102614758|WP_071585858.1	0.0
ParA	Paraquat-inducible protein A	1227bp	409aa	99%	gi|739086601|WP_036957686.	0.0

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ParB	Paraquat-inducible protein B	1650bp	550aa	99%	gi|490376536|WP_004256135.1	0.0
ParB	Paraquat-inducible protein B	2340bp	780aa	99%	gi|490374304|WP_004253906.1	0.0
hmuS	Hemin transport protein HmuS	1050bp	350aa	99%	gi|491051296|WP_004912947.1	0.0
hmuS	Hemin transport protein HmuS	1050bp	350aa	99%	gi|739087580|WP_036958663.1	0.0
PP_7	Hemin ABC transporter, permease protein	1002bp	334aa	99%	gi|491051302|WP_004912953.1	0.0
PP_7	Hemin ABC transporter, permease protein	1017bp	339aa	100%	gi|1042402962|OBY37242.1	0.0
ATPb	ABC-type hemin transport system, ATPase component	789bp	263aa	98%	gi|1172252176|WP_080641516.1	0.0
ATPb	ABC-type hemin transport system, ATPase component	768bp	256aa	99%	gi|1042402961|OBY37241.1	2E-178
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	744bp	248aa	97%	gi|490382765|WP_004262277.1	1E-162
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	966bp	322aa	98%	gi|490378848|WP_004258445.1	0.0
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	720bp	240aa	99%	gi|739086610|WP_036957695.1	6E-173
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	783bp	261aa	99%	gi|739087479|WP_036958564.1	3E-179
TonB	Ferric siderophore transport system, periplasmic binding protein TonB	756bp	252aa	97%	gi|490373999|WP_004253601.1	1E-165

Phages, Prophages

Sigla	Gene	Tamanho	Aminoácidos	Identidade	Sequenciamento	E. value
Transposable elements - CBSS-203122.12.peg.188						
R1	TniB NTP-binding protein	510bp	170aa	100%	gi|213054790|ACJ39692.1	2E-120
R8	MG(2+) CHELATASE FAMILY PROTEIN ComM-related protein	1527bp	509aa	99%	gi|491044471|WP_004906131.1	0.0
R9	MG(2+) CHELATASE FAMILY PROTEIN ComM-related protein	1527bp	509aa	99%	gi|491044471|WP_004906131.1	0.0
Phages, Prophages, Transposable elements, Plasmids - Integrons						
IntI2	Integron integrase IntI2	537bp	179aa	100%	gi|445994041|WP_000071896.1	8E-125
IntI2	Integron integrase IntI2	537bp	179aa	100%	gi|446419664|WP_000497519.1	9E-75
IntIPac	Integron integrase IntIPac	1014bp	338bp	100%	gi|471237918|EMR15449.1	0.0
Phages, Prophages - Phage tail proteins						
TP	Phage tail protein	429bp	143aa	100%	gi|739091102|WP_036962064.1	2E-98
*Measure	Phage tail length tape-measure protein	2700bp	900aa	98%	gi|873900395|WP_048606828.1	0.0
*Tube	Phage major tail tube protein	516bp	172aa	100%	gi|1101998870|WP_071548731.1	8E-120
*Sheath	Phage tail sheath monomer	1530bp	510aa	100%	gi|1101998871|WP_071548732.1	0.0
Phages, Prophages - Phage replication						
*Rep	Phage replication protein	2424bp	808aa	93%	gi|1101998888|WP_071548749.1	0.0
*dPol_3	DNA polymerase III alpha subunit (EC 2.7.7.7)	3483bp	1161aa	100%	gi|739086905|WP_036957990.1	0.0
Phages, Prophages - Phage tail proteins 2						
TMP1_1	Phage tape measure	447bp	149aa	99%	gi|873900393|WP_048606826.1	1E-99
TSM	Phage tail sheath monomer	1530bp	510aa	100%	gi|1101998871|WP_071548732	0.0

TMP	Phage tail length tape-measure protein	2700bp	900aa	98%	gi|873900395|WP_048606828.1	0.0
	Phages, Prophages - Phage tail fiber proteins					
TFP	Phage tail fiber protein	1530bp	510aa	99%	gi|1101502589|APC13982.1	0.0
TFAP	Phage tail fiber assembly protein	645bp	215aa	100%	gi|1101502588|APC13981.1	2E-149
TFP2	Phage tail fibers	612bp	204aa	100%	gi|873900403|WP_048606836.1	2E-146
	Phages, Prophages - Phage capsid proteins					
*Generic	Phage capsid and scaffold	444bp	148aa	100%	gi|739091104|WP_036962066.1	3.00E-108
MajCap	Phage major capsid protein	1095bp	365aa	99%	gi|1101998881|WP_071548742.1	0.0
*Scaffolding	Phage capsid scaffolding protein	828bp	276aa	99%	gi|1101998882|WP_071548743.1	0.0
HCSP	Phage head completion-stabilization protein	477bp	159aa	100%	gi|1101998879|WP_071548740.1	4.0E-108

Motility and Chemotaxis

Sigla	Gene	Tamanho	Aminoácidos	Identidade	Sequenciamento	E. value
			Bacterial Chemotaxis			
aer	Aerotaxis sensor receptor protein	1533bp	511aa	98%	gi|739086922|WP_036958007.1	0.0
tsr	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	1653bp	551aa	98%	gi|490373823|WP_004253426.1	0.0
tsr	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	1569bp	523aa	99%	gi|490376118|WP_004255718.1	0.0
tsr	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	1602bp	534aa	99%	gi|490376121|WP_004255721.1	0.0
tsr	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	1488bp	496aa	99%	gi|490378843|WP_004258440.1	0.0
*cheW-V	Positive regulator of CheA protein activity (CheW)	498bp	166aa	100%	gi|491048180|WP_004909833.1	3E-111
cheA	Signal transduction histidine kinase CheA (EC 2.7.3.-)	2058bp	686aa	99%	gi|739086771|WP_036957856.1	0.0
cheY	Chemotaxis regulator - transmits chemoreceptor signals to flagelllar motor components CheY	393bp	131aa	100%	gi|490376105|WP_004255705.1	7E-85
cheZ	Chemotaxis response - phosphatase CheZ	639bp	213aa	99%	gi|1042399717|OBY34011.1	8E-142
cheB	Chemotaxis response regulator protein-glutamate methylesterase CheB (EC 3.1.1.61)	1068bp	356aa	99%	gi|490376109|WP_004255709.1	0.0
fliG	Flagellar motor switch protein FliG	993bp	331aa	100%	gi|490376000|WP_004255600.1	0.0
fliM	Flagellar motor switch protein FliM	1008bp	336aa	99%	gi|490376019|WP_004255619.1	0.0
fliN	Flagellar motor switch protein FliN	417bp	139aa	100%	gi|490376021|WP_004255621.1	1E-90
malE	Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein MalE	1191bp	397aa	92%	gi|1057035456|WP_068445917.1	0.0
dppA	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	1608bp	536aa	100%	gi|490383128|WP_004262639.1	0.0
dppA	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	1560bp	520aa	99%	gi|739086975|WP_036958060.1	0.0

cheR	Chemotaxis protein methyltransferase CheR (EC 2.1.1.80)	837bp	279aa	100%	gi|490376113|WP_004255713.1	0.0
			Flagellum			
flgB	Flagellar basal-body rod protein FlgB	414bp	138aa	100%	gi|490376069|WP_004255669.1	2E-91
flgC	Flagellar basal-body rod protein FlgC	405bp	135aa	100%	gi|491048215|WP_004909868.1	3E-89
FlgD	Flagellar basal-body rod modification protein FlgD	858bp	286aa	99%	gi|490376064|WP_004255664.1	0.0
flgE	Flagellar hook protein FlgE	1221bp	407aa	96%	gi|873900357|WP_048606790.1	0.0
flgF	Flagellar basal-body rod protein FlgF	756bp	252aa	100%	gi|490376059|WP_004255659.1	2E-174
flgG	Flagellar basal-body rod protein FlgG	783bp	261aa	99%	gi|490376057|WP_004255657.1	0.0
FlgH	Flagellar L-ring protein FlgH	750bp	250aa	100%	gi|291314697|EFE55150.1	0.0
flgI	Flagellar P-ring protein FlgI	1104bp	368aa	100%	gi|490376051|WP_004255651.1	0.0
flgJ	Flagellar protein FlgJ [peptidoglycan hydrolase] (EC 3.2.1.-)	981bp	327aa	98%	gi|490376048|WP_004255648.1	0.0
flgK	Flagellar hook-associated protein FlgK	1644bp	548aa	99%	gi|739086767|WP_036957852.1	0.0
flgL	Flagellar hook-associated protein FlgL	936bp	312aa	98%	gi|491048236|WP_004909889.1	0.0
FlhA	Flagellar biosynthesis protein FlhA	2100bp	700aa	100%	gi|490376087|WP_004255687.1	0.0
fliE	Flagellar hook-basal body complex protein FliE	312bp	104aa	100%	gi|490375994|WP_004255594.1	4E-64
fliF	Flagellar M-ring protein FliF	1686bp	562aa	99%	gi|490375997|WP_004255597.1	0.0
fliG	Flagellar motor switch protein FliG	993bp	331aa	100%	gi|490376000|WP_004255600.1	0.0
fliH	Flagellar assembly protein FliH	729bp	243aa	99%	gi|490376003|WP_004255603.1	8E-177
FliI	Flagellum-specific ATP synthase FliI	1311bp	437aa	99%	gi|490376006|WP_004255606.1	0.0
fliK	Flagellar hook-length control protein FliK	1368bp	456aa	97%	gi|490376013|WP_004255613.1	0.0
fliJ	Flagellar protein FliJ	444bp	148aa	99%	gi|490376009|WP_004255609.1	3E-100
fliM	Flagellar motor switch protein FliM	1008bp	336aa	99%	gi|490376019|WP_004255619.1	0.0
fliN	Flagellar motor switch protein FliN	417bp	139aa	100%	gi|490376021|WP_004255621.1	1E-90
fliP	Flagellar biosynthesis protein FliP	744bp	248aa	99%	gi|739086765|WP_036957850.1	3E-167
fliQ	Flagellar biosynthesis protein FliQ	270bp	90aa	99%	gi|490376030|WP_004255630.1	2E-52
FliR	Flagellar biosynthesis protein FliR	780bp	260aa	99%	gi|490376033|WP_004255633.1	7E-180

*Flagellar-Regulation	RNA polymerase sigma factor RpoD	1854bp	618aa	100%	gi|1102614763|WP_071585863.1	0.0
*Flagellar-Regulation	Flagellar transcriptional activator FlhC	591bp	197aa	100%	gi|490376132|WP_004255732.1	1E-140
*Flagellar-Regulation	Flagellar biosynthesis protein FliZ	519bp	173aa	100%	gi|490376157|WP_004255757.1	4E-123
*Flagellar-Regulation	RNA polymerase sigma-54 factor RpoN	1446bp	482aa	99%	gi|490378708|WP_004258305.1	0.0
*Flagellar-Regulation	RNA polymerase sigma factor for flagellar operon	726bp	242aa	99%	gi|291314661|EFE55114.1	0.0
*Flagellin	Flagellar biosynthesis protein FliC	1170bp	390aa	87%	gi|1055836465|WP_067424616.1	0.0
fliD	Flagellar hook-associated protein FliD	1437bp	479aa	90%	gi|1057031755|WP_068442704.1	0.0
fliS	Flagellar biosynthesis protein FliS	399bp	133aa	100%	gi|491048316|WP_004909969.1	1E-86
fliT	Flagellar biosynthesis protein FliT	390bp	130aa	99%	gi|490375964|WP_004255564.1	2E-85
*fliO	Flagellar biosynthesis protein FliO	459bp	153aa	99%	gi|490376024|WP_004255624.1	7E-102
FlhB	Flagellar biosynthesis protein FlhB	1152bp	384aa	99%	gi|490376088|WP_004255688.1	0.0
MotA	Flagellar motor rotation protein MotA	954bp	318aa	99%	gi|291314724|EFE55177.1	0.0
MotB	Flagellar motor rotation protein MotB	918bp	306aa	99%	gi|490376126|WP_004255726.1	0.0
*flhD	Flagellar transcriptional activator FlhD	351bp	117aa	100%	gi|739086775|WP_036957860.1	3E-74
fliL	Flagellar biosynthesis protein FliL	480bp	160aa	99%	gi|490376015|WP_004255615.1	3E-107
		Flagellar motility				
FlhA	Flagellar biosynthesis protein FlhA	2100bp	700aa	100%	gi|490376087|WP_004255687.1	0.0
fliM	Flagellar motor switch protein FliM	1008bp	336aa	99%	gi|490376019|WP_004255619.1	0.0
fliN	Flagellar motor switch protein FliN	417bp	139aa	100%	gi|490376021|WP_004255621.1	1E-90
cheY	Chemotaxis regulator - transmits chemoreceptor signals to flagelllar motor components CheY	393bp	131aa	100%	gi|490376105|WP_004255705.1	7E-85
cheA	Signal transduction histidine kinase CheA (EC 2.7.3.-)	2058bp	686aa	99%	gi|739086771|WP_036957856.1	0.0
FlhB	Flagellar biosynthesis protein FlhB	1152bp	384aa	99%	gi|490376088|WP_004255688.1	0.0

FliI	Flagellum-specific ATP synthase FliI	1311bp	437aa	99%	gi|490376006|WP_004255606.1	0.0
FliR	Flagellar biosynthesis protein FliR	780bp	260aa	99%	gi|490376033|WP_004255633.1	7E-180
FlgD	Flagellar basal-body rod modification protein FlgD	858bp	286aa	99%	gi|490376064|WP_004255664.1	0.0
FlgH	Flagellar L-ring protein FlgH	750bp	250aa	100%	gi|291314697|EFE55150.1	0.0
MotA	Flagellar motor rotation protein MotA	954bp	318aa	99%	gi|291314724|EFE55177.1	0.0
MotB	Flagellar motor rotation protein MotB	918bp	306aa	99%	gi|490376126|WP_004255726.1	0.0
FliA	RNA polymerase sigma factor for flagellar operon	726bp	242aa	99%	gi|291314661|EFE55114.1	9E-167
RpoN	RNA polymerase sigma-54 factor RpoN	1446bp	482aa	99%	gi|490378708|WP_004258305.1	0.0

Suplemento II

Localização das Ilhas genômicas PR01

Island start	Island end	Length	Method	Gene ID	Locus	Gene start	Gene end	Strand	Product
121511	130328	8817	Predicted by at least one method		Predicted_04029	121511	121912	1	hypothetical protein
121511	130328	8817	Predicted by at least one method	mrpA_4	Predicted_04030	121905	122438	1	Major MR/P fimbria protein precursor
121511	130328	8817	Predicted by at least one method		Predicted_04330	123815	124828	1	hypothetical protein
121511	130328	8817	Predicted by at least one method		Predicted_04358	126856	127881	-1	hypothetical protein
121511	130328	8817	Predicted by at least one method		Predicted_04359	127897	128157	-1	hypothetical protein
121511	130328	8817	Predicted by at least one method	papD_11	Predicted_04180	129618	130328	-1	Chaperone protein PapD precursor
1629087	1715575	86488	Predicted by at least one method	hcpC_6	Predicted_04197	1629087	1630115	-1	Putative beta-lactamase HcpC precursor
1629087	1715575	86488	Predicted by at least one method	rhsC	Predicted_00766	1631840	1634869	-1	Putative deoxyribonuclease RhsC
1629087	1715575	86488	Predicted by at least one method		Predicted_00765	1635002	1635727	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00764	1636462	1636701	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00763	1636774	1637052	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00762	1637039	1638766	-1	Zinc-binding domain of primase-helicase
1629087	1715575	86488	Predicted by at least one method		Predicted_00761	1638944	1639330	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00760	1639437	1639583	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00759	1639788	1640639	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00758	1640714	1641271	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00757	1641345	1641563	-1	hypothetical protein
162908	1715575	86488	Predicted by at least		Predicted_0075	164157	164184	-1	hypothetical protein

7			one method		6	7	6		
1629087	1715575	86488	Predicted by at least one method	yfbR_1	Predicted_00755	164183	164244	-1	5'-deoxynucleotidase YfbR
1629087	1715575	86488	Predicted by at least one method		Predicted_00754	164251	164271	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00753	164292	164537	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00752	164546	164584	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00751	164608	164663	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00750	164670	164700	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method	hhaIM	Predicted_00749	164720	164882	-1	Modification methylase HhaI
1629087	1715575	86488	Predicted by at least one method		Predicted_00748	164890	164920	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00747	164928	164962	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00746	164982	165017	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00745	165024	165043	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00744	165049	165076	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00743	165077	165122	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00742	165121	165160	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method	ascD_2	Predicted_00741	165166	165188	-1	CDP-6-deoxy-L-threo-D-glycero-4-hexulose-3-dehydrase reductase
1629087	1715575	86488	Predicted by at least one method		Predicted_00740	165195	165283	-1	DNA methylase
1629087	1715575	86488	Predicted by at least one method		Predicted_00739	165291	165341	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00738	165350	165404	-1	hypothetical protein

1629087	1715575	86488	Predicted by at least one method		Predicted_00737	1654307	1654642	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00736	1654704	1656500	-1	von Willebrand factor type A domain
1629087	1715575	86488	Predicted by at least one method		Predicted_00735	1656585	1657862	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00734	1658062	1659072	-1	YqaJ-like viral recombinase domain
1629087	1715575	86488	Predicted by at least one method		Predicted_00733	1659135	1660124	-1	RecT family
1629087	1715575	86488	Predicted by at least one method	ssb_2	Predicted_00732	1660219	1660746	-1	Single-stranded DNA-binding protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00731	1660810	1661718	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method	cobS_3	Predicted_00730	1661729	1662697	-1	Aerobic cobaltochelatase subunit CobS
1629087	1715575	86488	Predicted by at least one method		Predicted_00729	1662917	1663102	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00728	1663406	1663726	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00727	1664020	1664661	1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00726	1664784	1665644	1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00725	1665683	1668481	-1	conjugal transfer mating pair stabilization protein TraN
1629087	1715575	86488	Predicted by at least one method		Predicted_00724	1668597	1669604	-1	TraU protein
1629087	1715575	86488	Predicted by at least one method	yfgF	Predicted_00723	1669601	1670272	-1	Cyclic di-GMP phosphodiesterase YfgF
1629087	1715575	86488	Predicted by at least one method		Predicted_00722	1670269	1671534	-1	Type-F conjugative transfer system pilin assembly protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00721	1671497	1672027	-1	Peptidase S26
1629087	1715575	86488	Predicted by at least one method		Predicted_00720	1672024	1672341	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00719	1672356	1674803	-1	F pilus assembly Type-IV secretion system for plasmid

									transfer
1629087	1715575	86488	Predicted by at least one method	dsbC_3	Predicted_00718	1674800	1675507	-1	Thiol:disulfide interchange protein DsbC precursor
1629087	1715575	86488	Predicted by at least one method		Predicted_00717	1675656	1681187	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00716	1681388	1681771	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00715	1681784	1682362	-1	Type IV conjugative transfer system lipoprotein (TraV)
1629087	1715575	86488	Predicted by at least one method		Predicted_00714	1682359	1683675	-1	Bacterial conjugation TrbI-like protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00713	1683672	1684589	-1	TraK protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00712	1684573	1685199	-1	TraE protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00711	1685622	1685999	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00710	1685999	1686142	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00709	1686323	1686985	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00708	1686985	1687362	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00707	1687372	1687818	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00706	1687828	1688457	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00705	1688414	1688959	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00704	1689009	1690874	-1	AAA-like domain
1629087	1715575	86488	Predicted by at least one method		Predicted_00703	1690871	1693849	-1	Putative helicase
1629087	1715575	86488	Predicted by at least one method		Predicted_00702	1694017	1694634	1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method	topB_1	Predicted_00701	1694849	1697041	1	DNA topoisomerase 3

1629087	1715575	86488	Predicted by at least one method		Predicted_00700	1697056	1697544	1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00699	1697636	1697914	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00698	1698093	1699367	-1	Transposase DDE domain
1629087	1715575	86488	Predicted by at least one method		Predicted_00697	1699546	1700163	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00696	1700257	1700475	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00695	1700479	1700742	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00694	1700681	1701337	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method	ydiO	Predicted_00693	1701337	1702764	-1	putative BsuMI modification methylase subunit YdiO
1629087	1715575	86488	Predicted by at least one method		Predicted_00692	1702768	1703268	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00691	1703277	1703588	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00690	1703594	1704100	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00689	1704093	1704767	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00688	1704742	1705023	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00687	1705016	1705393	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00686	1705712	1705855	1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00685	1705947	1706582	1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method	korB	Predicted_00684	1706956	1708137	-1	Transcriptional repressor protein KorB
1629087	1715575	86488	Predicted by at least one method	soj	Predicted_00683	1708141	1708926	-1	Sporulation initiation inhibitor protein Soj
1629087	1715575	86488	Predicted by at least one method		Predicted_00682	1709100	1709411	-1	hypothetical protein

