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IDENTIFICAÇÃO DE BACTÉRIAS PRODUTORAS DE COMPOSTOS ATIVOS DE SUPERFÍCIE, ISOLADAS DE SEDIMENTOS DE MANGUE

WALLACE RIBEIRO NUNES NETO

São Luís – MA

2022

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Tese de doutorado apresentada ao Curso de Doutorado do Programa de Pós-Graduação em Biodiversidade e Biotecnologia - Rede BIONORTE, na UNIVERSIDADE CEUMA, como requisito parcial para a obtenção do Título de Doutor em Biodiversidade e Biotecnologia.

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DEDICATÓRIA

Dedico essa tese as pessoas que tiveram ao meu lado, amigos de laboratório, professores e familiares pelo apoio.

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RESUMO

Os manguezais são zonas de transições de sedimentos, favorecendo a ciclagem de materiais, associada a alta concentração de microrganismos, apresentando vulnerabilidade as ações antropogênicas. Este estudo teve como objetivo avaliar a capacidade da microbiota em sedimentos de manguezal do rio Anil, na cidade de São Luís - MA para a produção de compostos ativos de superfície (CASs). As amostras foram inoculadas no meio Bushnell Haas, contendo 1 grama da amostra para 250ml de meio acrescido de querosene, a 3% (v/v). Sendo identificada pelo método MALDI-QTOF MS como *Pseudomonas aeruginosa*, capaz de produzir compostos ativos de superfície, PSA39. Submetido a análises de E_{24}, espalhamento da gota, estabilidade térmica/pressão, variação de pH e estabilidade iônica. O genoma da PSA39, foi sequenciado pela plataforma Illumina – MiSeq e as sequências de DNA genômico pré-montadas foram anotadas usando o software Prokka. A sequência genômica obtida foi analisada pelo Rapid Annotation using Subsystem Technology para identificação de vias metabólicas associadas com a degradação de hidrocarbonetos e produção de biossurfactante A construção da árvore filogenética foi realizada partir dos dados do sequenciamento de nucleotídeos de PSA39 utilizando como base no método de filogenia a distância do genoma BLAST, o genoma de PSA39 foi submetido a análise comparativa por MAUVE, utilizando outras linhagens de depositadas no GenBank. Os clusters de genes ortólogos foram identificados usando o OrthoVenn 2. Neste estudo foram isoladas cerca de 32 linhagens de bactérias a partir das amostras de sedimento de mangue, dos 32 isolados 9 apresentaram atividade emulsificante (E_{24}). Os valores de E24 variaram de 13% a 57,30% analisado. O isolado PSA39 foi selecionado para estudos de crescimento e produção de biossurfactante com atividade emulsificante. A máxima produção de compostos com atividade emulsificante ocorreu no tempo de 100 horas. Os ensaios de atividade emulsificante e estabilidade com o biossurfactante recuperado com acetato de etila demonstraram valores de E_{24} variando entre 57% a 69,2% de rendimento, com incremento na estabilidade em pHs básico, chegando a 79%, além de resistir ao teste de autoclavagem de pressão e temperatura. A análise do genoma da estirpe *P. aeruginosa* PSA39 pelo RAST indicou a presença de subsistemas genéticos num total de 2062 genes sendo 1946

relacionados com proteínas não hipotéticas e 571 genes relacionados a proteínas hipotéticas. O genoma de *P. aeruginosa* PSA39 apresentou genes relacionados com vias responsáveis pela produção do ramnolípideos como metabólitos secundários, muitos genes estavam relacionados com a degradação de hidrocarbonetos aromáticos e linfáticos, além de vários genes relacionados com a produção de sideróforos, como pioverdina e pioquelina. Ademais, as análises realizadas pelo RAST indicaram que *P. aeruginosa* PSA39 apresenta diversos mecanismos moleculares para adaptação a metais pesados, como a proteína, cobalto-zinco-cádmio (CzcC). Sendo identificado no isolado PSA39 cento e quinze grupos únicos (exclusivos) com proteínas de funções definidas, associadas a conjugação, a processos celulares e metabólicos de hidrocarbonetos como alcools e aromáticos visualidados pela análise comparativa genômica "orthovenns" associado com a plataforma RAST. Os resultados deste trabalho permitiram demonstrar a viabilidade de utilização de microrganismos regionais presentes nos manguezais para produção de compostos ativos de superfície com atividade emulsificante, a partir de fontes de carbono distintas, por possuir bons índices de emulsificação e estabilidade perante a diversidade de fatores ambientais.

Palavras-chave: Biossurfactantes; Pseudomonas aeruginosa; análises genômicas; resistência a metais pesados.

NETO, Wallace Ribeiro Nunes. **Identification of surface active compounds producing bacteria isolated from mangrove sediments.** 2022. 145 f. Thesis (Doctorate in Biotechnology) - Federal University of Maranhão, São Luis, 2022.

ABSTRACT

Mangroves are zones of sediment transitions, favoring the cycling of materials, associated with a high concentration of microorganisms, presenting vulnerability to anthropogenic actions. This study aimed to evaluate the capacity of the microbiota in mangrove sediments from the river Anil, in the city of São Luís - MA for the production of surface active compounds (CASs). The sediment samples were collected according to the EMBRAPA 2006 methodology, being inoculated in Bushnell Haas medium, containing 1 gram of the sample for 250ml of medium plus 3% (v/v) kerosene. Being identified by the MALDI-QTOF MS method as Pseudomonas aeruginosa, capable of producing surface active compounds, PSA39. Submitted to E24 analysis, drop scattering, thermal/pressure stability, pH variation and ionic stability. The PSA39 genome was sequenced by the Illumina – MiSeq platform and the pre-assembled genomic DNA sequences were annotated using the Prokka software. The genomic sequence obtained was analyzed by Rapid Annotation using Subsystem Technology (RAST) to identify metabolic pathways associated with hydrocarbon degradation and biosurfactant production. BLAST genome distance phylogeny method (GBDP), in addition to mean nucleotide identity (ANI). Also, the genome of PSA39 was submitted to comparative analysis by MAUVE, using other strains deposited in GenBank. Orthologous gene clusters were identified using OrthoVenn 2. In this study, approximately 32 strains of bacteria were isolated from mangrove sediment samples, of which 32 isolates 9 showed emulsifying activity (E24). E24 values ranged from 13% to 57.30% analyzed. Isolate PSA39 was selected for studies of growth and production of a biosurfactant with emulsifying activity. The maximum production of compounds with emulsifying activity occurred within 100 hours. The emulsifying activity and stability tests with the biosurfactant recovered with ethyl acetate showed E24 values ranging from 57% to 69.2% of yield, with an increase in stability at basic pHs, reaching 79%, in addition to resisting the test of pressure and temperature autoclaving. Genome analysis of the P. aeruginosa PSA39 strain by RAST indicated the presence of genetic subsystems in a total of 2062 genes, 1946 of which related to non-hypothetical proteins and 571 genes related to hypothetical proteins. The genome

of P. aeruginosa PSA39 showed genes related to pathways responsible for the production of rhamnolipids as secondary metabolites, many genes were related to the degradation of aromatic and lymphatic hydrocarbons, in addition to several genes related to the production of siderophores, such as pyoverdine and pyochelin. Furthermore, the analyzes performed by RAST indicated that P. aeruginosa PSA39 has several molecular mechanisms for adaptation to heavy metals, such as the protein, cobalt-zinc-cadmium (CzcC). One hundred and fifteen unique (exclusive) groups were identified in isolate PSA39 with proteins with defined functions, associated with conjugation, cellular and metabolic processes of hydrocarbons such as alcohols and aromatics visualized by the comparative genomic analysis "orthovenns" associated with the RAST platform. The results of this work allowed to demonstrate the viability of using regional microorganisms present in mangroves for the production of surface active compounds with emulsifying activity, from different carbon sources, as they have good emulsification rates and stability against the diversity of environmental factors.

Keywords: Biosurfactants; Pseudomonas aeruginosa; genomic analysis; heavy metal resistance.

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1. INTRODUÇÃO

Os hidrocarbonetos derivados de petróleo (HC) possuem grande relevância para a sociedade atual, uma vez que são comumente utilizados na produção de combustíveis usados em meios de transporte, produção de energia, indústria petroquímica, o que acarretou uma grande procura e utilização desse recurso natural (ZENG *et al*., 2018). Contudo, os HC´s são contaminantes comuns dos ecossistemas terrestres e marinhos, pois ocasionam uma poluição severa em decorrência do uso e descarte sem tratamento no ambiente desses derivados em grande quantidade nos rio, mares e no solo (WANG *et al*., 2018).

A concentração de químicos tóxicos presente no ambiente após derramamentos de óleos podem ser altas, em decorrência da incapacidade dos micro-organismos em fragmentar e consumir os HC, como fonte de carbono (JIMOH *et al*., 2019). Gerando assim, uma redução da capacidade do solo de suportar o crescimento das plantas, aumentando a presença de metais pesados que podem bioacumular e biomagnificar causando efeitos adversos à saúde humana em decorrência dos efeitos tóxicos dos HC´s provocarem mudanças imediatas nas funções e estruturas das comunidades microbianas juntamente com efeitos nocivos ás níveis tróficos (WITTGENS *et al*., 2017;GONZÁLEZ *et al*., 2019; JIMOH *et al*.,2019). A existência de micro-organismos capazes de lidar com a exposição a hidrocarbonetos utilizando-os como fontes de energia, em ambientes contaminados promovento a limpeza do ambiente, rhavendo uma ciclagem de nutrientes para o ambiente (WITTGENS *et al*., 2017;JIMOH *et al*.,2019).

A atuação dos micro-rganismos degradadores de hidrocarbonetos é restrita em face a disponibilidade de substratos, sendo fortemente influenciada por solubilidade em fase aquosa (WANG *et al*., 2019) .Os micro-organismos degradadores de hidrocarbonetos estão presentes em diversos habitats contaminados por essas moléculas, embora em baixa quantidade, fazendo parte da chamada biosfera rara e enriquecida (JIMOH *et al*.,2019). Os micro-organismos degradadores de hidrocarbonetos são filogeneticamente e fisiologicamente diferentes e possuem mecanismos próprios para detectar hidrocarbonetos, tais degradadores se movem em direção de áreas contaminadas por hidrocarbonetos visando produzir biopolímeros e surfactantes que aumentam a biodisponibilidade de hidrocarbonetos (KARLAPUDI *et al*., 2018; RAZA *et al*., 2020)

As biomoleculas são principalmente proteínas e polissacarídeos, além dessas duas classes de polímeros, os microorganismos têm o potencial para produzir outras moléculas, como biossurfactantes, polímeros anfifílicos e polímeros polifílicos, ideais para interagir com interfaces, água ar, e água hidrocarbonetos (JIMOH *et al*.,2020), biosurfactantes possuem

frações hidrofílicas e hidrofóbicas, tendo características anfifílicas participando na interface entre fases fluidas com diferentes polaridades e ligações de hidrogênio, tais como interfaces óle/água ou ar/água, pertencente a classe de Compostos Ativos de Superficie CAS (AMER *et al*., 2015; BARTAL *et al*., 2018).

Os CAS são de fundamental importância atualmente, vez que os surfactantes são produtos químicos de utilização comum, sendo muito utilizados em processos do dia-a-dia, como limpeza de superfícies e como componentes de sabonetes e sabões, além de apresentarem grande variedade de aplicações, tanto na indústria, como também na agricultura e saúde (WITTGENS *et al*., 2017; BANERJEE *et al*., 2018).

Os surfactantes são comercializados quase exclusivamente sintéticos, havendo um interesse crescente em biossurfactantes especialmente surfactantes microbianos (CATTER *et al*., 2016). Os biossurfactantes são intessantes do ponto de vista ambiental pois são compatíveis com o meio ambiente, uma vez que são relativamente não-tóxicos e biodegradáveis (ARAÚJO *et al*., 2020). Os biossurfactantes são compostos de propriedades estruturais únicas, muito importantes por seu potencial aplicação em muitas atividades industriais, desde a biotecnologia até a limpeza do meio ambiente, formação de espuma, alta seletividade e atividade específica em condições ambientais extremas de temperatura, pH e salinidade, além de serem sintetizados a partir de matérias-primas renováveis, como resíduos agro-industriais

Por constituírem metabólicos secundários os compostos ativos de superfície, microbianos são produzidos na fase estacionária do crescimento microbiano (SINGH, 2018), podendo ser classificados como glicolipídeos, lipoproteínas, lipopeptídeos, fosfolipídios, ácidos graxos, e ainda como surfactantes poliméricos e surfactantes de baixo peso molceular (WITTGENS *et al*., 2017; KAKOLI *et al*., 2020).

A capacidade de biossintetizar SACs é, freqüentemente, associada à capacidade desses microrganismos de crescer em fontes de carbono imiscíveis, como hidrocarbonetos. Diferentes mecanismos estão envolvidos nas interações dos CASs entre células microbianas e hidrocarbonetos imiscíveis, incluindo: (i) emulsificação, (ii) micelarização, (iii) aderência-barreira de microrganismos para e de hidrocarbonetos e (iv) dessorção de contaminantes.

Entre os biosurfactantes, os ramnolipídeos (RLs) podem ser produzidos por linhagens de *Pseudomonas aeruginosa*, que vendo sendo ao longo dos anos extensivamente estudados e relatados em várias aplicações industriais e ambientais (PARASZKIEWICZ *et al*., 2018). RLs, produzidos por *P. aeruginosa* apresentam regiões hidrofílica constituída de duas molceculs do

açúcar rhaminose, e uma região lipofílica de cadeia carbônica, sendo classificado como glicolípideo (RATTES *et al*., 2019).

A biossíntese de Rls por *P. aeruginosa* é regulada por fatores ambientais, juntamente com o *quórum sensing system* (QS) (WITTGENS *et al*., 2017; SINGH, 2018). Esse sistema é responsável por aproximadamente 10% dos genes de regulação em *P. aeruginosa*, no que tange a capacidade das bactérias de detectar e responder, por meio da regulação gênica à densidade celular (FRANZETTI *et al*.,2010; WITTGENS *et al*., 2017) . Esta comunicação permite às bactérias restringir a expressão de genes específicos de forma que está expressão ocorra somente na presença de um elevado número de bactérias, onde o fenótipo resultante será o mais benéfico para a população (WITTGENS *et al*., 2017; ROCHA *et al*., 2020). Alguns dos fenótipos em bactérias mais comuns regulados por meio de QS incluem a constituição de biofilmes, a expressão de fatores de virulência, motilidade, regulação da bioluminescência, fixação de azoto e a esporulação em bactérias Gram-positivas (SINGH, 2018).

Este estudo visou destacar a importância dos micro-organismos produtores de RL´s, por representarem uma alternativa promissora para o desenvolvimento de pesquisas auxiliadoras do desenvolvimento biotecnológico, industrial. O estudo tem como objetivo principal identificar de bactérias produtoras de compostos ativos de superfície com potencial de aplicação no controle de biofilmes e atividade antimicrobianas e caracterizar as vias metabólicas do CAS, produzido por *P. aeruginosa linhgem PA39,* isolado de uma área de mangue do rio Anil localizado na cidade de são Luís do Maranhão.

1.1 OBJETIVO GERAL

Identificar de bactérias produtoras de compostos ativos de superfície com potencial de aplicação no controle de biofilmes e atividade antimicrobianas

1.2 OBJETIVOS ESPECÍFICOS

Identificar de bactérias produtoras de compostos ativos de superfície com potencial de aplicação no controle de biofilmes e atividade antimicrobianas

Isolar e identificar as bactérias produtoras de BS e emulsificantes.

Correlacionar os gêneros bacterianos com a capacidade de produção de BS e emulsificantes.

Caracterizar a atividade dos BS, produzido pelos isolados de melhor resultado de biodegradação em condições físico-químicas distintas.

Determinar a concentração micelar critica (CMC).

Caracterizar vias metabólicas e genes relacionados a produção de BS´

2 REFERENCIAL TEÓRICO

2.1 MEIO AMBIENTE

O desenvolvimento industrial tem sido acompanhado da interferência humana nos ambientes naturais, incluindo interferências físicas e principalmente químicas mediante a geração de resíduos e poluentes diversos (GARGOURI *et al*., 2017; RATTES *et al*., 2019).

Entende-se por ambiente o "conjunto de condições que envolvem e sustentam os seres vivos na biosfera, como um todo ou em parte desta, abrangendo elementos do clima, solo, água e de organismos"(RATTES *et al*., 2019), e por meio ambiente " a "soma total das condições externas circundantes no interior das quais um organismo, uma condição, uma comunidade ou um objeto existe.

O Art. 225 da Constituição Federal afirma que "Todos têm direito ao meio ambiente ecologicamente equilibrado, bem de uso comum do povo e essencial à qualidade de vida impondo-se ao Poder público e à coletividade o dever de defendê-lo e preservá-lo para as presentes e futuras gerações". Assim, a população e os seus governantes se tornam responsáveis pelo meio ambiente para que suas intervenções sejam realizadas com o objetivo de não atingirem o meio de forma negativa, para não acarretar em uma diminuição no bem-estar de todos e das gerações futuras (ALMANSOORY *et al*., 2017; KARLAPUDI *et al*., 2018; LIAO *et al*., 2019).

Grande parte da poluição presente no meio ambiente é fruto do armazenamento impróprio da grande quantidade de resíduos produzidos pelos indivíduos, resultando na proliferação de vetores, deterioração do meio ambiente, queda no valor de mercado dos imóveis vizinhos em áreas degradadas e queda na qualidade de vida (PEELE *et al*., 2018). O aumento do resíduo é uma das consequências provenientes da relação consumista de produtos, concomitante com os resíduos domésticos, hospitalares e industriais que entram em contato com o solo contaminando-o, alterando assim suas propriedades físico-químicas, modificando os processos catabólicos dos microrganismos viventes naquela região, tornando necessário meios de proteger o local onde residem, afim de manter segura sua microbiota (ALMANSOORY *et al*., 2017).

A preocupação com o meio ambiente ainda é tratada como fardo para a maioria das empresas, sendo obrigadas a tomarem medidas para diminuir a poluição proveniente de suas indústrias com o intuito somente de não sofrerem embargos oriundos das leis ambientais, ou meramente para promover campanhas de marketing buscando atingir um público alvo. E assim também, por pessoas comuns como pré-requisito para serem considerados politicamente

corretos, porém incapazes de abrirem mão do seu estilo de vida consumista, com a finalidade de contribuírem com o meio ambiente de forma efetiva (ALMANSOORY *et al*., 2017).

2.2 DEFINIÇÃO DO MANGUE NA ILHA DE *UPAON-AÇU*

> A Zona Costeira do Brasil é uma unidade territorial que se estende, na sua porção terrestre, por mais de 8500 km, abrangendo 17 estados e mais de quatrocentos municípios, distribuídos do Norte equatorial ao Sul temperado do país. Inclui ainda a faixa marítima formada por mar territorial, com largura de 12 milhas náuticas a partir da linha da costa. Possuímos uma das maiores faixas costeiras do mundo, entre a foz do rio Oiapoque, no Amapá e Chuí, no Rio Grande do Sul (MINISTÉRIO DO MEIO AMBIENTE, 2012).

A zona costeira brasileira é considerada uma das maiores do mundo em extensão, apresentando uma quantidade significativa de paisagens distintas como dunas, ilhas, recifes, costões rochosos, baías, falésias, brejos e estuários. Já estuário é definido como "uma massa de água costeira parcialmente fechada que é permanente ou periodicamente aberta ao mar e dentro da qual existe uma variação mensurável de salinidade devido à mistura de água do mar com água doce derivada da drenagem da terra" (FALCÃO, 2016). Forma-se assim, um ecossistema ímpar, com extrema sensibilidade e dependente das variações de marés, salinidade, temperatura. Sendo considerando os estuários tropicais regiões com teor de sal e densidade maior que no oceano, tais características únicas proporcionam são essenciais para a biodiversidade costeira (HRUDAYANATH *et al* 2013).

A Zona Costeira e Estuarina do Maranhão (ZCEM) possui 5 setores: Golfão Maranhense, Litoral Oriental, Litoral Ocidental, Baixada Maranhense e Parque Estadual Marinho do Parcel Manuel Luís. O Golfão maranhense consiste em um complexo estuarino, onde deságuam os afluentes dos rios Mearim, Itapecuru e Munim, entre outros menos relevantes. Ele está localizado no extremo norte do estado, abrangendo as regiões tropicais úmidas, as quais se estendem entre as latitudes de 15ºN e 15ºS, em uma posição em ângulo reto em relação ao litoral (TEIXEIRA, 2009). Sendo fundamental a relevância para o meio ambiente da região, pois é possuidor de metade da água doce, partículas e solutos desembocados no oceano (TEIXEIRA 2009).

Cerca de 90% da área de mangue está localizada em países em desenvolvimento, sendo o Brasil possuidor de 15% do mangue mundial, o Golfão maranhense juntamente com os rios do Pará e do Maranhão é considerado o maior cinturão contínuo desse ecossistema no mundo (WITTGENS *et al*., 2017; DINIZ *et al*., 2019). Os manguezais são ambientes que apresentam uma ciclagem rápida associada a alta concentração de compostos bacterianos, sendo vulneráveis e facilmente impactados pela poluição antropogênica.

Os manguezais são sistemas jovens que apresentam uma dinâmica das marés das áreas onde se localizam, produzindo varias modificações na topografia local resultando numa sequência de recuos e avanços da cobertura vegetal (DINIZ *et al*., 2019). A importância desse bioma se deve a sua função como refúgio de animais marinhos para sua procriação, contenção e filtração dos diversos tipos de sedimentos e absorção do impacto das ondas do mar (DINIZ *et al*., 2019).

2.3 CONTAMINAÇÃO DOS MANGUEZAIS POR ÓLEOS

A colonização de modo geral sempre se iniciou em regiões litorâneas, tendo como efeito os maiores agrupamentos de pessoas no decorrer do tempo em áreas ao longo do litoral, ações antropogênicas na costa do mar culminou em uma deterioração tanto do solo quanto das águas deixando-os contaminados (FERREIRA 2016; DINIZ *et al*., 2019). Um dos principais causadores de poluição no ambientes costeiros são os derramamentos dos mais variados tipos de óleos, devido ao seu potencial hidrofóbico e a pouca solubilidade em meio aquoso, causando uma simples adsorção no material particulado e nos seus sedimentos. No decorrer das últimas décadas, uma quantidade significativa de impactos ambientais provenientes de vazamentos de óleos, afetara principalmente regiões estuarinas (FERREIRA, 2016).

Os dejetos produzidos pelo homem podem ser classificados em domésticos, que são gerados em residências tendo em sua composição um alto índice de matéria orgânica. Nos resíduos industriais a sua composição depende do tipo de atividade exercida pelas empresas, podendo conter alto teor de matéria orgânica, substâncias químicas, metais pesados, óleos e dentre outros (KAKOLI BANERJEE *et al* , 2020). A maioria dos óleos derramados em águas estuarinas são oriundos dos derivados de petróleo e pirólise de matéria orgânica, chegando aos estuários por vias de descargas de efluentes, drenagem urbana, transporte atmosférico e despejo direto (BANERJEE *et al*., 2018; KARLAPUDI *et al*., 2018).

A localização geográfica dos manguezais propicia a ocupação e uso dos solos, que vem ocorrendo de modo desordenado nas cidades, tornando-os mais vulneráveis aos impactos antrópicos. O lançamento de esgotos domésticos, efluentes industriais, lubrificantes e combustíveis fósseis provenientes da manutenção ou acidentes com embarcações são os tipos de contaminação mais comuns nos ambientes estuarinos (KARLAPUDI *et al*., 2018; MAIA *et al*., 2018).

O resultado do derramamento de óleos originados tanto de hidrocarbonetos de petróleo quanto de origem vegetal, acarretam um saldo negativo por serem hidrofóbicos, alterarem o pH, a salinidade, sua textura, a própria composição, o teor de densidade e seu ponto de fluidez

da região contaminada (VARJANI, 2017). Fatores esses determinantes para interferirem no equilíbrio do meio ambiente e que têm sua intensidade ampliada devido à fragilidade do equilíbrio ambiental no estuário. Desta forma o reconhecimento destas causas é essencial para a escolha da tecnologia de remediação mais adequada para a recuperação da área contaminada como exemplo a biorremediação (GARGOURI *et al*., 2017).

Mesmo em condições anóxicas, os contaminantes oleosos se acumulam facilmente nos terrenos de mangue podendo causar problemas futuros na conservação e preservação do ecossistema (KAKOLI,2020). Dependendo da intensidade do impacto, efeitos nocivos poderão ser observados tanto a curto prazo, como recobrimento das lenticelas (órgão de arejamento no formato poroso que possibilitam trocas gasosas diretamente com o ar) e pneumatóforos (raízes adaptadas para realizar as trocas gasosas com o ambiente) causadores de asfixia dos vegetais, quanto problemáticas mais acentuadas durante longos períodos como a alta toxicidade que dependendo do tipo de óleo, alterará as populações microbianas prejudicando a ciclagem dos nutrientes (BANERJEE *et al*., 2018).

As consequências dos derramamentos de óleos em áreas de manguezais ocasionam danos físicos e biológicos, como à aderência do contaminante atingindo a fisiologia do ambiente, afetando a respiração e sistema de eliminação do sal do meio. Tendo efeitos toxicológicos como a entrada de meios químicos nos seres vivos relacionado a formação do hidrocarboneto (DEEPIKA *et al*., 2016; KAKOLI, 2020). Após danos a curto prazo (asfixia mecânica) e longo prazo (toxicidade química), o ambiente entra em estado de autodepuração, ou recuperação devido a sua ciclagem periódica ocasionada pela variação das marés (BANERJEE *et al*., 2018).

2.4 BIORREMEDIAÇÃO

Podemos defi ni-la como conjunto de processos para o tratamento de solos ou águas, visando degradar, minimizar ou eliminar compostos xenobióticos que proporcionam riscos ao meio ambiente, aplicando o uso de microrganismos por meio de técnicas fermentativas ou pelo manuseio de enzimas na catálise da reação de transformação do elemento tóxico (JENNERJAHN *et al*., 2017; PEREIRA *et al*., 2017). Os microrganismos em geral, são os principais agentes biológicos utilizados, devido a sua capacidade de consumir fontes de carbono, também podem ser utilizados com o objetivo de degradar substâncias tóxicas (PEREIRA *et al*., 2017).

Entre os métodos de remediação a utilização da biorremediação é uma das mais prósperas, devido ao uso dos agentes biológicos oriundos da região afetada. Podendo abranger

uma considerável quantidade de contaminantes orgânicos, em específico os hidrocarbonetos de petróleo. Possuindo uma alta capacidade de eliminar ou mitigar os impactos gerados pelos poluentes ambientais na região afetada (PEREIRA *et al*., 2017). Baseando-se na utilização dos componentes nocivos como fonte primária de energia por meio de fermentação, respiração aeróbica ou respiração anaeróbica, para a biodegradação dos compostos durante o método escolhido (ARAÚJO *et al*., 2020).

Tendo a biorremediação uma das técnicas mais usada para descontaminação de solo e água, independentemente do local de aplicação, em duas categorias: in situ e *ex situ* (PEREIRA *et al*., 2017). Os procedimentos *in situ* são tratamentos realizados sobre o solo ou água contaminados no próprio local, já o modelo *ex situ* remete a retirada do solo ou transporte da água para realizar o tratamento em outro local (CHARLES *et al*., 2017).

A diversidade de agentes biológicos aumenta a eficácia no processo de biorremediação, pois uma única espécie de microrganismo pode metabolizar apenas uma faixa limitada de um determinado meio tóxico, porém um conjunto composto de diversos agentes distintos e com diferentes capacidades enzimáticas, resultam na degradação dos mais variados contaminantes (CHARLES *et al*., 2017; GARGOURI *et al*., 2017; KARLAPUDI *et al*., 2018). Entre as vantagens de uso da técnica de biorremediação temos a simplicidade do processo, baixo custo, eliminação permanente dos contaminantes, realização do procedimento no local sendo utiliza como base em mecanismos biológicos, afim de evitar riscos relacionados com resíduos sintéticos perigosos, eficiência em meios homogêneos de textura arenosa e pode associar-se com outros métodos de tratamento (CHARLES *et al*., 2017; PEREIRA *et al*., 2017).

Para a escolha do método de biorremediação devem ser considerados fatores que impeçam ou dificultam a sua utilização como a escolha da seleção das linhagens, a ecologia microbiana, tipo e concentração do contaminante, restrições ambientais, procedimento de inoculação dos microrganismos, a existência de compostos recalcitrantes a biodegradação, o tempo de operação, que pode ser mais longo em comparação aos métodos físico-químicos de tratamento, a toxidade do poluente, que pode inibir a atividade microbiana e a bioconversão dos poluentes que pode resultar em produtos mais tóxicos que o composto original, intervindo no efeito real do processo (CHARLES *et al*., 2017; GEETHA, 2018) .

2.5 COMPOSTOS ATIVOS DE SUPERFÍCIE

Os microrganismos cultivados em hidrocarbonetos são capazes de produzir e excretar moléculas com atividades emulsificantes e surfactantes, conhecidos como compostos ativos de superfície (CASs). Os micro-organismos são capazes de sintetizar vários tipos de CAS

(GEETHA, 2018).. De acordo com Furthmuller (1996), esses compostos podem ser classificados em três grupos: os de baixo peso molecular, comumente denominados de biosurfactantes, os que possuem alto peso molecular com uma região hidrofóbica em uma extremidade da molécula, neste caso a terminologia mais adequada utilizada é “polímeros anfifílicos” e por fim, os polímeros polifílicos são aqueles que possuem regiões hidrofóbicas ao longo de toda a molécula polimérica (KRESSE, 1996). Com uma classificação de acordo com a composição química os CASs de origem microbiana, são divididos em baixo peso molecular, conhecidos como biossurfactantes, englobando os glicolipídeos, lipopeptídeos e fosfolipídeos, de outra forma, os CASs de alto peso molecular abrangem os polissacarídeos, proteínas, lipopolissacarídeos, lipoproteínas ou misturas desses biopolímeros (DEEPIKA *et al*., 2016; KARLAPUDI *et al*., 2018). Sendo definido como surfactantes de baixo peso molecular os glicolipídios e peptidolipídeos produzido por microorganismo como metabólicos secundários (KATARZYNA, 2018). Par.a CASs de alto peso molecular com uma região hidrofóbica em uma extremidade da molécula, por exemplo, lipopolissacarídeos e ácidos lipoteicóicos, o termo "polímeros anfifílicos" é mais adequado. Caso os grupos hidrofóbicos estiverem distribuídos por toda a molécula polimérica, os CASs serão idênticos aos polímeros hidrofóbicos sendo chamados de polímeros polifílicos; os exemplos incluem polissacarídeos hidrofóbicos emulsão (MNIF, 2015; RATTES *et al*., 2019).

Os biossurfactantes podem ser produzidos por metabolismo microbiano, sua atividade pode ser definida por meio de mudanças nas tensões interfaciais de alguns meios combinados como água/óleo ou ar/água com suas mudanças sendo medidas com auxílio de tensiômetro (DEEPIKA *et al*., 2016; MAIA *et al*., 2018). Os biossurfactantes agem cobrindo hidrocarbonetos hidrofóbicos com um envelopamento para que ocorra o transporte através da membrana celular, micelas. Isso permitirá que o metabolismo dos compostos hidrofóficos aconteça no citoplasma.

A fração polar do biosurfactante é derivada de carboidratos, amino ácidos, ácidos carboxílicos, fosfatos ou álcool (SINGH, 2018). Enquanto, que a porção apolar da molécula consiste em cadeias de hidrocarnentos como ácidos graxos (SINGH, 2018). Tais propriedades químicas se tornam essenciais nas aplicações que exigem, emulsificação, lubrificação, formação de espuma, e solubilização de fases imiscíveis (CHARLES *et al*., 2017).

Os biossurfactantes também possuem aplicação na biorremediação sendo utilizado na dispersão no derramamento de óleos, remoção e mobilização de resíduos de óleo em tanques de estocagem por ser biodegradável na água e no solo, tornando-o melhor que os surfactantes de origem química (MAIA *et al*., 2018). Emulsificação é a dispersão de um líquido em outro,

sendo assim os biossurfactantes com sua propriedade de criar e estabilizar emulsões de óleos em água, se tornam capazes de reduzir as forças de repulsão entre líquidos com diferentes graus de polaridade permitindo que as duas fases se misturem (DEEPIKA, 2017; MAIA *et al*., 2018).

2.6 MICRORGANISMOS PRODUTORES DE SACS

"Os microrganismos representam a forma de vida mais abundante e diversificada no planeta" (KARLAPUDI *et al*., 2018). Os microrganismos do solo, são representados pelas bactérias, fungos, algas, virus e protozoários (AMER *et al*., 2015). O correto conhecimento sobre a variedade da microbiota serve principalmente para as tomadas de decisões sobre métodos para conservar a biomassa, devido as alterações ambientais e a precária utilização dos solos (CHARLES *et al*., 2017).

A microbiota presente nos manguezais desempenham mudanças bioquímicas de nutrientes, sendo necessárias para o consumo da matéria orgânica e meios tóxicos apresentando assim um papel fundamental no equilíbrio deste ecossistema (WITTGENS *et al*., 2017). O domínio Bacteria exerce função significativa relacionadas à decomposição, á síntese de nutrientes e aos outros processos biogeoquímicos ligados a preservação da capacidade de produção dos solos em situações do ambiente (BARTAL *et al*., 2018).

Processos importantes como a ciclagem dos nutrientes no ambiente estão diretamente relacionadas às atividades e diversidades das comunidades microbianas do solo. Poluentes de origem antrópica podem alterar a estrutura das comunidades microbianas e causar desequilíbrios ecológicos que podem levar à extinção de espécies importantes ou diminuir a ciclagem de nutrientes para a manutenção do ecossistema (ANTONIOU *et al*., 2015). A poluição no solo também pode conduzir a um decréscimo na diversidade microbiana em termos de abundância de espécies, devido à extinção causada pelo processo de seleção natural por meio do estresse imposto, e ao mesmo tempo ocasionar o enriquecimento de espécies particulares mais adaptadas a esse estresse (CHARLES *et al*., 2017; JOY, 2017).

Poluentes de origem antrópica podem alterar a estrutura das comunidades microbianas, e causar desequilíbrios ecológicos (FERREIRA, 2016), onde os danos causados pelo homem em relação ao manejo incorreto do solo, afeta diretamente as culturas microbianas, gerando uma série de problemáticas, pois entre 90 − 95% dos microrganismos do solo não conseguem serem cultivados utilizando os métodos convencionais (HRUDAYANATH, 2013; PRAMANIK, 2018).

Os diversos microrganismos, entre bactérias e fungos, possuem eficiência em degradar os hidrocarbonetos do petróleo, variando entre uma parcela de degradadores de alcanos, outros

de aromáticos e alguns com capacidade para os dois. Podemos encontrar uma gama de variedades destes microrganismos deterioradores de hidrocarbonetos do petróleo em oceanos (CATTER *et al*., 2016). Entre eles temos como representante de gêneros produtoras de CAS, Pseudomonas, Rhodococcus entre outros (FERREIRA;2016; VARJANI, 2017; KAKOLI, 2020).

Os microrganismos são capazes de produzir diversos CASs, que são caracterizadas pela presença de porções hidrofílicas e hidrofóbicas. Tais características estruturais permite-lhes a capacidade de interagir com superfícies e tensões interfaciais, formar micelas e emulsionar substâncias imiscíveis (VARJANI; 2019). Diversas outras macromoléculas podem ser encontradas entre os polímeros excretados pelas bactérias, porém os CASs são facilmente detectados, permitindo um crivo dos isolados produtores das biomoléculas de interesse (VARJANI; 2019).

2.7 VIAS METABOLICAS E GENÔMICA PARA SÍNTESE DE RAMNOLIPÍDEOS

Os ramnolipídios são os biossurfactante produzidos principalmente por espécies do gênero *Pseudomonas,* e são os mais intensamente investigado, com a biossíntese interligada com a formação de várias espécies de polissacarídeos. No entanto, a maioria das estirpes produtoras de ramnolipídeos são patógenos oportunistas para humanos e representando um risco para a saúde na produção em larga escala, sem o tratamento e analise adequada na biomolecula (WITTGENS *et al*., 2017; RAZA *et al*., 2020).

Por conseguinte, com fulcro no aumento da produção de ramnolipídios em linhagens de espécies bacterianas não patogênicas, a engenharia genética tem buscado cada vez mais atenção, mantendo o foco sobre a expressão do operon *RhlA*, para a conformação de mono-congêneres (WANG *et al*., 2016; WITTGENS *et al*., 2017). A *Escherichia coli* tem sido usada como base para a biossíntese de ramnolipídeos, tirando vantagens de seu background genômico e técnicas de manipulação genética bem estabelecidas (CHARLES *et al*., 2017; CHEN *et al*., 2018)

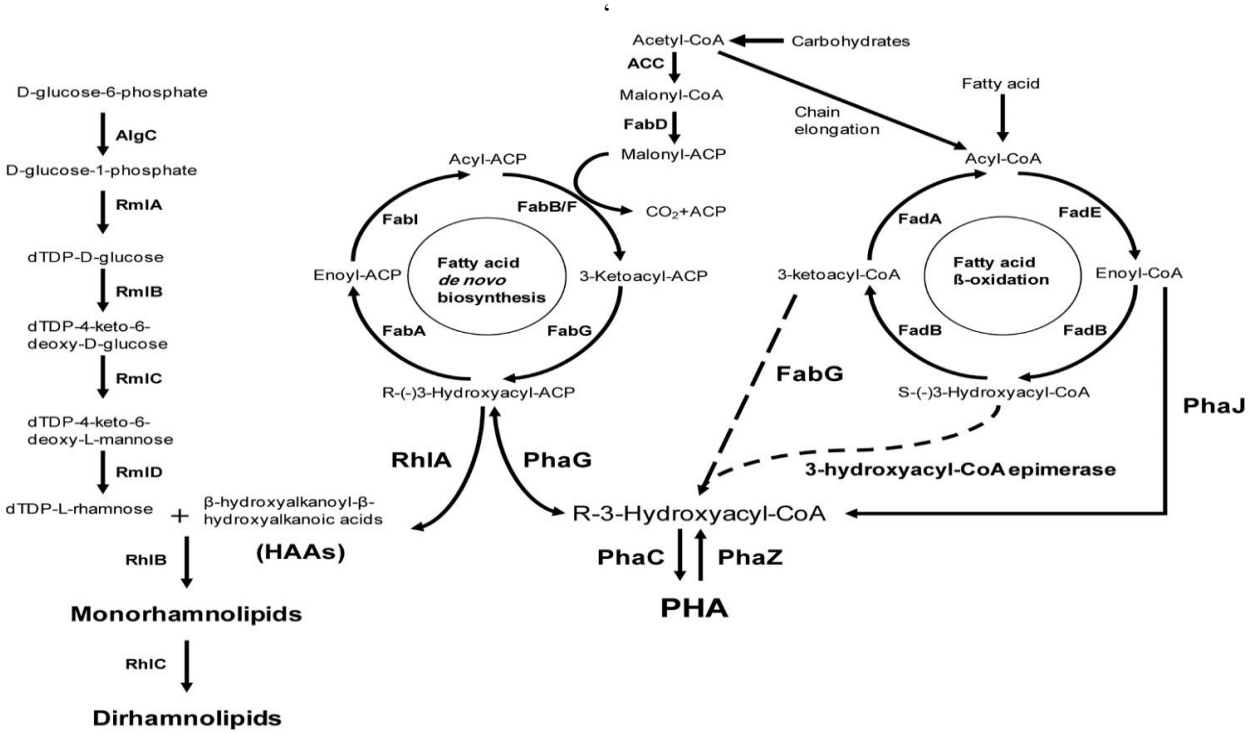
A biossíntese de rhaminolipidio por *P. aeruginosa* é efetuada através de três reações enzimáticas importantes, originando-se os mono-ramnolipídios ou di-ramnolipídios (WITTGENS *et al*., 2017). Via de regra, os micro-organismos usufruem de substratos hidrofílicos na síntese da porção polar da molécula de biossurfactante, compostos por um ácido carboxílico, um álcool ou um aminoácido, ao mesmo tempo que os substratos hidrofóbicos são utilizados exclusivamente na porção hidrocarboneto, formada por um ácido graxo de cadeia longa, um hidroxiácido ou um ácido graxo na-alquil-â-hidroxi (WITTGENS *et al*., 2017).

A síntese da porção hidrofóbica dos ramnolipídeos, sucede por uma sintetases clássicas do ácido graxo tipo II (FAS II). As sínteses da fração ácido graxo de N-acil homoserina lactonas (AHL) e 4-hidroxil-2-alquilquinolenos (HAQ) estão estreitamente ligadas entre si (DULCEY *et al*., 2019). Em que o RhlA desempenha função essencial na conversão de intermediários β-D-hidroxiacil-ACP a partir da síntese de ácidos graxos no componente β-hidroxidecanoil-β-hidroxidecanoato de ramnolipídeos (GUTIÉRREZ-GÓMEZ *et al.,* 2019). Observações estereoquímicas dos β-hidroxiácidos presentes nos componentes de ácidos graxos de ramnolipídeos sugerem que essa fração se inicia nos intermediários na via biossintética dos ácidos graxos. A porção lipídica de ramnolipídeos, logo é sintetizada novamente (WITTGENS *et al*., 2017).

Óleos metabolizados através da β-oxidação podem causar aumento da produção de ramnolipídeos (IBRAHIM, 2018), sugeriram a existência de potencial para uma conexão metabólica entre a a proteína β-oxidação e a biossíntese de ramnolipídeos. Nos estudos de sobre as vias enzimáticas foi obervado um vinculo direto entre os números de carbono dos ácidos graxos β-hidroxi com a síntese de ramnolipídeos (DULCEY *et al*., 2019). Os estudos demonstraram que o papel da β-oxidação na produção de ramnolipídios é constitutivo, e deve ter ocorrência não apenas quando ácidos graxos que são fornecidos como fontes de carbono (DEEPIKA *et al*., 2016; GEETHA *et al*.,2018). Sugerindo, assim, que a β-oxidação é o principal fornecedor de precursores lipídicos para a biossíntese de ramnolipídeos além da D-glucose proveniente da biosíntese da raminose (DEEPIKA *et al*., 2016; DULCEY *et al*., 2019).

A ramnose é um açúcar que é encontrando em diferentes componentes estruturais de diversas estirpes de *Pseudomonas* spp., por exemplo um componente do lipopolissacarídeo da parede celular (LPS) (TAZDAÏT *et al.,* 2018). Entretanto, pode ser constituinte de exopolissacarideos e biossurfactantes, sendo identificado que o dTDP-L-ramnose é a porção hidrofílica dos ramnolipídios derivado diretamente da via Entner-Doudoroff e da gliconeogênese (FANG *et al*., 2017). A geração de L-ramnose activa (*dTDP-L-ramnose*) inicia-se através da conversão de D-glucose-6-fosfato em D-glucose-1-fosfato pela Algof de fosfoglucomutase (LI *et al*., 2019; SOMOZA *et al*., 2020) seguida do operon *rmlBDAC* (figura 1).

Figura 1 Biossíntese completa da produção de biosurfactantes do tipo ramnolipídeo produzido por *Pseudomonas aeruginosa*



Fonte: GUTIERREZ, Merced *et al*. 2013. Legenda: RmlA Oxygen-dependent upregulation of transcription of alginate, RmlABCD Glucose-1-phosphate thymidylyltransferase, RhLABC Rhamnosyl transferase, FabABlGE 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase

2.8 IMPORTÂNCIA BIOTECNOLÓGICA

O momento industrial na atualidade tem como um de seus objetivos alcançar o desenvolvimento tecnológico atrelado ao bem-estar ecológico, buscando um crescimento harmônico entre tecnologia e meio ambiente, uma vez que a exploração de recursos naturais é valiosa e contribui para o avanço da produção de produtos que não apresentem malefícios para o ecossistema (SINGH, 2018). Os micro-organismos produzem uma variedade de metabólitos secundários, que são de interesse para a indústrias biotecnológica e farmacêutica (KUBICKI *et al*., 2019). Tais divergências tem incentivado a comunidade cientifica a buscar biomoléculas, que apresentem benefícios ambientais, como a complexação de íons metálicos, baixa toxicidade, alta degradabilidade, baixas Concentração Micelar Crítica CMC, forte redução de tensão superficial e alta estabilidade que seja capaz de interagir com a microbiota de cada bioma sem causar lesões (DANG *et al*., 2016; SNGH, 2018)

Um exemplo relevante trata-se dos biossurfactantes, um grupo variado de compostos ativos de superfície compostos anfipáticos constituídos de ácidos graxos, monossacarídeos ou aminoácidos, que têm um caráter hidrofóbico e hidrofílico na mesma (ROCHA *et al*., 2020). Na natureza, a biossíntese de compostos ativos de superfície como os biossurfactantes por micro-organismos podem levar a vantagens competitivas, além de promover a adaptação nichos

ecológicos específicos, como aqueles ricos em substratos hidrofóbicos (WITTGENS *et al*., 2017).

Em vista que consumidores cada vez mais se preocupam com o uso de mercadorias ambientalmente corretos, além do fator que a legislação vem trazendo novos incentivos para o desenvolvimento de produtos naturais, em decorrência das diversas vantagens das propriedades biológicas e físico-químicas proporcionadas pelo uso dos biosurfactantes, abrangendo efeitos antibacterianos, antifúngicos e antitumorais (CAO *et al*., 2016; WITTGENS *et al*., 2017). Ao mesmo tempo, aspectos ecológicos são considerados importantes, pois os biossurfactantes podem ser produzidos a partir de recursos renováveis e exibem baixa eco-toxicidade em conexão com a degradabilidade biológica suprema acumulação ambiental (KUBICKI *et al*., 2019; ROCHA *et al*., 2020).

Embora as melhorias advindas da biotecnologia permitam a produção de biomoléculas, é provável que novos avanços significativos (mesmo que de menor magnitude) são necessários para tornar esta tecnologia comercialmente viável.

3 .MATERIAL E MÉTODOS

3.1 AMOSTRAGEM, ISOLAMENTO E SELEÇÃO DOS MICROORGANISMOS HIDROCARBONOCLÁSTICOS

As amostras de sedimento de mangue para o isolamento de bactérias foram coletadas na região do Rio Anil no município de São Luís do estado do Maranhão de coordenadas 2°31'22.0"S 44°17'29.7"W // -2.522770 -44.291583 (Figura 2).

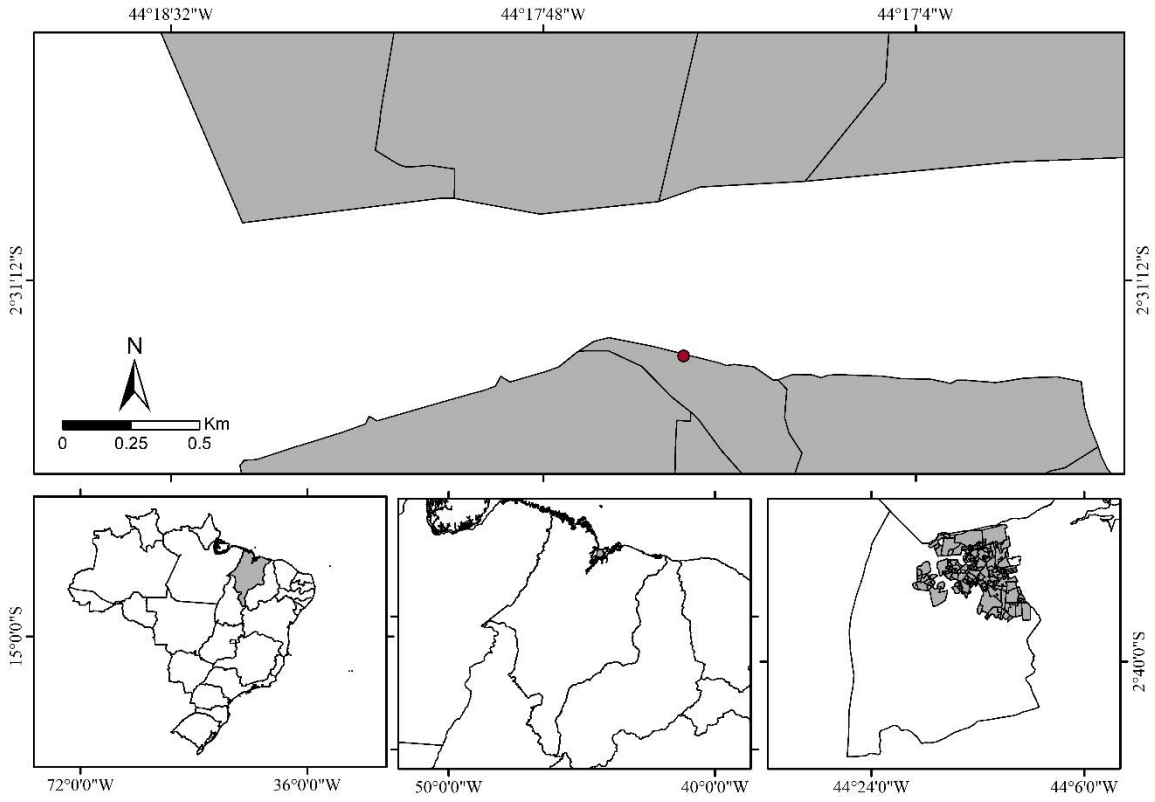


Figura 2 Área de coleta localizada as margens do Rio Anil em São Luis do Maranhão.

Foram coletadas cinco amostras randômicas de 100 gramas cada em frascos estéreis, dentro de uma poligonal de 20m x 20m no ponto referenciado, por ser uma área de alta interação antropogênica. As amostras foram peneiradas em peneiras, no laboratório de microbiologia aplicada da universidade CEUMA em malha 2 mm, com a finalidade de eliminação de pedregulhos e material orgânico parcialmente decomposto (MENYAILO *et al*., 2003).

Para o isolamento das bactérias produtoras de biossurfactantes ou bioemulsificantes foi formado uma amostra composta contendo 5 gramas de cada coleta realizada, totalizando vinte e cinco gramas da amostra para realização do ensaio, contendo todas as cinco parcelas no ponto de coleta dentro da poligonal.

Isolamento do Microrganismos

As amostras foram acondicionadas em sacos hermeticamente vedados e transportadas em uma caixa térmica com temperatura constante, para o laboratório de Microbiologia Aplicada da Universidade CEUMA.

Para o isolamento de bactérias capazes de degradar compostos hidrofóbicos de origem vegetal ou querosene, cerca de 20 gramas da amostra composta do sedimento foi inoculada em frascos Erlenmeyer adicionados de 180 mL do meio mineral Bushnell Haas Broth (BHB) (Hi-Media. Laboratories, Mumbai, India) contendo por litro 0,2 g de sulfato de magnésio, 0,02 g de cloreto de cálcio, 1,0 g de fosfato monobásico de potássio, 1,0 g de fosfato dibásico de potássio, 1,0 g de nitrato de amônia, 0,05 g de cloreto de ferro, final pH 7, acrescido de 5% de oléo de girassol, querosene ou glicerol como única fonte de carbono (RATTES *et al*., 2019). Após a inoculação, os fracos foram incubados a 30 ºC em agitação de 140 rpm por até 12 dias. Após uma sequência de dois, oito e doze dias de incubação1 ml das culturas foram diluídas serialmente em uma solução salina estéril (NaCl a 0,85%) e alíquotas de 100 µL das diluições de 10^{-1} até 10^{-9} foram inoculadas pela técnica *spread plate* em meio Brain Heart Infusion (BHI - Difco) acrescido de 1,5% de ágar para a caracterização das colônias, seguido de quantificação e isolamento dos diferentes morfotipos observados. Os microorganismos triados foram considerados como potencialmente degradadores dos compostos adicionados ao meio como fonte de carbono e energia.

As amostras das colônias representantes dos diferentes morfotipos foram purificadas por meio de estrias compostas em o meio agar BHI. Amostras das culturas puras obtidas foram submetidas à coloração de Gram. A manutenção das culturas foi feita por meio do estoque em tubos inclinados com meio BHI sólido a 4 ºC e em criotubos com caldo BHI acrescido de 20% de glicerol a –80 ºC (KHADEMOLHOSSEINI *et al*., 2019).

3.2 IDENTIFICAÇÃO DOS ISOLADOS BACTERIANOS

Os diferentes morfotipos foram identificados pelo sistema Matrix-Assisted Laser Desorption Ionization –Time of Flight Mass Spectrometry (MALDI-TOF MS) utilizando o sistema Biotyper (Biotyper; Bruker Daltonics, Billerica, MA). As bactérias foram cultivadas em meio ágar Trypticase soy (TSA; Difco Laboratories, Detroit, Mich. USA) durante 24 h a uma temperatura de 30 °C. Em seguida, uma amostra da colônia foi transferida com auxílio de uma alça bacteriológica calibrada de 1 µL para uma placa, e seguida, foram adicionados a amostra 1 µL de da matriz ácido α-ciano-4-hidroxicinâmico. A amostra foi submetida à incidência de um feixe de laser para extração dos peptídeos ribossomais energizados.

Finalmente, os espectros de massa adquiridos foram comparados com os espectros de massa conhecida contidas no software para classificação (Versão 3.1, Library 1.0). Os valores dos escores foram analisados de acordo com as recomendações do fabricante: um escore ≥2 indica confiança para o nível de espécie, 1,7 a 1,99 indica confiança para o gênero e <1,7 ausência de identificação.

3.3 IDENTIFICAÇÃO DA ATIVIDADE TENSOATIVA E EMULSIFICANTE DO SOBRENADANTE DAS CULTURAS

Os isolados bacterianos obtidos foram inoculados na concentração inicial de 0,1 unidade de densidade ótica a 600 nm (D.O $_{600nm}$) em frascos Erlenmeyer contendo 50 mL do meio BHB adicionado de 5% de oléo de girassol, querosene ou glicerol como única fonte de carbono (GARGOURI *et al*., 2017). Os frascos foram incubados por até 5 dias a 30 ºC sob agitação de 144 rpm. Após o período de incubação, as culturas foram centrifugadas a 5.000 g por 15 min e os sobrenadantes utilizados nos testes de detecção de atividade surfactante, pelo método de espalhamento da gota, e emulsificante aplicando o método de E_{24} (GARGOURI *et al*., 2017).

Para a medida da atividade surfactante, 1 mL de cada sobrenadante de crescimento bacteriano foi adicionado a uma superfície hidrofóbica para analisar o diâmetro de dispersão de gotas. Todos os resultados foram comparados como uma amostra contendo apenas o MM mínimo (RUGGERI *et al*., 2009; VARJANI, 2017).