1629087	1715575	86488	Predicted by at least one method		Predicted_00681	1709510	1709734	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method	bin3_2	Predicted_00680	1709731	1710468	-1	Putative transposon Tn552 DNA-invertase bin3
1629087	1715575	86488	Predicted by at least one method		Predicted_00679	1710575	1711066	1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method	dhfrI	Predicted_00200	1712632	1713105	1	Dihydrofolate reductase type 1
1629087	1715575	86488	Predicted by at least one method		Predicted_00201	1713200	1713724	1	TDP-fucosamine acetyltransferase
1629087	1715575	86488	Predicted by at least one method	ant1_2	Predicted_00202	1713782	1714570	1	Streptomycin 3''-adenylyltransferase
1629087	1715575	86488	Predicted by at least one method		Predicted_00203	1714646	1715143	1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method		Predicted_00204	1715204	1715575	1	hypothetical protein
1690871	1705023	14152	Predicted by at least one method		Predicted_00704	1689009	1690874	-1	AAA-like domain
1690871	1705023	14152	Predicted by at least one method		Predicted_00703	1690871	1693849	-1	Putative helicase
1690871	1705023	14152	Predicted by at least one method		Predicted_00702	1694017	1694634	1	hypothetical protein
1690871	1705023	14152	Predicted by at least one method	topB_1	Predicted_00701	1694849	1697041	1	DNA topoisomerase 3
1690871	1705023	14152	Predicted by at least one method		Predicted_00700	1697056	1697544	1	hypothetical protein
1690871	1705023	14152	Predicted by at least one method		Predicted_00699	1697636	1697914	-1	hypothetical protein
1690871	1705023	14152	Predicted by at least one method		Predicted_00698	1698093	1699367	-1	Transposase DDE domain
1690871	1705023	14152	Predicted by at least one method		Predicted_00697	1699546	1700163	-1	hypothetical protein
1690871	1705023	14152	Predicted by at least one method		Predicted_00696	1700257	1700475	-1	hypothetical protein
1690871	1705023	14152	Predicted by at least one method		Predicted_00695	1700479	1700742	-1	hypothetical protein
1690871	1705023	14152	Predicted by at least one method		Predicted_00694	1700681	1701337	-1	hypothetical protein

1690871	1705023	14152	Predicted by at least one method	ydiO	Predicted_00693	1701337	1702764	-1	putative BsuMI modification methylase subunit YdiO
1690871	1705023	14152	Predicted by at least one method		Predicted_00692	1702768	1703268	-1	hypothetical protein
1690871	1705023	14152	Predicted by at least one method		Predicted_00691	1703277	1703588	-1	hypothetical protein
1690871	1705023	14152	Predicted by at least one method		Predicted_00690	1703594	1704100	-1	hypothetical protein
1690871	1705023	14152	Predicted by at least one method		Predicted_00689	1704093	1704767	-1	hypothetical protein
1690871	1705023	14152	Predicted by at least one method		Predicted_00688	1704742	1705023	-1	hypothetical protein
1690871	1705023	14152	Predicted by at least one method		Predicted_00687	1705016	1705393	-1	hypothetical protein
1708141	1717256	9115	Predicted by at least one method	soj	Predicted_00683	1708141	1708926	-1	Sporulation initiation inhibitor protein Soj
1708141	1717256	9115	Predicted by at least one method		Predicted_00682	1709100	1709411	-1	hypothetical protein
1708141	1717256	9115	Predicted by at least one method		Predicted_00681	1709510	1709734	-1	hypothetical protein
1708141	1717256	9115	Predicted by at least one method	bin3_2	Predicted_00680	1709731	1710468	-1	Putative transposon Tn552 DNA-invertase bin3
1708141	1717256	9115	Predicted by at least one method		Predicted_00679	1710575	1711066	1	hypothetical protein
1708141	1717256	9115	Predicted by at least one method	dhfrI	Predicted_00200	1712632	1713105	1	Dihydrofolate reductase type 1
1708141	1717256	9115	Predicted by at least one method		Predicted_00201	1713200	1713724	1	TDP-fucosamine acetyltransferase
1708141	1717256	9115	Predicted by at least one method	ant1_2	Predicted_00202	1713782	1714570	1	Streptomycin 3''-adenylyltransferase
1708141	1717256	9115	Predicted by at least one method		Predicted_00203	1714646	1715143	1	hypothetical protein
1708141	1717256	9115	Predicted by at least one method		Predicted_00204	1715204	1715575	1	hypothetical protein
1708141	1717256	9115	Predicted by at least one method		Predicted_00205	1716048	1717256	1	Transposase DDE domain
1708141	1717256	9115	Predicted by at least one method		Predicted_00206	1717253	1717831	1	hypothetical protein

1730364	1799760	69396	Predicted by at least one method		Predicted_00218	1729735	1730367	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00219	1730364	1730924	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00220	1731267	1731755	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00221	1731778	1732104	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00222	1732091	1732522	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00223	1732529	1732783	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00224	1732780	1733337	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00225	1733334	1733798	-1	ASCH domain
1730364	1799760	69396	Predicted by at least one method		Predicted_00226	1733795	1734097	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00227	1734424	1735473	1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00228	1735625	1736710	1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00229	1736728	1737057	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00230	1737054	1737827	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00231	1737814	1738392	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00232	1738501	1739025	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00233	1739025	1739399	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method	hpaIIM	Predicted_00234	1739414	1740319	-1	Modification methylase HpaII
1730364	1799760	69396	Predicted by at least one method		Predicted_00235	1740574	1740762	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00236	1740774	1741178	-1	hypothetical protein

1730364	1799760	69396	Predicted by at least one method	nrdH_1	Predicted_00237	1741192	1741521	-1	Glutaredoxin-like protein NrdH
1730364	1799760	69396	Predicted by at least one method		Predicted_00238	1741699	1742010	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00239	1742068	1742442	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00240	1742521	1743201	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method	dinG_1	Predicted_00241	1743242	1745302	-1	putative ATP-dependent helicase DinG
1730364	1799760	69396	Predicted by at least one method		Predicted_00242	1745409	1745717	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00243	1745735	1746013	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method	virB	Predicted_00244	1746290	1747309	-1	Virulence regulon transcriptional activator VirB
1730364	1799760	69396	Predicted by at least one method	parA_1	Predicted_00245	1747312	1748559	-1	Plasmid partition protein A
1730364	1799760	69396	Predicted by at least one method		Predicted_00246	1748775	1749053	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00247	1749110	1749454	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00248	1749560	1749820	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00249	1749851	1750087	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00250	1750084	1750353	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00251	1750404	1750607	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00252	1750671	1751111	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00253	1751320	1751523	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00254	1751533	1751868	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00255	1751914	1752141	-1	hypothetical protein

1730364	1799760	69396	Predicted by at least one method		Predicted_00256	175216	175239	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00257	175256	175308	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00258	175325	175355	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00259	175362	175429	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00260	175436	175474	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method	ascD_1	Predicted_00261	175494	175520	-1	CDP-6-deoxy-L-threo-D-glycero-4-hexulose-3-dehydrase reductase
1730364	1799760	69396	Predicted by at least one method		Predicted_00262	175538	175568	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00263	175588	175630	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00264	175642	175676	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00265	175700	175760	1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00266	175748	175797	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00267	175804	175847	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00268	175948	176051	1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00269	176053	176106	1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00270	176109	176165	1	Transglycosylase SLT domain
1730364	1799760	69396	Predicted by at least one method		Predicted_00271	176164	176217	1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method	flhC_1	Predicted_00272	176217	176269	1	Flagellar transcriptional regulator FlhC
1730364	1799760	69396	Predicted by at least one method		Predicted_00273	176269	176311	1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00274	176325	176400	1	hypothetical protein

1730364	1799760	69396	Predicted by at least one method		Predicted_00275	1764054	1766768	-1	conjugal transfer mating pair stabilization protein TraN
1730364	1799760	69396	Predicted by at least one method		Predicted_00276	1766961	1767137	1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00277	1767190	1770348	-1	TraG-like protein, N-terminal region
1730364	1799760	69396	Predicted by at least one method		Predicted_00278	1770363	1771799	-1	Conjugative relaxosome accessory transposon protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00279	1771821	1772882	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00280	1772860	1773198	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00281	1773448	1773621	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00282	1773688	1773900	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00283	1773943	1774452	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00284	1774490	1774879	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00285	1774915	1775175	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00286	1775219	1775446	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00287	1775450	1775764	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00288	1775825	1776310	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00289	1776409	1778187	-1	von Willebrand factor type A domain
1730364	1799760	69396	Predicted by at least one method		Predicted_00290	1778239	1778520	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00291	1778573	1779838	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method	cobS_1	Predicted_00292	1779938	1780999	-1	Aerobic cobaltochelatase subunit CobS
1730364	1799760	69396	Predicted by at least one method		Predicted_00293	1781066	1781440	-1	hypothetical protein

1730364	1799760	69396	Predicted by at least one method		Predicted_00294	178180	178292	-1	YqaJ-like viral recombinase domain
1730364	1799760	69396	Predicted by at least one method		Predicted_00295	178298	178452	-1	recombination and repair protein RecT
1730364	1799760	69396	Predicted by at least one method		Predicted_00296	178461	178530	-1	Single-strand binding protein family
1730364	1799760	69396	Predicted by at least one method		Predicted_00297	178577	178620	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00298	178628	178689	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00299	178740	178815	1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00300	178829	178882	1	Sel1 repeat
1730364	1799760	69396	Predicted by at least one method		Predicted_00301	178887	178996	-1	TraU protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00302	178996	179121	-1	Type-F conjugative transfer system pilin assembly protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00303	179121	179173	-1	signal peptidase I
1730364	1799760	69396	Predicted by at least one method		Predicted_00304	179175	179203	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00305	179202	179451	-1	AAA-like domain
1730364	1799760	69396	Predicted by at least one method	dsbC_1	Predicted_00306	179454	179528	-1	putative thiol:disulfide interchange protein DsbC precursor
1730364	1799760	69396	Predicted by at least one method		Predicted_00307	179569	179622	-1	Type IV conjugative transfer system lipoprotein (TraV)
1730364	1799760	69396	Predicted by at least one method		Predicted_00308	179622	179761	-1	Bacterial conjugation TrbI-like protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00309	179762	179871	-1	TraK protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00310	179888	179947	-1	TraE protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00311	179947	179976	-1	TraL protein
184302	1848130	5101	Predicted by at least		Predicted_0036	184302	184474	-1	hypothetical protein

9			one method		4	9	4		
1843029	1848130	5101	Predicted by at least one method		Predicted_00365	184486 9	184547	-1	hypothetical protein
1843029	1848130	5101	Predicted by at least one method		Predicted_00366	184555 0	184600 2	-1	hypothetical protein
1843029	1848130	5101	Predicted by at least one method		Predicted_00367	184601 5	184648 2	-1	hypothetical protein
1843029	1848130	5101	Predicted by at least one method		Predicted_00368	184657 1	184721 8	-1	hypothetical protein
1843029	1848130	5101	Predicted by at least one method		Predicted_00369	184725 6	184762 4	-1	hypothetical protein
1843029	1848130	5101	Predicted by at least one method		Predicted_00370	184762 1	184813 0	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00366	184555 0	184600 2	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00367	184601 5	184648 2	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00368	184657 1	184721 8	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00369	184725 6	184762 4	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00370	184762 1	184813 0	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method	rdgC_1	Predicted_00371	184818 4	184942 2	-1	Recombination-associated protein RdgC
1845550	1871329	25779	Predicted by at least one method	dam_1	Predicted_00372	184941 9	185024 0	-1	DNA adenine methylase
1845550	1871329	25779	Predicted by at least one method		Predicted_00373	185029 5	185093 6	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method	dnaN_1	Predicted_00374	185116 3	185243 1	-1	DNA polymerase III subunit beta
1845550	1871329	25779	Predicted by at least one method		Predicted_00375	185258 0	185291 2	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00376	185290 9	185337 0	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00377	185342 5	185394 6	-1	hypothetical protein
184555	1871329	25779	Predicted by at least		Predicted_0037	185405	185447	-1	hypothetical protein

0			one method		8	3	8		
1845550	1871329	25779	Predicted by at least one method		Predicted_00379	185464	185493	1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00380	185497	185530	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00381	185533	185581	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00382	185591	185611	1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00383	185623	185658	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method	ssb_1	Predicted_00384	185665	185717	-1	Single-stranded DNA-binding protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00385	185742	185785	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00386	185786	185815	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method	hflK_1	Predicted_00387	185826	185918	-1	Modulator of FtsH protease HflK
1845550	1871329	25779	Predicted by at least one method		Predicted_00388	185920	185963	-1	NfeD-like C-terminal, partner-binding
1845550	1871329	25779	Predicted by at least one method		Predicted_00389	185992	186008	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00390	186013	186104	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00391	186104	186153	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00392	186157	186220	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00393	186220	186295	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00394	186324	186350	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00395	186381	186588	-1	AAA-like domain
1845550	1871329	25779	Predicted by at least one method		Predicted_00396	186587	186727	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method	tnpR_1	Predicted_00397	186734	186792	-1	Transposon gamma-delta

0			one method		7	7	8		resolvase
1845550	1871329	25779	Predicted by at least one method		Predicted_00398	186811 3	186846 3	1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method	higA_1	Predicted_00399	186846 5	186876 4	1	Antitoxin HigA
1845550	1871329	25779	Predicted by at least one method		Predicted_00400	186890 5	186992 1	1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00401	186997 2	187037 3	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00402	187080 5	187132 9	-1	LexA repressor
1880359	1892698	12339	Predicted by at least one method	comR_1	Predicted_00417	188035 9	188094 0	-1	HTH-type transcriptional repressor ComR
1880359	1892698	12339	Predicted by at least one method		Predicted_00418	188108 9	188166 1	-1	hypothetical protein
1880359	1892698	12339	Predicted by at least one method		Predicted_00419	188179 7	188248 9	-1	hypothetical protein
1880359	1892698	12339	Predicted by at least one method	tus_1	Predicted_00420	188254 5	188342 6	-1	DNA replication terminus site-binding protein
1880359	1892698	12339	Predicted by at least one method		Predicted_00421	188383 3	188582 1	-1	Tn3 transposase DDE domain
1880359	1892698	12339	Predicted by at least one method		Predicted_00422	188587 0	188609 4	1	hypothetical protein
1880359	1892698	12339	Predicted by at least one method		Predicted_00179	188808 7	188847 0	1	Transposase
1880359	1892698	12339	Predicted by at least one method		Predicted_00180	188923 2	188996 0	1	Tn3 transposase DDE domain
1880359	1892698	12339	Predicted by at least one method	aacA4_1	Predicted_00527	189135 3	189195 8	-1	Aminoglycoside N(6')-acetyltransferase type 1
1880359	1892698	12339	Predicted by at least one method	tnpR_2	Predicted_00526	189214 1	189269 8	-1	Transposon Tn3 resolvase
1889232	1896303	7071	Predicted by at least one method		Predicted_00180	188923 2	188996 0	1	Tn3 transposase DDE domain
1889232	1896303	7071	Predicted by at least one method	aacA4_1	Predicted_00527	189135 3	189195 8	-1	Aminoglycoside N(6')-acetyltransferase type 1
1889232	1896303	7071	Predicted by at least one method	tnpR_2	Predicted_00526	189214 1	189269 8	-1	Transposon Tn3 resolvase
188923	1896303	7071	Predicted by at least		Predicted_0052	189286	189586	1	Tn3 transposase DDE domain

2			one method		5	0	5		
1889232	1896303	7071	Predicted by at least one method		Predicted_00524	1896214	1896303	1	hypothetical protein
1889232	1896303	7071	Predicted by at least one method	dmlR_1	Predicted_00523	1896281	1897150	-1	HTH-type transcriptional regulator DmlR
1903585	1915816	12231	Predicted by at least one method		Predicted_00516	1903585	1903809	1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00515	1904357	1904641	1	Transposase
1903585	1915816	12231	Predicted by at least one method		Predicted_00514	1904671	1905495	1	Integrase core domain
1903585	1915816	12231	Predicted by at least one method		Predicted_00513	1905885	1906526	-1	DNA replication terminus site-binding protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00512	1906615	1906710	-1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00511	1906786	1907013	-1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method	pir	Predicted_00510	1907016	1907852	-1	PI protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00509	1909188	1909679	-1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00508	1909690	1910070	-1	Plasmid stability protein
1903585	1915816	12231	Predicted by at least one method	parM	Predicted_00507	1910075	1911034	-1	Plasmid segregation protein ParM
1903585	1915816	12231	Predicted by at least one method		Predicted_00506	1911331	1912143	-1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00505	1912467	1912886	1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00504	1913222	1913680	-1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00503	1914167	1914715	1	Transglycosylase SLT domain
1903585	1915816	12231	Predicted by at least one method		Predicted_00502	1914738	1915259	1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00501	1915256	1915816	1	transcriptional activator FlhC
1904355	1910070	5713	Predicted by at least		Predicted_0051	1904355	1904641	1	Transposase

7			one method		5	7	1		
1904357	1910070	5713	Predicted by at least one method		Predicted_00514	1904671	1905495	1	Integrase core domain
1904357	1910070	5713	Predicted by at least one method		Predicted_00513	1905885	1906526	-1	DNA replication terminus site-binding protein
1904357	1910070	5713	Predicted by at least one method		Predicted_00512	1906615	1906710	-1	hypothetical protein
1904357	1910070	5713	Predicted by at least one method		Predicted_00511	1906786	1907013	-1	hypothetical protein
1904357	1910070	5713	Predicted by at least one method	pir	Predicted_00510	1907016	1907852	-1	PI protein
1904357	1910070	5713	Predicted by at least one method		Predicted_00509	1909188	1909679	-1	hypothetical protein
1904357	1910070	5713	Predicted by at least one method		Predicted_00508	1909690	1910070	-1	Plasmid stability protein
1923186	1932903	9717	Predicted by at least one method		Predicted_00496	1923186	1924595	-1	Conjugative relaxosome accessory transposon protein
1923186	1932903	9717	Predicted by at least one method		Predicted_00495	1924611	1925642	-1	hypothetical protein
1923186	1932903	9717	Predicted by at least one method		Predicted_00494	1925878	1927653	-1	von Willebrand factor type A domain
1923186	1932903	9717	Predicted by at least one method		Predicted_00493	1927718	1928905	-1	hypothetical protein
1923186	1932903	9717	Predicted by at least one method	cobS_2	Predicted_00492	1929004	1930011	-1	Aerobic cobaltochelatase subunit CobS
1923186	1932903	9717	Predicted by at least one method		Predicted_00491	1930065	1930433	-1	hypothetical protein
1923186	1932903	9717	Predicted by at least one method		Predicted_00490	1930471	1931565	-1	YqaJ-like viral recombinase domain
1923186	1932903	9717	Predicted by at least one method		Predicted_00489	1931614	1932903	-1	recombination and repair protein RecT
1961683	2089481	127798	Predicted by at least one method		Predicted_00458	1961683	1964370	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00457	1964402	1966432	1	Helicase conserved C-terminal domain
1961683	2089481	127798	Predicted by at least one method		Predicted_00456	1966436	1967695	1	T5orf172 domain
1961683	2089481	12779	Predicted by at least	mrr_1	Predicted_0045	1967706	1968701	1	Mrr restriction system protein

3		8	one method		5	8	6		
196168	2089481	12779	Predicted by at least		Predicted_0045	196887	197142	-1	hypothetical protein
3		8	one method		4	7	9		
196168	2089481	12779	Predicted by at least		Predicted_0045	197157	197204	1	hypothetical protein
3		8	one method		3	8	5		
196168	2089481	12779	Predicted by at least		Predicted_0045	197204	197249	1	hypothetical protein
3		8	one method		2	2	1		
196168	2089481	12779	Predicted by at least		Predicted_0045	197253	197296	1	hypothetical protein
3		8	one method		1	0	1		
196168	2089481	12779	Predicted by at least		Predicted_0045	197302	197322	-1	Prophage CP4-57 regulatory
3		8	one method		0	0	9		protein (AlpA)
196168	2089481	12779	Predicted by at least	engB_1	Predicted_0044	197330	197429	1	GTP-binding protein EngB
3		8	one method		9	7	6		
196168	2089481	12779	Predicted by at least		Predicted_0044	197440	197485	1	hypothetical protein
3		8	one method		8	6	2		
196168	2089481	12779	Predicted by at least		Predicted_0044	197489	197553	-1	hypothetical protein
3		8	one method		7	4	8		
196168	2089481	12779	Predicted by at least		Predicted_0044	197598	197691	1	hypothetical protein
3		8	one method		6	5	7		
196168	2089481	12779	Predicted by at least		Predicted_0044	197714	197747	-1	Resolvase, N terminal domain
3		8	one method		5	2	1		
196168	2089481	12779	Predicted by at least		Predicted_0044	197763	198062	1	Tn3 transposase DDE domain
3		8	one method		4	9	6		
196168	2089481	12779	Predicted by at least		Predicted_0044	198089	198243	1	DNA-dependent helicase II
3		8	one method		3	8	3		
196168	2089481	12779	Predicted by at least		Predicted_0044	198252	198360	-1	hypothetical protein
3		8	one method		2	9	5		
196168	2089481	12779	Predicted by at least		Predicted_0044	198365	198421	-1	hypothetical protein
3		8	one method		1	9	3		
196168	2089481	12779	Predicted by at least		Predicted_0044	198427	198523	-1	hypothetical protein
3		8	one method		0	2	4		
196168	2089481	12779	Predicted by at least		Predicted_0043	198532	198625	-1	Restriction endonuclease
3		8	one method		9	4	9		
196168	2089481	12779	Predicted by at least		Predicted_0043	198627	198684	-1	hypothetical protein
3		8	one method		8	7	6		
196168	2089481	12779	Predicted by at least		Predicted_0043	198683	198718	-1	hypothetical protein
3		8	one method		7	3	3		
196168	2089481	12779	Predicted by at least	sipT	Predicted_0043	198717	198791	-1	Signal peptidase I T