Para determinar o índice de emulsificação (E_{24}), 3 mL do meio de cultura e 1 mL de querosene foram adicionados em um tubo de ensaio, os quais foram agitados por dois minutos em Vortex e incubados a temperatura ambiente por 24 horas. A seguir, procedeu-se a medida da altura da camada de óleo emulsificada e camada total que foram usadas para o cálculo do E24, segundo a equação (1);

$$Te_0 = (\frac{HE}{HT}\text{x}100) - Te_b \qquad (1)$$

Onde;

Teo – índice de emulsificação da camada do oléo

HE – Camada total da emulsificação formada

HT - Altura total de caldo nutritivo e oléo;

Teb - Taxa de emulsificação do ensaio em branco (emulsificação na fase do meio de cultura sem crescimento bacteriano).

3.4. ESTABILIDADE DA ATIVIDADE EMULSIFICANTE À TEMPERATURA, PRESSÃO E PH.

Para avaliar a estabilidade das biomoléculas com atividades tensoativas, os sobrenadantes foram submetidos a temperatura de 121ºC e pressão de 1 atm por 30 min usandoa autoclave (VARJANI, 2017). Após o tratamento térmico, cada solução foi arrefecida à temperatura ambiente e novamente avaliada quanto a atividade emulsificante (E_{24}).

Para a avaliar a estabilidade frente a diferentes valores de pH, os sobrenadantes foram submetidos ao ajuste do pH nos valores de 3, 4, 5, 6, 7, 8, 9, 10 pela adição de HCl (0,1N) ou NaOH (1 e 0,1N), e mantidos em banho-maria por 30 min a uma temperatura de 25 ± 1 ºC. Todos os tratamentos foram realizados em triplicada e as medidas das taxas de emulsificação foram repetidas após cada tratamento.

3.5 DETERMINAÇÃO DA CONCENTRAÇÃO MICELAR CRÍTICA (CMC).

Para determinação da concentração micelar crítica (CMC), os compostos tensoativos foram precipitados a partir do sobrenadante pela adição de 4 volumes de etanol absoluto gelado e mantido em geladeira por cerca de 12h. O material foi centrifugado, o precipitado obtido foi seco a temperatura de 40 ºC e pesado. Em seguida, o precipitado foi diluído em água tipo Milli Q e soluções de diferentes concentrações foram submetidas a medição da tensão superficial em tensiômetro KRÜSS® GmbH K100C-MK2 acoplado com placa de platina, à temperatura ambiente. As medidas foram feitas em triplicata. O CMC foi determinado a partir do ponto de estabilização da tensão superficial versus o logaritmo de sua concentração (VARJANI; 2019).

3.6 MÉTODO DO ESPALHAMENTO DA GOTA

Após oito dias de incubação das amostras foi realizado o método do espalhamento da gota com o objetivo de determinar a capacidade de redução da tensão superficial. Para tal, 1 mL de cada sobrenadante com crescimento bacteriano foi colocado na placa de Petri para análise do resultado da dispersão da gota sobre a uma superfície hidrofóbica (CHARLES *et al*., 2017; VARJANI, 2017).

3.7 ANÁLISE GENÔMICA E PREDIÇÃO DE GENES RELACIONADOS A CARACTERISTICAS IMPORTANTES PARA A BIORREMEDIAÇÃO.

Nesta etapa foi utilizada a bactéria *Pseudomonas aeruginosa* denominada PSA39, slecionada por apresentar alta atividade emulsificante e surfacatante. A bactéria foi cultivada em caldo BHI por 18 h de incubação a 30ºC e alíquotas de 500 µL foram centrifugadas a 10.000 rpm por 20 min e o pellet submetido a extração de DNA usando o KIT de Purificação de DNA Genômico Wizard® (Promega Corp, Madison, WI, EUA), seguindo o protocolo original do fabricante. O DNA genômico foi quantificado com o espectrofotômetro NanodropTM 1000 a 260 nm.

O genoma foi sequenciado usando a plataforma Illumina MiSeq™ usando a estratégia paired-end. A biblioteca foi preparada usando o Kit de Preparação de Biblioteca Nextera XT DNA (Illumina, San Diego, CA, EUA). As leituras de sequência foram montadas com o software A5 para filtrar adaptadores, análise de qualidade e correção de erros para gerar contigs e andaimes (POIREL *et al*., 2014). Além disso, o software CAP3 foi usado para melhorar a montagem de andaimes, cortar regiões de baixa qualidade e corrigir ligaçoes erradas entre os contigs (CAO *et al*., 2016). As sequências de DNA genômico pré-montadas foram anotadas usando a ferramenta de software Prokka (EDWARDS, 2013).

O genoma de *P. aeruginosa* PSA39 foi submetido 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 deposito da sequência foi realizada no (National Center For Biotechnology Information, (NCBI), Sequence READ Archive (SRA) Bioproject PRJNA563020.

3.8 CONSTRUÇÃO DA ÁRVORE FILOGENÉTICA

A análise de alta semelhança filogenética foi realizada com base no método de filogenia a distância do genoma BLAST (GBDP), conforme implementado na plataforma TYGS (Type Strain Genome Server) (https://tygs.dsmz.de/).

3.9 ANÁLISE DE SEQUENCIAMENTO DE GENOMA, ANI, CÁLCULOS E FILOGENIA DO DDH IN SILICOIN

A relação genômica bacteriana foi investigada por diferentes algoritmos para comparação genoma-genoma. Os valores médios da identidade nucleotídica (ANI) foram calculados com base no BLAST (ANIb) usando o servidor online JSpeciesWS do serviço da web (**http://jspecies.ribohost.com/jspeciesws/**) (RICHTER *et al*., 2016). Para a análise *in sílico*

de hibridação DNA-DNA (DDH), os resultados foram obtidos no serviço da web da calculadora distância genoma-genoma (GGDC) usando a fórmula 2 (identidades / comprimento do HSP) (**http://ggdc.dsmz.de**) (AUCH *et al*., 2010).

3.10 ANÁLISE COMPARATIVA DO GENOMA DE *P. AERUGINOSA* PSA39

O genoma de *P. aeruginosa* PSA39 foi submetidos à análise na anotação Rapid usando o banco de dados do Subsystem Technologu (RAST) (http://rast.nmpdr.org).

O alinhamento de múltiplas sequências genômicas foi realizado usando o algoritmo Mauve progressivo (http://darlinglab.org/mauve/mauve.html). Também realizamos uma comparação entre os genomas de microorganismos produtores de biosurfactante, NCTC10332, DMS50071 e PAO1 presentes no banco de genes do Genbank, NCBI.

Para comparar todos os genomas de *P. aeruginosa* em nível de proteína, usamos o OrthoVenn2 (http://orthovenn2.bioinfortoolkits.net/home), uma plataforma web para comparação e análise de clusters de genomas ortólogos.

3.11 CURVA DE CRESCIMENTO E PRODUÇÃO DE CASS POR *P. AERUGINOSA* PSA39.

A produção de biossurfactantes\bioemulsificantes foi realizada em frascos Erlenmeyer de 250 mL contendo 100 mL de meio BHB adicionadonfraçoes de 2 a 5% de querosene, glicerol e óleo de girassol. O inóculo bacteriano foi padronizado para 0,02 D.O. 560nm e os frascos incubados por até 48 horas em shaker com mesa rotatória a 140 rpm e temperatura 30°C. Amostras de 100 µL foram retirados em intervalos de tempo de 12 em 12 horas regular para a análise do índice de emulsificação (E_{24}), produção de surfactante (g/L), crescimento microbianono meio BHI para quantificação (UFC\mL). Todos os ensaios foram realizados em duplicata.

4.RESULTADOS E DISCUSSÃOe

4.1 TRIAGEM E IDENTIFICAÇÃO DE MICROORGANISMOS PRODUTORES DE SAC´S

A triagem inicial de linhagens de bactérias capazes crescer em meio mínimo mineral adicionado de querose e óleos vegetais como única fonte de carbono a 2%, foi realizada em duas etapas, de 2 e 8 dias de incubação, apresentando uma densidade microbiana máxima de 11,94 UFC/g de sedimento com 2 dias de incubação para fonte de óleo de girassol e mínima de 5,7 UFC/g de sedimento com 8 dias de incubação para glicerol e querosene (Tabela 1). A capacidade de crescimento microbiano em meios mínimos contendo óleos vegetais ou derivados do petróleo como única fonte de carbono e energia depende das vias enzimáticas específicas associadas ao tipo de hidrocarboneto disponível, paralelamente com a habilidade de produção de BS´s (VARJANI; 2019).

Dos 32 isolados bacterianos obtidos na triagem inicial de microrganismos capazes de se desenvolver em meio de cultura mínimo com hidrocarbonetos como única fonte de carbono, somente nove estirpes, A-4-3, B-2-1, A-2-3, A-2-1, PSA39, A-2-11, C-3-5, B-2-9 E C-2-11 sendo identificados como Serratia marcescens, Serratia marcescens, Ochrabactrum anthropi, Ochrabactrum anthropi, Pseudomonas aeruginosa, Ochrabactrum anthropi, Ochrabactrum anthropi, Ochrabactrum anthropi, e Ochrabactrum intermedium respectivamente que apresentaram atividades emulsificantes (Tabela 2). As fontes de carbono são um dos fatores físico-químicos que influenciam de forma direta na produção de biossurfactantes (MA *et al*., 2016). Desta forma, o resultado apresentado na tabela 2 demonstram a capacidade dos noves isolados na produção de diferentes BS´s capazes de utilizarem uma diversidade de fonte de carbono indisponível, como nutriente.

Com soluções solúveis em água, por exemplo os substratos como a glicose, existe uma variedade de infrequentes substratos insolúveis, que têm sido utilizados para aumentar o crescimento bem como a produção de RLs (MA *et al*., 2016; CHARLES *et al*., 2017; TIWARY, 2018). A incorporação de glicose, querosene e óleo de girassol pode causar aumento significativa no rendimento de BS´s. Outras condições que favorecem maior nível de produção incluem alta proporção de carbono/nitrogênio, exaustão fonte de nitrogênio, condições de estresse e altas densidades celulares (MA *et al*., 2016).

Tabela 1: Densidade microbiana em função do tempo e fonte de carbono

Tempo de Incubação	Fonte	UFC/g de Solo
2 Dias	Controle	11,94
2 Dias	2% Glicerol	11,85
2 Dias	2% Querosene	9,40
2 Dias	2% Oleo de Girassol	11,90
8 Dias	2% Glicerol	11,52
8 Dias	2% Querosene	11,52
8 Dias	2% Oleo de Girassol	5,70

Tabela 2: Isolados da seleção de microorganismos em diversas fontes de carbono e suas atividades emulsificante E_{24}

Isolado	Fontes de crescimento	% V/V fonte de carbono	Atividade emulsificante
A-4-3	Óleo de Girassol	5%	40%
B-2-1	Glicerol	5%	27%
A-2-3	Glicerol	5%	47%
A-2-1	Glicerol	5%	31%
PSA39	Querosene	5%	57,30%
A-2-11	Glicerol	5%	22%
C-3-5	Querosene	5%	13%
B-2-9	Glicerol	5%	36%
C-2-11	Glicerol	5%	48%
A-3-5	Querosene	5%	0
A-3-7	Querosene	5%	0
A-3-11	Querosene	5%	0
B-3-5	Querosene	5%	0
B-3-7	Querosene	5%	0
B-3-9	Querosene	5%	0
B-3-11	Querosene	5%	0
C-3-7	Querosene	5%	0
C-3-11	Querosene	5%	0
D-3-5	Querosene	5%	0
D-3-11	Querosene	5%	0
A-2-7	Glicerol	5%	0
B-2-3	Glicerol	5%	0
B-2-7	Glicerol	5%	0
B-2-11	Glicerol	5%	0
A-2-5	Glicerol	5%	0
C-2-7	Glicerol	5%	0
D-2-11	Glicerol	5%	0
A-4-1	Óleo de Girassol	5%	0
A-4-5	Óleo de Girassol	5%	0
B-4-1	Óleo de Girassol	5%	0
B-4-3	Óleo de Girassol	5%	0
B-4-5	Óleo de Girassol	5%	0

Somente a estirpe PSA39, que foi identificado como *Pseudomona aeruginosa*, através do sistema (MALDI-TOF/MS) foi utilizada para testes relacionados as atividades emulsificantes, por ser a única entre os nove isolados capaz de crescer e produzir BS´s nas três variações das fontes de enriquecimento, querosene, glicerol e óleo de girassol. *Pseudomonas* é um gênero bacteriano pertencente *a* família Pseudomonadaceae, composta por bacilos Gram-negativos que podem ser encontrados em diversos ambientes, como água, solo e ambientes, também habitam tecidos de plantas e tecidos de diferentes animais (CHARLES *et al*., 2017; WITTGENS *et al*., 2017).

Diferentes espécies do gênero *Pseudomonas* podem produzir biossurfactantes e outros CAS, sendo a espécie *P. aeruginosa* a mais promissora na produção de de BS´s, sendo relatado um ótimo desempenho no que tange a produtividade e eficácia de suas biomolecula produzidas. Entre as espécies os isolados *P. aeruginosa* PAO1, *P. aeruginosa* L10, *P. aeruginosa* NCTC10332 e *P. aeruginosa* DN1, todas reladas por apresentarem vias de degradação de hidrocarbonetos e produção de CAS´s (MA *et al*., 2016).

4.2 ATIVIDADE EMULSIFICANTE DOS DO SOBRENADANTE DAS CULTURAS

Para compreender a aplicação dos BS´s em condições ambientais, é necessário o estudo da estabilidade da emulsão e sua eficiência frente a variações de temperatura e pressão, pH resistência a salinidade (GARGOURI *et al*., 2017). As taxas de emulsificação do teste E_{24} do isolado *P. aeruginosa* PSA39, para as fontes glicerol, óleo de girassol e querosene foram de 69%, 60% e 58%, respectivamente.

Os BS´s produzidos por *P. aeruginosa* PSA39 em cada fonte de enriquecimento após submetido a 1 atm e 135°C, apresentaram valores da taxa emulsificação (E_{24}) de 53% e 49% para o enriquecimento utilizando glicerol e óleo de girassol, respectivamente (Tabela 3), sendo classificados como termoestáveis, e não estável para o de querosene. Após o teste de estabilidade térmica alguns estudos de linhagens produtoras de biossurfactantes, como *P. aeruginosa*, apresentaram decaimento nos valores de emulsificação, abaixo de 50% (CHARLES *et al*., 2017; DEEPIKA *et al*., 2017).

A atividade emulsificante do biossurfactante produzido pela PSA39 variou conforme a fonte de carbono utilizado no meio de crescimento, foram observados valores de E_{24} de 75% e 65,2%, quando glicerol e óleo de girassol, foram utilizados no meio de crescimento, respectivamente (Tabela 3). O pH é relatado como um fator significativo para a produção de

biossurfactante por *P. aeruginosa* (SOMOZA *et al*., 2020). Em nosso estudo, a produção de biossurfactante foi visto como sendo mais alto em pH básico e instável em pH ácidos. Esses resultados comparados á estudos anteriores, apresentam uma maior eficácia do BS produzido por *P. aeruginosa* PSA39 por estar com numa faixa de variação de pH 7,8 (DEEPIKA *et al*., 2017) e corroborando com a instabilidade de Biosurfactantes produzidos por pseudômonas para pH´s ácidos (DEEPIKA,. 2017; LI *et al*., 2019). Para a linhagens de *P. aeruginosa*, o pH ótimo para atividade emulsificante de biossurfactantes aumenta significativamente com o incremento dos valores de pH (SOMOZA *et al*., 2020). Resultados semelhantes já foram relatados para biossurfactantes produzidos por outras linhagens de bactérias utilizando outras fontes de carbono, como óleo cru, dextrose, melaço e óleo de cozinha .(WITTGENS *et al*., 2017; TIWARY; DUBEY, 2018; LI *et al*., 2019; SOMOZA *et al*., 2020) .

A estabilidade iônica do biossurfactante produzido perante sais distintos, foi observada que para NaCl 10 a 30% M/V, somente o BS produzido pela fonde de glicerol foi capaz de produzir emulsões estáveis, com valores de E_{24} variando de 53% a 75% já para $CaCl_2$ foi observado que todas as emulsões foram instáveis. Entretanto, para as demais fontes de querosene e óleo de girassol, as emulsões produzidas foram instáveis na presença de NaCl. Também, foi observado que o biossurfactante recuperado do meio de crescimento adicionado de querosene, óleo de girassol e glicerol produziram emulsões estáveis em todas as concentrações de $CaCl_2$ utilizadas nos ensaios, onde o querosene apresentou uma redução da sua atividade com o aumento da concentração do sal apresentando um valor mínimo de 62% para E_{24}, e o de óleo de girassol com 79%, ambos rendimentos na concentração máxima do sal de 50% (Tabela 3).

De acordo resultados observados nos ensaios de estabilidade da emulsão na presença de sais, a salinidade não afeta as propriedades tensoativas do biossurfactantes , portanto, esta BS possui propriedades tensoativas que podem ser aplicadas sob mesófilos ou condições ambientais com variações de temperatura e pressão (SOMOZA *et al*., 2020). Biossurfactantes em comparação com surfactantes sintéticos, apresentam baixa ecotoxicidade, estabilidade a condições extremas de pH, temperatura e salinidade e além disso são biodegradáveis (AGARWAL *et al*., 2018; SOMOZA *et al*., 2020). Nossos resultados indicam que o biossurfactante produzido por *P. aeruginosa* PSA39 utilizando três fontes de carbono utilizadas possuem potencial para aplicação em uma ampla faixa de temperatura, valores de pH e ambiente salinidade.

4.3 DETERMINAÇÃO DA CONCENTRAÇÃO MICELAR CRÍTICA, CMC.

A concentração micelar crítica (CMC) do biossurfactante foi avaliada em soluções aquosas, variando-se a concentração do composto. Neste ensaio foram obtidas da curva isotérmica um valor mínimo de 29,78 mNm^{-1} (Figura 3). A tendência dos biossurfactantes em adsorver na interface água-ar e agregar na fase hidrofóbica pode ser prevista, tendo base nos parâmetros termodinâmicos, no processo de adsorção e micelização (ZENG *et al*., 2018).

O valor do CMC encontrado está na faixa de declarada pelos outros autores que investigam BS´s (mono- e di-ramnolipídios) e surfactantes sintéticos (WITTGENS *et al*., 2017). O valor de CMC para o biossurfactante de *P. aeruginosa* PA39 indicou que o isolado bacteriano produz moléculas com menor tendência à adsorção, predispondo uma densidade menor nas interfaces saturadas de água/ar (IBRAHIM, 2018; TIWARY *et al*., 2018; ZENG *et al*., 2018). As moléculas de mono- e di-ramnolipídios já são relatadas por apresentarem a capacidade de redução da tensão superficial da água de 72 a ≤30 mN/m, com valor valor crítico de concentração de micelas (CMC) na faixa de 10 a 200 mg/L (ZENG *et al*., 2018). A atividade superficial dos ramnolipídios pode ser mantida mesmo sob condições extremas de temperatura (capazes de suportar 90 °C até 120 min e até 120 ° C por 15 min) e variação de pH entre 5 a 11 (DEEPIKA *et al*., 2017; ZENG *et al*., 2018).

4.4 MÉTODO DO ESPALHAMENTO DA GOTA

No ensaio de espalhamento da gota, para verificar a redução da tensão superficial, obteve-se os resultados de 83%, 133% e 17% de incremento no diâmetro de cada gota, para as fontes de óleo de girassol, glicerol e querosene respectivamente (Tabela 3). Indicando a presença da produção de BS´s, e a alta capacidade de redução da tensão superficial para 29,78 $mN\ m^{-1,}$ uma vez que os RLs produzido na fonte de enriquecimento glicerol apresentou o maior incremento no diâmetro da gota. Por outro lado, baixos valores de incremento do diâmetro da gota >30% estão relacionados com emulsões que apresentam agregados maiores e menos compactos, portanto, de menor qualidade .(MA *et al*., 2016) A capacidade de redução da tensão superficial é formada quando o meio atinge uma concentração crítica do surfactante (CMC) e a forma das micelas, (esférica, bicamada, etc.), estão relacionadas com o tipo de surfactante presente no meio (DEEPIKA *et al*., 2016).

Tabela 3: Resultados do teste E_{24} para o biossurfactante produzido por *P. aeruginosa* PSA39 com variações de condições químicas e físicas

Variaveis	Querosene	Glicerol	Óleo de Girassol
Autoclave	-	53%	49%
pH	-	-	-
6	-	62.6%	-
7	57.3%	65.5%	59.2%
8	56.7%	68.1%	63.7%
9	57.6%	68.9%	64.3%
10	55.7%	69.2%	65.2%
Salinidade.g/mL	-	-	-
NaCl 10%	-	46%	-
NaCl 20%	-	20.4%	-
NaCl30%	-	6.8%	-
NaCl40%	-	-	-
NaCl50%	-	-	-
CaCl2 10%	67.3%	-	58.3%
CaCl2 20%	66.7%	-	58.3%
CaCl2 30%	66.3%	-	76.2%
CaCl2 40%	65%	-	76.2%
CaCl2 50%	62%	-	79%
Incremento de Diametro da gota	17%	83%	133%

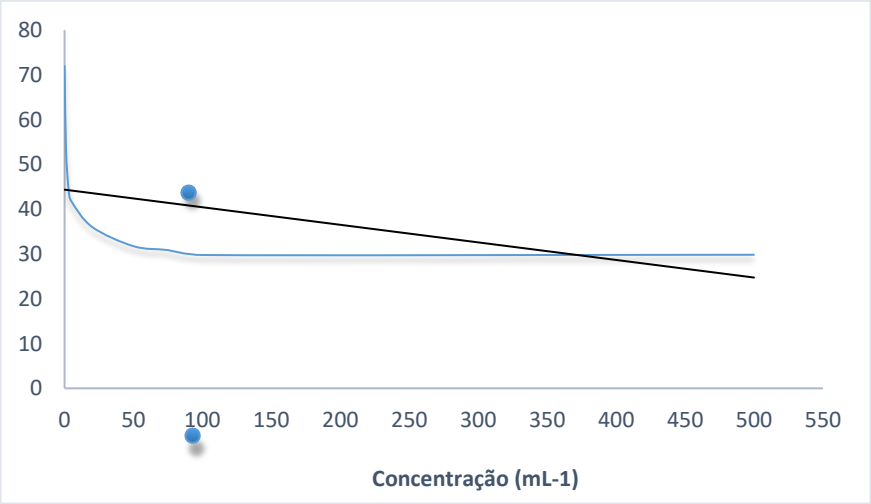


Figura 3- CMC do biosurfactante produzido por *P. aeruginosa* PSA39 e curva de tendência

4.5 CURVA DE PRODUÇÃO DE BIOSURFACTANTE E CRESCIMENTO DE *P. AERUGINOSA* PSA39

Nos ensaios de crescimento foram obtidas curvas e produção de biossurfactante em g/L pela estirpe *P. aeruginosa* PSA39 utilizando glicerol, óleo de girassol e querosene como única fonte de carbonoo. A produção de biossurfactante por *P. aeruginosa* PSA39 apresentou um aumento de 2% na presença de glicerol, sendo observado um pico máximo de produção entre 15 horas e 35 horas de crescimento, e se mantendo constante após esse período (Figura 4). As propriedades físicas e químicas dos BS´s produzidos por isolados microbianos apresentam uma alta variabilidade em suas características devido à fonte utilizada, condições ambientais e gênero/espécie de isolado que o produz (BARTAL *et al*., 2018; EL-SHESHTAWY *et al*., 2017).

Quando utilizado a produção de biosurfactante em óleo de girassol, a concentração máxima de biossurfactante foi observada no tempo de 100 horas, sendo posteriormente degradado (Figura 5), pois a concentração teve um decréscimo após este período. Em adição, no meio mínimo adicionado de querosene foi o observado uma produção máxima de BS entre o período de 20 e 48 horas (Figura 6). Para todas as fontes utilizadas, a curva de crescimento de *P. aeruginosa* PSA39 apresentou uma fase estacionária entre 24 e 35 horas (Figura 4,5 e 6). Já foi verificado que meios de cultivo contendo hidrocarbonetos como única fonte de carbono são capazes de promover o crescimento bacteriano de linhagens de *P. aeruginosa* , ao comparar (CHARLES *et al*., 2017; MORRIS *et al*., 2019)com ax' produção de biossurfactantes por cepas *Bacillus subtilis e Clostridium perfringens* utilizando óleos vegetais e hidrocarbonetos, dentre eles o querosene e glicerol, observa-se que os melhores valores de emulsão encontrados para esse hidrocarbonetos variaram entre 52% e 55% para os ambos os gêneros *Bacillus* e *Clostridium* (MORRIS *et al*., 2019; JIMOH, 2020).

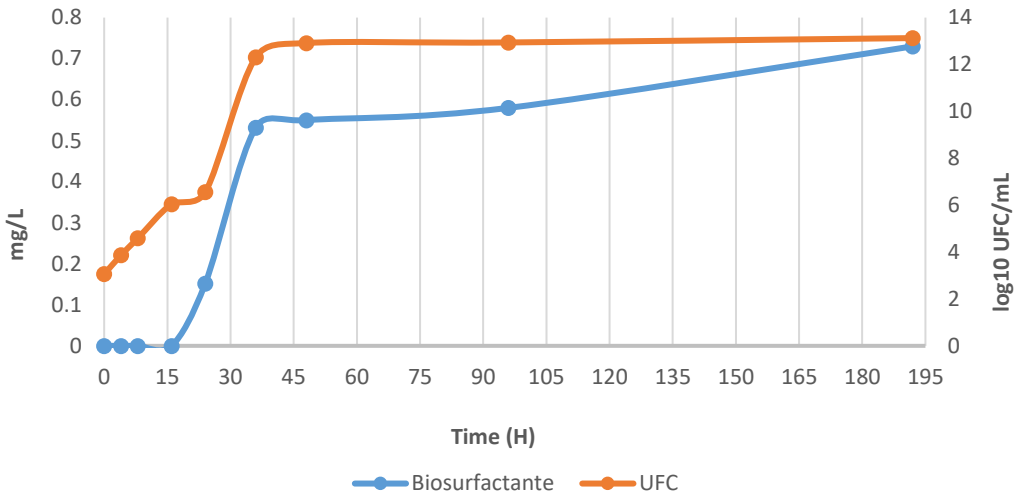


Figura 4. Curva de crescimento e produção de biossurfactante em meio mínimo adicionado 5%(v/v) de glicerol de *P. aeruginosa* PSA39

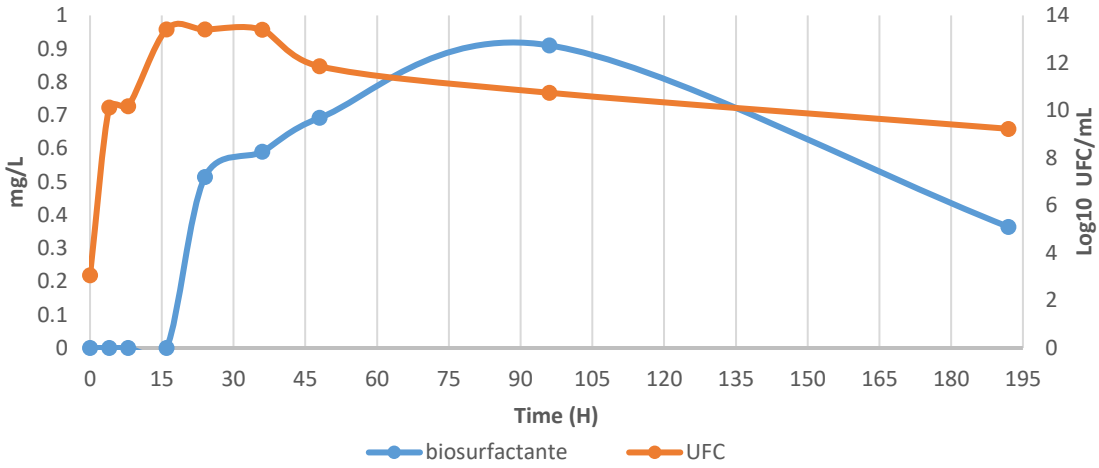


Figura 5- Curva de crescimento e produção de biossurfactante em meio mínimo adicionado 5%(v/v) de óleo de girassol de *P. aeruginosa* PSA39

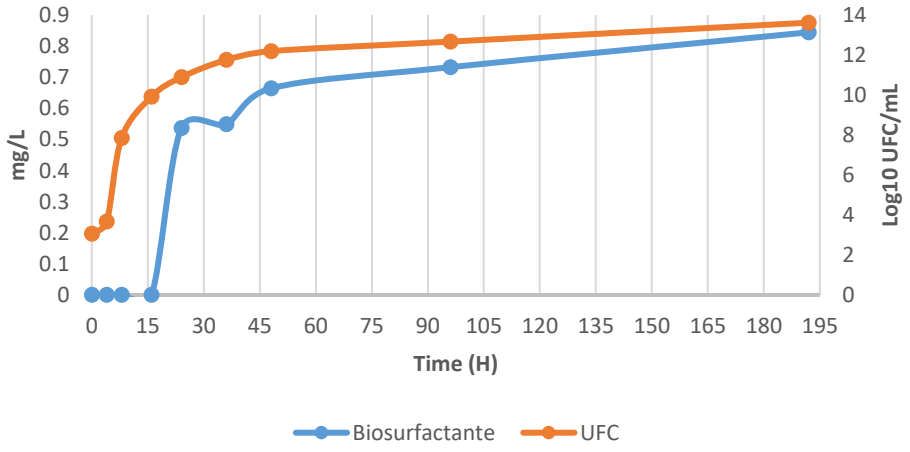


Figura 6. Curva de crescimento e produção de biossurfactante em meio mínimo adicionado 5%(v/v) de querosene de *P. aeruginosa* PSA39

4.6 ANÁLISE GENÔMICA E DE VIAS METABÓLICAS

A análise do genoma da estirpe *P. aeruginosa* PSA39 pelo RAST indicou a presença de subsistemas genéticos divididos em genes tabulados no sistema com 30% tabulados e 70% de genes que não constam na biblioteca do programa. Na categorização dos genes obtidos pelos sub-sistemas, a estirpe *P. aeruginosa* PSA39 apresentou um total de 2062 genes sendo 1946 relacionados a proteínas não hipotéticas e 571 genes relacionados a proteínas hipotéticas (Figura 7, Tabela 4).

Tabela 4 Dados do Sequenciamento do Isolado PSA39

ID´s	DADOS BASE
Specie	PSA39
TAXONOMOMIA	Bacteria: *Pseudomonas aeruginosa*
Tamanho	7.160.969
GC	65.7
N50	280366
L50	9
Número de Contigs (com PEGs)	79
Número de Subsistemas	432
Número de Sequencias Codificadas	6949
Número de RNAs	65

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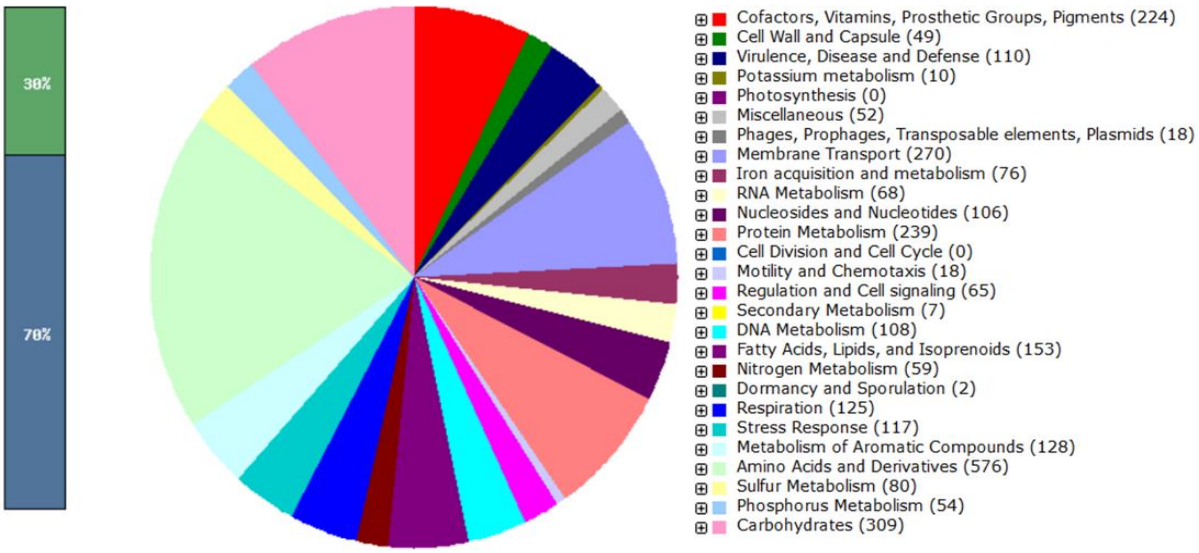

Figura 7 Categorização e distribuição dos subsistemas da linhagem *P. aeruginosa* PSA39

Os genes presentes na estirpe *P. aeruginosa* PSA39, que são responsáveis pela produção do ramnolípideos, também participam das vias metabólicas, glicosídicas e de ácidos graxos que compõem as funções presentes no isolado, (Figura 8, suplemento 1).

Os ramnolipídios são os biossurfactante mais intensamente investigados, com a biossíntese interligada com a formação de vários tipos de polissacarídeos. A biossíntese de raminolipidios por linhagens de *P. aeruginosa* é efetuada através de três reações enzimáticas importantes, originando-se o mono-ramnolipídios ou di-ramnolipídios (WITTGENS *et al*., 2017). Via de regra, microrganismos usufruem de substratos hidrofílicos na síntese da porção polar da molécula de biossurfactante, compostos por um ácido carboxílico, um álcool ou um aminoácido, ao mesmo tempo que os substratos hidrofóbicos são utilizados exclusivamente na porção hidrocarboneto, formada por um ácido graxo de cadeia longa, um hidroxiácido ou um ácido graxo na-alquil-â-hidroxi (WITTGENS *et al*., 2017).

Os estudos recentes indicaram que os óleos metabolizados através da β-oxidação podem causar aumento da produção de ramnolipídeos (PIAST *et al*., 2005; IBRAHIM, 2018; TIWARY; DUBEY, 2018). Ademais, foi sugerido a existência de potencial para uma conexão metabólica entre a β-oxidação e a biossíntese de ramnolipídeos (IBRAHIM, 2018). Analisando-se as vias de síntese biológica dos ramnolipídeos foi verificado um vínculo direto entre os números de carbono dos ácidos graxos β-hidroxi com a síntese dos biossurfactantes. Recentemente, as analises bioquímicas indicaram que o papel da β-oxidação na produção de ramnolipídios é constitutivo, e deve ter ocorrência não apenas quando ácidos graxos são fornecidos como fontes de carbono (DEEPIKA *et al*., 2016; GEETHA *et al*., 2018). Sugerindo, assim, que a β-oxidação é o principal fornecedor de precursores lipídicos para a biossíntese de ramnolipídeos alem da D-glucose proveniente da biosintese da raminose (DEEPIKA *et al*., 2016; GEETHA *et al*., 2018).

A ramnose é um açúcar encontrado em diferentes componentes e estruturas celulares de bactérias pertencentes ao gênero *Pseudomonas*, como por exemplo o lipopolissacarídeo da parede celular (LPS) (TAZDAÏT *et al*., 2018). O dTDP-L-ramnose é a porção hidrofílica dos ramnolipídios que é derivado diretamente da via Entner-Doudoroff e da gliconeogênese (LI *et al*., 2019). A geração de L-ramnose ativa dTDP-L-ramnose inicia-se através da conversão de D-glucose-6-fosfato em D-glucose-1-fosfato pela Algof de fosfoglucomutase (LI *et al*., 2019; SOMOZA *et al*., 2020) seguida do operon rmlBDAC (Figura 8).

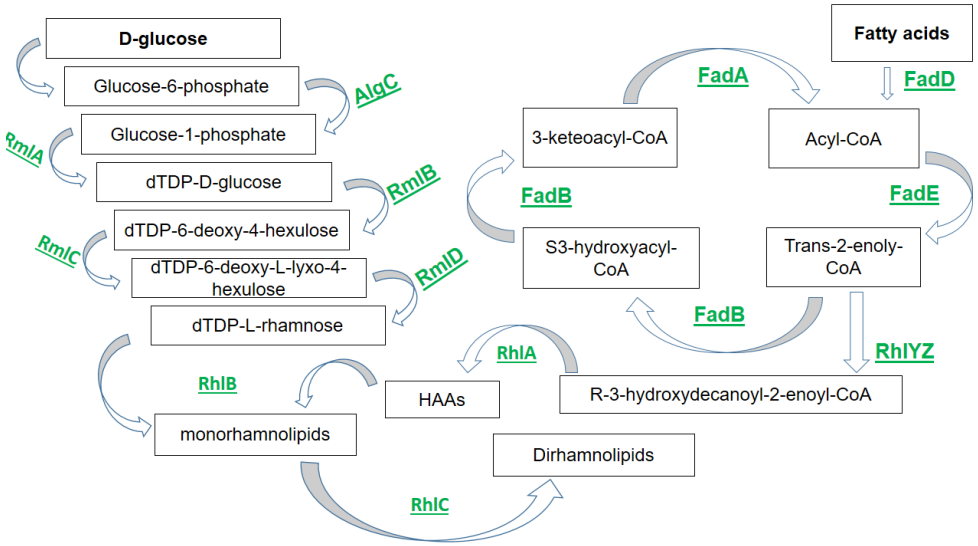

Figura 8 Via metabólica de rhamnolipidios presentes na estirpe P. aeruginosa PSA39

4.7 ANÁLISE COMPARATIVA TYGS, MAUVE, ANIB E ORTHOVENN

Na análise do *Type (Strain) Genome Server, TYGS* (Figura 9) foi observda uma alta semelhança entre especieis produtoras de BS, RLs na espécie *P. aeruginosa* devido à sua capacidade inerente de utilizar uma gama de substratos como fonte de carbono; particularmente isolados ambientais (MORRIS *et al*., 2019). Além disso, o estudo anterior também demonstrou claramente a alta semelhança entre a *P. aeruginosa* produtoras de BS e semelhança relativamente mediana entre o género.

Utilizamos o banco de dados TYGS para estimar a hibridação digital DNA-DNA (dDDH) (MEIER *et al*., 2019). Os resultados indicaram alta similaridade entre P. aeruginosa PSA39 e P. aeruginosa NCTC10332, DN1, PAO1e NBRC respectivamente com 98,25% 98,41%, 98,39% e 98,26%. As diferenças fenotípicas e genotípicas e as relações clonais são suportadas pela relação genômica (ANI e dDDH), sendo consideradas meios adaptativos para sobrevivência de cada estirpe de acordo com o meio a qual se encontra (MEIER *et al*., 2019; MORRIS *et al*., 2019). A análise filogenética da sequência do esboço do genoma de P. eruginosa PSA39 com outras cepas de Pseudomonas revelou um agrupamento da estirpe PSA39 com P. aeruginosa de referência (Figura 9). De acordo com esses resultados, a análise do genoma confirmou que PSA39, realmente pertence a P. aeruginosa com valores de ANI de 98,41 (Tabela 5 e apêndice 2).

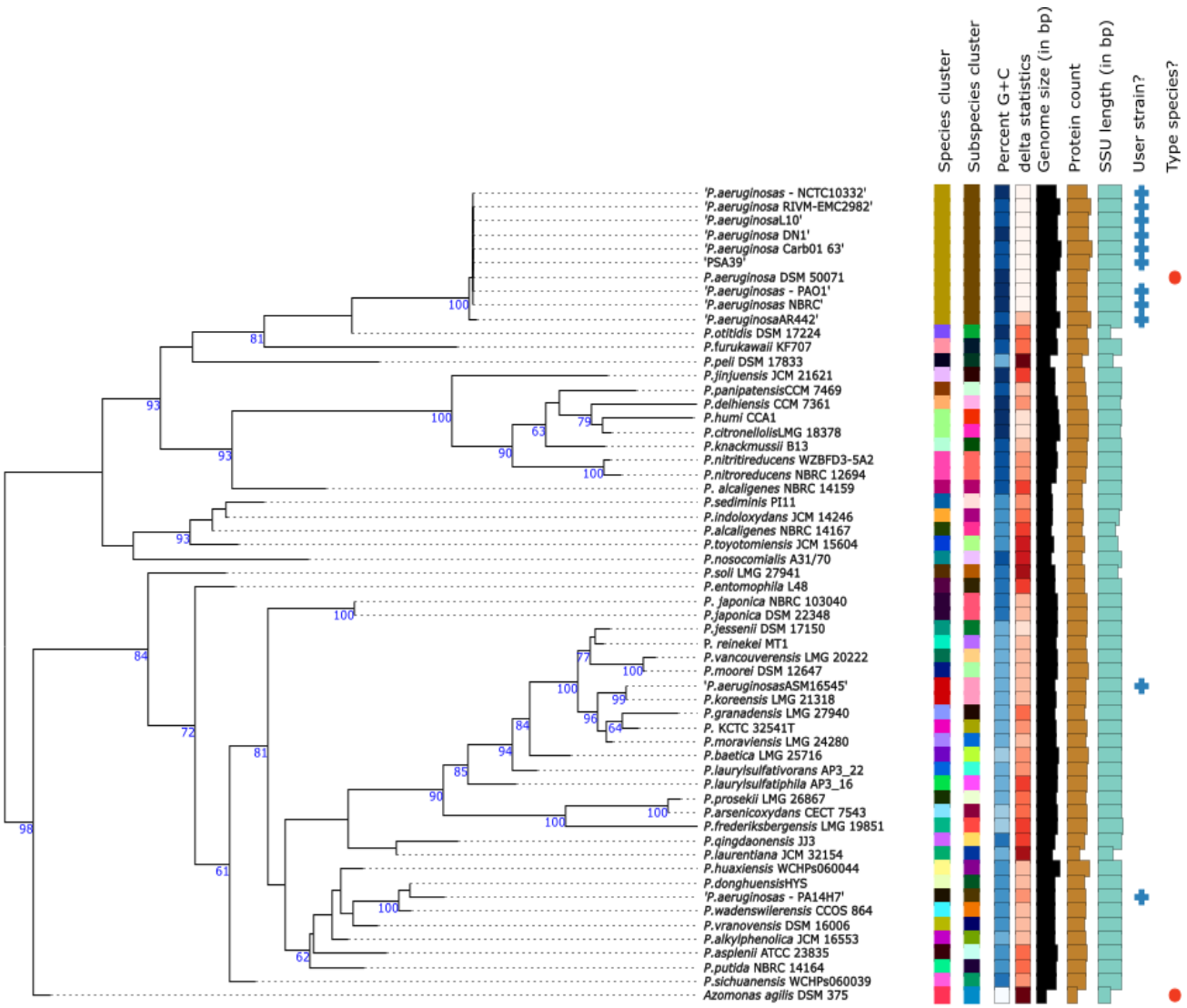

Figura 9 A árvore filogenómica de Pseudomonas aeruginosa PSA39 e estirpes tipo relacionadas do género Pseudomonas disponíveis na base de dados TYGS. A árvore inferida com FastME 2.1.6.1 a partir do método Genome BLAST Distance Phylogeny (GBDP) mostra as distâncias calculadas a partir das sequências do genoma. Os comprimentos das ramificações são dimensionados em termos da fórmula de distância GBDP d5. Os números acima das ramificações são valores de suporte de pseudo-bootstrap GBDP de 100 réplicas, com um suporte médio de ramificação de 95,5%.

Tabela 5 Os valores médios pareados de identidade de nucleotídeo (ANI) (%) entre as cepas de *Pseudomonas aeruginosa.*

Genoma	ANIb [%]	Alinhamento [%]	Alinhamento [bp]	Total [bp]
Pseudomonas aeruginosa DN1	98.41	85.35	6111571	7160969
Pseudomonas aeruginosa PAO1	98.39	83.19	5957088	7160969
Pseudomonas aeruginosa NBRC	98.26	83.11	5951579	7160969
Pseudomonas aeruginosa NCTC10332	98.25	83.12	5952289	7160969
Pseudomonas aeruginosa L10	98.15	85.41	6116118	7160969
Pseudomonas aeruginosa AR442	97.97	87.20	6244700	7160969
Pseudomonas aeruginosa Carb01	97.91	87.89	6293720	7160969
Pseudomonas aeruginosa RIVM-EMC2982	97.89	87.87	6292153	7160969
Pseudomonas aeruginosa PA14H7	75.77	40.68	2913425	7160969
Pseudomonas aeruginosa ASM16545	75.11	40.01	2865150	7160969

A análise comparativa genômica entre as linagens *P. aeruginosa* PSA39, *P. aeruginosa* NCTC10332, *P. aeruginosa* DMS50071 e *P. aeruginosa* PAO1, indicou que existem regiões reversas em todo o código genômico comparado ao genoma de interesse, apesar da alta similaridade observada, a movimentação entre regiões também é notada, havendo além de inversões e sobreposições dos blocos gênicos entre as estirpes (Figura 10).

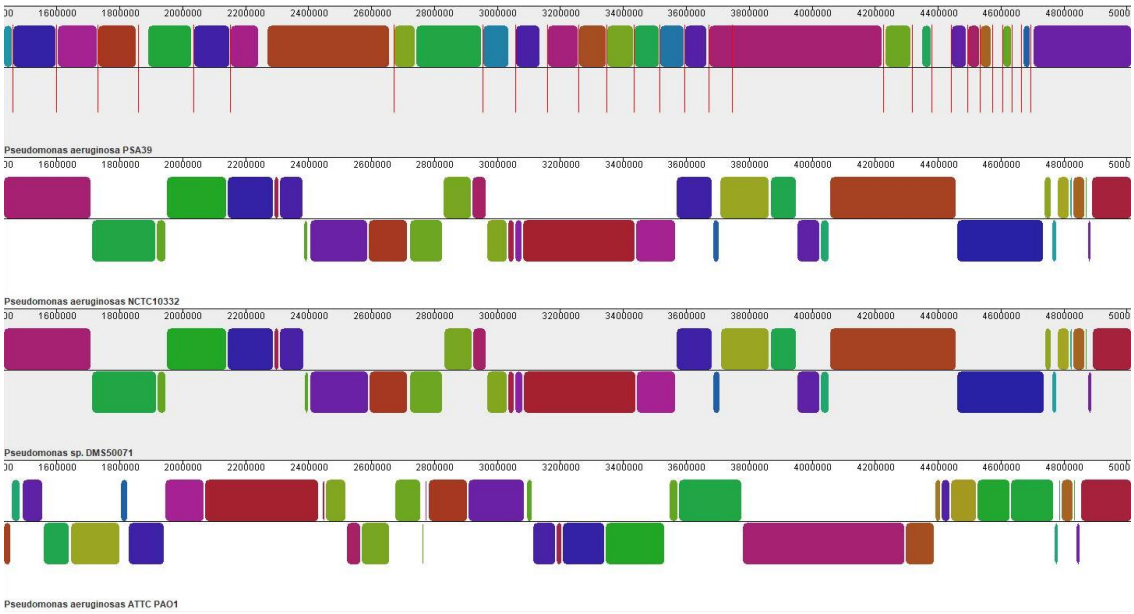

Figura 10. Alinhamento de genoma múltiplo gerado pelo software Mauve (http://asap.ahabs.wisc.edu/mauve/). Foram comparados os cromossomos do genoma dos estirpes de *P. aeruginosa* PSA39, PA01, DM550071 e NCTC10332. A similaridade do genoma é representada pela altura da

barra, que corresponde ao nível conservador médio nessa região da sequência. Uma região completamente branca indica um fragmento que não está alinhado ou contém um elemento de sequência específico do genoma específico. Caixas com cores idênticas representam blocos colineares locais (LCB), indicando regiões de DNA homólogas compartilhadas por dois ou mais cromossomos sem rearranjos de sequência.

A semelhança observada nas análises do genoma das linhagens de *P. aeruginosa* é atribuída a funções importantes, como genes de captação de ferro, vias metabólicas primárias e secundárias capazes de degradar o uso de hidrocarbonetos e aromáticos ou determinantes de antibióticos de resistência presentes nos isolados (GUDIÑA *et al.*, 2016; MORRIS *et al*., 2019).

Verificando as figuras obtidas pelo MAUVE foi observado a presença de sobreposições de blocos gênicos entre as estirpes de *P. aeruginosa*. Os arranjos identificados podem ser explicados pelas características evolutivas de cada micro-organismo, sendo que estes apresentam adaptações genéticas oriundas da pressão seletiva e das características de cada ambiente, ou características particulares de cada nicho em que estas linhagens de *Pseudomonas* se encontravam (SANTOS *et al*., 2020). Muitos fatores ambientais podem estar correlacionados com a evolução adaptativa microbiana, como por exemplo a existência de fatores de estress distintos, e fontes de carbono disponíveis para a geração de energia e geração de metabólitos primários e secundários, servindo como um sistema de defesa de menor consumo de energia do organismo (GUDIÑA *et al.*, 2016; MORRIS *et al*., 2019).

A pressão seletiva exercida por de metais pesados no ambiente pode ser um fator relacionado com a apresença micro-organimos adaptados a ambientes impactados. Ademains, as análises realizadas pelo RAST indicaram que *P. aeruginosa* PSA39 apresenta diversos mecanismos moleculares para adaptação a metais pesados, como a proteína, cobalto-zinco-cádmio (CzcC), que é associada ao sistema de efluxo de membrana denominado de *resistance-nodulation-division* (RND) (Suplemento 1). Proteínas classificadas como pertencentes ao sistema RND, são uma família de proteínas exportadoras de metais pesados que juntamente com muitos sistemas de efluxo desintoxicam o citoplasma, uma defesa bacteriana eficiente contra cátions de metais de transição.

Em adição, as análises moleculares *in sílico* indicaram a presença proteínas associadas a genes do operon de resistência a mercúrio, designadas como MerT, MerP e MerA (EL-SHESHTAWY *et al*., 2017). Estas proteínas estão diretamente relacionadas ao transporte de mercuúrio (íon Hg^{2+}) através da membrana citoplasmática bacteriana, já MerR é um regulador dos operons de resistência ao mercúrio em bactérias gram-negativas. MerR é um regulador que demonstrou ser um ativador dos genes *mer* na presença de sais de Hg (II) e um

repressor fraco na ausência de Hg (II) (ZHANG *et al.*,2019). O determinante de resistência à czc (cobalto-zinco-cádmio) geralmente está localizado em um plasmídeo, no entanto esta análise não foi realizada para *P. aeruginosa* PSA39. O genoma de *P. aeruginosa* PSA39, ainda apresenta o gene *chrA*, responsável por codificar o transportador Cr, este confere capacidade de bombear cromo do meio intracelular, sendo importante na tolerância a este metal (LEUNGTONGKAM *et al*., 2018).

Os genes *czc*, *chr*, *mer* são responsáveis pela resistência ao Zn, Cr, e Hg, respectivamente. A presença destes genes em *P. aeruginosa* PSA39 sugere uma capacidade adaptativa da linhagem a ambientes impactados por metais oriundos de despejos de esgotos industriais ou associados a atividades de mineração (AMER *et al*., 2015).

O espectro de aquisição de ferro como Fe (III), e outros componentes associados em *P. aeruginosa* PSA39 também foi avaliado considerando a análise de sub-sistemas pelo RAST. Nestas analise foram detectados 8 genes associados aos síderoforos enterobactina associados a proteína reguladora PfeR (do inglês, Two-component response regulator ou regulador de resposta de dois componentes), a proteína PfeS (do inglês, Two-component sensor histidine kinase, ou sensor de histidina quinase de dois componentes) (Suplemento 2). Além das proteínas FepC (do inglês, Ferric enterobactin transport ATP-binding protein), FepB (do inglês, Ferric enterobactin-binding periplasmic protein), FepD (do inglês, Ferric enterobactin transport system permease protein FepD) e FepG (do inglês, Ferric enterobactin transport system permease protein). Também, foram detectados no genoma de *P. aeruginosa* PSA39 genes associados a ao sideróforos pioquelina e pioverdina, que em conjunto são considerados os sideróforos mais abudantes produzidos por bactérias do gênero *Pseudomonas* (BRANDEL *et al*., 2012).

Os elementos genéticos para pioverdina foram os mais abundantes no genoma de *P. aeruginosa* PSA39, indicados pelo RAST constituindo cerca de 39 proteínas associadas. As pioverdinas produzidas por linhagens de *P. aeruginosa* compreende um cromóforo fluorescente de di-hidroxiquinolina unido a um peptídeo de comprimento e composição variáveis (GANNE *et al*., 2017). As poverdinas são interessantes do ponto de vista ecológico, pois podem estar relacionadas a adaptação bacteriana em solos, no que tange a captação de ferro e outros ions metálicos, e também por seu possível envolvimento no controle biológico de patógenos vegetais (DREHE *et al*., 2018; KRON *et al*., 2020).

Os clusters ortólogos nas linhagens *P. aeruginosa* PSA39, DMS_50071, PA01, CRS05_R5 e NCTC100332 foram analisados usando o software OrthoVenn 2. A análise das

cepas indicou que elas formam 5979 aglomerados ortólogos, que incluem 3316 ortólogos do genoma do núcleo (Figura 11 e 12). *P. aeruginosa* PSA39 apresentou cento e quinze grupos únicos (exclusivos) com proteínas de funções definidas, associadas a conjugação, a processos celulares e metabólicos de hidrocarbonetos como alcools e aromáticos (Tabela 5). Os genes contendo seqüências das quatro linhagens de *Pseudomonas*, das quais 3316 (55,46%), 2009 (33,60%), 211 (3,52%), 252 (6,33%) e 191 (1,09%) foram compartilhadas por cinco, quatro, três, duas e uma dessas espécies, respectivamente.