3		8	one method		6	0	9		
1961683	2089481	127798	Predicted by at least one method		Predicted_004305	198800	198842	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_004304	198841	198942	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_004303	198944	199026	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	xerC_1	Predicted_004302	199027	199122	-1	Tyrosine recombinase XerC
1961683	2089481	127798	Predicted by at least one method		Predicted_004301	199152	199179	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_004300	199183	199208	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_004299	199218	199264	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_004298	199296	199310	1	small toxic polypeptide
1961683	2089481	127798	Predicted by at least one method		Predicted_004297	199319	199357	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	mazF_1	Predicted_004296	199360	199393	-1	mRNA interferase MazF
1961683	2089481	127798	Predicted by at least one method	mazE	Predicted_004295	199393	199417	-1	Antitoxin MazE
1961683	2089481	127798	Predicted by at least one method	parA_2	Predicted_004294	199448	199511	1	Chromosome partitioning protein ParA
1961683	2089481	127798	Predicted by at least one method		Predicted_004293	199523	199546	1	ParG
1961683	2089481	127798	Predicted by at least one method		Predicted_043402	199758	199781	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	xerC_6	Predicted_043403	199844	199898	-1	Tyrosine recombinase XerC
1961683	2089481	127798	Predicted by at least one method		Predicted_011904	200098	200148	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_011903	200148	200197	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_011902	200206	200240	1	hypothetical protein
1961683	2089481	127798	Predicted by at least		Predicted_011901	200241	200288	-1	hypothetical protein

3		8	one method		1	8	8		
1961683	2089481	127798	Predicted by at least one method		Predicted_01190	200288 1	200325 2	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01189	200326 3	200345 7	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01188	200345 7	200370 8	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01187	200379 8	200434 6	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01186	200450 9	200485 9	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	higA_4	Predicted_01185	200486 4	200516 6	1	Antitoxin HigA
1961683	2089481	127798	Predicted by at least one method		Predicted_01184	200519 3	200548 6	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	hupB_1	Predicted_01183	200557 4	200584 6	-1	DNA-binding protein HU-beta
1961683	2089481	127798	Predicted by at least one method	yncB	Predicted_01182	200590 4	200643 1	-1	Endonuclease YncB precursor
1961683	2089481	127798	Predicted by at least one method		Predicted_01181	200644 8	200663 6	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01180	200666 2	200751 9	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01179	200750 6	200773 3	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01178	200773 6	200825 4	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01177	200825 1	200869 7	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01176	200869 7	200905 6	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01175	200911 3	200954 1	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	bdbD_2	Predicted_01174	200957 5	201043 5	-1	Disulfide bond formation protein D precursor
1961683	2089481	127798	Predicted by at least one method	sppA_1	Predicted_01173	201045 1	201141 0	-1	Putative signal peptide peptidase SppA
1961683	2089481	12779	Predicted by at least		Predicted_0117	201141	201226	-1	hypothetical protein

3		8	one method	2	0	4		
1961683	2089481	127798	Predicted by at least one method	Predicted_01171	201226	201256	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01170	201257	201304	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01169	201314	201366	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01168	201366	201418	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01167	201419	201480	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01166	201507	201618	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01165	201620	201663	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01164	201704	201732	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01163	201767	201873	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01162	201875	201904	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01161	201905	201959	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01160	202008	202107	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01159	202108	202138	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01158	202138	202180	1	H-NS histone family
1961683	2089481	127798	Predicted by at least one method	Predicted_01157	202186	202241	-1	transcriptional activator FlhC
1961683	2089481	127798	Predicted by at least one method	Predicted_01156	202241	202307	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	Predicted_01155	202303	202356	-1	Transglycosylase SLT domain
1961683	2089481	127798	Predicted by at least one method	Predicted_01154	202356	202383	-1	DNA-binding transcriptional regulator Nlp
1961683	2089481	127798	Predicted by at least	Predicted_0115	202455	202491	1	hypothetical protein

3		8	one method		3	1	3		
1961683	2089481	127798	Predicted by at least one method		Predicted_01152	202495	202856	-1	TraG-like protein, N-terminal region
1961683	2089481	127798	Predicted by at least one method		Predicted_01151	202857	203001	-1	Conjugative relaxosome accessory transposon protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01150	203001	203104	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01149	203116	203267	-1	DNA helicase IV
1961683	2089481	127798	Predicted by at least one method		Predicted_01148	203268	203296	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	smc_2	Predicted_01147	203296	203400	-1	Chromosome partition protein Smc
1961683	2089481	127798	Predicted by at least one method	tus_3	Predicted_01146	203415	203503	-1	DNA replication terminus site-binding protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01145	203535	203584	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	dnaQ_1	Predicted_01144	203584	203671	-1	DNA polymerase III subunit epsilon
1961683	2089481	127798	Predicted by at least one method	xerD_2	Predicted_01143	203671	203755	-1	Tyrosine recombinase XerD
1961683	2089481	127798	Predicted by at least one method		Predicted_01142	203773	203826	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01141	203826	203854	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01140	203856	203888	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01139	203911	203971	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01138	203972	204018	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01137	204034	204064	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01136	204094	204121	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01135	204151	204244	-1	Transposase DDE domain
196168	2089481	12779	Predicted by at least		Predicted_0113	204253	204286	1	hypothetical protein

3		8	one method		4	8	4		
1961683	2089481	127798	Predicted by at least one method	dinB_3	Predicted_01133	2042900	2044177	-1	DNA polymerase IV
1961683	2089481	127798	Predicted by at least one method	lexA_3	Predicted_01132	2044183	2044611	-1	LexA repressor
1961683	2089481	127798	Predicted by at least one method		Predicted_01131	2044707	2044979	-1	Helix-turn-helix domain
1961683	2089481	127798	Predicted by at least one method		Predicted_01130	2045104	2045454	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01129	2045475	2045864	1	Transposase DDE domain
1961683	2089481	127798	Predicted by at least one method		Predicted_01128	2045932	2046483	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01127	2046705	2046944	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01126	2047007	2047837	-1	Integrase core domain
1961683	2089481	127798	Predicted by at least one method		Predicted_01125	2047834	2048145	-1	Transposase
1961683	2089481	127798	Predicted by at least one method	tmrB	Predicted_01124	2048198	2048491	-1	Tunicamycin resistance protein
1961683	2089481	127798	Predicted by at least one method	yokD	Predicted_01123	2048504	2049364	-1	SPBc2 prophage-derived aminoglycoside N(3')-acetyltransferase-like protein YokD
1961683	2089481	127798	Predicted by at least one method	bla_1	Predicted_01122	2049506	2050366	-1	Beta-lactamase TEM precursor
1961683	2089481	127798	Predicted by at least one method	tnpR_4	Predicted_01121	2050549	2051106	-1	Transposon Tn3 resolvase
1961683	2089481	127798	Predicted by at least one method		Predicted_01120	2051270	2054278	1	Tn3 transposase DDE domain
1961683	2089481	127798	Predicted by at least one method		Predicted_00097	2056678	2058219	1	Putative transposase
1961683	2089481	127798	Predicted by at least one method	trpF	Predicted_00098	2058775	2059245	-1	N-(5'-phosphoribosyl)anthranilate isomerase
1961683	2089481	127798	Predicted by at least one method		Predicted_00099	2059355	2059906	1	hypothetical protein

1961683	2089481	127798	Predicted by at least one method	blaNDM-1	Predicted_00100	2059787	2060599	-1	Beta-lactamase NDM-1 precursor
1961683	2089481	127798	Predicted by at least one method		Predicted_00101	2060700	2061710	-1	Integrase core domain
1961683	2089481	127798	Predicted by at least one method	aphA_1	Predicted_00102	2061877	2062656	-1	Aminoglycoside 3'-phosphotransferase
1961683	2089481	127798	Predicted by at least one method		Predicted_00103	2062762	2062992	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00104	2062982	2063425	-1	Transposase
1961683	2089481	127798	Predicted by at least one method		Predicted_00105	2063716	2065977	-1	Tn3 transposase DDE domain
1961683	2089481	127798	Predicted by at least one method	hin	Predicted_00106	2065980	2066612	-1	DNA-invertase hin
1961683	2089481	127798	Predicted by at least one method	ttgC	Predicted_00107	2066668	2068155	-1	Toluene efflux pump outer membrane protein TtgC precursor
1961683	2089481	127798	Predicted by at least one method		Predicted_00108	2068142	2068615	-1	Cytochrome C'
1961683	2089481	127798	Predicted by at least one method	lolD_1	Predicted_00109	2068644	2069354	-1	Lipoprotein-releasing system ATP-binding protein LolD
1961683	2089481	127798	Predicted by at least one method		Predicted_00110	2069359	2070561	-1	FtsX-like permease family
1961683	2089481	127798	Predicted by at least one method	mdtA_1	Predicted_00111	2070558	2071709	-1	Multidrug resistance protein MdtA precursor
1961683	2089481	127798	Predicted by at least one method	slmA_1	Predicted_00112	2071706	2072314	-1	Nucleoid occlusion factor SlmA
1961683	2089481	127798	Predicted by at least one method		Predicted_00113	2072395	2073069	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00114	2073624	2073971	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00115	2074016	2077042	-1	Tn3 transposase DDE domain
1961683	2089481	127798	Predicted by at least one method	bin3_1	Predicted_00116	2077204	2077848	1	Putative transposon Tn552 DNA-invertase bin3
1961683	2089481	127798	Predicted by at least one method	betT_1	Predicted_00117	2078032	2078361	1	High-affinity choline transport protein

1961683	2089481	127798	Predicted by at least one method	merR	Predicted_00118	207835	207880	-1	Mercuric resistance operon regulatory protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00119	207887	207924	1	MerT mercuric transport protein
1961683	2089481	127798	Predicted by at least one method	merP	Predicted_00120	207925	207953	1	Mercuric transport protein periplasmic component precursor
1961683	2089481	127798	Predicted by at least one method	merC	Predicted_00121	207956	207998	1	Mercuric resistance protein MerC
1961683	2089481	127798	Predicted by at least one method	merA	Predicted_00122	208002	208171	1	Mercuric reductase
1961683	2089481	127798	Predicted by at least one method		Predicted_00123	208172	208209	1	zinc-responsive transcriptional regulator
1961683	2089481	127798	Predicted by at least one method		Predicted_00124	208209	208232	1	MerE protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00125	208239	208260	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00126	208286	208368	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00127	208414	208463	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	folP_1	Predicted_00128	208474	208558	-1	Dihydropteroate synthase
1961683	2089481	127798	Predicted by at least one method	emrE_1	Predicted_00129	208557	208592	-1	Multidrug transporter EmrE
1961683	2089481	127798	Predicted by at least one method	ant1_1	Predicted_00130	208608	208686	-1	Streptomycin 3''-adenylyltransferase
1961683	2089481	127798	Predicted by at least one method	dfrA	Predicted_00131	208728	208778	-1	Dihydrofolate reductase
1961683	2089481	127798	Predicted by at least one method	xerD_1	Predicted_00132	208792	208894	1	Tyrosine recombinase XerD
1961683	2089481	127798	Predicted by at least one method		Predicted_00133	208892	208948	-1	hypothetical protein
1973020	1980626	7606	Predicted by at least one method		Predicted_00450	197302	197322	-1	Prophage CP4-57 regulatory protein (AlpA)
1973020	1980626	7606	Predicted by at least one method	engB_1	Predicted_00449	197330	197429	1	GTP-binding protein EngB
197302	1980626	7606	Predicted by at least		Predicted_0044	197440	197485	1	hypothetical protein

0			one method		8	6	2		
1973020	1980626	7606	Predicted by at least one method		Predicted_00447	197489	197553	-1	hypothetical protein
1973020	1980626	7606	Predicted by at least one method		Predicted_00446	197598	197691	1	hypothetical protein
1973020	1980626	7606	Predicted by at least one method		Predicted_00445	197714	197747	-1	Resolvase, N terminal domain
1973020	1980626	7606	Predicted by at least one method		Predicted_00444	197763	198062	1	Tn3 transposase DDE domain
1985324	1990261	4937	Predicted by at least one method		Predicted_00439	198532	198625	-1	Restriction endonuclease
1985324	1990261	4937	Predicted by at least one method		Predicted_00438	198627	198684	-1	hypothetical protein
1985324	1990261	4937	Predicted by at least one method		Predicted_00437	198683	198718	-1	hypothetical protein
1985324	1990261	4937	Predicted by at least one method	sipT	Predicted_00436	198717	198791	-1	Signal peptidase I T
1985324	1990261	4937	Predicted by at least one method		Predicted_00435	198800	198842	-1	hypothetical protein
1985324	1990261	4937	Predicted by at least one method		Predicted_00434	198841	198942	-1	hypothetical protein
1985324	1990261	4937	Predicted by at least one method		Predicted_00433	198944	199026	-1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method		Predicted_00431	199152	199179	1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method		Predicted_00430	199183	199208	1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method		Predicted_00429	199218	199264	1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method		Predicted_00428	199296	199310	1	small toxic polypeptide
1991523	2001971	10448	Predicted by at least one method		Predicted_00427	199319	199357	-1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method	mazF_1	Predicted_00426	199360	199393	-1	mRNA interferase MazF
1991523	2001971	10448	Predicted by at least one method	mazE	Predicted_00425	199393	199417	-1	Antitoxin MazE
1991523	2001971	10448	Predicted by at least	parA_2	Predicted_0042	199448	199511	1	Chromosome partitioning

3			one method		4	9	2		protein ParA
1991523	2001971	10448	Predicted by at least one method		Predicted_00423	199523 7	199546 4	1	ParG
1991523	2001971	10448	Predicted by at least one method		Predicted_04342	199758 0	199781 9	1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method	xerC_6	Predicted_04343	199844 8	199898 4	-1	Tyrosine recombinase XerC
1991523	2001971	10448	Predicted by at least one method		Predicted_01194	200098 3	200148 0	-1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method		Predicted_01193	200148 3	200197 1	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01191	200241 8	200288 8	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01190	200288 1	200325 2	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01189	200326 3	200345 7	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01188	200345 7	200370 8	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01187	200379 8	200434 6	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01186	200450 9	200485 9	1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method	higA_4	Predicted_01185	200486 4	200516 6	1	Antitoxin HigA
2002881	2009541	6660	Predicted by at least one method		Predicted_01184	200519 3	200548 6	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method	hupB_1	Predicted_01183	200557 4	200584 6	-1	DNA-binding protein HU-beta
2002881	2009541	6660	Predicted by at least one method	yncB	Predicted_01182	200590 4	200643 1	-1	Endonuclease YncB precursor
2002881	2009541	6660	Predicted by at least one method		Predicted_01181	200644 8	200663 6	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01180	200666 2	200751 9	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01179	200750 6	200773 3	-1	hypothetical protein
200288	2009541	6660	Predicted by at least		Predicted_0117	200773	200825	-1	hypothetical protein

1			one method		8	6	4			
2002881	2009541	6660	Predicted by at least one method		Predicted_01177	2008251	2008697	-1	hypothetical protein	
2002881	2009541	6660	Predicted by at least one method		Predicted_01176	2008697	2009056	-1	hypothetical protein	
2002881	2009541	6660	Predicted by at least one method		Predicted_01175	2009113	2009541	-1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method	sppA_1	Predicted_01173	2010451	2011410	-1	Putative signal peptide peptidase SppA	
2010451	2024913	14462	Predicted by at least one method		Predicted_01172	2011410	2012264	-1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01171	2012269	2012562	-1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01170	2012573	2013046	-1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01169	2013143	2013664	-1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01168	2013667	2014188	-1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01167	2014193	2014801	-1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01166	2015070	2016185	1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01165	2016203	2016637	1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01164	2017047	2017328	-1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01163	2017674	2018738	-1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01162	2018759	2019046	-1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01161	2019051	2019590	-1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01160	2020089	2021072	1	hypothetical protein	
2010451	2024913	14462	Predicted by at least one method		Predicted_01159	2021089	2021382	1	hypothetical protein	
2010451	2024913	14462	Predicted by at least		Predicted_01158	2021382	2021802	1	H-NS histone family	

1			one method		8	4	3		
2010451	2024913	14462	Predicted by at least one method		Predicted_01157	202186 3	202241 4	-1	transcriptional activator FlhC
2010451	2024913	14462	Predicted by at least one method		Predicted_01156	202241 1	202307 6	-1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01155	202303 0	202356 3	-1	Transglycosylase SLT domain
2010451	2024913	14462	Predicted by at least one method		Predicted_01154	202356 3	202383 5	-1	DNA-binding transcriptional regulator Nlp
2010451	2024913	14462	Predicted by at least one method		Predicted_01153	202455 1	202491 3	1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01150	203001 3	203104 1	-1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01149	203116 4	203267 5	-1	DNA helicase IV
2030013	2060599	30586	Predicted by at least one method		Predicted_01148	203268 4	203296 2	-1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method	smc_2	Predicted_01147	203296 2	203400 2	-1	Chromosome partition protein Smc
2030013	2060599	30586	Predicted by at least one method	tus_3	Predicted_01146	203415 5	203503 0	-1	DNA replication terminus site-binding protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01145	203535 7	203584 8	-1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method	dnaQ_1	Predicted_01144	203584 5	203671 4	-1	DNA polymerase III subunit epsilon
2030013	2060599	30586	Predicted by at least one method	xerD_2	Predicted_01143	203671 9	203755 2	-1	Tyrosine recombinase XerD
2030013	2060599	30586	Predicted by at least one method		Predicted_01142	203773 2	203826 8	-1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01141	203826 1	203854 8	-1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01140	203856 7	203888 4	-1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01139	203911 0	203971 2	1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01138	203972 8	204018 0	-1	hypothetical protein
203001	2060599	30586	Predicted by at least		Predicted_0113	204034	204064	-1	hypothetical protein

3			one method		7	7	6		
2030013	2060599	30586	Predicted by at least one method		Predicted_01136	204094	204121	-1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01135	204151	204244	-1	Transposase DDE domain
2030013	2060599	30586	Predicted by at least one method		Predicted_01134	204253	204286	1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method	dinB_3	Predicted_01133	204290	204417	-1	DNA polymerase IV
2030013	2060599	30586	Predicted by at least one method	lexA_3	Predicted_01132	204418	204461	-1	LexA repressor
2030013	2060599	30586	Predicted by at least one method		Predicted_01131	204470	204497	-1	Helix-turn-helix domain
2030013	2060599	30586	Predicted by at least one method		Predicted_01130	204510	204545	1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01129	204547	204586	1	Transposase DDE domain
2030013	2060599	30586	Predicted by at least one method		Predicted_01128	204593	204648	1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01127	204670	204694	-1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01126	204700	204783	-1	Integrase core domain
2030013	2060599	30586	Predicted by at least one method		Predicted_01125	204783	204814	-1	Transposase
2030013	2060599	30586	Predicted by at least one method	tmrB	Predicted_01124	204819	204849	-1	Tunicamycin resistance protein
2030013	2060599	30586	Predicted by at least one method	yokD	Predicted_01123	204850	204936	-1	SPBc2 prophage-derived aminoglycoside N(3')-acetyltransferase-like protein YokD
2030013	2060599	30586	Predicted by at least one method	bla_1	Predicted_01122	204950	205036	-1	Beta-lactamase TEM precursor
2030013	2060599	30586	Predicted by at least one method	tnpR_4	Predicted_01121	205054	205110	-1	Transposon Tn3 resolvase
2030013	2060599	30586	Predicted by at least one method		Predicted_01120	205127	205427	1	Tn3 transposase DDE domain
203001	2060599	30586	Predicted by at least		Predicted_0009	205667	205821	1	Putative transposase

3			one method		7	8	9		
2030013	2060599	30586	Predicted by at least one method	trpF	Predicted_00098	205877 5	205924 5	-1	N-(5'-phosphoribosyl)anthranilate isomerase
2030013	2060599	30586	Predicted by at least one method		Predicted_00099	205935 5	205990 6	1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method	blaNDM-1	Predicted_00100	205978 7	206059 9	-1	Beta-lactamase NDM-1 precursor
2082861	2089481	6620	Predicted by at least one method		Predicted_00126	208286 1	208368 2	1	hypothetical protein
2082861	2089481	6620	Predicted by at least one method		Predicted_00127	208414 2	208463 6	1	hypothetical protein
2082861	2089481	6620	Predicted by at least one method	folP_1	Predicted_00128	208474 2	208558 1	-1	Dihydropteroate synthase
2082861	2089481	6620	Predicted by at least one method	emrE_1	Predicted_00129	208557 5	208592 2	-1	Multidrug transporter EmrE
2082861	2089481	6620	Predicted by at least one method	ant1_1	Predicted_00130	208608 6	208686 5	-1	Streptomycin 3''-adenylyltransferase
2082861	2089481	6620	Predicted by at least one method	dfrA	Predicted_00131	208728 5	208778 2	-1	Dihydrofolate reductase
2082861	2089481	6620	Predicted by at least one method	xerD_1	Predicted_00132	208792 7	208894 0	1	Tyrosine recombinase XerD
2082861	2089481	6620	Predicted by at least one method		Predicted_00133	208892 7	208948 1	-1	hypothetical protein
2591142	2599539	8397	Predicted by at least one method		Predicted_00637	259114 2	259415 0	-1	Tn3 transposase DDE domain
2591142	2599539	8397	Predicted by at least one method	tnpR_3	Predicted_00638	259431 4	259488 6	1	Transposon Tn3 resolvase
2591142	2599539	8397	Predicted by at least one method	fdtC	Predicted_00639	259500 6	259545 8	1	dTDP-3-amino-3,6-dideoxy-alpha-D- galactopyranose 3-N-acetyltransferase
2591142	2599539	8397	Predicted by at least one method	hapE	Predicted_00640	259549 0	259702 2	-1	4-hydroxyacetophenone monooxygenase
2591142	2599539	8397	Predicted by at least one method		Predicted_00641	259701 9	259728 8	-1	PQ loop repeat
2591142	2599539	8397	Predicted by at least one method	ntdC	Predicted_00642	259729 0	259830 6	-1	Glucose-6-phosphate 3-dehydrogenase
259114	2599539	8397	Predicted by at least	ntdB	Predicted_00643	259830	259913	-1	Kanosamine-6-phosphate