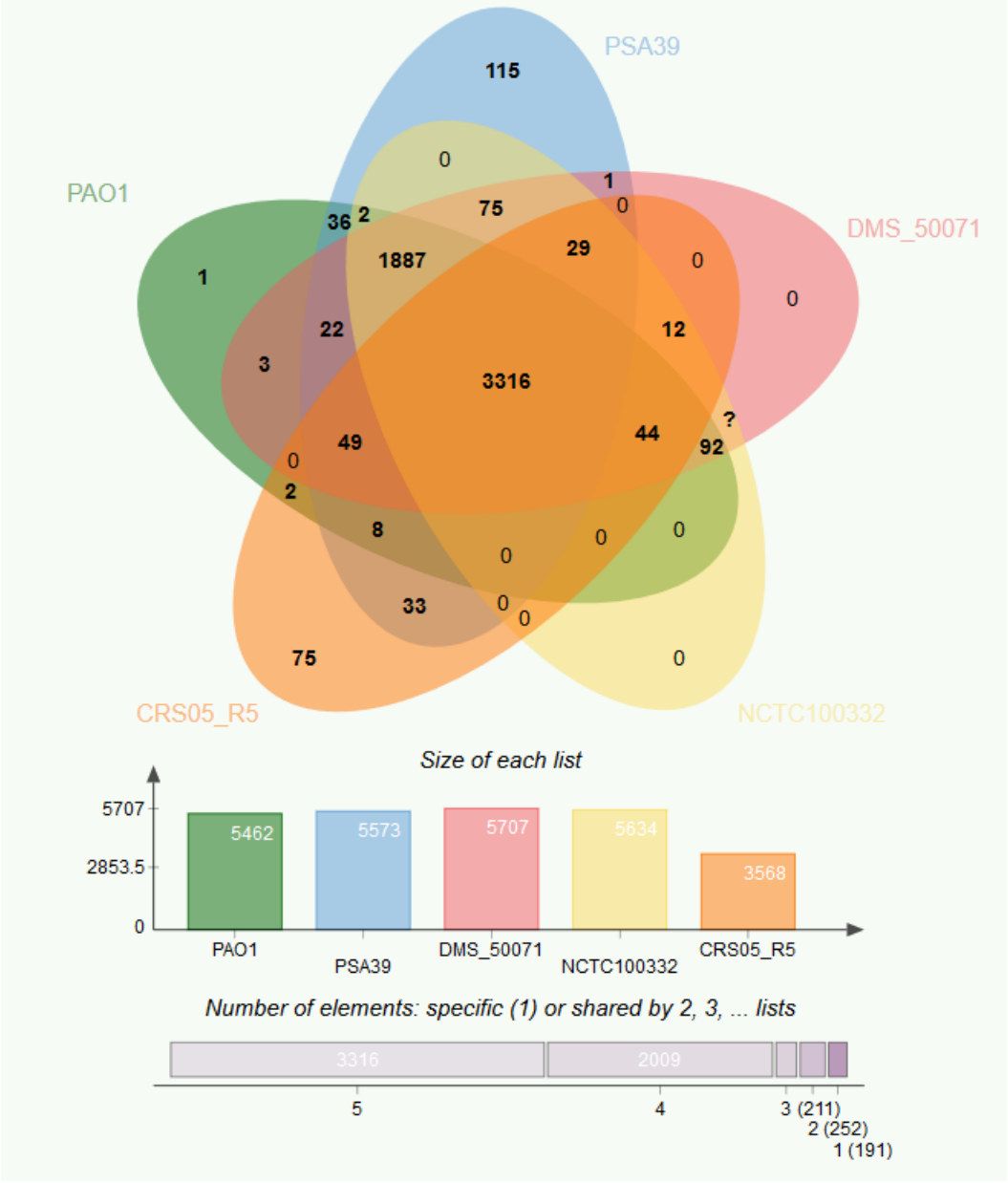

Figura 10. Diagrama de Venn representando os agrupamentos de proteínas ortólogas compartilhados entre os isolados de *P. aeruginosa* PSA39, PA01, DM550071, NCTC10332 e CRS05_R5.

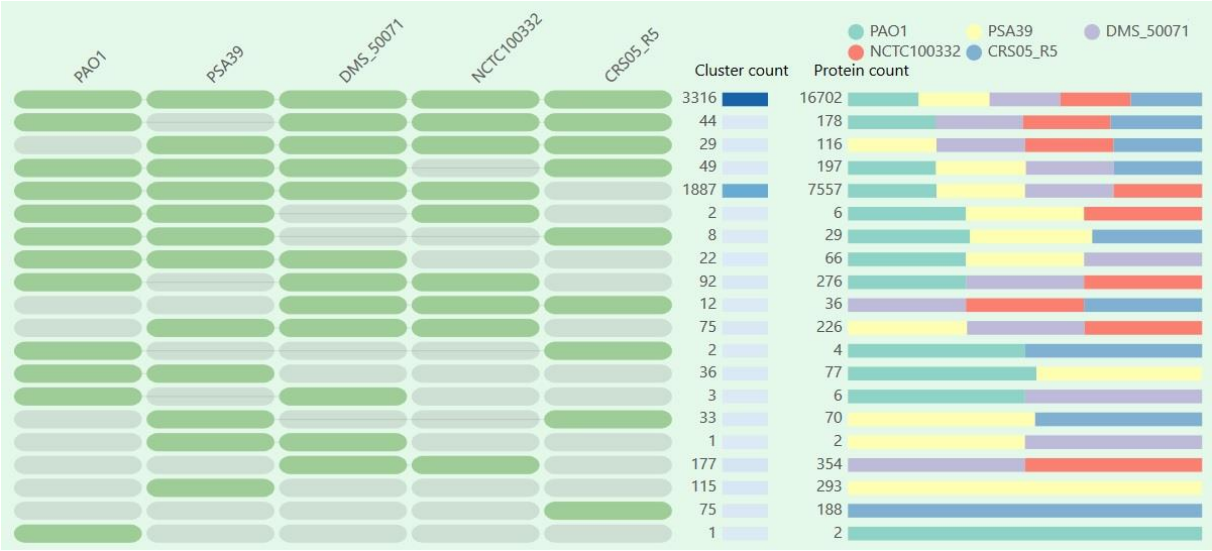

Figura 12 Overlaps presentes na analise orthoVenns dos isolados de *P. aeruginosa* PSA39, ATTC PA01, DM550071, NCTC10332 e CRS05_R5.

Tabela 6- Processos biológicos exclusivos detectados em *P. aeruginosa* PSA39 utilizando o OrthoVenn 2

Slimmed_GO	Name	Count of Unique input accessions
GO:0000746	conjugation	7
GO:0006066	alcohol metabolic process	1
GO:0006139	nucleobase-containing compound metabolic process	5
GO:0006259	DNA metabolic process	5
GO:0006304	DNA modification	2
GO:0006725	cellular aromatic compound metabolic process	6
GO:0006807	nitrogen compound metabolic process	6
GO:0006810	transport	1
GO:0008150	biological_process	17
GO:0008152	metabolic process	9
GO:0009292	genetic transfer	1
GO:0009987	cellular process	5
GO:0015031	protein transport	1
GO:0016032	viral process	1
GO:0017144	drug metabolic process	2
GO:0019748	secondary metabolic process	1
GO:0032196	transposition	6
GO:0032502	developmental process	2
GO:0042180	cellular ketone metabolic process	1
GO:0043170	macromolecule metabolic process	5
GO:0044237	cellular metabolic process	9
GO:0044238	primary metabolic process	5
GO:0044419	interspecies interaction between organisms	1
GO:0046483	heterocycle metabolic process	7
GO:0046903	secretion	1
GO:0050896	response to stimulus	7
GO:0051179	localization	1
GO:0051186	cofactor metabolic process	1
GO:0051234	establishment of localization	1
GO:0051704	multi-organism process	1
GO:0065007	biological regulation	1

5.CONCLUSÃO

O trabalho demonstra a presença de bactérias em sedimentos de mangue capazes de produzir compostos tensoativos. Os resultados reforçam a capacidade que microrganismos presentes nos ecossistemas de manguezais do Rio Anil na cidade de São Luís podem apresentar variabilidade nas propriedades dos SACs. Tal representatividade desta característica se deve à presença de uma diversidade de micro e macronutrientes presentes em ambientes de mangue, e a biodiversidade microbiana presente, facilitando a troca de material genético, para melhor desenvolvimento e crescimento de isolados, seleção natural. Tais dados demonstram a capacidade de áreas afetadas ou degradadas antropogenicamente como promissoras para encontrar microrganismos capazes de apresentar potencial biotecnológico. Produzir biomoléculas com atributos capazes de substituir moléculas sintéticas, com maior estabilidade, funcionalidade e biodegradabilidade.

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APÊNDICE 1

Tabela de Genes da estirpe PSA39- aquisição e metabolismo de ferro, Degradação de compostos aromáticos, Hidrocarbonetos e virulência, patogenicidade e sistema de defesa.

Gene ou sistema	Função predita	Subsistemas	pb	aa
	Iron acquisition and metabolism - Siderophores			
*PchA	Isochorismate synthase (EC 5.4.4.2) [pyochelin] siderophore Isochorismate synthase (EC 5.4.4.2) of siderophore biosynthesis	Siderophore pyochelin	1431	477
*PchC	Pyochelin biosynthetic protein PchC, predicted thioesterase Thioesterase in siderophore biosynthesis gene cluster	Siderophore pyochelin	756	252
*PchD	2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58) [pyochelin] siderophore 2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58) of siderophore biosynthesis	Siderophore pyochelin	1002	334
*PchD	2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58) [pyochelin] siderophore 2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58) of siderophore biosynthesis	Siderophore pyochelin	522	174
PchG	Pyochelin biosynthetic protein PchG, oxidoreductase (NAD-binding) Thiazolinyl imide reductase in siderophore biosynthesis gene cluster	Siderophore pyochelin	1050	350

PchE	Dihydroaeruginoate synthetase PchE, non-ribosomal peptide synthetase modules Siderophore biosynthesis non-ribosomal peptide synthetase modules	Siderophore pyochelin	4317	1439
*PchF	Pyochelin synthetase PchF, non-ribosomal peptide synthetase module Siderophore biosynthesis non-ribosomal peptide synthetase modules	Siderophore pyochelin	5436	1812
*FptA	Outer membrane receptor for ferric-pyochelin FptA Outer membrane receptor for ferric siderophore	Siderophore pyochelin	2163	721
FptB	Hypothetical protein FtpB in pyochelin gene cluster Hypothetical protein FtpB in siderophore gene cluster	Siderophore pyochelin	282	94
FptC	Putative iron-regulated membrane protein FtpC in pyochelin gene cluster Putative iron-regulated membrane protein in siderophore cluster	Siderophore pyochelin	1506	502
FptX	Inner-membrane permease FptX, ferripyochelin Inner-membrane permease for ferric siderophore	Siderophore pyochelin	1245	415
ABCeff	ABC efflux pump, fused inner membrane and ATPase subunits in pyochelin gene cluster Putative ABC iron siderophore transporter, fused permease and ATPase domains	Siderophore pyochelin	1725	575
ABCeff	ABC efflux pump, fused inner membrane and ATPase subunits in pyochelin gene cluster	Siderophore pyochelin	1713	571

	Putative ABC iron siderophore transporter, fused permease and ATPase domains			
PchR	Transcriptional regulator PchR	Siderophore pyochelin	891	297
iutA	Aerobactin siderophore receptor IutA Rhizobactin 1021 siderophore outer membrane receptor Schizokinen siderophore outer membrane receptor	Siderophore Aerobactin	2229	743
Iron acquisition and metabolism - no subcategory				
pitA	Ferric iron ABC transporter, iron-binding protein	Iron acquisition in Streptococcus	999	333
pitD	Ferric iron ABC transporter, ATP-binding protein	Iron acquisition in Streptococcus	1083	361
pitC	Ferric iron ABC transporter, permease protein	Iron acquisition in Streptococcus	1620	540
*Heme_oxygenases	Heme oxygenase HemO, associated with heme uptake	Heme, hemin uptake and utilization systems in GramPositives	510	170
*Heme_oxygenases	Heme oxygenase HemO, associated with heme uptake	Heme, hemin uptake and utilization systems in GramPositives	603	201
*Heme_oxygenases	Heme oxygenase HemO, associated with heme uptake	Heme, hemin uptake and utilization systems in GramPositives	399	133
*Heme_oxygenases	Hemin transport protein HmuS	Heme, hemin uptake and utilization systems in GramPositives	1065	355
*HmuTUV	Heme ABC transporter, cell surface heme and hemoprotein receptor HmuT	Heme, hemin uptake and utilization systems in GramPositives	894	298
*HmuTUV	Heme ABC transporter, permease protein HmuU	Heme, hemin uptake and utilization systems in GramPositives	984	328
*HmuTUV	Heme ABC transporter, ATPase component HmuV	Heme, hemin uptake and utilization systems in GramPositives	768	256

R4	Outer membrane (iron.B12.siderophore.hemin) receptor	ABC transporter [iron.B12.siderophore.hemin]	2163	721
*Rec	Outer membrane receptor proteins, mostly Fe transport	Hemin transport system	2109	703
hmuS	Hemin transport protein HmuS	Hemin transport system	1065	355
HO	Heme oxygenase HemO, associated with heme uptake	Hemin transport system	510	170
HO	Heme oxygenase HemO, associated with heme uptake	Hemin transport system	603	201
HO	Heme oxygenase HemO, associated with heme uptake	Hemin transport system	399	133
DyP	Predicted dye-decolorizing peroxidase (DyP), encapsulated subgroup	Encapsulating protein for DyP-type peroxidase and ferritin-like protein oligomers	945	315
YfeX	Predicted dye-decolorizing peroxidase (DyP), YfeX-like subgroup	Encapsulating protein for DyP-type peroxidase and ferritin-like protein oligomers	882	294
*Iron_Reg	Ferric uptake regulation protein FUR	Transport of Iron	405	135
*Feo	Ferrous iron-sensisng transcriptional regulator FeoC	Transport of Iron	243	81
*Feo	Ferrous iron transport protein B	Transport of Iron	2301	767
*Feo	Ferrous iron transport protein A	Transport of Iron	228	76
IrpA	Iron-regulated protein A precursor	Transport of Iron	1341	447
IrpA	Iron-regulated protein A precursor	Transport of Iron	1065	355
*Fbp	Ferric iron ABC transporter, ATP-binding protein	Transport of Iron	1083	361
*Fbp	Ferric iron ABC transporter, permease protein	Transport of Iron	1620	540
*Fbp	Ferric iron ABC transporter, iron-binding protein	Transport of Iron	999	333
*Piu	Uncharacterized iron-regulated membrane protein Iron-uptake factor PiuB	Transport of Iron	1416	472

*Piu	Uncharacterized iron-regulated membrane protein Iron-uptake factor PiuB	Transport of Iron	2553	851
OMR1	Ferrichrome-iron receptor Iron siderophore receptor protein	Transport of Iron	2442	814
OMR2	Ferrichrome-iron receptor	Transport of Iron	2301	767
OMR3	Ferrichrome-iron receptor	Transport of Iron	2127	709
OMR4	Ferrichrome-iron receptor	Transport of Iron	2415	805
OMR5	Ferrichrome-iron receptor Iron siderophore receptor protein	Transport of Iron	2388	796
OMR6	Ferrichrome-iron receptor Iron siderophore receptor protein	Transport of Iron	2463	81
OMR7	Ferrichrome-iron receptor	Transport of Iron	2199	733
Gene ou sistema	Função predita	Subsistemas	pb	aa
Metabolism of Aromatic Compounds - Peripheral pathways for catabolism of aromatic compounds				
*QuiB	3-dehydroquinate dehydratase II (EC 4.2.1.10)	Quinate degradation	444	148
*QuiB	3-dehydroquinate dehydratase II (EC 4.2.1.10)	Quinate degradation	447	149
FadA	3-ketoacyl-CoA thiolase (EC 2.3.1.16)	n-Phenylalkanoic acid degradation	1176	392
FadA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	n-Phenylalkanoic acid degradation	1185	395
FadA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	n-Phenylalkanoic acid degradation	1185	395
FadA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	n-Phenylalkanoic acid degradation	1176	392
FadA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	n-Phenylalkanoic acid degradation	1188	396

FadA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	n-Phenylalkanoic acid degradation	1206	402
FadA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	n-Phenylalkanoic acid degradation	1191	397
FadA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9), FadA2	n-Phenylalkanoic acid degradation	1278	426
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17)	n-Phenylalkanoic acid degradation	762	254
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17)	n-Phenylalkanoic acid degradation	969	323
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	n-Phenylalkanoic acid degradation	2148	716
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	n-Phenylalkanoic acid degradation	2148	716
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	n-Phenylalkanoic acid degradation	2148	716

*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	n-Phenylalkanoic acid degradation	2148	716
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) Enoyl-CoA hydratase EchA5 (EC 4.2.1.17)	n-Phenylalkanoic acid degradation	771	257
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17)	n-Phenylalkanoic acid degradation	789	263
*FadB	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	n-Phenylalkanoic acid degradation	1530	510
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	n-Phenylalkanoic acid degradation	792	264
*FadB	17hydroxysteroid dehydrogenase type 10 (HSD10)-like	n-Phenylalkanoic acid degradation	768	256
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17)	n-Phenylalkanoic acid degradation	774	258
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	n-Phenylalkanoic acid degradation	1236	412
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	n-Phenylalkanoic acid degradation	1236	412

*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	n-Phenylalkanoic acid degradation	1236	412
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	n-Phenylalkanoic acid degradation	1236	412
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	n-Phenylalkanoic acid degradation	2145	715
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	n-Phenylalkanoic acid degradation	2145	715
*FadB	Enoyl-CoA hydratase (EC 4.2.1.17) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	n-Phenylalkanoic acid degradation	2145	715
*FadB	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 17hydroxysteroid dehydrogenase type 10 (HSD10)-like	n-Phenylalkanoic acid degradation	768	256
FadD	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	n-Phenylalkanoic acid degradation	1689	563
FadD	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	n-Phenylalkanoic acid degradation	1689	563
FadD	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	n-Phenylalkanoic acid degradation	1899	633

FadD	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	n-Phenylalkanoic acid degradation	1566	522
FadD	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	n-Phenylalkanoic acid degradation	1668	556
phaJ1	enoyl-CoA hydratase, R-specific	n-Phenylalkanoic acid degradation	471	157
BenB	Benzoate 1,2-dioxygenase beta subunit (EC 1.14.12.10)	Benzoate degradation	489	163
BenA	Benzoate 1,2-dioxygenase alpha subunit (EC 1.14.12.10)	Benzoate degradation	1395	465
BenA	Benzoate 1,2-dioxygenase alpha subunit (EC 1.14.12.10)	Benzoate degradation	1368	456
BenC	Benzoate 1,2-dioxygenase, ferredoxin reductase component	Benzoate degradation	1014	338
BenD	1,2-dihydroxycyclohexa-3,5-diene-1-carboxylate dehydrogenase (EC 1.3.1.25)	Benzoate degradation	762	254
BenK	benzoate MFS transporter BenK	Benzoate degradation	1254	418
BenE2	Benzoate transport protein	Benzoate degradation	1197	399
*RP	benABC operon transcriptional activator BenR	Benzoate degradation	1002	334
*RP	benABC operon transcriptional activator BenR	Benzoate degradation	957	319
BFD	Benzoylformate decarboxylase (EC 4.1.1.7)	Benzoate degradation	1587	529
pobA	P-hydroxybenzoate hydroxylase (EC 1.14.13.2)	p-Hydroxybenzoate degradation	1185	395
HT	4-hydroxybenzoate transporter	p-Hydroxybenzoate degradation	1347	449
HT	4-hydroxybenzoate transporter	p-Hydroxybenzoate degradation	1347	449
Metabolism of Aromatic Compounds - Metabolism of central aromatic intermediates				
*CatA	Catechol 1,2-dioxygenase (EC 1.13.11.1)	Catechol branch of beta-ketoadipate pathway	933	311

CatB	Muconate cycloisomerase (EC 5.5.1.1)	Catechol branch of beta-ketoadipate pathway	1122	374
*CatC	Muconolactone isomerase (EC 5.3.3.4)	Catechol branch of beta-ketoadipate pathway	291	97
*CatD	Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24)	Catechol branch of beta-ketoadipate pathway	798	266
*CatD	Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24)	Catechol branch of beta-ketoadipate pathway	792	264
*CoTa	Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5)	Catechol branch of beta-ketoadipate pathway	699	33
*CoTa	3-oxoadipate CoA-transferase subunit A (EC 2.8.3.6)	Catechol branch of beta-ketoadipate pathway	852	284
*CoTb	Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5)	Catechol branch of beta-ketoadipate pathway	657	219
*CoTb	3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6)	Catechol branch of beta-ketoadipate pathway	783	261
*SH	Gentisate 1,2-dioxygenase (EC 1.13.11.4)	Salicylate and gentisate catabolism	1062	354
*TP	4-hydroxybenzoate transporter	Salicylate and gentisate catabolism	1347	449
*TP	4-hydroxybenzoate transporter	Salicylate and gentisate catabolism	1347	449
*MI	Maleylacetoacetate isomerase (EC 5.2.1.2) Glutathione S-transferase, zeta (EC 2.5.1.18)	Salicylate and gentisate catabolism	639	213
*MI	Maleylacetoacetate isomerase (EC 5.2.1.2) Glutathione S-transferase, zeta (EC 2.5.1.18)	Salicylate and gentisate catabolism	645	215
*FAA	Fumarylacetoacetase (EC 3.7.1.2)	Salicylate and gentisate catabolism	1299	433
*FAA	Fumarylacetoacetase (EC 3.7.1.2)	Salicylate and gentisate catabolism	699	233

pcaQ	Pca regulon regulatory protein PcaR	Protocatechuate branch of beta-ketoadipate pathway	840	280
pcaQ	Pca regulon regulatory protein PcaR	Protocatechuate branch of beta-ketoadipate pathway	780	260
pcaH	Protocatechuate 3,4-dioxygenase beta chain (EC 1.13.11.3)	Protocatechuate branch of beta-ketoadipate pathway	720	240
pcaG	Protocatechuate 3,4-dioxygenase alpha chain (EC 1.13.11.3)	Protocatechuate branch of beta-ketoadipate pathway	606	202
pcaB	3-carboxy-cis,cis-muconate cycloisomerase (EC 5.5.1.2)	Protocatechuate branch of beta-ketoadipate pathway	1380	460
*pcaC	4-carboxymuconolactone decarboxylase (EC 4.1.1.44)	Protocatechuate branch of beta-ketoadipate pathway	387	129
*pcaC	4-carboxymuconolactone decarboxylase (EC 4.1.1.44)	Protocatechuate branch of beta-ketoadipate pathway	402	134
*pcaD	Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24)	Protocatechuate branch of beta-ketoadipate pathway	798	266
*pcaD	Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24)	Protocatechuate branch of beta-ketoadipate pathway	792	264
pcaI	3-oxoadipate CoA-transferase subunit A (EC 2.8.3.6)	Protocatechuate branch of beta-ketoadipate pathway	852	284
pcaJ	3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6)	Protocatechuate branch of beta-ketoadipate pathway	783	261
pcaI2	Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5)	Protocatechuate branch of beta-ketoadipate pathway	699	233

pcaJ2	Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5)	Protocatechuate branch of beta-ketoadipate pathway	657	219
PcaT	dicarboxylic acid transporter PcaT	Protocatechuate branch of beta-ketoadipate pathway	1299	433
HpaX	4-hydroxyphenylacetate symporter, major facilitator superfamily (MFS)	4-Hydroxyphenylacetic acid catabolic pathway	1305	435
HpaA	Transcriptional activator of 4-hydroxyphenylacetate 3-monooxygenase operon, XylS/AraC family	4-Hydroxyphenylacetic acid catabolic pathway	912	304
HpaC	4-hydroxyphenylacetate 3-monooxygenase, reductase component (EC 1.6.8.-)	4-Hydroxyphenylacetic acid catabolic pathway	513	171
HpaH	2-oxo-hepta-3-ene-1,7-dioic acid hydratase (EC 4.2.-.-)	4-Hydroxyphenylacetic acid catabolic pathway	804	268
HpaF	5-carboxymethyl-2-hydroxymuconate delta-isomerase (EC 5.3.3.10)	4-Hydroxyphenylacetic acid catabolic pathway	393	131
HpaD	3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15)	4-Hydroxyphenylacetic acid catabolic pathway	924	308
HpaE	5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (EC 1.2.1.60)	4-Hydroxyphenylacetic acid catabolic pathway	1461	487
*HpaG	5-carboxymethyl-2-oxo-hex-3- ene-1,7-dioate decarboxylase (EC 4.1.1.68)	4-Hydroxyphenylacetic acid catabolic pathway	660	220
*HpaG	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (EC 5.3.3.-)	4-Hydroxyphenylacetic acid catabolic pathway	780	260
HpaR	Homoprotocatechuate degradative operon repressor	4-Hydroxyphenylacetic acid catabolic pathway	423	141

IQOb	Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16)	N-heterocyclic aromatic compound degradation	2316	772
IQOb	Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16)	N-heterocyclic aromatic compound degradation	2247	749
IQOb	Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16)	N-heterocyclic aromatic compound degradation	1302	434
IQOb	Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16)	N-heterocyclic aromatic compound degradation	2196	732
IQOa	Isoquinoline 1-oxidoreductase alpha subunit (EC 1.3.99.16)	N-heterocyclic aromatic compound degradation	471	157
IQOa	Isoquinoline 1-oxidoreductase alpha subunit (EC 1.3.99.16)	N-heterocyclic aromatic compound degradation	492	164
IQOa	Isoquinoline 1-oxidoreductase alpha subunit (EC 1.3.99.16)	N-heterocyclic aromatic compound degradation	462	154
*RingCl	3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15)	Central meta-cleavage pathway of aromatic compound degradation	924	308
*HMSD	5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (EC 1.2.1.60)	Central meta-cleavage pathway of aromatic compound degradation	1461	487
*4-OT	5-carboxymethyl-2-hydroxymuconate delta-isomerase (EC 5.3.3.10)	Central meta-cleavage pathway of aromatic compound degradation	393	131
OHA	2-oxo-hepta-3-ene-1,7-dioic acid hydratase (EC 4.2.-.-)	Central meta-cleavage pathway of aromatic compound degradation	804	268
PPH_55	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	Central meta-cleavage pathway of aromatic compound degradation	927	309

PPH_55	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases CDP-6-deoxy-delta-3,4-glucoseen reductase-like	Central meta-cleavage pathway of aromatic compound degradation	969	323
HD	Homogentisate 1,2-dioxygenase (EC 1.13.11.5)	Homogentisate pathway of aromatic compound degradation	1299	433
HPPD	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)	Homogentisate pathway of aromatic compound degradation	1074	358
HPPD	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)	Homogentisate pathway of aromatic compound degradation	1905	635
*MAI	Maleylacetoacetate isomerase (EC 5.2.1.2) Glutathione S-transferase, zeta (EC 2.5.1.18)	Homogentisate pathway of aromatic compound degradation	639	213
*MAI	Maleylacetoacetate isomerase (EC 5.2.1.2) Glutathione S-transferase, zeta (EC 2.5.1.18)	Homogentisate pathway of aromatic compound degradation	645	215
FAA	Fumarylacetoacetase (EC 3.7.1.2)	Homogentisate pathway of aromatic compound degradation	1299	433
FAA	Fumarylacetoacetase (EC 3.7.1.2)	Homogentisate pathway of aromatic compound degradation	699	233
*AAA	Biosynthetic Aromatic amino acid aminotransferase alpha (EC 2.6.1.57) Aromatic-amino-acid aminotransferase (EC 2.6.1.57)	Homogentisate pathway of aromatic compound degradation	1197	399
*AAA	Aspartate aminotransferase (EC 2.6.1.1) Aromatic-amino-acid aminotransferase (EC 2.6.1.57)	Homogentisate pathway of aromatic compound degradation	1200	400
HmgR	Transcriptional regulator, IclR family	Homogentisate pathway of aromatic compound degradation	801	267

HmgR	Transcriptional regulator, IclR family	Homogentisate pathway of aromatic compound degradation	315	105
HmgR	Transcriptional regulator, IclR family	Homogentisate pathway of aromatic compound degradation	834	278
HmgR	Transcriptional regulator, IclR family	Homogentisate pathway of aromatic compound degradation	729	243
HmgR	Transcriptional regulator, IclR family	Homogentisate pathway of aromatic compound degradation	867	289
HmgR	Transcriptional regulator, IclR family	Homogentisate pathway of aromatic compound degradation	819	273
HmgR	Transcriptional regulator, IclR family	Homogentisate pathway of aromatic compound degradation	771	257
HmgR	Transcriptional regulator, IclR family	Homogentisate pathway of aromatic compound degradation	804	268
Metabolism of Aromatic Compounds - no subcategory				
HPADO	3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15)	Aromatic Amin Catabolism	924	308
feaB	Phenylacetaldehyde dehydrogenase (EC 1.2.1.39)	Aromatic Amin Catabolism	1488	496
*HPAHb	4-hydroxyphenylacetate 3-monooxygenase, reductase component (EC 1.6.8.-)	Aromatic Amin Catabolism	513	171
GD	Gentisate 1,2-dioxygenase (EC 1.13.11.4)	Gentisate degradation	1062	354
MI	Maleylacetoacetate isomerase (EC 5.2.1.2) Glutathione S-transferase, zeta (EC 2.5.1.18)	Gentisate degradation	639	213
MI	Maleylacetoacetate isomerase (EC 5.2.1.2) Glutathione S-transferase, zeta (EC 2.5.1.18)	Gentisate degradation	645	215