2			one method		3	3	6		phosphatase
2591142	2599539	8397	Predicted by at least one method	ntdA_1	Predicted_00644	2599120	2599539	-1	3-oxo-glucose-6-phosphate:glutamate aminotransferase
2594314	2599539	5225	Predicted by at least one method	tnpR_3	Predicted_00638	2594314	2594886	1	Transposon Tn3 resolvase
2594314	2599539	5225	Predicted by at least one method	fdtC	Predicted_00639	2595006	2595458	1	dTDP-3-amino-3,6-dideoxy-alpha-D- galactopyranose 3-N-acetyltransferase
2594314	2599539	5225	Predicted by at least one method	hapE	Predicted_00640	2595490	2597022	-1	4-hydroxyacetophenone monooxygenase
2594314	2599539	5225	Predicted by at least one method		Predicted_00641	2597019	2597288	-1	PQ loop repeat
2594314	2599539	5225	Predicted by at least one method	ntdC	Predicted_00642	2597290	2598306	-1	Glucose-6-phosphate 3-dehydrogenase
2594314	2599539	5225	Predicted by at least one method	ntdB	Predicted_00643	2598303	2599136	-1	Kanosamine-6-phosphate phosphatase
2594314	2599539	5225	Predicted by at least one method	ntdA_1	Predicted_00644	2599120	2599539	-1	3-oxo-glucose-6-phosphate:glutamate aminotransferase
3267726	3284238	16512	Predicted by at least one method	ppnK_2	Predicted_02302	3267726	3268625	1	putative inorganic polyphosphate/ATP-NAD kinase
3267726	3284238	16512	Predicted by at least one method	recN	Predicted_02303	3268712	3270373	1	DNA repair protein RecN
3267726	3284238	16512	Predicted by at least one method	bamE	Predicted_02304	3270486	3270878	1	Outer membrane protein assembly factor BamE precursor
3267726	3284238	16512	Predicted by at least one method	pasI	Predicted_02305	3271052	3271357	-1	Persistence and stress-resistance antitoxin PasI
3267726	3284238	16512	Predicted by at least one method	pasT	Predicted_02306	3271341	3271775	-1	Persistence and stress-resistance toxin PasT
3267726	3284238	16512	Predicted by at least one method	smpB	Predicted_02307	3271929	3272411	1	SsrA-binding protein
3267726	3284238	16512	Predicted by at least one method	intA_4	Predicted_02309	3272989	3274197	1	Prophage CP4-57 integrase
3267726	3284238	16512	Predicted by at least one method		Predicted_02310	3274243	3276297	1	hypothetical protein

3267726	3284238	16512	Predicted by at least one method		Predicted_02311	3276399	3277670	-1	hypothetical protein
3267726	3284238	16512	Predicted by at least one method	era_2	Predicted_03129	3279073	3279945	1	GTPase Era
3267726	3284238	16512	Predicted by at least one method	klcA_3	Predicted_03128	3280037	3280462	1	Antirestriction protein KlcA
3267726	3284238	16512	Predicted by at least one method		Predicted_03127	3280476	3280907	1	hypothetical protein
3267726	3284238	16512	Predicted by at least one method	xerD_4	Predicted_03126	3280993	3282003	-1	Tyrosine recombinase XerD
3267726	3284238	16512	Predicted by at least one method	xerC_4	Predicted_03125	3281996	3282961	-1	Tyrosine recombinase XerC
3267726	3284238	16512	Predicted by at least one method	xerC_3	Predicted_03124	3282961	3284238	-1	Tyrosine recombinase XerC
3296833	3302010	5177	Predicted by at least one method		Predicted_04334	3296833	3297108	-1	InsA C-terminal domain
3296833	3302010	5177	Predicted by at least one method		Predicted_04335	3297222	3297341	1	hypothetical protein
3296833	3302010	5177	Predicted by at least one method		Predicted_02210	3299136	3299243	-1	hypothetical protein
3296833	3302010	5177	Predicted by at least one method		Predicted_02209	3299279	3299545	-1	hypothetical protein
3296833	3302010	5177	Predicted by at least one method		Predicted_02208	3299535	3300593	-1	hypothetical protein
3296833	3302010	5177	Predicted by at least one method	hcpA_5	Predicted_02207	3300611	3301090	-1	Major exported protein
3296833	3302010	5177	Predicted by at least one method	intA_3	Predicted_02206	3301576	3302010	1	Prophage CP4-57 integrase
3623549	3629520	5971	Predicted by at least one method		Predicted_00860	3623549	3623920	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method		Predicted_00861	3623979	3624461	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method		Predicted_00862	3624647	3625042	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method		Predicted_00863	3625141	3625626	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method	repA	Predicted_00864	3626145	3627017	-1	Replication protein RepA

3623549	3629520	5971	Predicted by at least one method		Predicted_00865	3627321	3627626	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method		Predicted_00866	3627623	3627940	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method		Predicted_00867	3628060	3628626	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method	higA_2	Predicted_00868	3629104	3629520	1	Antitoxin HigA
4097099	4102094	4995	Predicted by at least one method		Predicted_01114	4097099	4097785	-1	hypothetical protein
4097099	4102094	4995	Predicted by at least one method		Predicted_01113	4097789	4101121	-1	ATP-dependent helicase HepA
4097099	4102094	4995	Predicted by at least one method		Predicted_01112	4101159	4102094	-1	hypothetical protein
4468672	4477529	8857	Predicted by at least one method	arsD_2	Predicted_03796	4468672	4469037	-1	Arsenical resistance operon trans-acting repressor ArsD
4468672	4477529	8857	Predicted by at least one method	arsR_3	Predicted_03797	4469085	4469420	-1	Arsenical resistance operon repressor
4468672	4477529	8857	Predicted by at least one method		Predicted_03798	4469903	4470646	-1	hypothetical protein
4468672	4477529	8857	Predicted by at least one method		Predicted_03799	4470648	4471184	-1	hypothetical protein
4468672	4477529	8857	Predicted by at least one method		Predicted_03421	4472613	4472939	1	hypothetical protein
4468672	4477529	8857	Predicted by at least one method		Predicted_03420	4472936	4474015	1	hypothetical protein
4468672	4477529	8857	Predicted by at least one method		Predicted_03419	4474019	4474963	-1	hypothetical protein
4468672	4477529	8857	Predicted by at least one method	thyA_2	Predicted_03418	4474967	4475944	-1	Thymidylate synthase
4468672	4477529	8857	Predicted by at least one method	intA_5	Predicted_03417	4476255	4477529	-1	Prophage CP4-57 integrase
4469085	4475944	6859	Predicted by at least one method	arsR_3	Predicted_03797	4469085	4469420	-1	Arsenical resistance operon repressor
4469085	4475944	6859	Predicted by at least one method		Predicted_03798	4469903	4470646	-1	hypothetical protein
4469085	4475944	6859	Predicted by at least one method		Predicted_03799	4470648	4471184	-1	hypothetical protein

4469085	4475944	6859	Predicted by at least one method		Predicted_03421	4472613	4472939	1	hypothetical protein
4469085	4475944	6859	Predicted by at least one method		Predicted_03420	4472936	4474015	1	hypothetical protein
4469085	4475944	6859	Predicted by at least one method		Predicted_03419	4474019	4474963	-1	hypothetical protein
4469085	4475944	6859	Predicted by at least one method	thyA_2	Predicted_03418	4474967	4475944	-1	Thymidylate synthase
4803320	4810555	7235	Predicted by at least one method		Predicted_02454	4802716	4803327	-1	Phage tail protein (Tail_P2_I)
4803320	4810555	7235	Predicted by at least one method		Predicted_02455	4803320	4804231	-1	Baseplate J-like protein
4803320	4810555	7235	Predicted by at least one method		Predicted_02456	4804234	4804575	-1	Gene 25-like lysozyme
4803320	4810555	7235	Predicted by at least one method		Predicted_02457	4804572	4805195	-1	Phage-related baseplate assembly protein
4803320	4810555	7235	Predicted by at least one method		Predicted_02458	4805202	4805582	-1	hypothetical protein
4803320	4810555	7235	Predicted by at least one method		Predicted_02459	4805671	4806288	-1	Phage virion morphogenesis family
4803320	4810555	7235	Predicted by at least one method		Predicted_02460	4806285	4806728	-1	P2 phage tail completion protein R (GpR)
4803320	4810555	7235	Predicted by at least one method		Predicted_02461	4806697	4807257	-1	hypothetical protein
4803320	4810555	7235	Predicted by at least one method		Predicted_02462	4807291	4807734	-1	hypothetical protein
4803320	4810555	7235	Predicted by at least one method		Predicted_02463	4807727	4808032	-1	hypothetical protein
4803320	4810555	7235	Predicted by at least one method		Predicted_02464	4808036	4808239	-1	Phage Tail Protein X
4803320	4810555	7235	Predicted by at least one method		Predicted_02465	4808236	4808712	-1	Phage head completion protein (GPL)
4803320	4810555	7235	Predicted by at least one method		Predicted_02466	4808801	4809457	-1	Phage small terminase subunit
4803320	4810555	7235	Predicted by at least one method		Predicted_02467	4809461	4810555	-1	Phage major capsid protein, P2 family
4951197	5040496	89299	Predicted by at least one method		Predicted_04263	4951197	4951985	-1	hypothetical protein

4951197	5040496	89299	Predicted by at least one method		Predicted_03994	495345	495369	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_03995	495426	495525	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_03996	495538	495638	-1	Reverse transcriptase (RNA-dependent DNA polymerase)
4951197	5040496	89299	Predicted by at least one method		Predicted_03997	495648	495745	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_03998	495752	495945	-1	chromosome segregation protein
4951197	5040496	89299	Predicted by at least one method	mdaB_1	Predicted_04399	496104	496119	1	Modulator of drug activity B
4951197	5040496	89299	Predicted by at least one method	mdaB_2	Predicted_04400	496119	496136	1	Modulator of drug activity B
4951197	5040496	89299	Predicted by at least one method		Predicted_04391	496277	496323	-1	Replication protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04403	496483	496503	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	wbbD	Predicted_04340	496801	496884	-1	UDP-Gal:alpha-D-GlcNAc-diphosphoundecaprenol beta-1,3-galactosyltransferase
4951197	5040496	89299	Predicted by at least one method		Predicted_04341	496896	496983	-1	Polysaccharide pyruvyl transferase
4951197	5040496	89299	Predicted by at least one method		Predicted_00176	497449	497489	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_00177	497518	497582	1	Pentapeptide repeats (8 copies)
4951197	5040496	89299	Predicted by at least one method		Predicted_00178	497646	497690	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04203	498032	498082	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04204	498083	498359	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04401	498711	498737	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04408	499536	499555	-1	hypothetical protein
495119	5040496	89299	Predicted by at least		Predicted_0439	499679	499754	-1	TcdA/TcdB pore forming

7			one method		2	4	6		domain
4951197	5040496	89299	Predicted by at least one method		Predicted_04298	5001994	5002113	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	epsE	Predicted_04390	5005779	5006264	1	Putative glycosyltransferase EpsE
4951197	5040496	89299	Predicted by at least one method		Predicted_04354	5011714	5011806	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04267	5014092	5014322	1	Prophage CP4-57 regulatory protein (AlpA)
4951197	5040496	89299	Predicted by at least one method	papC_6	Predicted_03857	5018927	5021290	1	Outer membrane usher protein PapC precursor
4951197	5040496	89299	Predicted by at least one method	papD_6	Predicted_03858	5021297	5022022	1	Chaperone protein PapD precursor
4951197	5040496	89299	Predicted by at least one method		Predicted_03859	5022026	5023003	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	rcsB_2	Predicted_03860	5023073	5023726	1	Transcriptional regulatory protein RcsB
4951197	5040496	89299	Predicted by at least one method	rcsC_2	Predicted_03861	5023704	5026910	-1	Sensor histidine kinase RcsC
4951197	5040496	89299	Predicted by at least one method		Predicted_04394	5028347	5029108	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	epsJ_2	Predicted_04356	5030150	5031004	-1	putative glycosyltransferase EpsJ
4951197	5040496	89299	Predicted by at least one method	gtf1	Predicted_04357	5031178	5031606	-1	Glycosyltransferase Gtf1
4951197	5040496	89299	Predicted by at least one method		Predicted_04319	5033279	5034010	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04320	5034029	5034379	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04321	5034528	5034683	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_03779	5039708	5040154	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	hrsA	Predicted_03780	5040176	5040496	1	Heat-responsive suppressor HrsA
4951197	5040496	89299	Predicted by at least one method	fruA_2	Predicted_03781	5040483	5041601	1	PTS system fructose-specific EIIBC component
496119	4968844	7650	Predicted by at least	mdaB_1	Predicted_0439	496104	496119	1	Modulator of drug activity B

4			one method		9	8	7		
4961194	4968844	7650	Predicted by at least one method	mdaB_2	Predicted_04400	4961194	4961361	1	Modulator of drug activity B
4961194	4968844	7650	Predicted by at least one method		Predicted_04391	4962775	4963239	-1	Replication protein
4961194	4968844	7650	Predicted by at least one method		Predicted_04403	4964839	4965030	1	hypothetical protein
4961194	4968844	7650	Predicted by at least one method	wbbD	Predicted_04340	4968011	4968844	-1	UDP-Gal:alpha-D-GlcNAc-diphosphoundecaprenol beta-1,3-galactosyltransferase
4995363	5006264	10901	Predicted by at least one method		Predicted_04408	4995363	4995554	-1	hypothetical protein
4995363	5006264	10901	Predicted by at least one method		Predicted_04392	4996794	4997546	-1	TcdA/TcdB pore forming domain
4995363	5006264	10901	Predicted by at least one method		Predicted_04298	5001994	5002113	-1	hypothetical protein
4995363	5006264	10901	Predicted by at least one method	epsE	Predicted_04390	5005779	5006264	1	Putative glycosyltransferase EpsE
5073122	5079853	6731	Predicted by at least one method	aacA4_2	Predicted_04218	5073122	5073721	-1	Aminoglycoside N(6')-acetyltransferase type 1
5073122	5079853	6731	Predicted by at least one method		Predicted_04256	5075851	5076714	-1	hypothetical protein
5073122	5079853	6731	Predicted by at least one method	ant1_4	Predicted_04257	5077043	5077987	-1	Streptomycin 3''-adenylyltransferase
5073122	5079853	6731	Predicted by at least one method		Predicted_04327	5079515	5079853	1	hypothetical protein
5079946	5085829	5883	Predicted by at least one method	smfA_7	Predicted_04328	5079946	5080479	1	Fimbria A protein precursor
5079946	5085829	5883	Predicted by at least one method	papH_6	Predicted_04329	5080526	5081083	1	PAP fimbrial minor pilin protein precursor
5079946	5085829	5883	Predicted by at least one method	xerD_6	Predicted_04021	5083027	5083629	-1	Tyrosine recombinase XerD
5079946	5085829	5883	Predicted by at least one method		Predicted_04022	5083868	5084329	1	hypothetical protein
5079946	5085829	5883	Predicted by at least one method		Predicted_04023	5085335	5085829	-1	hypothetical protein

Localização das Ilhas genômicas PR02

Island start	Island end	Length	Method	Gene ID	Locus	Gene start	Gene end	Strand	Product
121511	130328	8817	Predicted by at least one method		Predicted_04029	121511	121912	1	hypothetical protein
121511	130328	8817	Predicted by at least one method	mrpA_4	Predicted_04030	121905	122438	1	Major MR/P fimbria protein precursor
121511	130328	8817	Predicted by at least one method		Predicted_04330	123815	124828	1	hypothetical protein
121511	130328	8817	Predicted by at least one method		Predicted_04358	126856	127881	-1	hypothetical protein
121511	130328	8817	Predicted by at least one method		Predicted_04359	127897	128157	-1	hypothetical protein
121511	130328	8817	Predicted by at least one method	papD_11	Predicted_04180	129618	130328	-1	Chaperone protein PapD precursor
1629087	1715575	86488	Predicted by at least one method	hcpC_6	Predicted_04197	1629087	1630115	-1	Putative beta-lactamase HcpC precursor
1629087	1715575	86488	Predicted by at least one method	rhsC	Predicted_00766	1631840	1634869	-1	Putative deoxyribonuclease RhsC
1629087	1715575	86488	Predicted by at least one method	yfbR_1	Predicted_00755	1641839	1642444	-1	5'-deoxynucleotidase YfbR
1629087	1715575	86488	Predicted by at least one method	hhaIM	Predicted_00749	1647201	1648826	-1	Modification methylase HhaI
1629087	1715575	86488	Predicted by at least one method		Predicted_00742	1651213	1651602	-1	hypothetical protein
1629087	1715575	86488	Predicted by at least one method	ascD_2	Predicted_00741	1651664	1651888	-1	CDP-6-deoxy-L-threo-D-glycero-4-hexulose-3-dehydrase reductase
1629087	1715575	86488	Predicted by at least one method	ssb_2	Predicted_00732	1660219	1660746	-1	Single-stranded DNA-binding protein
1629087	1715575	86488	Predicted by at least one method	cobS_3	Predicted_00730	1661729	1662697	-1	Aerobic cobaltochelatase subunit CobS
1629087	1715575	86488	Predicted by at least one method	yfgF	Predicted_00723	1669601	1670272	-1	Cyclic di-GMP phosphodiesterase YfgF
1629087	1715575	86488	Predicted by at least one method	dsbC_3	Predicted_00718	1674800	1675507	-1	Thiol:disulfide interchange protein DsbC precursor
1629087	1715575	86488	Predicted by at least one method	topB_1	Predicted_00701	1694849	1697041	1	DNA topoisomerase 3

1629087	1715575	86488	Predicted by at least one method	ydiO	Predicted_00693	1701337	1702764	-1	putative BsuMI modification methylase subunit YdiO
1629087	1715575	86488	Predicted by at least one method	korB	Predicted_00684	1706956	1708137	-1	Transcriptional repressor protein KorB
1629087	1715575	86488	Predicted by at least one method	soj	Predicted_00683	1708141	1708926	-1	Sporulation initiation inhibitor protein Soj
1629087	1715575	86488	Predicted by at least one method	bin3_2	Predicted_00680	1709731	1710468	-1	Putative transposon Tn552 DNA-invertase bin3
1629087	1715575	86488	Predicted by at least one method	dhfrI	Predicted_00200	1712632	1713105	1	Dihydrofolate reductase type 1
1629087	1715575	86488	Predicted by at least one method	ant1_2	Predicted_00202	1713782	1714570	1	Streptomycin 3''-adenylyltransferase
1690871	1705023	14152	Predicted by at least one method	topB_1	Predicted_00701	1694849	1697041	1	DNA topoisomerase 3
1690871	1705023	14152	Predicted by at least one method	ydiO	Predicted_00693	1701337	1702764	-1	putative BsuMI modification methylase subunit YdiO
1708141	1717256	9115	Predicted by at least one method	soj	Predicted_00683	1708141	1708926	-1	Sporulation initiation inhibitor protein Soj
1708141	1717256	9115	Predicted by at least one method		Predicted_00682	1709100	1709411	-1	hypothetical protein
1708141	1717256	9115	Predicted by at least one method		Predicted_00681	1709510	1709734	-1	hypothetical protein
1708141	1717256	9115	Predicted by at least one method	bin3_2	Predicted_00680	1709731	1710468	-1	Putative transposon Tn552 DNA-invertase bin3
1708141	1717256	9115	Predicted by at least one method		Predicted_00679	1710575	1711066	1	hypothetical protein
1708141	1717256	9115	Predicted by at least one method	dhfrI	Predicted_00200	1712632	1713105	1	Dihydrofolate reductase type 1
1708141	1717256	9115	Predicted by at least one method		Predicted_00201	1713200	1713724	1	TDP-fucosamine acetyltransferase
1708141	1717256	9115	Predicted by at least one method	ant1_2	Predicted_00202	1713782	1714570	1	Streptomycin 3''-adenylyltransferase
1730364	1799760	69396	Predicted by at least one method	hpaIIM	Predicted_00234	1739414	1740319	-1	Modification methylase HpaII
1730364	1799760	69396	Predicted by at least one method		Predicted_00235	1740574	1740762	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00236	1740774	1741178	-1	hypothetical protein

1730364	1799760	69396	Predicted by at least one method	nrdH_1	Predicted_00237	1741192	1741521	-1	Glutaredoxin-like protein NrdH
1730364	1799760	69396	Predicted by at least one method		Predicted_00238	1741699	1742010	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00239	1742068	1742442	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00240	1742521	1743201	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method	dinG_1	Predicted_00241	1743242	1745302	-1	putative ATP-dependent helicase DinG
1730364	1799760	69396	Predicted by at least one method		Predicted_00242	1745409	1745717	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00243	1745735	1746013	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method	virB	Predicted_00244	1746290	1747309	-1	Virulence regulon transcriptional activator VirB
1730364	1799760	69396	Predicted by at least one method	parA_1	Predicted_00245	1747312	1748559	-1	Plasmid partition protein A
1730364	1799760	69396	Predicted by at least one method	ascD_1	Predicted_00261	1754946	1755203	-1	CDP-6-deoxy-L-threo-D-glycero-4-hexulose-3-dehydrase reductase
1730364	1799760	69396	Predicted by at least one method	flhC_1	Predicted_00272	1762176	1762691	1	Flagellar transcriptional regulator FlhC
1730364	1799760	69396	Predicted by at least one method		Predicted_00275	1764054	1766768	-1	conjugal transfer mating pair stabilization protein TraN
1730364	1799760	69396	Predicted by at least one method		Predicted_00277	1767190	1770348	-1	TraG-like protein, N-terminal region
1730364	1799760	69396	Predicted by at least one method		Predicted_00278	1770363	1771799	-1	Conjugative relaxosome accessory transposon protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00289	1776409	1778187	-1	von Willebrand factor type A domain
1730364	1799760	69396	Predicted by at least one method	cobS_1	Predicted_00292	1779938	1780999	-1	Aerobic cobaltochelatase subunit CobS
1730364	1799760	69396	Predicted by at least one method		Predicted_00293	1781066	1781440	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00294	1781808	1782923	-1	YqaJ-like viral recombinase domain
1730364	1799760	69396	Predicted by at least		Predicted_00295	1782983	1784527	-1	recombination and repair

			one method						protein RecT
1730364	1799760	69396	Predicted by at least one method		Predicted_00296	1784613	1785302	-1	Single-strand binding protein family
1730364	1799760	69396	Predicted by at least one method		Predicted_00297	1785770	1786207	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00298	1786286	1786894	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00299	1787404	1788153	1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00300	1788297	1788827	1	Sel1 repeat
1730364	1799760	69396	Predicted by at least one method		Predicted_00301	1788878	1789963	-1	TraU protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00302	1789960	1791219	-1	Type-F conjugative transfer system pilin assembly protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00303	1791213	1791737	-1	signal peptidase I
1730364	1799760	69396	Predicted by at least one method		Predicted_00304	1791755	1792030	-1	hypothetical protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00305	1792027	1794516	-1	AAA-like domain
1730364	1799760	69396	Predicted by at least one method	dsbC_1	Predicted_00306	1794540	1795283	-1	putative thiol:disulfide interchange protein DsbC precursor
1730364	1799760	69396	Predicted by at least one method		Predicted_00307	1795691	1796224	-1	Type IV conjugative transfer system lipoprotein (TraV)
1730364	1799760	69396	Predicted by at least one method		Predicted_00308	1796227	1797615	-1	Bacterial conjugation TrbI-like protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00309	1797623	1798717	-1	TraK protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00310	1798886	1799476	-1	TraE protein
1730364	1799760	69396	Predicted by at least one method		Predicted_00311	1799473	1799760	-1	TraL protein
1845550	1871329	25779	Predicted by at least one method	rdgC_1	Predicted_00371	1848184	1849422	-1	Recombination-associated protein RdgC
1845550	1871329	25779	Predicted by at least one method	dam_1	Predicted_00372	1849419	1850240	-1	DNA adenine methylase

1845550	1871329	25779	Predicted by at least one method		Predicted_00373	1850295	1850936	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method	dnaN_1	Predicted_00374	1851163	1852431	-1	DNA polymerase III subunit beta
1845550	1871329	25779	Predicted by at least one method		Predicted_00383	1856238	1856588	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method	ssb_1	Predicted_00384	1856656	1857177	-1	Single-stranded DNA-binding protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00385	1857426	1857857	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00386	1857866	1858150	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method	hflK_1	Predicted_00387	1858261	1859181	-1	Modulator of FtsH protease HflK
1845550	1871329	25779	Predicted by at least one method		Predicted_00388	1859205	1859636	-1	NfeD-like C-terminal, partner-binding
1845550	1871329	25779	Predicted by at least one method		Predicted_00396	1865879	1867270	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method	tnpR_1	Predicted_00397	1867347	1867928	-1	Transposon gamma-delta resolvase
1845550	1871329	25779	Predicted by at least one method		Predicted_00398	1868113	1868463	1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method	higA_1	Predicted_00399	1868465	1868764	1	Antitoxin HigA
1845550	1871329	25779	Predicted by at least one method		Predicted_00400	1868905	1869921	1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00401	1869972	1870373	-1	hypothetical protein
1845550	1871329	25779	Predicted by at least one method		Predicted_00402	1870805	1871329	-1	LexA repressor
1880359	1892698	12339	Predicted by at least one method	comR_1	Predicted_00417	1880359	1880940	-1	HTH-type transcriptional repressor ComR
1880359	1892698	12339	Predicted by at least one method		Predicted_00418	1881089	1881661	-1	hypothetical protein
1880359	1892698	12339	Predicted by at least one method		Predicted_00419	1881797	1882489	-1	hypothetical protein
1880359	1892698	12339	Predicted by at least one method	tus_1	Predicted_00420	1882545	1883426	-1	DNA replication terminus site-binding protein

1880359	1892698	12339	Predicted by at least one method		Predicted_00180	1889232	1889960	1	Tn3 transposase DDE domain
1880359	1892698	12339	Predicted by at least one method	aacA4_1	Predicted_00527	1891353	1891958	-1	Aminoglycoside N(6')-acetyltransferase type 1
1880359	1892698	12339	Predicted by at least one method	tnpR_2	Predicted_00526	1892141	1892698	-1	Transposon Tn3 resolvase
1889232	1896303	7071	Predicted by at least one method		Predicted_00180	1889232	1889960	1	Tn3 transposase DDE domain
1889232	1896303	7071	Predicted by at least one method	aacA4_1	Predicted_00527	1891353	1891958	-1	Aminoglycoside N(6')-acetyltransferase type 1
1889232	1896303	7071	Predicted by at least one method	tnpR_2	Predicted_00526	1892141	1892698	-1	Transposon Tn3 resolvase
1889232	1896303	7071	Predicted by at least one method		Predicted_00525	1892860	1895865	1	Tn3 transposase DDE domain
1889232	1896303	7071	Predicted by at least one method		Predicted_00524	1896214	1896303	1	hypothetical protein
1889232	1896303	7071	Predicted by at least one method	dmlR_1	Predicted_00523	1896281	1897150	-1	HTH-type transcriptional regulator DmlR
1903585	1915816	12231	Predicted by at least one method		Predicted_00516	1903585	1903809	1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00515	1904357	1904641	1	Transposase
1903585	1915816	12231	Predicted by at least one method		Predicted_00514	1904671	1905495	1	Integrase core domain
1903585	1915816	12231	Predicted by at least one method		Predicted_00513	1905885	1906526	-1	DNA replication terminus site-binding protein
1903585	1915816	12231	Predicted by at least one method	pir	Predicted_00510	1907016	1907852	-1	PI protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00509	1909188	1909679	-1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00508	1909690	1910070	-1	Plasmid stability protein
1903585	1915816	12231	Predicted by at least one method	parM	Predicted_00507	1910075	1911034	-1	Plasmid segregation protein ParM
1903585	1915816	12231	Predicted by at least one method		Predicted_00506	1911331	1912143	-1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00505	1912467	1912886	1	hypothetical protein

1903585	1915816	12231	Predicted by at least one method		Predicted_00504	1913222	1913680	-1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00503	1914167	1914715	1	Transglycosylase SLT domain
1903585	1915816	12231	Predicted by at least one method		Predicted_00502	1914738	1915259	1	hypothetical protein
1903585	1915816	12231	Predicted by at least one method		Predicted_00501	1915256	1915816	1	transcriptional activator FlhC
1904357	1910070	5713	Predicted by at least one method		Predicted_00515	1904357	1904641	1	Transposase
1904357	1910070	5713	Predicted by at least one method		Predicted_00514	1904671	1905495	1	Integrase core domain
1904357	1910070	5713	Predicted by at least one method		Predicted_00513	1905885	1906526	-1	DNA replication terminus site-binding protein
1904357	1910070	5713	Predicted by at least one method		Predicted_00512	1906615	1906710	-1	hypothetical protein
1904357	1910070	5713	Predicted by at least one method		Predicted_00511	1906786	1907013	-1	hypothetical protein
1904357	1910070	5713	Predicted by at least one method	pir	Predicted_00510	1907016	1907852	-1	PI protein
1904357	1910070	5713	Predicted by at least one method		Predicted_00509	1909188	1909679	-1	hypothetical protein
1904357	1910070	5713	Predicted by at least one method		Predicted_00508	1909690	1910070	-1	Plasmid stability protein
1923186	1932903	9717	Predicted by at least one method		Predicted_00496	1923186	1924595	-1	Conjugative relaxosome accessory transposon protein
1923186	1932903	9717	Predicted by at least one method		Predicted_00495	1924611	1925642	-1	hypothetical protein
1923186	1932903	9717	Predicted by at least one method		Predicted_00494	1925878	1927653	-1	von Willebrand factor type A domain
1923186	1932903	9717	Predicted by at least one method		Predicted_00493	1927718	1928905	-1	hypothetical protein
1923186	1932903	9717	Predicted by at least one method	cobS_2	Predicted_00492	1929004	1930011	-1	Aerobic cobaltochelatase subunit CobS
1923186	1932903	9717	Predicted by at least one method		Predicted_00491	1930065	1930433	-1	hypothetical protein
1923186	1932903	9717	Predicted by at least one method		Predicted_00490	1930471	1931565	-1	YqaJ-like viral recombinase domain

1923186	1932903	9717	Predicted by at least one method		Predicted_00489	1931614	1932903	-1	recombination and repair protein RecT
1961683	2089481	127798	Predicted by at least one method		Predicted_00458	1961683	1964370	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00457	1964402	1966432	1	Helicase conserved C-terminal domain
1961683	2089481	127798	Predicted by at least one method		Predicted_00456	1966436	1967695	1	T5orf172 domain
1961683	2089481	127798	Predicted by at least one method	mrr_1	Predicted_00455	1967708	1968706	1	Mrr restriction system protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00454	1968877	1971429	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00453	1971578	1972045	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00452	1972042	1972491	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00451	1972530	1972961	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00450	1973020	1973229	-1	Prophage CP4-57 regulatory protein (AlpA)
1961683	2089481	127798	Predicted by at least one method	engB_1	Predicted_00449	1973307	1974296	1	GTP-binding protein EngB
1961683	2089481	127798	Predicted by at least one method		Predicted_00448	1974406	1974852	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00447	1974894	1975538	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00446	1975985	1976917	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00445	1977142	1977471	-1	Resolvase, N terminal domain
1961683	2089481	127798	Predicted by at least one method		Predicted_00444	1977639	1980626	1	Tn3 transposase DDE domain
1961683	2089481	127798	Predicted by at least one method		Predicted_00443	1980898	1982433	1	DNA-dependent helicase II
1961683	2089481	127798	Predicted by at least one method		Predicted_00442	1982529	1983605	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00441	1983659	1984213	-1	hypothetical protein

1961683	2089481	127798	Predicted by at least one method		Predicted_00440	1984272	1985234	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00439	1985324	1986259	-1	Restriction endonuclease
1961683	2089481	127798	Predicted by at least one method		Predicted_00438	1986277	1986846	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00437	1986833	1987183	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	sipT	Predicted_00436	1987170	1987919	-1	Signal peptidase I T
1961683	2089481	127798	Predicted by at least one method		Predicted_00435	1988000	1988422	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00434	1988412	1989422	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00433	1989443	1990261	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	xerC_1	Predicted_00432	1990275	1991228	-1	Tyrosine recombinase XerC
1961683	2089481	127798	Predicted by at least one method		Predicted_00431	1991523	1991792	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00430	1991831	1992085	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00429	1992182	1992640	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00428	1992961	1993104	1	small toxic polypeptide
1961683	2089481	127798	Predicted by at least one method		Predicted_00427	1993191	1993571	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	mazF_1	Predicted_00426	1993602	1993934	-1	mRNA interferase MazF
1961683	2089481	127798	Predicted by at least one method	mazE	Predicted_00425	1993934	1994179	-1	Antitoxin MazE
1961683	2089481	127798	Predicted by at least one method	parA_2	Predicted_00424	1994489	1995112	1	Chromosome partitioning protein ParA
1961683	2089481	127798	Predicted by at least one method		Predicted_00423	1995237	1995464	1	ParG
1961683	2089481	127798	Predicted by at least one method		Predicted_04342	1997580	1997819	1	hypothetical protein

1961683	2089481	127798	Predicted by at least one method	xerC_6	Predicted_04343	1998448	1998984	-1	Tyrosine recombinase XerC
1961683	2089481	127798	Predicted by at least one method		Predicted_01194	2000983	2001480	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01193	2001483	2001971	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01192	2002068	2002403	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01191	2002418	2002888	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01190	2002881	2003252	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01189	2003263	2003457	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01188	2003457	2003708	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01187	2003798	2004346	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01186	2004509	2004859	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	higA_4	Predicted_01185	2004864	2005166	1	Antitoxin HigA
1961683	2089481	127798	Predicted by at least one method		Predicted_01184	2005193	2005486	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	hupB_1	Predicted_01183	2005574	2005846	-1	DNA-binding protein HU-beta
1961683	2089481	127798	Predicted by at least one method	yncB	Predicted_01182	2005904	2006431	-1	Endonuclease YncB precursor
1961683	2089481	127798	Predicted by at least one method		Predicted_01181	2006448	2006636	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01180	2006662	2007519	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01179	2007506	2007733	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01178	2007736	2008254	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01177	2008251	2008697	-1	hypothetical protein

1961683	2089481	127798	Predicted by at least one method		Predicted_01176	2008697	2009056	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01175	2009113	2009541	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	bdbD_2	Predicted_01174	2009575	2010435	-1	Disulfide bond formation protein D precursor
1961683	2089481	127798	Predicted by at least one method	sppA_1	Predicted_01173	2010451	2011410	-1	Putative signal peptide peptidase SppA
1961683	2089481	127798	Predicted by at least one method		Predicted_01159	2021089	2021382	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01158	2021384	2021803	1	H-NS histone family
1961683	2089481	127798	Predicted by at least one method		Predicted_01157	2021863	2022414	-1	transcriptional activator FlhC
1961683	2089481	127798	Predicted by at least one method		Predicted_01156	2022411	2023076	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01155	2023030	2023563	-1	Transglycosylase SLT domain
1961683	2089481	127798	Predicted by at least one method		Predicted_01154	2023563	2023835	-1	DNA-binding transcriptional regulator Nlp
1961683	2089481	127798	Predicted by at least one method		Predicted_01153	2024551	2024913	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01152	2024951	2028565	-1	TraG-like protein, N-terminal region
1961683	2089481	127798	Predicted by at least one method		Predicted_01151	2028578	2030011	-1	Conjugative relaxosome accessory transposon protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01150	2030013	2031041	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01149	2031164	2032675	-1	DNA helicase IV
1961683	2089481	127798	Predicted by at least one method		Predicted_01148	2032684	2032962	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	smc_2	Predicted_01147	2032962	2034002	-1	Chromosome partition protein Smc
1961683	2089481	127798	Predicted by at least one method	tus_3	Predicted_01146	2034155	2035030	-1	DNA replication terminus site-binding protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01145	2035357	2035848	-1	hypothetical protein

1961683	2089481	127798	Predicted by at least one method	dnaQ_1	Predicted_01144	2035845	2036714	-1	DNA polymerase III subunit epsilon
1961683	2089481	127798	Predicted by at least one method	xerD_2	Predicted_01143	2036719	2037552	-1	Tyrosine recombinase XerD
1961683	2089481	127798	Predicted by at least one method		Predicted_01135	2041517	2042449	-1	Transposase DDE domain
1961683	2089481	127798	Predicted by at least one method		Predicted_01134	2042538	2042864	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	dinB_3	Predicted_01133	2042900	2044177	-1	DNA polymerase IV
1961683	2089481	127798	Predicted by at least one method	lexA_3	Predicted_01132	2044183	2044611	-1	LexA repressor
1961683	2089481	127798	Predicted by at least one method		Predicted_01131	2044707	2044979	-1	Helix-turn-helix domain
1961683	2089481	127798	Predicted by at least one method		Predicted_01130	2045104	2045454	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01129	2045475	2045864	1	Transposase DDE domain
1961683	2089481	127798	Predicted by at least one method		Predicted_01128	2045932	2046483	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01127	2046705	2046944	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_01126	2047007	2047837	-1	Integrase core domain
1961683	2089481	127798	Predicted by at least one method		Predicted_01125	2047834	2048145	-1	Transposase
1961683	2089481	127798	Predicted by at least one method	tmrB	Predicted_01124	2048198	2048491	-1	Tunicamycin resistance protein
1961683	2089481	127798	Predicted by at least one method	yokD	Predicted_01123	2048504	2049364	-1	SPBc2 prophage-derived aminoglycoside N(3')-acetyltransferase-like protein YokD
1961683	2089481	127798	Predicted by at least one method	bla_1	Predicted_01122	2049506	2050366	-1	Beta-lactamase TEM precursor
1961683	2089481	127798	Predicted by at least one method	tnpR_4	Predicted_01121	2050549	2051106	-1	Transposon Tn3 resolvase
1961683	2089481	127798	Predicted by at least one method		Predicted_01120	2051270	2054278	1	Tn3 transposase DDE domain

1961683	2089481	127798	Predicted by at least one method		Predicted_00097	2056678	2058219	1	Putative transposase
1961683	2089481	127798	Predicted by at least one method	trpF	Predicted_00098	2058775	2059245	-1	N-(5'-phosphoribosyl)anthranilate isomerase
1961683	2089481	127798	Predicted by at least one method		Predicted_00099	2059355	2059906	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	blaNDM-1	Predicted_00100	2059787	2060599	-1	Beta-lactamase NDM-1 precursor
1961683	2089481	127798	Predicted by at least one method		Predicted_00101	2060700	2061710	-1	Integrase core domain
1961683	2089481	127798	Predicted by at least one method	aphA_1	Predicted_00102	2061877	2062656	-1	Aminoglycoside 3'-phosphotransferase
1961683	2089481	127798	Predicted by at least one method		Predicted_00103	2062762	2062992	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00104	2062982	2063425	-1	Transposase
1961683	2089481	127798	Predicted by at least one method		Predicted_00105	2063716	2065977	-1	Tn3 transposase DDE domain
1961683	2089481	127798	Predicted by at least one method	hin	Predicted_00106	2065980	2066612	-1	DNA-invertase hin
1961683	2089481	127798	Predicted by at least one method	ttgC	Predicted_00107	2066668	2068155	-1	Toluene efflux pump outer membrane protein TtgC precursor
1961683	2089481	127798	Predicted by at least one method		Predicted_00108	2068142	2068615	-1	Cytochrome C'
1961683	2089481	127798	Predicted by at least one method	lolD_1	Predicted_00109	2068644	2069354	-1	Lipoprotein-releasing system ATP-binding protein LolD
1961683	2089481	127798	Predicted by at least one method		Predicted_00110	2069359	2070561	-1	FtsX-like permease family
1961683	2089481	127798	Predicted by at least one method	mdtA_1	Predicted_00111	2070558	2071709	-1	Multidrug resistance protein MdtA precursor
1961683	2089481	127798	Predicted by at least one method	slmA_1	Predicted_00112	2071706	2072314	-1	Nucleoid occlusion factor SlmA
1961683	2089481	127798	Predicted by at least one method		Predicted_00113	2072395	2073069	-1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00114	2073624	2073971	1	hypothetical protein