HT	4-hydroxybenzoate transporter	Gentisate degradation	1347	449
HT	4-hydroxybenzoate transporter	Gentisate degradation	1347	449
PHBT	putative 4-hydroxybenzoyl-CoA thioesterase	Gentisate degradation	444	148
Gene ou sistema	Função predita	Subsistemas	pb	aa
Carbohydrates - Central carbohydrate metabolism				
		Peripheral Glucose Catabolism Pathways		
		Peripheral Glucose Catabolism Pathways		
		Peripheral Glucose Catabolism Pathways		
		Peripheral Glucose Catabolism Pathways		
		Peripheral Glucose Catabolism Pathways		
		Peripheral Glucose Catabolism Pathways		
		Peripheral Glucose Catabolism Pathways		
		Peripheral Glucose Catabolism Pathways		
GloA	Lactoylglutathione lyase (EC 4.4.1.5)	Methylglyoxal Metabolism	387	129
GloA	Lactoylglutathione lyase (EC 4.4.1.5)	Methylglyoxal Metabolism	396	132
GloA	Lactoylglutathione lyase (EC 4.4.1.5)	Methylglyoxal Metabolism	531	177
GloA	Lactoylglutathione lyase (EC 4.4.1.5)	Methylglyoxal Metabolism	471	157
GloA	Lactoylglutathione lyase (EC 4.4.1.5)	Methylglyoxal Metabolism	447	149
GloB	Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	Methylglyoxal Metabolism	777	259

AldB	Aldehyde dehydrogenase B (EC 1.2.1.22)	Methylglyoxal Metabolism	1494	498
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1494	498
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1494	498
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3) Probable coniferyl aldehyde dehydrogenase (EC 1.2.1.68)	Methylglyoxal Metabolism	1431	477
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3) Probable coniferyl aldehyde dehydrogenase (EC 1.2.1.68)	Methylglyoxal Metabolism	1431	477
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1479	493
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1479	493
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1491	497
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1491	497
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1491	497
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1491	497
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1035	345
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1035	345
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1443	481
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1443	481
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	969	323
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	969	323
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	741	247
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	741	247
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1491	497
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1491	497

ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1443	481
ALDH2a	Aldehyde dehydrogenase (EC 1.2.1.3)	Methylglyoxal Metabolism	1491	497
*PyrDH	Pyruvate dehydrogenase E1 component (EC 1.2.4.1)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	2649	883
*PyrDH	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1644	548
PAT	BioD-like N-terminal domain Phosphate acetyltransferase (EC 2.3.1.8)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	2115	705
ACK	Acetate kinase (EC 2.7.2.1)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1185	395
APH	Acylphosphate phosphohydrolase (EC 3.6.1.7), putative	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	276	92
ActP	Acetate permease ActP (cation/acetate symporter)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1656	552
ActP	Acetate permease ActP (cation/acetate symporter)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1650	550
*ACS-ADP	Acetyl-CoA synthetase (ADP-forming) alpha and beta chains, putative	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	2148	716
*ACS-ADP	Acetyl-CoA synthetase (ADP-forming) alpha and beta chains, putative	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	561	187
*ACS_Sir2_regulation	NAD-dependent protein deacetylase of SIR2 family	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	753	251
*ACS_Sir2_regulation	NAD-dependent protein deacetylase of SIR2 family	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	771	257

ADH	Aldehyde dehydrogenase (EC 1.2.1.3)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1494	498
ADH	Aldehyde dehydrogenase (EC 1.2.1.3) Probable coniferyl aldehyde dehydrogenase (EC 1.2.1.68)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1431	477
ADH	Aldehyde dehydrogenase (EC 1.2.1.3)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1479	493
ADH	Aldehyde dehydrogenase (EC 1.2.1.3)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1491	497
ADH	Aldehyde dehydrogenase (EC 1.2.1.3)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1491	497
ADH	Aldehyde dehydrogenase (EC 1.2.1.3)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1035	345
ADH	Aldehyde dehydrogenase (EC 1.2.1.3)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1035	345
ADH	Aldehyde dehydrogenase (EC 1.2.1.3)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1443	481
ADH	Aldehyde dehydrogenase (EC 1.2.1.3)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1479	493
ADH	Aldehyde dehydrogenase (EC 1.2.1.3)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	969	323
ADH	Aldehyde dehydrogenase (EC 1.2.1.3)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	741	247
ADH	Aldehyde dehydrogenase (EC 1.2.1.3)	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	1491	497

*AlaR	Alanine racemase (EC 5.1.1.1)	Pyruvate Alanine Serine Interconversions	1077	359
*AlaR	Alanine racemase (EC 5.1.1.1)	Pyruvate Alanine Serine Interconversions	1074	358
*SerDL	L-serine dehydratase, beta subunit (EC 4.3.1.17) L-serine dehydratase, alpha subunit (EC 4.3.1.17)	Pyruvate Alanine Serine Interconversions	1377	459
*SerDL	L-serine dehydratase, beta subunit (EC 4.3.1.17) L-serine dehydratase, alpha subunit (EC 4.3.1.17)	Pyruvate Alanine Serine Interconversions	1377	459
*SerDL	L-serine dehydratase, beta subunit (EC 4.3.1.17) L-serine dehydratase, alpha subunit (EC 4.3.1.17)	Pyruvate Alanine Serine Interconversions	1377	459
*SerDL	L-serine dehydratase, beta subunit (EC 4.3.1.17) L-serine dehydratase, alpha subunit (EC 4.3.1.17)	Pyruvate Alanine Serine Interconversions	1377	459
*LAlaAT	Omega-amino acid--pyruvate aminotransferase (EC 2.6.1.18)	Pyruvate Alanine Serine Interconversions	1335	445
*LAlaAT	Omega-amino acid--pyruvate aminotransferase (EC 2.6.1.18)	Pyruvate Alanine Serine Interconversions	1371	457
*LAlaAT	Omega-amino acid--pyruvate aminotransferase (EC 2.6.1.18)	Pyruvate Alanine Serine Interconversions	1347	449
*LAlaAT	Omega-amino acid--pyruvate aminotransferase (EC 2.6.1.18)	Pyruvate Alanine Serine Interconversions	1383	461
*LAlaAT	Valine--pyruvate aminotransferase (EC 2.6.1.66)	Pyruvate Alanine Serine Interconversions	1173	391
BCAAT	Branched-chain amino acid aminotransferase (EC 2.6.1.42)	Pyruvate Alanine Serine Interconversions	924	308

CycA	D-serine/D-alanine/glycine transporter	Pyruvate Alanine Serine Interconversions	1434	478
*CitS	Citrate synthase (si) (EC 2.3.3.1)	Glyoxylate bypass	1287	429
*AH	Aconitate hydratase (EC 4.2.1.3) 2-methylisocitrate dehydratase (EC 4.2.1.99)	Glyoxylate bypass	2733	911
*AH	Aconitate hydratase 2 (EC 4.2.1.3) 2-methylisocitrate dehydratase (EC 4.2.1.99)	Glyoxylate bypass	2610	870
IsDH_reg	Isocitrate dehydrogenase phosphatase (EC 2.7.11.5)/kinase (EC 3.1.3.-)	Glyoxylate bypass	1734	578
*ICL	Isocitrate lyase (EC 4.1.3.1)	Glyoxylate bypass	1596	532
*MS	Malate synthase G (EC 2.3.3.9)	Glyoxylate bypass	2178	726
PDHAB	Pyruvate dehydrogenase E1 component (EC 1.2.4.1)	Dehydrogenase complexes	2649	883
DATP	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Dehydrogenase complexes	1644	548
LeuAP	Cytosol aminopeptidase PepA (EC 3.4.11.1)	Dehydrogenase complexes	1488	496
TRBCKDH	Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4)	Dehydrogenase complexes	1233	411
TRBCKDH	Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4)	Dehydrogenase complexes	1098	
BCKDHB	Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)	Dehydrogenase complexes	1053	351
BCKDHB	Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)	Dehydrogenase complexes	1002	334

BCKDHB	Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168)	Dehydrogenase complexes	1287	429
BCKDHB	Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168)	Dehydrogenase complexes	1113	371
ODHAB	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2)	Dehydrogenase complexes	2832	944
DSTO	Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61)	Dehydrogenase complexes	1242	414
DDHO	Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4)	Dehydrogenase complexes	1437	479
DDHB	Dihydrolipoamide dehydrogenase of branched-chain alpha-keto acid dehydrogenase (EC 1.8.1.4)	Dehydrogenase complexes	1395	465
gltA	Citrate synthase (si) (EC 2.3.3.1)	TCA Cycle	1287	429
*AcoH	Aconitate hydratase (EC 4.2.1.3) 2-methylisocitrate dehydratase (EC 4.2.1.99)	TCA Cycle	2733	911
*AcoH	Aconitate hydratase 2 (EC 4.2.1.3) 2-methylisocitrate dehydratase (EC 4.2.1.99)	TCA Cycle	2610	870
sucA	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2)	TCA Cycle	2832	944
*sucB	Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61)	TCA Cycle	1242	414

*lpdA	Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4)	TCA Cycle	1437	479
*lpdA	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	TCA Cycle	1401	467
*sucD	Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5)	TCA Cycle	888	296
*sucS	Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5)	TCA Cycle	1167	389
*Fum	Fumarate hydratase class II (EC 4.2.1.2)	TCA Cycle	1395	465
*Fum	Fumarate hydratase class I, aerobic (EC 4.2.1.2)	TCA Cycle	1524	508
*Fum	Fumarate hydratase class II (EC 4.2.1.2)	TCA Cycle	1377	459
*MD	Malate:quinone oxidoreductase (EC 1.1.5.4)	TCA Cycle	1542	508
*MD	Malate:quinone oxidoreductase (EC 1.1.5.4)	TCA Cycle	1572	524
*icd	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	TCA Cycle	1257	419
*icd	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42) Monomeric isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	TCA Cycle	2226	742
GPDH	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	Pentose phosphate pathway	1470	490
GPDH	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	Pentose phosphate pathway	1467	489
*PGL	6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type	Pentose phosphate pathway	717	239
*Ris	Ribose 5-phosphate isomerase A (EC 5.3.1.6)	Pentose phosphate pathway	672	224
Repi	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Pentose phosphate pathway	675	225
*TK	Transketolase (EC 2.2.1.1)	Pentose phosphate pathway	1998	666
TA	Transaldolase (EC 2.2.1.2)	Pentose phosphate pathway	924	308

FPK	Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9) Fructose-6-phosphate phosphoketolase (EC 4.1.2.22)	Pentose phosphate pathway	2406	802
XPK	Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9) Fructose-6-phosphate phosphoketolase (EC 4.1.2.22)	Pentose phosphate pathway	2406	802
PRPPS	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	Pentose phosphate pathway	942	314
PyK	Pyruvate kinase (EC 2.7.1.40)	Pyruvate metabolism I: anaplerotic reactions, PEP	1434	478
PyK	Pyruvate kinase (EC 2.7.1.40)	Pyruvate metabolism I: anaplerotic reactions, PEP	1452	484
*pps	Phosphoenolpyruvate synthase (EC 2.7.9.2)	Pyruvate metabolism I: anaplerotic reactions, PEP	2322	774
*PEPC	Phosphoenolpyruvate carboxylase (EC 4.1.1.31)	Pyruvate metabolism I: anaplerotic reactions, PEP	2637	879
*PEPCK	Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)	Pyruvate metabolism I: anaplerotic reactions, PEP	672	224
*PEPCK	Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)	Pyruvate metabolism I: anaplerotic reactions, PEP	1542	514
*Malic_enzyme	NADP-dependent malic enzyme (EC 1.1.1.40)	Pyruvate metabolism I: anaplerotic reactions, PEP	1269	423
*Malic_enzyme	NAD-dependent malic enzyme (EC 1.1.1.38)	Pyruvate metabolism I: anaplerotic reactions, PEP	1695	565
GlcD	Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD	Glycolate, glyoxylate interconversions	1500	500
GlcE	Glycolate dehydrogenase (EC 1.1.99.14), FAD-binding subunit GlcE	Glycolate, glyoxylate interconversions	1080	360

GlcF	Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF	Glycolate, glyoxylate interconversions	1227	409
GlcG	Hypothetical protein GlcG in glycolate utilization operon	Glycolate, glyoxylate interconversions	402	134
GlcC	Glycolate utilization operon transcriptional activator GlcC	Glycolate, glyoxylate interconversions	756	252
GoxR(P)	Glyoxylate reductase (EC 1.1.1.79) Glyoxylate reductase (EC 1.1.1.26) Hydroxypyruvate reductase (EC 1.1.1.81) 2-ketoaldonate reductase, broad specificity (EC 1.1.1.215) (EC 1.1.1.-)	Glycolate, glyoxylate interconversions	978	326
GoxR	Glyoxylate reductase (EC 1.1.1.79) Glyoxylate reductase (EC 1.1.1.26) Hydroxypyruvate reductase (EC 1.1.1.81) 2-ketoaldonate reductase, broad specificity (EC 1.1.1.215) (EC 1.1.1.-)	Glycolate, glyoxylate interconversions	978	326
HPyrR	Glyoxylate reductase (EC 1.1.1.79) Glyoxylate reductase (EC 1.1.1.26) Hydroxypyruvate reductase (EC 1.1.1.81) 2-ketoaldonate reductase, broad specificity (EC 1.1.1.215) (EC 1.1.1.-)	Glycolate, glyoxylate interconversions	978	326
*2PGP	Phosphoglycolate phosphatase (EC 3.1.3.18)	Glycolate, glyoxylate interconversions	819	273
*2PGP	Phosphoglycolate phosphatase (EC 3.1.3.18)	Glycolate, glyoxylate interconversions	666	222

Carbohydrates - Aminosugars				
NagA	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	Chitin and N-acetylglucosamine utilization	1092	364
*NagB	Glucosamine-6-phosphate deaminase [isomerizing], alternative (EC 3.5.99.6)	Chitin and N-acetylglucosamine utilization	1023	341
*NagR	Predicted transcriptional regulator of N-Acetylglucosamine utilization, GntR family	Chitin and N-acetylglucosamine utilization	744	248
*Chitinolytic_Enz	Chitinase (EC 3.2.1.14)	Chitin and N-acetylglucosamine utilization	1452	484
Carbohydrates - Di- and oligosaccharides				
TS	Trehalose synthase (EC 5.4.99.16)	Trehalose Biosynthesis	3303	1101
TreY	Malto-oligosyltrehalose synthase (EC 5.4.99.15)	Trehalose Biosynthesis	2781	927
TreZ	Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141)	Trehalose Biosynthesis	1755	585
GBE	1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18)	Trehalose Biosynthesis	2199	733
*Amy	Alpha-amylase (EC 3.2.1.1)	Trehalose Biosynthesis	1995	665
*MalP	Glycogen phosphorylase (EC 2.4.1.1)	Maltose and Maltodextrin Utilization	2439	813
MalQ	4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)	Maltose and Maltodextrin Utilization	2055	685
MapA	Maltose phosphorylase (EC 2.4.1.8)	Maltose and Maltodextrin Utilization	2265	755
MTrS	Malto-oligosyltrehalose synthase (EC 5.4.99.15)	Maltose and Maltodextrin Utilization	2781	927
Amy	Alpha-amylase (EC 3.2.1.1)	Maltose and Maltodextrin Utilization	1995	665
Carbohydrates - One-carbon Metabolism				

*folD	Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5)	One-carbon metabolism by tetrahydropterines	855	285
*folD	Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5)	One-carbon metabolism by tetrahydropterines	855	285
FTFD	Formyltetrahydrofolate deformylase (EC 3.5.1.10)	One-carbon metabolism by tetrahydropterines	852	284
FTFD	Formyltetrahydrofolate deformylase (EC 3.5.1.10)	One-carbon metabolism by tetrahydropterines	858	286
MTFR	5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)	One-carbon metabolism by tetrahydropterines	873	291
*FTCL	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	One-carbon metabolism by tetrahydropterines	612	204
Carbohydrates - Carbohydrates - no subcategory				
CsrA	Carbon storage regulator	Carbon storage regulator	186	62
Carbohydrates - Polysaccharides				
Amse	4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)	Glycogen metabolism	2055	685
GP	Glycogen phosphorylase (EC 2.4.1.1)	Glycogen metabolism	2439	813
*GBr	1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18)	Glycogen metabolism	2199	733
*GS	Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21)	Glycogen metabolism	1605	535
Carbohydrates - Sugar alcohols				

GlpT	Glycerol-3-phosphate transporter	Glycerol and Glycerol-3-phosphate Uptake and Utilization	1362	454
GlpT	Glycerol-3-phosphate transporter	Glycerol and Glycerol-3-phosphate Uptake and Utilization	1347	449
GlpF	Glycerol uptake facilitator protein	Glycerol and Glycerol-3-phosphate Uptake and Utilization	840	280
GlpK	Glycerol kinase (EC 2.7.1.30)	Glycerol and Glycerol-3-phosphate Uptake and Utilization	1560	520
GlpK	Glycerol kinase (EC 2.7.1.30)	Glycerol and Glycerol-3-phosphate Uptake and Utilization	1518	506
GlpK	Glycerol kinase (EC 2.7.1.30)	Glycerol and Glycerol-3-phosphate Uptake and Utilization	1485	495
*GPD	Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	Glycerol and Glycerol-3-phosphate Uptake and Utilization	1581	527
*GPD	Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	Glycerol and Glycerol-3-phosphate Uptake and Utilization	1539	513
*GPD	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)	Glycerol and Glycerol-3-phosphate Uptake and Utilization	1023	341
GlpR	Glycerol-3-phosphate regulon repressor GlpR	Glycerol and Glycerol-3-phosphate Uptake and Utilization	756	252
GlpE	Thiosulfate sulfurtransferase GlpE (EC 2.8.1.1)	Glycerol and Glycerol-3-phosphate Uptake and Utilization	333	111
UdpQ	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	Glycerol and Glycerol-3-phosphate Uptake and Utilization	1152	384

UdpQ	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	Glycerol and Glycerol-3-phosphate Uptake and Utilization	1128	376
UdpQ	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	Glycerol and Glycerol-3-phosphate Uptake and Utilization	723	241
UdpQ	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	Glycerol and Glycerol-3-phosphate Uptake and Utilization	936	312
Carbohydrates - Organic acids				
AcnD	2-Methylcitrate dehydratase AcnD	2-methylcitrate to 2-methylaconitate metabolism cluster	1743	581
PrpE	Propionate--CoA ligase (EC 6.2.1.17)	Methylcitrate cycle	1887	629
PrpC	2-methylcitrate synthase (EC 2.3.3.5)	Methylcitrate cycle	1128	376
PrpD	2-methylcitrate dehydratase (EC 4.2.1.79)	Methylcitrate cycle	1485	495
PrpF	2-methylaconitate isomerase	Methylcitrate cycle	1188	396
MICDH	Aconitate hydratase (EC 4.2.1.3) 2-methylisocitrate dehydratase (EC 4.2.1.99)	Methylcitrate cycle	2733	911
MICDH	Aconitate hydratase 2 (EC 4.2.1.3) 2-methylisocitrate dehydratase (EC 4.2.1.99)	Methylcitrate cycle	2610	870
PrpB	Methylisocitrate lyase (EC 4.1.3.30)	Methylcitrate cycle	897	299
PrpE	Propionate--CoA ligase (EC 6.2.1.17)	Propionate-CoA to Succinate Module	1887	629
MCS	2-methylcitrate synthase (EC 2.3.3.5)	Propionate-CoA to Succinate Module	1128	376
MCDH	2-methylcitrate dehydratase (EC 4.2.1.79)	Propionate-CoA to Succinate Module	1485	495
PrpF	2-methylaconitate isomerase	Propionate-CoA to Succinate Module	1188	396
MICDH	Aconitate hydratase (EC 4.2.1.3) 2-methylisocitrate dehydratase (EC 4.2.1.99)	Propionate-CoA to Succinate Module	2733	911

MICDH	Aconitate hydratase 2 (EC 4.2.1.3) 2-methylisocitrate dehydratase (EC 4.2.1.99)	Propionate-CoA to Succinate Module	2610	870
MICLY	Methylisocitrate lyase (EC 4.1.3.30)	Propionate-CoA to Succinate Module	897	299
ACN	Aconitate hydratase (EC 4.2.1.3) 2-methylisocitrate dehydratase (EC 4.2.1.99)	Propionate-CoA to Succinate Module	2733	911
ACN2	Aconitate hydratase 2 (EC 4.2.1.3) 2-methylisocitrate dehydratase (EC 4.2.1.99)	Propionate-CoA to Succinate Module	2610	870
GK-I	Glycerate kinase (EC 2.7.1.31)	Glycerate metabolism	1146	382
GK-I	Glycerate kinase (EC 2.7.1.31)	Glycerate metabolism	1146	382
HPR	Glyoxylate reductase (EC 1.1.1.79) Glyoxylate reductase (EC 1.1.1.26) Hydroxypyruvate reductase (EC 1.1.1.81) 2-ketoaldonate reductase, broad specificity (EC 1.1.1.215) (EC 1.1.1.-)	Glycerate metabolism	978	326
GCL	Glyoxylate carboligase (EC 4.1.1.47)	Glycerate metabolism	1776	592
HOPR	2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)	Glycerate metabolism	891	297
HOPR	2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)	Glycerate metabolism	867	289
HPI	Hydroxypyruvate isomerase (EC 5.3.1.22)	Glycerate metabolism	783	261
HPI	Hydroxypyruvate isomerase (EC 5.3.1.22)	Glycerate metabolism	798	266
GlyP	D-glycerate transporter (predicted)	Glycerate metabolism	1359	453
Pyk	Pyruvate kinase (EC 2.7.1.40)	Glycerate metabolism	1434	478
Pyk	Pyruvate kinase (EC 2.7.1.40)	Glycerate metabolism	1452	484
Carbohydrates - Fermentation				
LDH_D	D-lactate dehydrogenase (EC 1.1.1.28)	Fermentations: Lactate	990	330

FPX	Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9) Fructose-6-phosphate phosphoketolase (EC 4.1.2.22)	Fermentations: Lactate	2406	802
XPK	Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9) Fructose-6-phosphate phosphoketolase (EC 4.1.2.22)	Fermentations: Lactate	2406	802
PTA	BioD-like N-terminal domain Phosphate acetyltransferase (EC 2.3.1.8)	Fermentations: Lactate	2115	705
ACK	Acetate kinase (EC 2.7.2.1)	Fermentations: Lactate	1185	395
AADH	Alcohol dehydrogenase (EC 1.1.1.1) Acetaldehyde dehydrogenase (EC 1.2.1.10)	Fermentations: Lactate	1164	388
R1	Acetolactate synthase large subunit (EC 2.2.1.6)	Acetolactate synthase subunits	1725	575
R2	Acetolactate synthase small subunit (EC 2.2.1.6)	Acetolactate synthase subunits	492	164
AtoB	Acetyl-CoA acetyltransferase (EC 2.3.1.9) 3-oxoadipyl-CoA thiolase (EC 2.3.1.174)	Acetyl-CoA fermentation to Butyrate	1206	402
AtoB	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Acetyl-CoA fermentation to Butyrate	1185	395
AtoB	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Acetyl-CoA fermentation to Butyrate	1185	395
AtoB	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Acetyl-CoA fermentation to Butyrate	1176	392
AtoB	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Acetyl-CoA fermentation to Butyrate	1188	396
AtoB	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Acetyl-CoA fermentation to Butyrate	1182	394
AtoB	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Acetyl-CoA fermentation to Butyrate	1206	402

AtoB	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Acetyl-CoA fermentation to Butyrate	1191	397
*HbdA	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	Acetyl-CoA fermentation to Butyrate	2148	716
*HbdA	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	Acetyl-CoA fermentation to Butyrate	852	284
*HbdA	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	Acetyl-CoA fermentation to Butyrate	1530	510
*HbdA	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	Acetyl-CoA fermentation to Butyrate	1530	510
*HbdA	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 17hydroxysteroid dehydrogenase type 10 (HSD10)-like	Acetyl-CoA fermentation to Butyrate	768	256
*HbdA	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	Acetyl-CoA fermentation to Butyrate	1236	412
*HbdA	Enoyl-CoA hydratase (EC 4.2.1.17) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	Acetyl-CoA fermentation to Butyrate	2145	715

*HbdA	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 17hydroxysteroid dehydrogenase type 10 (HSD10)-like Enoyl-CoA hydratase (EC 4.2.1.17)	Acetyl-CoA fermentation to Butyrate	768	256
FadB	Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	Acetyl-CoA fermentation to Butyrate	2148	716
FadB	3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3) Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	Acetyl-CoA fermentation to Butyrate	1236	412
FadB	3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3) Enoyl-CoA hydratase (EC 4.2.1.17) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	Acetyl-CoA fermentation to Butyrate	2145	715
EH	Enoyl-CoA hydratase (EC 4.2.1.17)	Acetyl-CoA fermentation to Butyrate	762	254
EH	Enoyl-CoA hydratase (EC 4.2.1.17) Enoyl-CoA hydratase (EC 4.2.1.17)	Acetyl-CoA fermentation to Butyrate	762	254
EH	Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	Acetyl-CoA fermentation to Butyrate	2148	716
EH	Enoyl-CoA hydratase (EC 4.2.1.17) Enoyl-CoA hydratase EchA5 (EC 4.2.1.17)	Acetyl-CoA fermentation to Butyrate	771	257

EH	Enoyl-CoA hydratase (EC 4.2.1.17)	Acetyl-CoA fermentation to Butyrate	789	263
EH	Enoyl-CoA hydratase (EC 4.2.1.17)	Acetyl-CoA fermentation to Butyrate	792	264
EH	Enoyl-CoA hydratase (EC 4.2.1.17)	Acetyl-CoA fermentation to Butyrate	774	258
EH	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	Acetyl-CoA fermentation to Butyrate	1236	412
EH	Enoyl-CoA hydratase (EC 4.2.1.17) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	Acetyl-CoA fermentation to Butyrate	2145	715
FixB	Electron transfer flavoprotein, alpha subunit	Acetyl-CoA fermentation to Butyrate	930	310
FixB	Electron transfer flavoprotein, alpha subunit	Acetyl-CoA fermentation to Butyrate	1233	411
FixA	Electron transfer flavoprotein, beta subunit	Acetyl-CoA fermentation to Butyrate	750	250
FixA	Electron transfer flavoprotein, beta subunit	Acetyl-CoA fermentation to Butyrate	774	258
FixC2	Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)	Acetyl-CoA fermentation to Butyrate	1656	552
ACA	Acetyl-CoA acetyltransferase (EC 2.3.1.9) 3-oxoadipyl-CoA thiolase (EC 2.3.1.174)	Butanol Biosynthesis	1206	402
ACA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Butanol Biosynthesis	1185	395
ACA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Butanol Biosynthesis	1185	395
ACA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Butanol Biosynthesis	1176	392