1961683	2089481	127798	Predicted by at least one method		Predicted_00115	2074016	2077042	-1	Tn3 transposase DDE domain
1961683	2089481	127798	Predicted by at least one method	bin3_1	Predicted_00116	2077204	2077848	1	Putative transposon Tn552 DNA-invertase bin3
1961683	2089481	127798	Predicted by at least one method	betT_1	Predicted_00117	2078032	2078361	1	High-affinity choline transport protein
1961683	2089481	127798	Predicted by at least one method	merR	Predicted_00118	2078351	2078806	-1	Mercuric resistance operon regulatory protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00119	2078878	2079243	1	MerT mercuric transport protein
1961683	2089481	127798	Predicted by at least one method	merP	Predicted_00120	2079259	2079534	1	Mercuric transport protein periplasmic component precursor
1961683	2089481	127798	Predicted by at least one method	merC	Predicted_00121	2079562	2079987	1	Mercuric resistance protein MerC
1961683	2089481	127798	Predicted by at least one method	merA	Predicted_00122	2080026	2081711	1	Mercuric reductase
1961683	2089481	127798	Predicted by at least one method		Predicted_00123	2081729	2082094	1	zinc-responsive transcriptional regulator
1961683	2089481	127798	Predicted by at least one method		Predicted_00124	2082091	2082327	1	MerE protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00125	2082393	2082605	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00126	2082861	2083682	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method		Predicted_00127	2084142	2084636	1	hypothetical protein
1961683	2089481	127798	Predicted by at least one method	folP_1	Predicted_00128	2084742	2085581	-1	Dihydropteroate synthase
1961683	2089481	127798	Predicted by at least one method	emrE_1	Predicted_00129	2085575	2085922	-1	Multidrug transporter EmrE
1961683	2089481	127798	Predicted by at least one method	ant1_1	Predicted_00130	2086086	2086865	-1	Streptomycin 3''-adenylyltransferase
1961683	2089481	127798	Predicted by at least one method	dfrA	Predicted_00131	2087285	2087782	-1	Dihydrofolate reductase
1961683	2089481	127798	Predicted by at least one method	xerD_1	Predicted_00132	2087927	2088940	1	Tyrosine recombinase XerD
1961683	2089481	127798	Predicted by at least		Predicted_00133	2088927	2089481	-1	hypothetical protein

			one method						
1973020	1980626	7606	Predicted by at least one method		Predicted_00450	1973020	1973229	-1	Prophage CP4-57 regulatory protein (AlpA)
1973020	1980626	7606	Predicted by at least one method	engB_1	Predicted_00449	1973307	1974296	1	GTP-binding protein EngB
1973020	1980626	7606	Predicted by at least one method		Predicted_00448	1974406	1974852	1	hypothetical protein
1973020	1980626	7606	Predicted by at least one method		Predicted_00447	1974894	1975538	-1	hypothetical protein
1973020	1980626	7606	Predicted by at least one method		Predicted_00446	1975985	1976917	1	hypothetical protein
1973020	1980626	7606	Predicted by at least one method		Predicted_00445	1977142	1977471	-1	Resolvase, N terminal domain
1973020	1980626	7606	Predicted by at least one method		Predicted_00444	1977639	1980626	1	Tn3 transposase DDE domain
1985324	1990261	4937	Predicted by at least one method		Predicted_00439	1985324	1986259	-1	Restriction endonuclease
1985324	1990261	4937	Predicted by at least one method		Predicted_00438	1986277	1986846	-1	hypothetical protein
1985324	1990261	4937	Predicted by at least one method		Predicted_00437	1986833	1987183	-1	hypothetical protein
1985324	1990261	4937	Predicted by at least one method	sipT	Predicted_00436	1987170	1987919	-1	Signal peptidase I T
1985324	1990261	4937	Predicted by at least one method		Predicted_00435	1988000	1988422	-1	hypothetical protein
1985324	1990261	4937	Predicted by at least one method		Predicted_00434	1988412	1989422	-1	hypothetical protein
1985324	1990261	4937	Predicted by at least one method		Predicted_00433	1989443	1990261	-1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method		Predicted_00431	1991523	1991792	1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method		Predicted_00430	1991831	1992085	1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method		Predicted_00429	1992182	1992640	1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method		Predicted_00428	1992961	1993104	1	small toxic polypeptide
1991523	2001971	10448	Predicted by at least		Predicted_00427	1993191	1993571	-1	hypothetical protein

			one method						
1991523	2001971	10448	Predicted by at least one method	mazF_1	Predicted_00426	1993602	1993934	-1	mRNA interferase MazF
1991523	2001971	10448	Predicted by at least one method	mazE	Predicted_00425	1993934	1994179	-1	Antitoxin MazE
1991523	2001971	10448	Predicted by at least one method	parA_2	Predicted_00424	1994489	1995112	1	Chromosome partitioning protein ParA
1991523	2001971	10448	Predicted by at least one method		Predicted_00423	1995237	1995464	1	ParG
1991523	2001971	10448	Predicted by at least one method		Predicted_04342	1997580	1997819	1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method	xerC_6	Predicted_04343	1998448	1998984	-1	Tyrosine recombinase XerC
1991523	2001971	10448	Predicted by at least one method		Predicted_01194	2000983	2001480	-1	hypothetical protein
1991523	2001971	10448	Predicted by at least one method		Predicted_01193	2001483	2001971	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01191	2002418	2002888	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01190	2002881	2003252	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01189	2003263	2003457	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01188	2003457	2003708	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01187	2003798	2004346	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01186	2004509	2004859	1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method	higA_4	Predicted_01185	2004864	2005166	1	Antitoxin HigA
2002881	2009541	6660	Predicted by at least one method		Predicted_01184	2005193	2005486	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method	hupB_1	Predicted_01183	2005574	2005846	-1	DNA-binding protein HU-beta
2002881	2009541	6660	Predicted by at least one method	yncB	Predicted_01182	2005904	2006431	-1	Endonuclease YncB precursor
2002881	2009541	6660	Predicted by at least		Predicted_01181	2006448	2006636	-1	hypothetical protein

			one method						
2002881	2009541	6660	Predicted by at least one method		Predicted_01180	2006662	2007519	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01179	2007506	2007733	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01178	2007736	2008254	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01177	2008251	2008697	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01176	2008697	2009056	-1	hypothetical protein
2002881	2009541	6660	Predicted by at least one method		Predicted_01175	2009113	2009541	-1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method	sppA_1	Predicted_01173	2010451	2011410	-1	Putative signal peptide peptidase SppA
2010451	2024913	14462	Predicted by at least one method		Predicted_01172	2011410	2012264	-1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01171	2012269	2012562	-1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01170	2012573	2013046	-1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01169	2013143	2013664	-1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01168	2013667	2014188	-1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01167	2014193	2014801	-1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01166	2015070	2016185	1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01165	2016203	2016637	1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01164	2017047	2017328	-1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01163	2017674	2018738	-1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01162	2018759	2019046	-1	hypothetical protein
2010451	2024913	14462	Predicted by at least		Predicted_01161	2019051	2019590	-1	hypothetical protein

			one method						
2010451	2024913	14462	Predicted by at least one method		Predicted_01160	2020089	2021072	1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01159	2021089	2021382	1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01158	2021384	2021803	1	H-NS histone family
2010451	2024913	14462	Predicted by at least one method		Predicted_01157	2021863	2022414	-1	transcriptional activator FlhC
2010451	2024913	14462	Predicted by at least one method		Predicted_01156	2022411	2023076	-1	hypothetical protein
2010451	2024913	14462	Predicted by at least one method		Predicted_01155	2023030	2023563	-1	Transglycosylase SLT domain
2010451	2024913	14462	Predicted by at least one method		Predicted_01154	2023563	2023835	-1	DNA-binding transcriptional regulator Nlp
2010451	2024913	14462	Predicted by at least one method		Predicted_01153	2024551	2024913	1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01150	2030013	2031041	-1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01149	2031164	2032675	-1	DNA helicase IV
2030013	2060599	30586	Predicted by at least one method		Predicted_01148	2032684	2032962	-1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method	smc_2	Predicted_01147	2032962	2034002	-1	Chromosome partition protein Smc
2030013	2060599	30586	Predicted by at least one method	tus_3	Predicted_01146	2034155	2035030	-1	DNA replication terminus site-binding protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01145	2035357	2035848	-1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method	dnaQ_1	Predicted_01144	2035845	2036714	-1	DNA polymerase III subunit epsilon
2030013	2060599	30586	Predicted by at least one method	xerD_2	Predicted_01143	2036719	2037552	-1	Tyrosine recombinase XerD
2030013	2060599	30586	Predicted by at least one method		Predicted_01135	2041517	2042449	-1	Transposase DDE domain
2030013	2060599	30586	Predicted by at least one method		Predicted_01134	2042538	2042864	1	hypothetical protein
2030013	2060599	30586	Predicted by at least	dinB_3	Predicted_01133	2042900	2044177	-1	DNA polymerase IV

			one method						
2030013	2060599	30586	Predicted by at least one method	lexA_3	Predicted_01132	2044183	2044611	-1	LexA repressor
2030013	2060599	30586	Predicted by at least one method		Predicted_01131	2044707	2044979	-1	Helix-turn-helix domain
2030013	2060599	30586	Predicted by at least one method		Predicted_01130	2045104	2045454	1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01129	2045475	2045864	1	Transposase DDE domain
2030013	2060599	30586	Predicted by at least one method		Predicted_01128	2045932	2046483	1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01127	2046705	2046944	-1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method		Predicted_01126	2047007	2047837	-1	Integrase core domain
2030013	2060599	30586	Predicted by at least one method		Predicted_01125	2047834	2048145	-1	Transposase
2030013	2060599	30586	Predicted by at least one method	tmrB	Predicted_01124	2048198	2048491	-1	Tunicamycin resistance protein
2030013	2060599	30586	Predicted by at least one method	yokD	Predicted_01123	2048504	2049364	-1	SPBc2 prophage-derived aminoglycoside N(3')-acetyltransferase-like protein YokD
2030013	2060599	30586	Predicted by at least one method	bla_1	Predicted_01122	2049506	2050366	-1	Beta-lactamase TEM precursor
2030013	2060599	30586	Predicted by at least one method	tnpR_4	Predicted_01121	2050549	2051106	-1	Transposon Tn3 resolvase
2030013	2060599	30586	Predicted by at least one method		Predicted_01120	2051270	2054278	1	Tn3 transposase DDE domain
2030013	2060599	30586	Predicted by at least one method		Predicted_00097	2056678	2058219	1	Putative transposase
2030013	2060599	30586	Predicted by at least one method	trpF	Predicted_00098	2058775	2059245	-1	N-(5'-phosphoribosyl)anthranilate isomerase
2030013	2060599	30586	Predicted by at least one method		Predicted_00099	2059355	2059906	1	hypothetical protein
2030013	2060599	30586	Predicted by at least one method	blaNDM-1	Predicted_00100	2059787	2060599	-1	Beta-lactamase NDM-1 precursor

2082861	2089481	6620	Predicted by at least one method		Predicted_00126	2082861	2083682	1	hypothetical protein
2082861	2089481	6620	Predicted by at least one method		Predicted_00127	2084142	2084636	1	hypothetical protein
2082861	2089481	6620	Predicted by at least one method	folP_1	Predicted_00128	2084742	2085581	-1	Dihydropteroate synthase
2082861	2089481	6620	Predicted by at least one method	emrE_1	Predicted_00129	2085575	2085922	-1	Multidrug transporter EmrE
2082861	2089481	6620	Predicted by at least one method	ant1_1	Predicted_00130	2086086	2086865	-1	Streptomycin 3"-adenylyltransferase
2082861	2089481	6620	Predicted by at least one method	dfrA	Predicted_00131	2087285	2087782	-1	Dihydrofolate reductase
2082861	2089481	6620	Predicted by at least one method	xerD_1	Predicted_00132	2087927	2088940	1	Tyrosine recombinase XerD
2082861	2089481	6620	Predicted by at least one method		Predicted_00133	2088927	2089481	-1	hypothetical protein
2591142	2599539	8397	Predicted by at least one method		Predicted_00637	2591142	2594150	-1	Tn3 transposase DDE domain
2591142	2599539	8397	Predicted by at least one method	tnpR_3	Predicted_00638	2594314	2594886	1	Transposon Tn3 resolvase
2591142	2599539	8397	Predicted by at least one method	fdtC	Predicted_00639	2595006	2595458	1	dTDP-3-amino-3,6-dideoxy-alpha-D- galactopyranose 3-N-acetyltransferase
2591142	2599539	8397	Predicted by at least one method	hapE	Predicted_00640	2595490	2597022	-1	4-hydroxyacetophenone monooxygenase
2591142	2599539	8397	Predicted by at least one method		Predicted_00641	2597019	2597288	-1	PQ loop repeat
2591142	2599539	8397	Predicted by at least one method	ntdC	Predicted_00642	2597290	2598306	-1	Glucose-6-phosphate 3-dehydrogenase
2591142	2599539	8397	Predicted by at least one method	ntdB	Predicted_00643	2598303	2599136	-1	Kanosamine-6-phosphate phosphatase
2591142	2599539	8397	Predicted by at least one method	ntdA_1	Predicted_00644	2599120	2599539	-1	3-oxo-glucose-6-phosphate:glutamate aminotransferase
2594314	2599539	5225	Predicted by at least one method	tnpR_3	Predicted_00638	2594314	2594886	1	Transposon Tn3 resolvase
2594314	2599539	5225	Predicted by at least one method	fdtC	Predicted_00639	2595006	2595458	1	dTDP-3-amino-3,6-dideoxy-alpha-D- galactopyranose 3-N-acetyltransferase

2594314	2599539	5225	Predicted by at least one method	hapE	Predicted_00640	2595490	2597022	-1	4-hydroxyacetophenone monooxygenase
2594314	2599539	5225	Predicted by at least one method		Predicted_00641	2597019	2597288	-1	PQ loop repeat
2594314	2599539	5225	Predicted by at least one method	ntdC	Predicted_00642	2597290	2598306	-1	Glucose-6-phosphate 3-dehydrogenase
2594314	2599539	5225	Predicted by at least one method	ntdB	Predicted_00643	2598303	2599136	-1	Kanosamine-6-phosphate phosphatase
2594314	2599539	5225	Predicted by at least one method	ntdA_1	Predicted_00644	2599120	2599539	-1	3-oxo-glucose-6-phosphate:glutamate aminotransferase
3267726	3284238	16512	Predicted by at least one method	ppnK_2	Predicted_02302	3267726	3268625	1	putative inorganic polyphosphate/ATP-NAD kinase
3267726	3284238	16512	Predicted by at least one method	recN	Predicted_02303	3268712	3270373	1	DNA repair protein RecN
3267726	3284238	16512	Predicted by at least one method	bamE	Predicted_02304	3270486	3270878	1	Outer membrane protein assembly factor BamE precursor
3267726	3284238	16512	Predicted by at least one method	pasI	Predicted_02305	3271052	3271357	-1	Persistence and stress-resistance antitoxin PasI
3267726	3284238	16512	Predicted by at least one method	pasT	Predicted_02306	3271341	3271775	-1	Prophage CP4-57 integrase
3267726	3284238	16512	Predicted by at least one method	smpB	Predicted_02307	3271929	3272411	1	SsrA-binding protein
3267726	3284238	16512	Predicted by at least one method	intA_4	Predicted_02309	3272989	3274197	1	Prophage CP4-57 integrase
3267726	3284238	16512	Predicted by at least one method		Predicted_02310	3274243	3276297	1	hypothetical protein
3267726	3284238	16512	Predicted by at least one method		Predicted_02311	3276399	3277670	-1	hypothetical protein
3267726	3284238	16512	Predicted by at least one method	era_2	Predicted_03129	3279073	3279945	1	GTPase Era
3267726	3284238	16512	Predicted by at least one method	klcA_3	Predicted_03128	3280037	3280462	1	Antirestriction protein KlcA
3267726	3284238	16512	Predicted by at least one method		Predicted_03127	3280476	3280907	1	hypothetical protein
3267726	3284238	16512	Predicted by at least	xerD_4	Predicted_03126	3280993	3282003	-1	Tyrosine recombinase XerD

			one method						
3267726	3284238	16512	Predicted by at least one method	xerC_4	Predicted_03125	3281996	3282961	-1	Tyrosine recombinase XerC
3267726	3284238	16512	Predicted by at least one method	xerC_3	Predicted_03124	3282961	3284238	-1	Tyrosine recombinase XerC
3296833	3302010	5177	Predicted by at least one method		Predicted_04334	3296833	3297108	-1	InsA C-terminal domain
3296833	3302010	5177	Predicted by at least one method		Predicted_04335	3297222	3297341	1	hypothetical protein
3296833	3302010	5177	Predicted by at least one method		Predicted_02210	3299136	3299243	-1	hypothetical protein
3296833	3302010	5177	Predicted by at least one method		Predicted_02209	3299279	3299545	-1	hypothetical protein
3296833	3302010	5177	Predicted by at least one method		Predicted_02208	3299535	3300593	-1	hypothetical protein
3296833	3302010	5177	Predicted by at least one method	hcpA_5	Predicted_02207	3300611	3301090	-1	Major exported protein
3296833	3302010	5177	Predicted by at least one method	intA_3	Predicted_02206	3301576	3302010	1	Prophage CP4-57 integrase
3623549	3629520	5971	Predicted by at least one method		Predicted_00860	3623549	3623920	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method		Predicted_00861	3623979	3624461	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method		Predicted_00862	3624647	3625042	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method		Predicted_00863	3625141	3625626	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method	repA	Predicted_00864	3626145	3627017	-1	Replication protein RepA
3623549	3629520	5971	Predicted by at least one method		Predicted_00865	3627321	3627626	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method		Predicted_00866	3627623	3627940	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method		Predicted_00867	3628060	3628626	-1	hypothetical protein
3623549	3629520	5971	Predicted by at least one method	higA_2	Predicted_00868	3629104	3629520	1	Antitoxin HigA
4097099	4102094	4995	Predicted by at least		Predicted_01114	4097099	4097785	-1	hypothetical protein

			one method						
4097099	4102094	4995	Predicted by at least one method		Predicted_01113	4097789	4101121	-1	ATP-dependent helicase HepA
4097099	4102094	4995	Predicted by at least one method		Predicted_01112	4101159	4102094	-1	hypothetical protein
4468672	4477529	8857	Predicted by at least one method	arsD_2	Predicted_03796	4468672	4469037	-1	Arsenical resistance operon trans-acting repressor ArsD
4468672	4477529	8857	Predicted by at least one method	arsR_3	Predicted_03797	4469085	4469420	-1	Arsenical resistance operon repressor
4468672	4477529	8857	Predicted by at least one method		Predicted_03798	4469903	4470646	-1	hypothetical protein
4468672	4477529	8857	Predicted by at least one method		Predicted_03799	4470648	4471184	-1	hypothetical protein
4468672	4477529	8857	Predicted by at least one method		Predicted_03421	4472613	4472939	1	hypothetical protein
4468672	4477529	8857	Predicted by at least one method		Predicted_03420	4472936	4474015	1	hypothetical protein
4468672	4477529	8857	Predicted by at least one method		Predicted_03419	4474019	4474963	-1	hypothetical protein
4468672	4477529	8857	Predicted by at least one method	thyA_2	Predicted_03418	4474967	4475944	-1	Thymidylate synthase
4468672	4477529	8857	Predicted by at least one method	intA_5	Predicted_03417	4476255	4477529	-1	Prophage CP4-57 integrase
4469085	4475944	6859	Predicted by at least one method	arsR_3	Predicted_03797	4469085	4469420	-1	Arsenical resistance operon repressor
4469085	4475944	6859	Predicted by at least one method		Predicted_03798	4469903	4470646	-1	hypothetical protein
4469085	4475944	6859	Predicted by at least one method		Predicted_03799	4470648	4471184	-1	hypothetical protein
4469085	4475944	6859	Predicted by at least one method		Predicted_03421	4472613	4472939	1	hypothetical protein
4469085	4475944	6859	Predicted by at least one method		Predicted_03420	4472936	4474015	1	hypothetical protein
4469085	4475944	6859	Predicted by at least one method		Predicted_03419	4474019	4474963	-1	hypothetical protein
4469085	4475944	6859	Predicted by at least one method	thyA_2	Predicted_03418	4474967	4475944	-1	Thymidylate synthase
4803320	4810555	7235	Predicted by at least		Predicted_02454	4802716	4803327	-1	Phage tail protein (Tail_P2_I)

			one method					
4803320	4810555	7235	Predicted by at least one method	Predicted_02455	4803320	4804231	-1	Baseplate J-like protein
4803320	4810555	7235	Predicted by at least one method	Predicted_02456	4804234	4804575	-1	Gene 25-like lysozyme
4803320	4810555	7235	Predicted by at least one method	Predicted_02457	4804572	4805195	-1	Phage-related baseplate assembly protein
4803320	4810555	7235	Predicted by at least one method	Predicted_02458	4805202	4805582	-1	hypothetical protein
4803320	4810555	7235	Predicted by at least one method	Predicted_02459	4805671	4806288	-1	Phage virion morphogenesis family
4803320	4810555	7235	Predicted by at least one method	Predicted_02460	4806285	4806728	-1	P2 phage tail completion protein R (GpR)
4803320	4810555	7235	Predicted by at least one method	Predicted_02461	4806697	4807257	-1	hypothetical protein
4803320	4810555	7235	Predicted by at least one method	Predicted_02462	4807291	4807734	-1	hypothetical protein
4803320	4810555	7235	Predicted by at least one method	Predicted_02463	4807727	4808032	-1	hypothetical protein
4803320	4810555	7235	Predicted by at least one method	Predicted_02464	4808036	4808239	-1	Phage Tail Protein X
4803320	4810555	7235	Predicted by at least one method	Predicted_02465	4808236	4808712	-1	Phage head completion protein (GPL)
4803320	4810555	7235	Predicted by at least one method	Predicted_02466	4808801	4809457	-1	Phage small terminase subunit
4803320	4810555	7235	Predicted by at least one method	Predicted_02467	4809461	4810555	-1	Phage major capsid protein, P2 family
4951197	5040496	89299	Predicted by at least one method	Predicted_04263	4951197	4951985	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	Predicted_03994	4953457	4953699	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	Predicted_03995	4954260	4955252	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	Predicted_03996	4955385	4956383	-1	Reverse transcriptase (RNA-dependent DNA polymerase)
4951197	5040496	89299	Predicted by at least one method	Predicted_03997	4956487	4957458	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least	Predicted_03998	4957527	4959452	-1	chromosome segregation

			one method						protein
4951197	5040496	89299	Predicted by at least one method	mdaB_1	Predicted_04399	4961048	4961197	1	Modulator of drug activity B
4951197	5040496	89299	Predicted by at least one method	mdaB_2	Predicted_04400	4961194	4961361	1	Modulator of drug activity B
4951197	5040496	89299	Predicted by at least one method		Predicted_04391	4962775	4963239	-1	Replication protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04403	4964839	4965030	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	wbbD	Predicted_04340	4968011	4968844	-1	UDP-Gal:alpha-D-GlcNAc-diphosphoundecaprenol beta-1,3-galactosyltransferase
4951197	5040496	89299	Predicted by at least one method		Predicted_04341	4968965	4969831	-1	Polysaccharide pyruvyl transferase
4951197	5040496	89299	Predicted by at least one method		Predicted_00176	4974491	4974892	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_00177	4975183	4975827	1	Pentapeptide repeats (8 copies)
4951197	5040496	89299	Predicted by at least one method		Predicted_00178	4976465	4976905	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04203	4980321	4980827	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04204	4980838	4983597	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04401	4987113	4987379	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04408	4995363	4995554	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04392	4996794	4997546	-1	TcdA/TcdB pore forming domain
4951197	5040496	89299	Predicted by at least one method		Predicted_04298	5001994	5002113	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	epsE	Predicted_04390	5005779	5006264	1	Putative glycosyltransferase EpsE
4951197	5040496	89299	Predicted by at least one method		Predicted_04354	5011714	5011806	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04267	5014092	5014322	1	Prophage CP4-57 regulatory protein (AlpA)

4951197	5040496	89299	Predicted by at least one method	papC_6	Predicted_03857	5018927	5021290	1	Outer membrane usher protein PapC precursor
4951197	5040496	89299	Predicted by at least one method	papD_6	Predicted_03858	5021297	5022022	1	Chaperone protein PapD precursor
4951197	5040496	89299	Predicted by at least one method		Predicted_03859	5022026	5023003	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	rcsB_2	Predicted_03860	5023073	5023726	1	Transcriptional regulatory protein RcsB
4951197	5040496	89299	Predicted by at least one method	rcsC_2	Predicted_03861	5023704	5026910	-1	Sensor histidine kinase RcsC
4951197	5040496	89299	Predicted by at least one method		Predicted_04394	5028347	5029108	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	epsJ_2	Predicted_04356	5030150	5031004	-1	putative glycosyltransferase EpsJ
4951197	5040496	89299	Predicted by at least one method	gtf1	Predicted_04357	5031178	5031606	-1	Glycosyltransferase Gtf1
4951197	5040496	89299	Predicted by at least one method		Predicted_04319	5033279	5034010	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04320	5034029	5034379	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_04321	5034528	5034683	-1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method		Predicted_03779	5039708	5040154	1	hypothetical protein
4951197	5040496	89299	Predicted by at least one method	hrsA	Predicted_03780	5040176	5040496	1	Heat-responsive suppressor HrsA
4951197	5040496	89299	Predicted by at least one method	fruA_2	Predicted_03781	5040483	5041601	1	PTS system fructose-specific EIIBC component
4961194	4968844	7650	Predicted by at least one method	mdaB_1	Predicted_04399	4961048	4961197	1	Modulator of drug activity B
4961194	4968844	7650	Predicted by at least one method	mdaB_2	Predicted_04400	4961194	4961361	1	Modulator of drug activity B
4961194	4968844	7650	Predicted by at least one method		Predicted_04391	4962775	4963239	-1	Replication protein
4961194	4968844	7650	Predicted by at least one method		Predicted_04403	4964839	4965030	1	hypothetical protein

4961194	4968844	7650	Predicted by at least one method	wbbD	Predicted_04340	4968011	4968844	-1	UDP-Gal:alpha-D-GlcNAc-diphosphoundecaprenol beta-1,3-galactosyltransferase
4995363	5006264	10901	Predicted by at least one method		Predicted_04408	4995363	4995554	-1	hypothetical protein
4995363	5006264	10901	Predicted by at least one method		Predicted_04392	4996794	4997546	-1	TcdA/TcdB pore forming domain
4995363	5006264	10901	Predicted by at least one method		Predicted_04298	5001994	5002113	-1	hypothetical protein
4995363	5006264	10901	Predicted by at least one method	epsE	Predicted_04390	5005779	5006264	1	Putative glycosyltransferase EpsE
5073122	5079853	6731	Predicted by at least one method	aacA4_2	Predicted_04218	5073122	5073721	-1	Aminoglycoside N(6')-acetyltransferase type 1
5073122	5079853	6731	Predicted by at least one method		Predicted_04256	5075851	5076714	-1	hypothetical protein
5073122	5079853	6731	Predicted by at least one method	ant1_4	Predicted_04257	5077043	5077987	-1	Streptomycin 3''-adenylyltransferase
5073122	5079853	6731	Predicted by at least one method		Predicted_04327	5079515	5079853	1	hypothetical protein
5079946	5085829	5883	Predicted by at least one method	smfA_7	Predicted_04328	5079946	5080479	1	Fimbria A protein precursor
5079946	5085829	5883	Predicted by at least one method	papH_6	Predicted_04329	5080526	5081083	1	PAP fimbrial minor pilin protein precursor
5079946	5085829	5883	Predicted by at least one method	xerD_6	Predicted_04021	5083027	5083629	-1	Tyrosine recombinase XerD
5079946	5085829	5883	Predicted by at least one method		Predicted_04022	5083868	5084329	1	hypothetical protein
5079946	5085829	5883	Predicted by at least one method		Predicted_04023	5085335	5085829	-1	hypothetical protein

Molecular characterization of *Providencia rettgeri* clinical strains carrying the *bla*$_{NDM}$ and *bla*$_{TEM}$ genes

Abstract

Providencia rettgeri is a Gram-negative bacillus widely distributed in the environment and is currently considered an emerging pathogen, mainly associated with nosocomial infections. The aim this study was to analyze the profile genomic of the two *P. rettgeri* strains isolated from clinical samples. The presence of the *bla*$_{NDM}$ and *bla*$_{TEM}$ genes was determined by *Multiplex-PCR*. The genomes of the PR01 and PR02 strains, characterized as carrier of the *bla*$_{NDM-1}$ and *bla*$_{TEM}$ genes were sequenced using the Illumina-MiSeq platform. After sequencing, the pre-assembled genomic DNA sequences were annotated using the Prokka software. A complementary genome analysis was performed using the Fast Annotation Subsystem (RAST) technology. A partial genomic characterization for the *P. rettgeri* PR01 and *P. rettgeri* PR02 strains using RAST indicated a wide range of genes related to efflux pumps of antimicrobial drugs (genetic systems were characterized, such as multiple drug extrusion (MATE), and the large family of the facilitator (MFS), in which a total of 91 genes were identified that were related to the virulence, disease and defense subsystem. In addition, several genetic systems were identified for the production and release of siderophores, which are associated with iron absorption, and other genes as receptors and transportes for heme ring and hemin. About 43 genes were identified and expressed proteins for uptake and metabolism Analysis of the genome of the *P. rettgeri* PR01 and *P. rettgeri* PR02 strains showed a high concentration of insertion sequences, mobile and *prophages* elements, suggesting the existence of a genome. It was also verified the presence of several genomic islands, associated with persistence markers in relation to chemical and nutritional stress, such as the toxin-antitoxin system, containing the Pasl and Past genes. The diversity of genetic elements in *P. rettgeri* related to mechanisms of antimicrobial resistance can lead in the short term to an inefficiency of antimicrobial therapies in the fight against infections caused by this microorganism and its rapid access as pathogen is a result of great genetic plasticity.

Introduction

The *Providencia* genus is part of the Enterobacteriaceae family that contain Gram-negative bacilli With mobility producers of urease. Currently, the genus *Providencia* genus is composed of nine species named *P. alcalifaciens*, *P. stuartii*, P*. rettgeri*, *P. rustigianii. P. heimbachae*, *P. vermicola*, *P. sneebia*, P burhodogranariea, and P. *thailandensis* (Shima et al., 2016). Some bacterial species of the genus contribute to a series of human infections, highlighting, among them the *P. stuartti* and *P. rettgeri* species (Washington and Barnhill, 2015).

The species *P. rettgeri* can be found in many environments such as water, soil and still inhabiting plant tissues, also part of the normal flora of the human gastrointestinal tract (Clifford et al.; 2012). *P. rettgeri* has been implicated in infections of the urinary tract, and in some cases these infections are associated with gastroenteritis and bacteremia frame (Yoh et al., 2005; Tada et al., 2014)**.** *P. rettgeri* It is considered an emerging pathogenic bacteria and can exhibit high antimicrobial resistance rates commonly used in medical practice (Tshisevhe et al., 2017). *P. rettgeri* has intrinsic resistance to antibiotics polymyxin B and E (colistin), which are antimicrobial drugs of last choice for the treatment of infections caused by bacteria resistant to β-lactam antibiotics such as carbapenems (Olaitan et al., 2016).

P. rettgeri is a bacterial species that have been described in recent years as a microorganism key to spread the gene New Delphi Metallo-β-lactamase (Commonly called *bla*$_{NDM}$) in South America (Carvalho-Assef et al, 2013; Marquez-Ortiz, 2017). Enzymes classified as NDM, are characterized as carbapenemases, currently featuring 16 variants detectable in Gram-negative bacteria. These enzymes are capable of inactivating some of the class of β-lactam antibiotics (Khan; Maryam; Zarrilli, 2017). The NDM enzyme variants are widely distributed among Gram-negative bacteria and are responsible for triggering an increased level of bacterial resistance to antimicrobials agents (Khan; Maryam; Zarrilli, 2017).

The NDM-1 enzyme, which is encoded by *bla*$_{NDM-1}$ gene was first detected in

of the *Escherichia coli* and *Klebsiella pneumoniae* strains isolated from clinical samples from a Swedish patient, whose medical history showed his hospitalization in India in the year of 2009 (PillaI; McGeer, Low, 2011). The spread of *bla*$_{NDM-1}$ gene and its variants presents a challenge for health professionals on how to deal with infected patients (Olaitan et al., 2016).

The high mobility *bla*$_{NDM}$ gene is related to the mechanisms of horizontal transfer of genes (THG), which occurs mainly via plasmid (conjugation events), coupled to the bacteria against the environment (Rolain; Parola; Cornaglia, 2010). These resistance genes are readily mobilized due to their location on m*obile genetic* elements (MGEs), as transposon Tn125 containing 10092 pb also found in *Acinetobacter baumannii* specie (Poirel et al, 2012). Germinally these meetings greatly contribute to bacterial survival (Jackson et al., 2011). The *bla*$_{NDM-1}$ gene has been detected in plasmid pMR0211 in *P. stuartii* (Gann et al, 2012), and the plasmid pPrY2001 carried by *P. rettgeri* M15628 (Mataseje, 2014). However, *bla*$_{NDM-1}$ gene in some bacterial strains may be integrated into the bacterial chromosome, as evidenced in *P. rettgeri* (Gefen-Halevi et al., 2013).

After his description in 2009, *bla*$_{NDM-1}$ gene It was identified in bacteria isolated from clinical samples of UK hospital patients, India and other regions of the world, especially in isolated *E. coli* and *K. pneumoniae* (PillaI; McGeer, Low, 2011). In Brazil in 2013 bacterial strains harboring the *bla*$_{NDM-1}$ gene have been detected in clinical samples of two patients in a hospital of Rio Grande do Sul State, strain CCBH11880 with Genbank accession number: GCA000805715.1 (Carvalho-Assef et al., 2013). The second detection *bla*$_{NDM-1}$ gene in bacteria circulating in patients was reported in Brazil in the São Paulo. In this description a patient was colonized and infected by another *P. rettgeri* (Carmo-Junior et al., 2015).

The study main objective characterization of the genes and molecular mechanisms involved in the spread of resistance to carbapenems and other antimicrobial drugs in clinical isolates of *P. rettgeri*. Further, characterizing the genes and proteins related to virulence in two strains of *P. rettgeri* PR01 and PR02 strains from partial sequencing of the genome.

Material and methods

Collection and identification of bacterial isolates

This study included eight (8) strains of *Providencia rettgeri o*btained from clinical specimens from blood culture and urinary sample from patients treated in Maranhão state hospitals. These micro-organisms were provided the routine service of Analysis Laboratory Clinica Cedar, located in São Luis-MA.

The identification of the bacterial species was obtained by MALDI-TOF MS system (Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry) using Biotyper system (Bruker, Billerica, MA). Bacterial cells were grown on TSB agar plates (Himedia, India) for 24 h at 37 ° C. For the test, a sample of colony was transferred with the aid of a bacteriological loop metered 1 uL to a metal blade so as to present a thin layer over the detection plate, and then were added to sample 1 µL of a solution of matrix (α-cyano-4-hydroxycinnamic acid). The samples were subjected to the incidence of a laser beam for extracting energized ribosomal peptides. Finally, the mass spectra acquired for each bacterial strain were compared with the known mass spectra contained in the classification software (Version 3.1, Library 1.0).

Susceptibility tests to antimicrobial agentes

The susceptibility profile to antimicrobial drugs of bacterial strains was determined on the AST No. 105 cards for automated VITEK 2 (CLSI, 2016) (BioMerieux SA, Marcy-l'Etoile, France). Using antibiotics, amikacin, ampicillin, ampicillin / sulbactam, cefepime, ceftazidime, ceftriaxone, cefuroxime, cefuroxime axetil, ciprofloxacin, ertapenem, gentamicin, imipenem, meropenem, piperacillin / tazobactam. The sensitivity analyzes were performed according to the manufacturer's recommendations. Bacteria were stored in BHI plus 20% glycerol and stored in cryovials at -80 ° C.

Molecular identification of the *bla*$_{KPC}$, *bla*$_{NDM-1}$ *bla*$_{TEM}$, and *bla*$_{SHV}$ *bla*$_{AmpC}$ genes

DNA Extraction

Research on the presence of genes related to β-lactamase enzymes was conducted by multiplex-PCR reactions. For this purpose, bacterial cultures obtained from bacterial growth were used at 37 °C for up to 18 hours in medium liquid BHI (Difco, Detroit, MI, USA). After incubation, 500 µL of culture was centrifuged at 10,000 rpm for 20 minutes to obtain a pellet for using DNA extraction kit "Wizard® Genomic DNA Purification" (Promega Corporation, Madison, WI USA), following the original protocol manufacturer. Genomic DNA was quantified in NanodropTM 1000-260 and 280 nm and used for amplification reactions related gene fragments resistance to β-lactams.

M*ultiplex-PCR*

M*ultiplex-PCR* reactions were performed using a specific pair of primers (primers) in a final volume of 25 µL reaction containing 12.5 µL of a solution of GoTaq® Green Master Mix (Promega, Madison, WI, USA). The sequences of the specific primers that were used in this study are listed in Table 1

Amplification reactions of the m*ultiplex-PCR* assay were performed according to standard methods by the following authors: Cunningham et al. (2013), Liu et al., (2012), Khalilzadegan et al., (2016) and Dallenne et al. (2010). PCR products were separated on agarose gel at a concentration of 1.5% and visualized under ultraviolet light exposure. For bla_{NDM} gene sequencing, the fragments were subjected to sequencing reactions using the DYEnamic ET Terminator Cycle Sequencing kit (GE Healthcare Life Sciences, Buckinghamshire, UK) according to the manufacturer's instructions. The fragments were analyzed on the automatic sequencing system ABI PRISM® 3100 Genetic Analyze (Applied Biosystems, USA). The quality of the sequences obtained electropherograms during the sequencing process was analyzed with the software ChromasPro (http://www.technelysium.com.au/chromas.html). For alignment, at least three consensus sequences of each sequenced fragment NDM type were selected from the database for alignments using MEGA 6.0 (Tamura et al., 2013). Similarities between the obtained nucleotide sequences were verified using available BLASTnhttps://blast.ncbi.nlm.nih.gov/Blast.cgi.

To identify the gene variants *bla*$_{NDM}$, all sequences were translated into amino acids using the software ExPASy [translation tool (http://web.expasy.org/translate/)]. The correct translation was chosen based on data available in GenBank. The amino acid sequences were compared with the sequences obtained from the GenBank protein NDM using BLASTx. The values of similarity to the amino acid sequences ranged 99 to 100%, indicating a highly conserved region.

2.4 Characterization of the incompatibility groups of plasmids

The determination of incompatibility groups of plasmids was performed according to the method described by Carattoli et al. (2005). Through several PCR reactions (5 multiplexes and 3 simplex) are tested the most representative types of plasmids of the Enterobacteriaceae family, such as FIA, FIB, FIC HI1, HI2, I1-Iγ L/M, N, P, W, T, A/C, K, B/O, X, Y, F and FIIA. PCR reactions were performed in a final volume of 25 µL reaction containing 12.5 µL of a solution of GoTaq® Green Master Mix (Promega, Madison, WI, USA) and 100 ng of template DNA per reaction. The thermocycler program, except for that used for simplex-F reaction (whose difference is the annealing temperature of 52 ° C), consisted of an initial step of 5 minutes at 94 ° C followed by 30 cycles of 1 minute at 94 ° C 30 seconds at 60 ° C and 1 min.

Polymerase chain reaction for the detection of multiplex-integrons class 1, 2 and 3

The characterization of integrons it was performed having as the target sequences intI1, intI2 and intI3, these were amplified by PCR reaction method, using multiplex primers described by Goldstein et al (2001). PCR reactions were performed using a specific pair of primers (primers) in a final volume of 25 µLlreaction containing 12.5 µL of a solution of GoTaq® Green Master Mix (Promega, Madison, WI, USA), 25 □mol of each primer and 1 µL DNA template (100 ng DNA/reaction). The PCR conditions were used as described by Khoramrooz et al. (2016). The amplified products 280 bp to integron class 1, class 233 bp to 600 bp integron 2 and the class 3 integron were separated by electrophoresis in 1% agarose gel containing 0.5 µg/mL ethidium bromide.

Sequencing of the genome and notes

The genome of lines PR01 and PR02 blaNDM carrying the gene were subjected to data obtained by the assembly process MiSeq as A5 pipeline aid (http://www.ncbi.nlm.nih.gov/pubmed/23028432). This uses a new sequencing approach for prokaryote genomes A5 (Andrew And Aaron's Awesome Assembly pipeline). The pipeline and associated programs are open source distributed under GPLv3 license, runs under Linux and is installed on the local server for bioinformatics analysis Neoprospecta (Setting: 03 Linux servers, Core i7, 64GB RAM, 2TB HD).

The genes were sequenced as predicted using the inference constant BLAST protein (http://www.ncbi.nlm.nih.gov/). From this analysis, it was identified related sequences in other bacterial species of interest listed in the database RAST (Rapid Annotation using Subsystem Technology), which is an important tool bioinformatics to predict putative genes (available on http: // rast.nmpdr.org).

Construction of the phylogenetic tree

The sequences of *P. rettgeri* PR01 and *P. rettgeri* PR02 strains were subjected to analysis to this RNAmmer software: http://www.cbs.dtu.dk/services/RNAmmer (Lagesen et al., 2007) for identification of the 16S ribosomal gene. The analyzes were performed with the*BLAST algorithm,* using at least one sequence of the 16S rDNA gene. Some sequences of 16S rDNA of the genus *Providencia* were used for the preparation of phylogenetic relationships. To determine the root of the tree (outgroup) was used partial sequence of the 16S rRNA (ribosomal RNA) Serratia plymuthica K-7 (NR_037111). The sequences obtained from bacterial species were aligned so the software MEGA 7.0 (Kumar; Stecher; Tamura, 2016). For construction of the phylogenetic tree was used the maximum likelihood method (*Maximum Likelihood)* MUSCLE applying the algorithm (Multiple Sequence Comparison by Log-Expectation) (Edgar; Drive; Valley, 2004).The values of *Bootstrap* lower 70% were hidden in forming the phylogenetic tree of Fig.

Analysis of genomic islands

The genomes of the *P. rettgeri* PR01 and *P. rettgeri* strains PR02 were analyzed for the presence of genomic islands, pathogenicity islands (PAIs) and antibiotic resistance (RIs). For these analyzes, the genome draft were worked in house using scripts to the concatenation of contigs / scaffolds. For these analyzes it was first a search for bacteria of the same genus genomes or as close as possible to the genomes of strains *P. rettgeri* PR01 and *P. rettgeri* PR02. In this quest came to *Providencia alcalifaciens* DSM 30120. The analyzes were conducted with *P. rettgeri* PR01 (query) and a reference genome, in this case *P. alcalifaciens* (subject) for prediction of genomic islands. After the islands predicted, a figure in BRIG was generated using *P. rettgeri* PR01 reference. In the same figure, They were added to the coordinates of the islands previously predicted. Additionally, most were plotted two rings contigs corresponding to the genome of *P. rettgeri* PR01, where the pairs contigs were marked in blue and the odd in green. A manual curation was made on the data generated by the Gipsy software. Thus, PAIs were identified, gels and mixed Islands (MSIs), these regions are predicted as much as PAIs, as IRs by Gipsy software. Parallel genomic islands *P. rettgeri* PR01 and *P. rettgeri* PR02. They were predicted using *software* IslandViewer 4 (BertelII et al., 2017) associated with the programs IslandPick, SIGI-HMM, and IslandPath-DIMOB.

Results

Determination of the susceptibility profile to antimicrobial agents

In this study it was observed that eight (08) strains of *P. rettgeri* designated as PR01, PR02, PR12, PR13, PR18, PR20, PR21 and RP27 showed resistance to multiple antimicrobial drugs of different classes (Table 2), amikacin, and gentamicin (aminoglycosides) resistance with an MIC≥16 µg/mL, cephalosporins MIC ≥ 8 µg/mL and with carbapenem MIC ≥ 4 µg/mL. Where PR27 was the only isolate that showed a pattern sensitivity to all tested antibiotics, including β-lactam antibiotics.

Detection of genes related enzymes β-lactamases

In this work, the *bla*$_{TEM}$ genes have been identified, and *bla*$_{AmpC}$ *bla*$_{NDM}$ in all strains of the *P. rettgeri*. However for *bla*$_{SHV}$ *blaKPC* genes and the results

were negative in all strains of *P. rettgeri*, as shown in Table 3.

Identification and characterization of the incompatibility groups and integrons

All strains of *P. rettgeri* presented integrons class 1 and 2 as well as the plasmid incompatibility group FIIA as seen in Table 3.

The characterization of plasmid incompatibility groups, it was observed that all isolates of *P. rettgeri* replicon were FIIA carriers with integrons class 1 and 2 (Table 3).