ACA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Butanol Biosynthesis	1188	396
ACA	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Butanol Biosynthesis	1182	394
ACA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Butanol Biosynthesis	1206	402
ACA	3-ketoacyl-CoA thiolase (EC 2.3.1.16) Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Butanol Biosynthesis	1191	397
3HCD	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	Butanol Biosynthesis	852	284
3HCD	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	Butanol Biosynthesis	1530	510
ECH	Enoyl-CoA hydratase (EC 4.2.1.17)	Butanol Biosynthesis	762	254
ECH	Enoyl-CoA hydratase (EC 4.2.1.17)	Butanol Biosynthesis	969	323
ECH	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	Butanol Biosynthesis	2148	716
ECH	Enoyl-CoA hydratase (EC 4.2.1.17) Enoyl-CoA hydratase EchA5 (EC 4.2.1.17)	Butanol Biosynthesis	771	257
ECH	Enoyl-CoA hydratase (EC 4.2.1.17)	Butanol Biosynthesis	789	263
ECH	Enoyl-CoA hydratase (EC 4.2.1.17)	Butanol Biosynthesis	792	264
ECH	Enoyl-CoA hydratase (EC 4.2.1.17)	Butanol Biosynthesis	774	258
ECH	Enoyl-CoA hydratase (EC 4.2.1.17) Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8)	Butanol Biosynthesis	1236	412

	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)			
ECH	Enoyl-CoA hydratase (EC 4.2.1.17) 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	Butanol Biosynthesis	2145	715
*AD	Alcohol dehydrogenase (EC 1.1.1.1)	Butanol Biosynthesis	1182	394
*AD	Cinnamyl alcohol dehydrogenase/reductase (EC 1.1.1.195)	Butanol Biosynthesis	1062	354
*AD	Alcohol dehydrogenase (EC 1.1.1.1) Alcohol dehydrogenase (EC 1.1.1.1) Acetaldehyde dehydrogenase (EC 1.2.1.10)	Butanol Biosynthesis	1164	388
*AD	Alcohol dehydrogenase (EC 1.1.1.1) Acetaldehyde dehydrogenase (EC 1.2.1.10)	Butanol Biosynthesis	1164	388
*AD	Alcohol dehydrogenase (EC 1.1.1.1)	Butanol Biosynthesis	1029	343
Gene ou sistema	Função predita	Subsistemas	pb	aa
Virulence, Disease and Defense - Bacteriocins, ribosomally synthesized antibacterial peptides				
CbrC-like		Tolerance to colicin E2	540	180
CreA	Conserved uncharacterized protein CreA	Tolerance to colicin E2	465	155
CreD	Inner membrane protein CreD	Tolerance to colicin E2	1359	453
Virulence, Disease and Defense - Invasion and intracellular resistance				
Rv1641	Translation initiation factor 3	Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins)	534	178

Rv1642	LSU ribosomal protein L35p	Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins)	195	65
Rv1643	LSU ribosomal protein L20p	Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins)	357	119
Rv1594	Quinolinate synthetase (EC 2.5.1.72)	Mycobacterium virulence operon possibly involved in quinolinate biosynthesis	1059	353
Rv1595	L-aspartate oxidase (EC 1.4.3.16)	Mycobacterium virulence operon possibly involved in quinolinate biosynthesis	1617	539
Rv1596	Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)	Mycobacterium virulence operon possibly involved in quinolinate biosynthesis	849	283
Rv0667	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	Mycobacterium virulence operon involved in DNA transcription	4074	1358
Rv0668	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	Mycobacterium virulence operon involved in DNA transcription	4200	1400
Rv0682	SSU ribosomal protein S12p (S23e)	Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins)	372	124
Rv0683	SSU ribosomal protein S7p (S5e)	Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins)	471	157

Rv0684	Translation elongation factor G	Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins)	2121	707
Rv0684	Translation elongation factor G	Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins)	2109	703
Rv0685	Translation elongation factor Tu	Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins)	306	102
Rv0685	Translation elongation factor Tu	Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins)	351	117
Rv0685	Translation elongation factor Tu	Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins)	351	117
Rv0685	Translation elongation factor Tu	Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins)	1194	398
Virulence, Disease and Defense - Resistance to antibiotics and toxic compounds				
NfxB	Transcriptional regulator NfxB	MexC-MexD-OprJ Multidrug Efflux System	564	188
NfxB	Transcriptional regulator NfxB	MexC-MexD-OprJ Multidrug Efflux System	519	173
vanW	Vancomycin B-type resistance protein VanW	Resistance to Vancomycin	822	274
MIR	Mercuric ion reductase (EC 1.16.1.1)	Mercuric reductase	1689	563

FosA	Fosfomycin resistance protein FosA	Fosfomycin resistance	408	136
ChrA	Chromate transport protein ChrA	Fosfomycin resistance protein FosA	1230	410
ChrA	Chromate transport protein ChrA	Fosfomycin resistance protein FosA	1206	402
CutE	Apolipoprotein N-acyltransferase Copper homeostasis protein CutE	Copper homeostasis: copper tolerance	1536	512
CorC	Magnesium and cobalt efflux protein CorC	Copper homeostasis: copper tolerance	840	280
ParC	Topoisomerase IV subunit A (EC 5.99.1.-)	Resistance to fluoroquinolones	2265	755
parE	Topoisomerase IV subunit B (EC 5.99.1.-)	Resistance to fluoroquinolones	1890	630
gyrA	DNA gyrase subunit A (EC 5.99.1.3)	Resistance to fluoroquinolones	2766	922
gyrB	DNA gyrase subunit B (EC 5.99.1.3)	Resistance to fluoroquinolones	2421	807
MerT	Mercuric transport protein, MerT	Mercury resistance operon	351	117
MerT	Mercuric transport protein, MerT	Mercury resistance operon	351	117
MerP	Periplasmic mercury(+2) binding protein	Mercury resistance operon	276	92
MerP	Periplasmic mercury(+2) binding protein	Mercury resistance operon	306	102
MerA	Mercuric ion reductase (EC 1.16.1.1)	Mercury resistance operon	1689	563
*MATE_family_MDR_Pump	Multidrug and toxin extrusion (MATE) family efflux pump YdhE/NorM, homolog	Multidrug Resistance Efflux Pumps	1467	489
*MATE_family_MDR_Pump	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	Multidrug Resistance Efflux Pumps	1434	478
MacA	Macrolide-specific efflux protein MacA	Multidrug Resistance Efflux Pumps	1176	392
AcrB	Acriflavin resistance protein	Multidrug Resistance Efflux Pumps	3105	1035
NfxB	Transcriptional regulator NfxB	Multidrug Resistance Efflux Pumps	564	188
NfxB	Transcriptional regulator NfxB	Multidrug Resistance Efflux Pumps	519	173
arsR	Arsenical resistance operon repressor	Arsenic resistance	351	117
arsR	Arsenical resistance operon repressor	Arsenic resistance	471	157

arsR	Arsenical resistance operon repressor	Arsenic resistance	348	116
arsD	Arsenical resistance operon trans-acting repressor ArsD	Arsenic resistance	360	120
arsB	Arsenic efflux pump protein	Arsenic resistance	1284	428
arsC	Arsenate reductase (EC 1.20.4.1)	Arsenic resistance	489	163
arsC	Arsenate reductase (EC 1.20.4.1)	Arsenic resistance	429	143
ACR3	Arsenical-resistance protein ACR3	Arsenic resistance	1062	354
ACR3	Arsenical-resistance protein ACR3	Arsenic resistance	1086	362
ACR3	Arsenical-resistance protein ACR3	Arsenic resistance	1113	371
arsH	Arsenic resistance protein ArsH	Arsenic resistance	693	231
arsH	Arsenic resistance protein ArsH	Arsenic resistance	717	239
arsH	Arsenic resistance protein ArsH	Arsenic resistance	723	241
CRTR	Cu(I)-responsive transcriptional regulator	Copper homeostasis	399	133
*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)	Copper homeostasis	2229	743
*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)	Copper homeostasis	2076	692
*CIA	Type cbb3 cytochrome oxidase biogenesis protein CcoI Copper-translocating P-type ATPase (EC 3.6.3.4)	Copper homeostasis	2436	812
*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)	Copper homeostasis	2379	793

CopZ	Copper chaperone	Copper homeostasis	198	66
CopZ	Copper chaperone	Copper homeostasis	195	65
ClfA	Multidrug resistance transporter, Bcr/CflA family	Copper homeostasis	1179	393
ClfA	Multidrug resistance transporter, Bcr/CflA family	Copper homeostasis	1209	403
MO	Multicopper oxidase	Copper homeostasis	1392	464
MO	Multicopper oxidase	Copper homeostasis	1902	634
MO	edit functional role	Copper homeostasis	1938	646
CT	Copper tolerance protein	Copper homeostasis	546	182
*HL	Cytochrome c heme lyase subunit CcmH	Copper homeostasis	1224	408
*HL	Cytochrome c heme lyase subunit CcmH	Copper homeostasis	417	139
*HL	Cytochrome c heme lyase subunit CcmF	Copper homeostasis	1974	658
CopC	Copper resistance protein CopC	Copper homeostasis	387	129
CopD	Copper resistance protein CopD	Copper homeostasis	927	309
CRB	Copper resistance protein B	Copper homeostasis	981	327
CopG	CopG protein	Copper homeostasis	486	162
CopG	CopG protein	Copper homeostasis	450	150
CusS	Copper sensory histidine kinase CusS	Copper homeostasis	1332	444
CusS	Copper sensory histidine kinase CusS	Copper homeostasis	1155	385
CusR	Copper-sensing two-component system response regulator CusR	Copper homeostasis	681	227
*CzcA?	Cobalt-zinc-cadmium resistance protein CzcA Cation efflux system protein CusA	Cobalt-zinc-cadmium resistance	3153	1051
*CzcA?	Cobalt-zinc-cadmium resistance protein CzcA Cation efflux system protein CusA	Cobalt-zinc-cadmium resistance	3156	1052

CzcC	Heavy metal RND efflux outer membrane protein, CzcC family	Cobalt-zinc-cadmium resistance	1308	436
CzcC	Heavy metal RND efflux outer membrane protein, CzcC family	Cobalt-zinc-cadmium resistance	1287	429
*CusB/CzsB	Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family	Cobalt-zinc-cadmium resistance	1473	491
*CusB/CzsB	Probable Co/Zn/Cd efflux system membrane fusion protein	Cobalt-zinc-cadmium resistance	1167	389
*CusB/CzsB	Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family	Cobalt-zinc-cadmium resistance	1455	485
*CusA	Cobalt-zinc-cadmium resistance protein CzcA Cation efflux system protein CusA	Cobalt-zinc-cadmium resistance	3153	1051
*CusA	Cobalt-zinc-cadmium resistance protein CzcA Cation efflux system protein CusA	Cobalt-zinc-cadmium resistance	3156	1052
*CzrR	DNA-binding heavy metal response regulator	Cobalt-zinc-cadmium resistance	690	230
*CzrR	Copper-sensing two-component system response regulator CusR	Cobalt-zinc-cadmium resistance	681	227
*CzrR	DNA-binding heavy metal response regulator	Cobalt-zinc-cadmium resistance	690	230
*CzrR	DNA-binding heavy metal response regulator	Cobalt-zinc-cadmium resistance	693	231
*CzrR	DNA-binding heavy metal response regulator	Cobalt-zinc-cadmium resistance	675	225
*HMHK	Heavy metal sensor histidine kinase	Cobalt-zinc-cadmium resistance	1392	464
*HMHK	Copper sensory histidine kinase CusS	Cobalt-zinc-cadmium resistance	1332	444
*HMHK	Heavy metal sensor histidine kinase	Cobalt-zinc-cadmium resistance	1416	472
*HMHK	Copper sensory histidine kinase CusS	Cobalt-zinc-cadmium resistance	1155	385
*HMHK	Heavy metal sensor histidine kinase	Cobalt-zinc-cadmium resistance	1419	473

*TR	Transcriptional regulator, MerR family	Cobalt-zinc-cadmium resistance	456	152
*TR	Transcriptional regulator, MerR family	Cobalt-zinc-cadmium resistance	471	157
*TR	Transcriptional regulator, MerR family	Cobalt-zinc-cadmium resistance	426	142
*TR	Transcriptional regulator, MerR family	Cobalt-zinc-cadmium resistance	408	136
*TR	Transcriptional regulator, MerR family	Cobalt-zinc-cadmium resistance	489	163
*TR	Transcriptional regulator, MerR family	Cobalt-zinc-cadmium resistance	399	133
*TR	Transcriptional regulator, MerR family	Cobalt-zinc-cadmium resistance	456	152
*CzcD	Cobalt-zinc-cadmium resistance protein CzcD	Cobalt-zinc-cadmium resistance	972	324
*CzcD	Cobalt-zinc-cadmium resistance protein CzcD	Cobalt-zinc-cadmium resistance	900	300

APÊNDICE 2

Tabela de Genes da estirpe PSA39- As ilhas genômicas previstas usando IslandPick, SIGI-HMM e IslandPath-DIMOB

Island start	Island end	Length	Method	Locus	Gene start	Gene end	Strand	Product
5861	25247	19386	Predicted by at least one method	KALEADPK_05634	5861	7468	1	hypothetical protein
5861	25247	19386	Predicted by at least one method	KALEADPK_05646	9152	11890	1	hypothetical protein
5861	25247	19386	Predicted by at least one method	KALEADPK_05647	15515	16207	1	Transposase IS200 like protein
5861	25247	19386	Predicted by at least one method	KALEADPK_06130	19117	21819	1	hypothetical protein
5861	25247	19386	Predicted by at least one method	KALEADPK_06131	22728	23015	1	Immunity protein 35
5861	25247	19386	Predicted by at least one method	KALEADPK_06132	23363	23716	1	Transposase IS200 like protein
5861	25247	19386	Predicted by at least one method	KALEADPK_06133	25011	25247	-1	hypothetical protein
249428	263490	14062	Predicted by at least one method	KALEADPK_06343	249428	250717	1	C-5 cytosine-specific DNA methylase
249428	263490	14062	Predicted by at least one method	KALEADPK_06344	251129	252469	-1	AAA domain protein
249428	263490	14062	Predicted by at least one method	KALEADPK_06345	252466	253869	-1	hypothetical protein
249428	263490	14062	Predicted by at least one method	KALEADPK_06346	253866	254915	-1	hypothetical protein
249428	263490	14062	Predicted by at least one method	KALEADPK_06347	254905	255669	-1	hypothetical protein
249428	263490	14062	Predicted by at least one method	KALEADPK_06348	255735	256682	-1	HNH endonuclease
249428	263490	14062	Predicted by at least one method	KALEADPK_06349	257485	257697	1	hypothetical protein
249428	263490	14062	Predicted by at least one method	KALEADPK_06350	258664	259503	-1	Integrase core domain protein
249428	263490	14062	Predicted by at least one method	KALEADPK_06351	259536	259799	-1	Transposase
249428	263490	14062	Predicted by at least one method	KALEADPK_06352	260196	260492	1	Transposase
249428	263490	14062	Predicted by at least one method	KALEADPK_06353	260729	262315	1	Transposase IS66 family protein
249428	263490	14062	Predicted by at least one method	KALEADPK_06354	262327	263490	-1	hypothetical protein
257485	287399	29914	Predicted by at least one method	KALEADPK_06349	257485	257697	1	hypothetical protein
257485	287399	29914	Predicted by at least one method	KALEADPK_06350	258664	259503	-1	Integrase core domain protein
257485	287399	29914	Predicted by at least one method	KALEADPK_06351	259536	259799	-1	Transposase
257485	287399	29914	Predicted by at least one method	KALEADPK_06352	260196	260492	1	Transposase

257485	287399	29914	Predicted by at least one method	KALEADPK_06353	260729	262315	1	Transposase IS66 family protein
257485	287399	29914	Predicted by at least one method	KALEADPK_06354	262327	263490	-1	hypothetical protein
257485	287399	29914	Predicted by at least one method	KALEADPK_06355	263640	265790	-1	hypothetical protein
257485	287399	29914	Predicted by at least one method	KALEADPK_06356	265787	266284	-1	hypothetical protein
257485	287399	29914	Predicted by at least one method	KALEADPK_06357	266288	267403	-1	hypothetical protein
257485	287399	29914	Predicted by at least one method	KALEADPK_06358	267379	269166	-1	Phage late control gene D protein (GPD)
257485	287399	29914	Predicted by at least one method	KALEADPK_06359	269348	269866	-1	Type VI secretion system effector, Hcp
257485	287399	29914	Predicted by at least one method	KALEADPK_04061	271231	271671	1	Integrase core domain protein
257485	287399	29914	Predicted by at least one method	KALEADPK_04062	271664	274123	1	hypothetical protein
257485	287399	29914	Predicted by at least one method	KALEADPK_04063	274142	274354	-1	Cro/C1-type HTH DNA-binding domain protein
257485	287399	29914	Predicted by at least one method	KALEADPK_04064	274502	274735	1	hypothetical protein
257485	287399	29914	Predicted by at least one method	KALEADPK_04065	274728	275888	1	Arm DNA-binding domain protein
257485	287399	29914	Predicted by at least one method	KALEADPK_04066	275900	276184	1	hypothetical protein
257485	287399	29914	Predicted by at least one method	KALEADPK_04067	276430	277911	1	Sigma-54 interaction domain protein
257485	287399	29914	Predicted by at least one method	KALEADPK_04068	277942	281343	1	Type III restriction enzyme, res subunit
257485	287399	29914	Predicted by at least one method	KALEADPK_04069	281376	282959	1	N-6 DNA Methylase
257485	287399	29914	Predicted by at least one method	KALEADPK_04070	282968	284155	1	Type I restriction modification DNA specificity domain protein
257485	287399	29914	Predicted by at least one method	KALEADPK_04071	284274	284420	1	hypothetical protein
257485	287399	29914	Predicted by at least one method	KALEADPK_04072	284469	287399	1	hypothetical protein
282968	287399	4431	Predicted by at least one method	KALEADPK_04070	282968	284155	1	Type I restriction modification DNA specificity domain protein
282968	287399	4431	Predicted by at least one method	KALEADPK_04071	284274	284420	1	hypothetical protein
282968	287399	4431	Predicted by at least one method	KALEADPK_04072	284469	287399	1	hypothetical protein

289550	301462	11912	Predicted by at least one method	KALEADPK_04074	289550	290368	1	von Willebrand factor type A domain protein
289550	301462	11912	Predicted by at least one method	KALEADPK_04075	290365	291069	1	Protein phosphatase 2C
289550	301462	11912	Predicted by at least one method	KALEADPK_04076	291066	292493	1	Protein kinase domain protein
289550	301462	11912	Predicted by at least one method	KALEADPK_04077	292501	295815	1	AAA domain protein
289550	301462	11912	Predicted by at least one method	KALEADPK_04078	295805	297268	1	hypothetical protein
289550	301462	11912	Predicted by at least one method	KALEADPK_04079	297270	299642	1	hypothetical protein
289550	301462	11912	Predicted by at least one method	KALEADPK_04080	299639	301462	1	hypothetical protein
625566	639016	13450	Predicted by at least one method	KALEADPK_05003	625566	625913	-1	hypothetical protein
625566	639016	13450	Predicted by at least one method	KALEADPK_05002	625903	626517	-1	hypothetical protein
625566	639016	13450	Predicted by at least one method	KALEADPK_05001	626708	629434	-1	Peptidase M60, enhancin and enhancin-like
625566	639016	13450	Predicted by at least one method	KALEADPK_05000	630114	630431	1	hypothetical protein
625566	639016	13450	Predicted by at least one method	KALEADPK_04999	630856	632883	-1	hypothetical protein
625566	639016	13450	Predicted by at least one method	KALEADPK_04998	633341	634468	-1	hypothetical protein
625566	639016	13450	Predicted by at least one method	KALEADPK_04997	634543	635313	-1	Nuclease-related domain protein
625566	639016	13450	Predicted by at least one method	KALEADPK_04996	635484	636605	-1	hypothetical protein
625566	639016	13450	Predicted by at least one method	KALEADPK_04995	636867	637028	-1	hypothetical protein
625566	639016	13450	Predicted by at least one method	KALEADPK_04993	637331	639016	-1	Reverse transcriptase (RNA-dependent DNA polymerase)
630114	639016	8902	Predicted by at least one method	KALEADPK_05000	630114	630431	1	hypothetical protein
630114	639016	8902	Predicted by at least one method	KALEADPK_04999	630856	632883	-1	hypothetical protein
630114	639016	8902	Predicted by at least one method	KALEADPK_04998	633341	634468	-1	hypothetical protein
630114	639016	8902	Predicted by at least one method	KALEADPK_04997	634543	635313	-1	Nuclease-related domain protein
630114	639016	8902	Predicted by at least one method	KALEADPK_04996	635484	636605	-1	hypothetical protein
630114	639016	8902	Predicted by at least one method	KALEADPK_04995	636867	637028	-1	hypothetical protein
630114	639016	8902	Predicted by at least one method	KALEADPK_04993	637331	639016	-1	Reverse transcriptase (RNA-dependent DNA polymerase)
843264	852172	8908	Predicted by at least one method	KALEADPK_00702	843264	843536	-1	hypothetical protein
843264	852172	8908	Predicted by at least one method	KALEADPK_00703	843700	843981	1	hypothetical protein

843264	852172	8908	Predicted by at least one method	KALEADPK_00704	844603	844926	1	Helix-turn-helix domain protein
843264	852172	8908	Predicted by at least one method	KALEADPK_00705	845303	846391	-1	hypothetical protein
843264	852172	8908	Predicted by at least one method	KALEADPK_00706	846408	847112	-1	hypothetical protein
843264	852172	8908	Predicted by at least one method	KALEADPK_00707	847109	847627	-1	PAAR motif protein
843264	852172	8908	Predicted by at least one method	KALEADPK_00708	848097	848441	1	Transposase
843264	852172	8908	Predicted by at least one method	KALEADPK_00709	848589	849410	1	Integrase core domain protein
843264	852172	8908	Predicted by at least one method	KALEADPK_00710	849341	849526	-1	TM2 domain protein
843264	852172	8908	Predicted by at least one method	KALEADPK_00711	849769	850407	-1	hypothetical protein
843264	852172	8908	Predicted by at least one method	KALEADPK_00713	851294	852172	-1	hypothetical protein
843264	850407	7143	Predicted by at least one method	KALEADPK_00702	843264	843536	-1	hypothetical protein
843264	850407	7143	Predicted by at least one method	KALEADPK_00703	843700	843981	1	hypothetical protein
843264	850407	7143	Predicted by at least one method	KALEADPK_00704	844603	844926	1	Helix-turn-helix domain protein
843264	850407	7143	Predicted by at least one method	KALEADPK_00705	845303	846391	-1	hypothetical protein
843264	850407	7143	Predicted by at least one method	KALEADPK_00706	846408	847112	-1	hypothetical protein
843264	850407	7143	Predicted by at least one method	KALEADPK_00707	847109	847627	-1	PAAR motif protein
843264	850407	7143	Predicted by at least one method	KALEADPK_00708	848097	848441	1	Transposase
843264	850407	7143	Predicted by at least one method	KALEADPK_00709	848589	849410	1	Integrase core domain protein
843264	850407	7143	Predicted by at least one method	KALEADPK_00710	849341	849526	-1	TM2 domain protein
843264	850407	7143	Predicted by at least one method	KALEADPK_00711	849769	850407	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_00885	1023875	1024318	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_00886	1024296	1025801	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_00887	1025785	1026171	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_05651	1027971	1028594	1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_05650	1029412	1029630	1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_05649	1029627	1029806	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_05648	1029878	1030108	-1	Integrase core domain protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04180	1031749	1033062	1	Aminotransferase class-III
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04179	1033590	1033841	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04178	1034057	1034731	1	hypothetical protein

1024296	1047804	23508	Predicted by at least one method	KALEADPK_04177	1034724	1035770	1	NAD dependent epimerase/dehydratase family protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04176	1035764	1038028	1	Glycosyl hydrolase family 65 central catalytic domain protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04175	1038025	1039266	1	Major Facilitator Superfamily protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04174	1039250	1040350	1	DegT/DnrJ/EryC1/StrS aminotransferase family protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04173	1040384	1040821	-1	Transposase DDE domain protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04172	1040980	1041243	1	Transposase
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04171	1041642	1041962	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04170	1042055	1042309	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04169	1042377	1042739	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04168	1042842	1043633	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04167	1043690	1044040	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04166	1044276	1044983	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04165	1045181	1045333	1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04164	1045468	1045665	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04163	1045739	1045897	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04162	1046035	1046523	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04161	1046849	1046983	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04160	1046985	1047161	-1	hypothetical protein
1024296	1047804	23508	Predicted by at least one method	KALEADPK_04159	1047238	1047804	-1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_00886	1024296	1025801	-1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_00887	1025785	1026171	-1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_05651	1027971	1028594	1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_05650	1029412	1029630	1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_05649	1029627	1029806	-1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_05648	1029878	1030108	-1	Integrase core domain protein

1025785	1045665	19880	Predicted by at least one method	KALEADPK_04180	1031749	1033062	1	Aminotransferase class-III
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04179	1033590	1033841	-1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04178	1034057	1034731	1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04177	1034724	1035770	1	NAD dependent epimerase/dehydratase family protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04176	1035764	1038028	1	Glycosyl hydrolase family 65 central catalytic domain protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04175	1038025	1039266	1	Major Facilitator Superfamily protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04174	1039250	1040350	1	DegT/DnrJ/EryC1/StrS aminotransferase family protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04173	1040384	1040821	-1	Transposase DDE domain protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04172	1040980	1041243	1	Transposase
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04171	1041642	1041962	-1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04170	1042055	1042309	-1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04169	1042377	1042739	-1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04168	1042842	1043633	-1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04167	1043690	1044040	-1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04166	1044276	1044983	-1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04165	1045181	1045333	1	hypothetical protein
1025785	1045665	19880	Predicted by at least one method	KALEADPK_04164	1045468	1045665	-1	hypothetical protein
1047238	1052900	5662	Predicted by at least one method	KALEADPK_04159	1047238	1047804	-1	hypothetical protein
1047238	1052900	5662	Predicted by at least one method	KALEADPK_04158	1048114	1049112	-1	Putative transposase, YhgA-like
1047238	1052900	5662	Predicted by at least one method	KALEADPK_04157	1049198	1049845	1	hypothetical protein
1047238	1052900	5662	Predicted by at least one method	KALEADPK_04156	1050117	1050554	-1	PilM
1047238	1052900	5662	Predicted by at least one method	KALEADPK_04155	1050572	1051951	-1	hypothetical protein
1047238	1052900	5662	Predicted by at least one method	KALEADPK_04154	1051944	1052900	-1	Type II/IV secretion system protein
1047238	1052900	5662	Predicted by at least one method	KALEADPK_04153	1052897	1053427	-1	hypothetical protein

1067070	1085416	18346	Predicted by at least one method	KALEADPK_04141	1067070	1068989	-1	DNA topoisomerase
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04140	1069840	1070328	-1	Single-strand binding protein family protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04139	1070358	1071188	-1	Phage regulatory protein Rha (Phage_pRha)
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04138	1071236	1071784	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04137	1071790	1072518	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04136	1072675	1072872	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04135	1073674	1075005	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04134	1075002	1075757	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04133	1075785	1077512	-1	ParB-like nuclease domain protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04132	1077515	1077784	-1	Arc-like DNA binding domain protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04131	1077805	1078695	-1	D12 class N6 adenine-specific DNA methyltransferase
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04130	1078692	1079714	-1	37-kD nucleoid-associated bacterial protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04129	1079714	1079947	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04128	1079940	1080434	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04127	1080427	1080594	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04126	1080591	1081118	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04125	1081108	1081293	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04124	1081471	1081896	1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04123	1082486	1082923	1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04122	1083045	1083149	1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04121	1084054	1084641	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04120	1084638	1084739	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04119	1084736	1085416	-1	hypothetical protein
1067070	1085416	18346	Predicted by at least one method	KALEADPK_04118	1085413	1086756	-1	hypothetical protein
1071236	1078695	7459	Predicted by at least one method	KALEADPK_04138	1071236	1071784	-1	hypothetical protein
1071236	1078695	7459	Predicted by at least one method	KALEADPK_04137	1071790	1072518	-1	hypothetical protein