Phylogenetic analysis of *P. rettgeri* PR01 and *P. rettgeri* PR02 strains

The evolutionary relationships among isolates *P. rettgeri* PR01 and *P. rettgeri* PR02 were determined by maximum likelihood method, the results indicated that the closer to *P. rettgeri* were isolated strains DSM4542 P. rettgeri NCTC11801 (89% bootstrap) and having a genetic similarity to strain RB151 as seen in figure 2.

Genomic characterization of *P. rettgeri* PR01 and *P. rettgeri* PR02 strains

The general data annotation of partial genomes of the *P. rettgeri* PR01 and *P. rettgeri* PR02 strains are shown in Table 04. The identification of genomic or coding sequences (CDS, coding sequence) was present in the lines 4425 and 4477 for PR01 and PR02 strains, respectively. In RAST analysis performed by several genes were observed associated with various categories of subsystems (Figures 3,4). However, this study highlight the proteins associated with efflux pumps to antibiotics and biocides, iron shot to proteins, proteins associated with motility and elements associated with the gene transfer mechanisms. These elements were compared by BLASTn and finally their identities were then given in Supplement I. In addition, We verified the presence of genes associated with mobility genome such as those related to protein mobilities and bacteriophages. Finally, the analysis of genes and related proteins were also directed to the related sub-system metabolism and capture iron.

Resistance profile characterization and virulence of the *P. rettgeri* PR01 and

P. rettgeri PR02 strains

Drug efflux pumps and biocides

For a more specific analysis of the genetic features of the *P. rettgeri* PR01 and *P. rettgeri* PR02 strains, these were characterized at the genomic level after the next generation sequencing using Illumina- Miseq system. In these analyzes were identified sixteen (16) types of efflux pumps antimicrobial agents and biocides (Figures 5 and 6).

Among the sixteen (16) efflux pumps present in *P. rettgeri* PR01 and *P. rettgeri* PR02 strains were identified apple (Macrolide-specific efflux protein apple), MACB (Macrolide export ATP-binding/permease protein Mac TolC (RND efflux system, outer membrane lipoprotein CMEC), AcrB (RND multidrug efflux transporter, Acriflavin resistance protein), MATE_Family_MDR_Pump (Multi antimicrobial extrusion protein (Na (+) / drug antiporter, MATE family of MDR efflux pumps).

Characterization of iron uptake system

The *P. rettgeri* PR01 and *P. rettgeri* PR02 presented six categories of genes related to iron uptake and metabolism, and in two major groups represented caputra categories heme proteins and related Hemia with 22 followed by 14 Hemin transport proteins. As seen in Figure 7, having the iutA genes associated proteins, and FhuC with the location in BLASTn gi |490378242| WP_004257840.1 with 99% identity to iutA, and two genes for FhuC with their locations gi | 490382157 |WP_004261670.1 and gi | 757595221 | WP_042843418.1 both with 100% identity. Introducing a wide range of systems siderophoros the type and aerobactin iron transport (TonB) shown in Supplement I.

The PR01 and PR02 strains, have the iutA genes associated proteins, and FhuC with the location in BLASTn gi | 490378242 | WP_004257840.1 with 99% identity to iutA, and two genes for FhuC with their locations gi | 490382157 | WP_004261670.1 and gi | 757595221 | WP_042843418.1 both with 100% identity.

Characterization Genomic Islands

In the analysis of genomic islands carried by IslandViewer program 4 was observed 22 genomic islands in the genomes of PR01 and PR02 lines as seen in Figures (11, 12) with a great diversity of genes related to bacterial virulence, drug resistance antimicrobial and mercury, toxin-antitoxin system, generic control, among others in the supplement II. The major identified genomic island in strain showed PR01 114 821 bp (> 10 kb) and harboring the gene for resistance to aminoglycosides and β-lactam. This genomic island are the *bla*TEM and *bla*NDM gene, and a gene for the transposon Tn3 resolvase associated. Parallel to the analysis program BRIG 6 pathogenicity islands compared with strains 6, 2 and 4 P.rettgeri P. stuartii with an identity of 100% as shown in Figure 10.

Analysis of bacterial mobiloma

Insertion Sequences

All analyzes the genome of the *P. rettgeri* PR01 strain using Issaga software (Sequence Insertion semi-automatic annotation genome were detected twelve (12) Putative types of insertion, with a total of 54 elements, with the largest percentage for inserts were to IS3 with 19.64% and 19.23% for PR01 to PR02 iS5 followed by 12.5% to 13.46 to *P. rettgeri* PR01 and *P. rettgeri* PR02. About 8.93% of insertion sequences and PR01 11.54% in PR02 were not identified by the database, being named ISNCY (English, IS not yet classified, unclassified IS).

All analyzes were also identified that about 10.71% and 13.46% of insertion elements PR01 and PR02, respectively, belonging to the transposon Tn3. The Tn3 transposon was characterized with an average variation 2306-3282bp presenting an identity of 99% (2892/2896) housed in sequence with the plasmid carried by pNDM15-1091 P rettgeri N15-01091 strain (Genbank code: CP012903.1). This nucleotide sequence, in turn mainly relates to a gene for a 1845 bp transposase.

DNA sequences associated with phage

In the analysis of CDs for bacteriophages sequences in genome

performed by PHSAST program were observed 6 regions related to these elements. Of the sequences found five (05) presenting was incomplete 2.4 Kb to 30 Kb in size, and related sequences found in bacteria of the family Enterobacteriaceae (such as *Salmonella* spp.), and as Gram-positive *Staphylococcus* spp. and mycobacteria. The only intact bacteriophage sequence found was related to phage (PHAGE_Salmon_RE_2010_NC_019488), a sequence of 33.7 kb (at genome position: 4233321-4267110). This sequence shows 49 CDs and the majority of these sequences are derived from a bacteriophage of *Salmonella* spp. (Code in GenBank NC019488).

Transposable elements

In analyzes performed by RAST, it was observed several genes associated with transposable elements or transposons. These elements had their identities compared by BLASTn algorithm. *P. rettgeri* PR01 and *P. rettgeri* PR02 harboring two types of transposable elements, these elements are responsible for implementing proteins, namely Tn7 and Tn21.

Still, it was possible to verify that sequences associated with Tn7 are present in both *P. rettgeri* PR01 and *P. rettgeri* PR02 strains being related tofragments of 1026 and 882 bp which are located integrons Tn7. These genes are responsible for the implementation of tnsA protein, and protein tnsB, respectively. Yet PR02 strains contains only one TN21 associated sequence indicated by the sequence 372 bp in PR01 already has three sequences related to TN21 fragments of 372, 252 and 240 bp with their respective locations and the% identity of BLASTn gi | 519733601 | EPP24804.1 and 98% ID, gi | 1119200185 | WP_072209121.1 100% ID gi | 1119200185 | WP_072209121.1 ID 99%.

Discussion

Profile susceptibility to antimicrobial agents

In this study, 8 isolates of *P. rettgeri* PR01, PR02, PR12, PR13, PR18, PR20 and PR21 were analyzed for antimicrobial agentes susceptibility profile. Six

bacterial isolates were resistant carbapenem antibiotics, namely ertapenem, imipenem and meropenem MIC was with in ≥16 µg/mL (CLSI, 2016). A particular feature of these bacterial isolates is that they originate from two hospitals located 300 km away. Focusing on an inter-hospital transmission, occurring by professionals or patients transferred between the units. Since carbapenems are among the best options for treatment of infections by Gram-negative microorganisms resistant to multiple antimicrobial drugs (Johnson, Woodford, 2017; Haciseyitoglu et al., 2017; Leylabadl et al., 2015), it is evident therefore an alarming situation public health, where these microorganisms are a common source of hospital-acquired infections (Rolain; Parola; Cornaglia, 2010). The profile arising MDR genes related efflux pumps, or more specific genes such as those coding for β-lactamase enzymes, such as *bla*$_{NDM}$ and bla$_{KPC}$ genes. These genes are commonly found in species of bacteria of the Enterobacteriaceae family (Wu et al., 2015).

β lactamases Genes related enzyme

The *bla*$_{TEM}$ and *bla*$_{AmpC}$ genes are responsible for the expression of a cephalosporinase ESBL type and a β-lactamase AmpC type, respectively. Resistance to antibiotics amikacin, gentamicin, ampicillin, sulbactam, cefepime, ceftazidime, cetriaxona, cefuroxma, ciprofloxacin, piperacillin, and tazobactam is given the correlation of various defense mechanisms that have MDR`s as efflux pumps, and specific enzymes (Li; Plésiat, Nikaido 2015).

The gene *bla*TEM expresses a cephalosporinase ESLB the type often detected in *E. coli* and *Klebsiella* spp. (Oduro-Mensah et al., 2016). The presence of the *bla*$_{TEM}$ in *P. rettgeri* indicates a high probability that this occurrence is being made possible by the transfer of movable horizontally transposable elements. A feature of the resistance genes and their association with a Cassette region of integrons region which is located between two recombination sites (ETTA and attC), initial recombination sites and termination, respectively, in this way the furniture genes may be integral DNA molecule (Deng et al., 2015).

The gene *bla*$_{NDM}$ has shown a clinical relevance in recent years, since this gene is responsible for the production of carbapenemase enzyme, a metallo-

β-lactamase zinc-dependent, acting in the hydrolysis of the carbapenem antibiotics (Galdiero et al., 2012). The carbapenemases are usually able to hydrolyse not only carbapenems, but also all β-lactam antibiotics such as cephalosporins, monobactams and penicillin (Bernabeu, et al., 2012).**Integrons and incompatibility groups**

Integrons class I and II were identified in strains of *P. rettgeri* all clinical samples obtained from the aspect of resistance presented possibly the resistance markers βlactam are present recombination between the sites of integrons, which are commonly drug resistance or pathogenicity genes (Rajpara et al., 2015). Such genes may be allocated in the chromosome since the presence of integrons class I together with Tn3 family of transposons enable such insertion gene (Deng et al, 2015; Rajpara et al, 2015).

The incompatibility group FIIA detected in strains *P. rettgeri strains* gives a unique pattern with respect to transconjugate barriers between these strains. The FIIA replicon (replicon typing) is called conjugative plasmid or incf incf is the reference for the design of primers (primer) (Carattoli et al., 2005). This incompatilibilidade group was first identified in *Salmonella enterica* (Typhimurium). The replicon FIIA has also been identified in a plasmid recovered from a strain of Salmonella enterica serovar Kentucky, isolated from chicken fecal samples (Fricke et al., 2009). The FIIA incompatibility group was related to virulence factors and resistance to streptomycin and tetracycline these Salmonella enterica strains (Fricke et al., 2009). However, there are few reports on the presence of the FIIA incompatibility group in other species of bacteria in the Enterobacteriaceae family.

Moreover, it is believed that the presence of *replicon*FIIA is rare in other species of Gram-negative bacteria, yet its acquisition by other species such as P. rettgeri may be possible, especially if these species relate in environments such as the gastrointestinal tract of animals such as birds or human hosts. Recently, FIIA replicon was identified in strains of *Enterobacte*r spp. clinical origin (Logan et al., 2016). These bacterial strains were carriers of blaACT / MIR genes that confer resistance to oxyimino-β-lactams and other β-lactam antibiotics (Logan et al., 2016). It appears then, that there is a possibility of replicon FIIA not

be restricted to Salmonella spp. as had previously been proposed, can circulate in other genera of bacteria, however with a lower transmission frequency.

Phylogenetic analysis of *P. rettgeri* PR01 and *P. rettgeri* PR02 strains

The *P. rettgeri* PR01 and *P. rettgeri* PR02 strains showed a large genetic similarity to *P. rettgeri* strain RB151 that is a pathogen carrier bla$_{NDM-1}$ gene was also related to the same group (89% bootstrap) and which is lineages, and PR01 PR02, the pathogen is one of the few strains of the species is described for carrying metallo-β-lactamase (Cardozo Castro et al., 2017).

The *P. rettgeri* RB151 strain was isolated in 2013, from a urine sample from a female patient of 58 years old. This patient was diagnosed with urinary tract infection and was being treated at the emergency department of a hospital in the Bucaramanga city, Colombia (Saavedra-Rojas et al., 2015). Interestingly, the *bla*$_{NDM-1}$ gene present in strainRB151, It is housed in a so-called plasmid pRB151-NDM (Marquez-Ortiz et al., 2017), which may not occur with the lines PR01 and PR02. It was observed in a first analysis after partial sequencing, the plasmid PR01 (pPR01 9.8 kb) showed no *bla*$_{NDM-1}$ the gene harbored only *bla*$_{TEM}$ (supplement II). This plasmid showed 99% identity with the pCR14_2 plasmid carried by *K. pneumoniae* strain CR14 (ID in the Genbank: CP015394.1). Possibly *bla*$_{NDM-1}$ gene may be integrated into the chromosome in *P. rettgeri* PR01 strain as has been previously reported for other species, as combination assays failed to demonstrate clinical transfer between the horizontal strains *E. coli* (positive NDM) and the permissive receptor strain *E. coli* J53 (Shaheen et al., 2013).

Analyzes of the subsystems of the *P. rettgeri* PR01 and *P. rettgeri* PR02 strains

In *P. rettgeri* PR01 and *P. rettgeri* PR02 strains the systems MATE, TolC, MacAB, AcrB RND are connected in a direct way resistance to antimicrobial drugs such, as fluoroquinolones (ciprofloxacin, norfloxacin, norfloxacin), rifampicin and macrolide antibiotics (ritromicina, azithromycin and clarithromycin). In addition, of bacterial resistance to cobalt and zinc, this evidence was correlated with the pattern of resistance in the MIC test.

In genomes of the PR01 and PR02 strains it was also possible to detect the presence of 04 (four) genes for β-lactamases, which are related to the resistance to penicillins ID BLASTn gi | 926465406 | ALD19783.1 100% identity, 1st and 2nd generation cephalosporins, BLASTn ID gi | 490383288 | WP_004262799.1 with 99% identity and gi |446804399 | WP_000881655.1 100% identity, 3rd and 4th generation BLASTn ID gi | 1002048020 | AMM70781.1 100% identity.

The iron-binding proteins in PR01 and PR02 isolates were iutA (aerobactin receptor), FhuB (ferrichrome permease) and FhuC (ATP binding protein), which are characterized as iron uptake receptors (Cabrera et al. 2001). Also, they are elements responsible for the breakdown of the microbial cell wall, consequently iron chelators such as enterobactin are released into the extracellular space (West et al., 1987).

The FhuC gene was previously identified in some species of Enterobacteriaceae such as *Edwardsiella ictaluri (*Abdelhamed et al., 2016) and Yersinia enterocolitica biovar 1 (Kanaujia; Bajaj; Virdi, 2015). E. ictaluri the FhuC protein contributes to the acquisition of ferric hidroxamate*(A*bdelhamed et al*.,* 2016*)*. The detection of a great diversity of genes in *P. rettgeri* that are responsible for production of many elements such as siderophores and transport and membrane proteins that contribute to the uptake and transport of iron, indicate that these products may be important in virulence and rapid multiplication of this bacterial species.

Analysis of genomic islands and islands of pathogenicity

The great diversity of genes acquired by horizontal transfer in *P. rettgeri* PR01 and *P. rettgeri* PR02, indicate a high resiliency with respect to the species

to survive adverse environments and stressful conditions, such as in the presence of oxidizing agents, biocides, and environments with nutrient limitation.

The toxin-antitoxin system represented by different genetic sequences in the supplement II. The *P. rettgeri* PR01 and *P. rettgeri* PR02 found in genomic islands can contribute to biofilm formation on abiotic surfaces and colonization of host tissues, such as urinary tract, as well as generating persistent cells in inhospitable conditions, as observed for cells that survive in the presence antimicrobial drugs (Page; Peti, 2016; Wang; Wood, 2011). These assumptions were raised, taking into account that the toxin-antitoxin system is an important factor in *E. coli* uropathogenic for niche-specific colonization (urinary tract), resistance to stress caused by ciprofloxacin in addition to the nitrite oxidation resistance sodium and other reactive nitrogen intermediates (Norton; Mulvey, 2012).

Analysis of insertion and transposon sequences in the bacterial mobiloma

The transponase of Tn7 is heteromeric, which distinguishes itself by the complexity of its target site insertion transposition att Tn7, it requires four proteins, Tn7, TnsABC + D and two substrate DNA (Young et al., 2013). The Tn7 transposase protein has two, TnsA and TnsB. TnsA performs cleavage of the donor at the 5 'transposition and transposition TnsB acting directly on the ends 3`, causing splitting and joining the target DNA (Holder; Craig, 2010; Young et al, 2013).

The presence of DNA sequences in *P. rettgeri* PR01 and *P. rettgeri* PR02, Tn7 transposon Related indicates a high versatility of these strains in the spread of antibiotic resistance genes for this micro-organism. The transposon Tn7 is a particularly sophisticated mobile element, and developed in some Gram microorganisms negative, such as *E. coli* and *Acidithiobacillus ferrooxidans*, which have completely different lifestyles (Oppon et al., 1998; Peters, Craig, 2001). The Tn7 transposon has alternative mechanisms to promote their spread among bacterial populations. The movable element can move to low frequency insertion sites, such as transposable other furniture elements, in that implements in many places without the existence of a specific sequence in the DNA recipient.

Moreover, this element can preferably move to an insertion sequence for Tn7 in some replicons, preferably in conjugative plasmids. The latter contributes significantly to the spread of the bacterial population Tn7, thus resulting in the acquisition of genes associated with antibiotic resistance in many bacterial species (Peters, Craig, 2001).

The Tn21, is a tranposon belonging to the Tn3 family, is an important determinant for resistance to antibiotics, for example aminoglcosídeos, mainly by the gene adduce for *2''-aminoglycoside nucleotidyl transferase* ANT (2 " ') (Schmidt; Nucken; Henschke 1988). More recently it has been linked to cAMP Tn21 gene, which confers resistance to penicillins and cephalosporins in the 1st and and K. *pneumoniae* strain LCT-KP214 and KP289-LCT (Guo et al., 2014). A particular feature of Tn21, is its high exchange capacity and resistance locus accumulation in plasmids and transposons other (Liebert*,* Hall*;* Summers*,* 1999*)*. The transposition occurs by the Tn21 TnpA (transponase A), with the insertion sequence, a 5 bp duplication of target DNA, usually rich in AT (Liebert, Hall; Summers, 1999). As the horizontal and vertical transfer of genes related to antibiotic resistance in Enterobacteriaceae genus are derived from plasmids and transposons, end up covering a high variety of bacterial hosts.

The Tn3 transposon has been related to the presence *bla*$_{\text{TEM-1D}}$ gene (a beta-lactamase class A) in some bacterial species of the family Enterobacteriaceae (Sandner-Miranda et al., 2016). The *P. rettgeri* PR01 and *P. rettgeri* PR02, characterized in this study *bla*$_{\text{TEM}}$ carrying the gene, and there is probably a good correlation being the presence of the transposon Tn3 and the spread of this gene.

The contribution of insertion sequences for the genetic plasticity in Providencia spp. It has not been thoroughly studied, but can provide that its contribution can be very similar to those observed for other species of bacteria of the family Enterobacteriaceae. In *E. coli* O157 (a burial-hemorrhagic serotype), for example, it has been suggested that IS elements may have a role in the inactivation and immobilization of phage and plasmids received by bacterial strains (Ooka et al., 2009).

The presence of bacteriophage sequences in bacterial genomes, especially in enterobacteria may be the result of the acquisition by horizontal transfer genetic material into more specific niches such as the gastrointestinal tract of the host animals (Huddleston, 2014). This assumption is based on the evidence of the existence of a greater availability of viral genetic material into the intestinal lumen after its release during the lytic cycle of the bacteria in this niche (Sunagawa; Koonin; Bork, 2014). Experimental evidence using quantitative PCR for DNA bacteriophages present in human faeces indicates that these elements. They carry a large amount of resistance genes such as genes for β-lactamases and *bla*$_{TEM}$ and *bla*$_{CTX\text{-}M\text{-}1}$ (Modi et al., 2013). These observations can corroborate to measure the impact of bacteriophage genomes in movement and placement of antibiotic resistance genes for the bacterial population (Modi et al., 2013). Finally, it is believed that the bacteriophages associated with transduction events can increase the contribution mechanisms in resistoma the bacterial population in the gastrointestinal tract especially among Enterobacteriaceae, so have a great impact on the development of emerging pathogens such as *P. rettger*

This work showed various molecular characteristics analyzed after partial sequencing of the genome of two isolates of *P. rettgeri* (PR01 and PR02). These characteristics are related to the ability of these strains to endure the presence of various antibiotics, especially beta-lactam clinical use as cephalosporins and carbapenems. The presence of a wide variety of efflux pumps, in addition to inactivating enzymes aminoglycosides, beta-lactamases are expressed from the *bla*$_{NDM}$ gene and are *bla*$_{TEM}$ contributing to the rapid dissemination and accession of this species in Brazilian nosocomial environment, here in the first instance detected in isolated Maranhenses hospitals. It was also found that strains of *P. rettgeri.* They can adapt to various environments characteristics, especially with respect to iron capitation and self-regulation systems such, as system toxin-antitoxin. In addition, partial genome analysis also indicated that the species has a highly dynamic genome consists of a mobiloma wherein several gene segments related to mobility and bacteriophage protein genes. Finally, the dissemination of genetic elements can contribute to transmission of genes associated with virulence and resistance to biocides and bacterial antibiotic drugs and *other species of the Enterobacteriaceae family.*

Conflict of Interest Statement

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interes

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