1071236	1078695	7459	Predicted by at least one method	KALEADPK_04136	1072675	1072872	-1	hypothetical protein
1071236	1078695	7459	Predicted by at least one method	KALEADPK_04135	1073674	1075005	-1	hypothetical protein
1071236	1078695	7459	Predicted by at least one method	KALEADPK_04134	1075002	1075757	-1	hypothetical protein
1071236	1078695	7459	Predicted by at least one method	KALEADPK_04133	1075785	1077512	-1	ParB-like nuclease domain protein
1071236	1078695	7459	Predicted by at least one method	KALEADPK_04132	1077515	1077784	-1	Arc-like DNA binding domain protein
1071236	1078695	7459	Predicted by at least one method	KALEADPK_04131	1077805	1078695	-1	D12 class N6 adenine-specific DNA methyltransferase
1071236	1078695	7459	Predicted by at least one method	KALEADPK_04130	1078692	1079714	-1	37-kD nucleoid-associated bacterial protein
1079714	1085416	5702	Predicted by at least one method	KALEADPK_04129	1079714	1079947	-1	hypothetical protein
1079714	1085416	5702	Predicted by at least one method	KALEADPK_04128	1079940	1080434	-1	hypothetical protein
1079714	1085416	5702	Predicted by at least one method	KALEADPK_04127	1080427	1080594	-1	hypothetical protein
1079714	1085416	5702	Predicted by at least one method	KALEADPK_04126	1080591	1081118	-1	hypothetical protein
1079714	1085416	5702	Predicted by at least one method	KALEADPK_04125	1081108	1081293	-1	hypothetical protein
1079714	1085416	5702	Predicted by at least one method	KALEADPK_04124	1081471	1081896	1	hypothetical protein
1079714	1085416	5702	Predicted by at least one method	KALEADPK_04123	1082486	1082923	1	hypothetical protein
1079714	1085416	5702	Predicted by at least one method	KALEADPK_04122	1083045	1083149	1	hypothetical protein
1079714	1085416	5702	Predicted by at least one method	KALEADPK_04121	1084054	1084641	-1	hypothetical protein
1079714	1085416	5702	Predicted by at least one method	KALEADPK_04120	1084638	1084739	-1	hypothetical protein
1079714	1085416	5702	Predicted by at least one method	KALEADPK_04119	1084736	1085416	-1	hypothetical protein
1079714	1085416	5702	Predicted by at least one method	KALEADPK_04118	1085413	1086756	-1	hypothetical protein
1086753	1094078	7325	Predicted by at least one method	KALEADPK_04118	1085413	1086756	-1	hypothetical protein
1086753	1094078	7325	Predicted by at least one method	KALEADPK_04117	1086753	1086971	-1	hypothetical protein
1086753	1094078	7325	Predicted by at least one method	KALEADPK_04116	1086955	1087662	-1	HNH endonuclease
1086753	1094078	7325	Predicted by at least one method	KALEADPK_04115	1087659	1088360	-1	hypothetical protein
1086753	1094078	7325	Predicted by at least one method	KALEADPK_04114	1088360	1089511	-1	hypothetical protein
1086753	1094078	7325	Predicted by at least one method	KALEADPK_04113	1089508	1090005	-1	hypothetical protein
1086753	1094078	7325	Predicted by at least one method	KALEADPK_04112	1090002	1090739	-1	hypothetical protein
1086753	1094078	7325	Predicted by at least one method	KALEADPK_04111	1090741	1091679	-1	AAA domain protein
1086753	1094078	7325	Predicted by at least one method	KALEADPK_02507	1093740	1094078	1	hypothetical protein

1100740	1108103	7363	Predicted by at least one method	KALEADPK_02502	1100740	1101405	-1	hypothetical protein
1100740	1108103	7363	Predicted by at least one method	KALEADPK_02501	1101512	1101967	1	MerR, DNA binding
1100740	1108103	7363	Predicted by at least one method	KALEADPK_02500	1103432	1104538	1	NADH:flavin oxidoreductase / NADH oxidase family protein
1100740	1108103	7363	Predicted by at least one method	KALEADPK_02499	1105100	1105504	1	Thioesterase superfamily protein
1100740	1108103	7363	Predicted by at least one method	KALEADPK_02498	1105625	1106185	-1	hypothetical protein
1100740	1108103	7363	Predicted by at least one method	KALEADPK_02497	1106562	1107266	-1	NUDIX domain protein
1100740	1108103	7363	Predicted by at least one method	KALEADPK_02496	1107462	1108103	-1	hypothetical protein
1216210	1223404	7194	Predicted by at least one method	KALEADPK_02390	1215083	1216213	1	Ring hydroxylating alpha subunit (catalytic domain)
1216210	1223404	7194	Predicted by at least one method	KALEADPK_02389	1216210	1216830	1	Bacterial transferase hexapeptide (six repeats)
1216210	1223404	7194	Predicted by at least one method	KALEADPK_02388	1216841	1217980	1	Methyltransferase FkbM domain protein
1216210	1223404	7194	Predicted by at least one method	KALEADPK_02387	1218108	1219382	1	hypothetical protein
1216210	1223404	7194	Predicted by at least one method	KALEADPK_02386	1219427	1220194	1	Cytidylyltransferase
1216210	1223404	7194	Predicted by at least one method	KALEADPK_02385	1220184	1220684	1	hypothetical protein
1216210	1223404	7194	Predicted by at least one method	KALEADPK_02384	1220681	1221784	1	Methyltransferase domain protein
1216210	1223404	7194	Predicted by at least one method	KALEADPK_02383	1221788	1223404	1	HMGL-like protein
1497671	1502143	4472	Predicted by at least one method	KALEADPK_02129	1497671	1498159	1	hypothetical protein
1497671	1502143	4472	Predicted by at least one method	KALEADPK_02128	1498134	1499312	1	Phage integrase family protein
1497671	1502143	4472	Predicted by at least one method	KALEADPK_02127	1499773	1501107	1	hypothetical protein
1497671	1502143	4472	Predicted by at least one method	KALEADPK_02126	1501100	1501405	1	GIY-YIG catalytic domain protein
1497671	1502143	4472	Predicted by at least one method	KALEADPK_02125	1501352	1502143	-1	hypothetical protein
1513380	1518265	4885	Predicted by at least one method	KALEADPK_02117	1512418	1513383	1	Fatty acid hydroxylase superfamily protein
1513380	1518265	4885	Predicted by at least one method	KALEADPK_02116	1513380	1513784	1	hypothetical protein
1513380	1518265	4885	Predicted by at least one method	KALEADPK_02115	1513922	1514713	1	hypothetical protein

1513380	1518265	4885	Predicted by at least one method	KALEADPK_02114	1514994	1516037	-1	Transposase IS116/IS110/IS902 family protein
1513380	1518265	4885	Predicted by at least one method	KALEADPK_02113	1516600	1517439	1	Pterin binding enzyme
1513380	1518265	4885	Predicted by at least one method	KALEADPK_02112	1517501	1518265	1	DDE domain protein
1967944	1974375	6431	Predicted by at least one method	KALEADPK_04779	1967944	1968165	1	hypothetical protein
1967944	1974375	6431	Predicted by at least one method	KALEADPK_04778	1968429	1968686	-1	hypothetical protein
1967944	1974375	6431	Predicted by at least one method	KALEADPK_04777	1969393	1969584	-1	hypothetical protein
1967944	1974375	6431	Predicted by at least one method	KALEADPK_04776	1969696	1969980	-1	hypothetical protein
1967944	1974375	6431	Predicted by at least one method	KALEADPK_04775	1969977	1970378	-1	hypothetical protein
1967944	1974375	6431	Predicted by at least one method	KALEADPK_04774	1970564	1971358	-1	SIR2-like domain protein
1967944	1974375	6431	Predicted by at least one method	KALEADPK_04773	1971912	1972841	-1	Adenosine/AMP deaminase
1967944	1974375	6431	Predicted by at least one method	KALEADPK_04772	1973455	1973769	1	hypothetical protein
1967944	1974375	6431	Predicted by at least one method	KALEADPK_04771	1974163	1974375	1	hypothetical protein
2295121	2303375	8254	Predicted by at least one method	KALEADPK_05686	2295121	2295501	1	hypothetical protein
2295121	2303375	8254	Predicted by at least one method	KALEADPK_05687	2296107	2297096	1	Aldo/keto reductase family protein
2295121	2303375	8254	Predicted by at least one method	KALEADPK_05688	2297093	2297683	1	Flavodoxin
2295121	2303375	8254	Predicted by at least one method	KALEADPK_05689	2297708	2298700	1	Aldo/keto reductase family protein
2295121	2303375	8254	Predicted by at least one method	KALEADPK_05690	2298760	2299227	1	Cupin domain protein
2295121	2303375	8254	Predicted by at least one method	KALEADPK_05691	2299458	2300231	1	Carboxymuconolactone decarboxylase family protein
2295121	2303375	8254	Predicted by at least one method	KALEADPK_05692	2300233	2301297	1	Alpha/beta hydrolase family protein
2295121	2303375	8254	Predicted by at least one method	KALEADPK_05693	2301347	2302399	1	Dienelactone hydrolase family protein
2295121	2303375	8254	Predicted by at least one method	KALEADPK_05694	2302482	2303375	1	LysR substrate binding domain protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05687	2296107	2297096	1	Aldo/keto reductase family protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05688	2297093	2297683	1	Flavodoxin
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05689	2297708	2298700	1	Aldo/keto reductase family protein

2296107	2326026	29919	Predicted by at least one method	KALEADPK_05690	2298760	2299227	1	Cupin domain protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05691	2299458	2300231	1	Carboxymuconolactone decarboxylase family protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05692	2300233	2301297	1	Alpha/beta hydrolase family protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05693	2301347	2302399	1	Dienelactone hydrolase family protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05694	2302482	2303375	1	LysR substrate binding domain protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05695	2303593	2304732	-1	Catalase
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05696	2304911	2306806	-1	Cytochrome C oxidase, cbb3-type, subunit III
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05697	2307011	2308210	1	Phage integrase family protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05698	2308207	2309271	1	hypothetical protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05699	2309624	2310016	1	hypothetical protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05700	2310100	2310357	1	Metal-sensitive transcriptional repressor
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05701	2310367	2311677	1	Major Facilitator Superfamily protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05702	2311946	2312296	1	hypothetical protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05703	2312362	2312640	1	hypothetical protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05704	2313352	2314176	1	hypothetical protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05705	2314255	2316306	1	ParB-like nuclease domain protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05706	2316368	2316577	1	hypothetical protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05707	2317681	2317995	1	hypothetical protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05708	2318059	2318364	-1	hypothetical protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05709	2318605	2318955	1	hypothetical protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05710	2319265	2320035	1	hypothetical protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05711	2320119	2320400	1	Helix-turn-helix domain protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05712	2320427	2321284	1	Replication initiator protein A
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05713	2321538	2322176	1	AAA domain protein

2296107	2326026	29919	Predicted by at least one method	KALEADPK_05714	2322173	2322457	1	hypothetical protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05715	2322454	2322978	1	hypothetical protein
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05716	2322975	2323574	1	Signal peptidase, peptidase S26
2296107	2326026	29919	Predicted by at least one method	KALEADPK_05717	2324023	2326026	1	hypothetical protein
2318605	2322978	4373	Predicted by at least one method	KALEADPK_05709	2318605	2318955	1	hypothetical protein
2318605	2322978	4373	Predicted by at least one method	KALEADPK_05710	2319265	2320035	1	hypothetical protein
2318605	2322978	4373	Predicted by at least one method	KALEADPK_05711	2320119	2320400	1	Helix-turn-helix domain protein
2318605	2322978	4373	Predicted by at least one method	KALEADPK_05712	2320427	2321284	1	Replication initiator protein A
2318605	2322978	4373	Predicted by at least one method	KALEADPK_05713	2321538	2322176	1	AAA domain protein
2318605	2322978	4373	Predicted by at least one method	KALEADPK_05714	2322173	2322457	1	hypothetical protein
2318605	2322978	4373	Predicted by at least one method	KALEADPK_05715	2322454	2322978	1	hypothetical protein
2318605	2322978	4373	Predicted by at least one method	KALEADPK_05716	2322975	2323574	1	Signal peptidase, peptidase S26
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05718	2326093	2326788	-1	ABC-type transport auxiliary lipoprotein component
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05719	2326785	2327714	-1	MlaD protein
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05720	2327806	2328627	-1	ABC transporter
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05721	2328624	2329742	-1	Permease MlaE
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05722	2329778	2330398	-1	hypothetical protein
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05723	2330842	2333946	-1	AcrB/AcrD/AcrF family protein
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05724	2333971	2335137	-1	HlyD family secretion protein
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05725	2335134	2335775	-1	Bacterial regulatory proteins, tetR family
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05726	2335876	2337279	1	Outer membrane efflux protein
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05727	2337373	2338278	1	LysR substrate binding domain protein
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05728	2338633	2338950	1	Small Multidrug Resistance protein
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05729	2339179	2339415	-1	Integrase core domain protein
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05730	2339460	2339990	-1	hypothetical protein

2326093	2343953	17860	Predicted by at least one method	KALEADPK_05731	2340272	2341177	-1	LysR substrate binding domain protein
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05732	2341483	2343480	1	Type IV secretory system Conjugative DNA transfer
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05733	2343477	2343953	1	hypothetical protein
2326093	2343953	17860	Predicted by at least one method	KALEADPK_05734	2343950	2345020	1	Type II/IV secretion system protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06008	2649295	2649507	-1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06009	2649515	2649790	-1	Heavy-metal-associated domain protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06010	2649803	2650153	-1	MerT mercuric transport protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06011	2650228	2650626	1	MerR, DNA binding
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06012	2650616	2651110	-1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06013	2651424	2651903	-1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06014	2651884	2652528	-1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06015	2652567	2653565	-1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06016	2653749	2654720	1	Phage integrase family protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06017	2654750	2655493	1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06018	2655515	2656831	1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06019	2657243	2658652	1	Saccharopine dehydrogenase NADP binding domain protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06020	2658668	2659396	1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06021	2659393	2660298	1	EamA-like transporter family protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06022	2660940	2661302	-1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06023	2661299	2663497	-1	Tn3 transposase DDE domain protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06024	2664187	2665455	-1	Reverse transcriptase (RNA-dependent DNA polymerase)
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06025	2666148	2666780	-1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06026	2666777	2667070	-1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06027	2667413	2668240	1	ABC transporter

2649295	2682507	33212	Predicted by at least one method	KALEADPK_06028	2668237	2669100	1	ABC transporter, phosphonate, periplasmic substrate-binding protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06029	2669109	2669936	1	Binding-protein-dependent transport system inner membrane component
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06030	2669945	2670955	1	D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06031	2670949	2671818	1	LysR substrate binding domain protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06032	2671926	2672219	1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06033	2672216	2672587	1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06034	2672610	2672900	-1	IS66 Orf2 like protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06035	2673813	2674115	-1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06036	2674206	2675606	-1	Type III restriction enzyme, res subunit
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06037	2675603	2676181	-1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06038	2676286	2676507	1	helix-turn-helix protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06039	2677071	2677631	-1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06040	2679116	2681044	-1	hypothetical protein
2649295	2682507	33212	Predicted by at least one method	KALEADPK_06041	2681041	2682507	-1	Phage integrase family protein
2649515	2656831	7316	Predicted by at least one method	KALEADPK_06009	2649515	2649790	-1	Heavy-metal-associated domain protein
2649515	2656831	7316	Predicted by at least one method	KALEADPK_06010	2649803	2650153	-1	MerT mercuric transport protein
2649515	2656831	7316	Predicted by at least one method	KALEADPK_06011	2650228	2650626	1	MerR, DNA binding
2649515	2656831	7316	Predicted by at least one method	KALEADPK_06012	2650616	2651110	-1	hypothetical protein
2649515	2656831	7316	Predicted by at least one method	KALEADPK_06013	2651424	2651903	-1	hypothetical protein
2649515	2656831	7316	Predicted by at least one method	KALEADPK_06014	2651884	2652528	-1	hypothetical protein
2649515	2656831	7316	Predicted by at least one method	KALEADPK_06015	2652567	2653565	-1	hypothetical protein
2649515	2656831	7316	Predicted by at least one method	KALEADPK_06016	2653749	2654720	1	Phage integrase family protein
2649515	2656831	7316	Predicted by at least one method	KALEADPK_06017	2654750	2655493	1	hypothetical protein

2649515	2656831	7316	Predicted by at least one method	KALEADPK_06018	2655515	2656831	1	hypothetical protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06030	2669945	2670955	1	D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06031	2670949	2671818	1	LysR substrate binding domain protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06032	2671926	2672219	1	hypothetical protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06033	2672216	2672587	1	hypothetical protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06034	2672610	2672900	-1	IS66 Orf2 like protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06035	2673813	2674115	-1	hypothetical protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06036	2674206	2675606	-1	Type III restriction enzyme, res subunit
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06037	2675603	2676181	-1	hypothetical protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06038	2676286	2676507	1	helix-turn-helix protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06039	2677071	2677631	-1	hypothetical protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06040	2679116	2681044	-1	hypothetical protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06041	2681041	2682507	-1	Phage integrase family protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06042	2682563	2685076	-1	hypothetical protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06043	2685218	2685634	1	hypothetical protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06044	2685723	2686619	1	Cation efflux family protein
2669945	2687316	17371	Predicted by at least one method	KALEADPK_06045	2686612	2687316	-1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01046	2768032	2768541	1	RadC-like JAB domain protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01047	2768583	2769320	-1	NADPH-dependent FMN reductase
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01048	2769298	2769738	-1	ArsC family protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01049	2769753	2770865	-1	Sodium Bile acid symporter family protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01050	2770862	2772628	-1	Anion-transporting ATPase
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01051	2772642	2773001	-1	Arsenical resistance operon trans-acting repressor ArsD

2768032	2808131	40099	Predicted by at least one method	KALEADPK_01052	2773043	2773540	-1	Low molecular weight phosphotyrosine protein phosphatase
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01053	2773552	2773998	-1	Cadmium-induced protein CadI
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01054	2774011	2774340	-1	Helix-turn-helix domain protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01055	2774710	2775060	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01056	2776108	2776932	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01057	2777011	2779062	1	ParB-like nuclease domain protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01058	2779713	2780513	-1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01059	2781271	2781585	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01060	2781631	2781921	-1	Helix-turn-helix domain protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01061	2782219	2782569	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01062	2782908	2783705	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01063	2783789	2784073	1	Helix-turn-helix domain protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01064	2784100	2784933	1	Replication initiator protein A
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01065	2785199	2785837	1	AAA domain protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01066	2785834	2786082	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01067	2786082	2786615	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01068	2786612	2787211	1	Signal peptidase, peptidase S26
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01069	2787672	2789636	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01070	2789853	2790128	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01071	2790218	2790847	1	Oxygenase, catalysing oxidative methylation of damaged DNA
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01072	2790850	2791500	1	2OG-Fe(II) oxygenase superfamily protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01073	2791580	2791771	1	hypothetical protein

2768032	2808131	40099	Predicted by at least one method	KALEADPK_01074	2791784	2792335	1	6-O-methylguanine DNA methyltransferase, DNA binding domain
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01075	2792506	2792994	1	HhH-GPD superfamily base excision DNA repair protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01076	2793078	2794139	1	6-O-methylguanine DNA methyltransferase, DNA binding domain
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01077	2794140	2794862	1	Oxygenase, catalysing oxidative methylation of damaged DNA
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01078	2795187	2795939	1	Oxygenase, catalysing oxidative methylation of damaged DNA
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01079	2796046	2796795	1	Enoyl-(Acyl carrier protein) reductase
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01080	2796866	2797810	1	LysR substrate binding domain protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01081	2797807	2798085	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01082	2798322	2800331	1	Type IV secretory system Conjugative DNA transfer
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01083	2800328	2800792	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01084	2800789	2801835	1	Type II/IV secretion system protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01085	2801832	2802224	1	TrbC/VIRB2 family protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01086	2802221	2802493	1	Type IV secretory pathway, VirB3-like protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01087	2802509	2804980	1	CagE, TrbE, VirB family, component of type IV transporter system
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01088	2804977	2805702	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01089	2805715	2806032	1	hypothetical protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01090	2806029	2807414	1	TrbL/VirB6 plasmid conjugal transfer protein

2768032	2808131	40099	Predicted by at least one method	KALEADPK_01091	2807427	2808131	1	VirB8 protein
2768032	2808131	40099	Predicted by at least one method	KALEADPK_01092	2808128	2809120	1	Conjugal transfer protein
2768032	2773540	5508	Predicted by at least one method	KALEADPK_01046	2768032	2768541	1	RadC-like JAB domain protein
2768032	2773540	5508	Predicted by at least one method	KALEADPK_01047	2768583	2769320	-1	NADPH-dependent FMN reductase
2768032	2773540	5508	Predicted by at least one method	KALEADPK_01048	2769298	2769738	-1	ArsC family protein
2768032	2773540	5508	Predicted by at least one method	KALEADPK_01049	2769753	2770865	-1	Sodium Bile acid symporter family protein
2768032	2773540	5508	Predicted by at least one method	KALEADPK_01050	2770862	2772628	-1	Anion-transporting ATPase
2768032	2773540	5508	Predicted by at least one method	KALEADPK_01051	2772642	2773001	-1	Arsenical resistance operon trans-acting repressor ArsD
2768032	2773540	5508	Predicted by at least one method	KALEADPK_01052	2773043	2773540	-1	Low molecular weight phosphotyrosine protein phosphatase
2789853	2798085	8232	Predicted by at least one method	KALEADPK_01070	2789853	2790128	1	hypothetical protein
2789853	2798085	8232	Predicted by at least one method	KALEADPK_01071	2790218	2790847	1	Oxygenase, catalysing oxidative methylation of damaged DNA
2789853	2798085	8232	Predicted by at least one method	KALEADPK_01072	2790850	2791500	1	2OG-Fe(II) oxygenase superfamily protein
2789853	2798085	8232	Predicted by at least one method	KALEADPK_01073	2791580	2791771	1	hypothetical protein
2789853	2798085	8232	Predicted by at least one method	KALEADPK_01074	2791784	2792335	1	6-O-methylguanine DNA methyltransferase, DNA binding domain
2789853	2798085	8232	Predicted by at least one method	KALEADPK_01075	2792506	2792994	1	HhH-GPD superfamily base excision DNA repair protein
2789853	2798085	8232	Predicted by at least one method	KALEADPK_01076	2793078	2794139	1	6-O-methylguanine DNA methyltransferase, DNA binding domain
2789853	2798085	8232	Predicted by at least one method	KALEADPK_01077	2794140	2794862	1	Oxygenase, catalysing oxidative methylation of damaged DNA

2789853	2798085	8232	Predicted by at least one method	KALEADPK_01078	2795187	2795939	1	Oxygenase, catalysing oxidative methylation of damaged DNA
2789853	2798085	8232	Predicted by at least one method	KALEADPK_01079	2796046	2796795	1	Enoyl-(Acyl carrier protein) reductase
2789853	2798085	8232	Predicted by at least one method	KALEADPK_01080	2796866	2797810	1	LysR substrate binding domain protein
2789853	2798085	8232	Predicted by at least one method	KALEADPK_01081	2797807	2798085	1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01195	2916391	2917413	1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01196	2917849	2918073	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01197	2918146	2918385	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01198	2918382	2918684	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01199	2919255	2919536	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01200	2919537	2920097	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01201	2920102	2920293	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01202	2920286	2920873	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01203	2920903	2922561	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01204	2922558	2922962	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01205	2922973	2923518	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01206	2923518	2923928	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01207	2923931	2925628	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01208	2925628	2926149	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_01209	2926189	2929275	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_05199	2930730	2930960	1	Integrase core domain protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_05200	2931004	2932842	1	PLD-like domain protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_05201	2933195	2933647	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_05202	2934219	2935613	1	Homeodomain-like domain protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_05203	2936102	2936749	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_05204	2936761	2937780	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_05205	2937813	2938541	-1	hypothetical protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_05206	2938790	2939206	-1	hypothetical protein

2916391	2941982	25591	Predicted by at least one method	KALEADPK_05207	2939785	2940762	-1	Helix-turn-helix domain protein
2916391	2941982	25591	Predicted by at least one method	KALEADPK_05208	2940771	2941982	-1	Beta-lactamase
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01197	2918146	2918385	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01198	2918382	2918684	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01199	2919255	2919536	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01200	2919537	2920097	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01201	2920102	2920293	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01202	2920286	2920873	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01203	2920903	2922561	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01204	2922558	2922962	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01205	2922973	2923518	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01206	2923518	2923928	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01207	2923931	2925628	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01208	2925628	2926149	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_01209	2926189	2929275	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_05199	2930730	2930960	1	Integrase core domain protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_05200	2931004	2932842	1	PLD-like domain protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_05201	2933195	2933647	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_05202	2934219	2935613	1	Homeodomain-like domain protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_05203	2936102	2936749	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_05204	2936761	2937780	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_05205	2937813	2938541	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_05206	2938790	2939206	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_05207	2939785	2940762	-1	Helix-turn-helix domain protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_05208	2940771	2941982	-1	Beta-lactamase
2918146	2948589	30443	Predicted by at least one method	KALEADPK_05209	2942933	2943652	1	MOSC domain protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_05210	2943769	2944365	1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_04259	2947143	2947424	-1	hypothetical protein
2918146	2948589	30443	Predicted by at least one method	KALEADPK_04258	2947421	2948386	-1	HEAT repeats

2918146	2948589	30443	Predicted by at least one method	KALEADPK_04257	2948383	2948589	-1	hypothetical protein
3076442	3082835	6393	Predicted by at least one method	KALEADPK_05656	3076442	3076732	1	hypothetical protein
3076442	3082835	6393	Predicted by at least one method	KALEADPK_05273	3078963	3079667	1	hypothetical protein
3076442	3082835	6393	Predicted by at least one method	KALEADPK_05272	3081468	3082835	1	hypothetical protein
3178426	3187327	8901	Predicted by at least one method	KALEADPK_05246	3178426	3179496	-1	Integrase core domain protein
3178426	3187327	8901	Predicted by at least one method	KALEADPK_05245	3181028	3187327	-1	hypothetical protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_01712	3311061	3311207	-1	hypothetical protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_01713	3311676	3312044	-1	PA-IL-like protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_01714	3313894	3314190	1	Putative exonuclease, RdgC
3311061	3324214	13153	Predicted by at least one method	KALEADPK_01715	3314227	3314709	1	Ftsk gamma domain protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_01716	3314706	3314915	1	LexA DNA binding domain protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_01717	3315032	3316159	-1	PBP superfamily domain protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_01718	3316399	3316896	1	D12 class N6 adenine-specific DNA methyltransferase
3311061	3324214	13153	Predicted by at least one method	KALEADPK_01719	3316896	3317075	1	hypothetical protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_04384	3318665	3318859	1	hypothetical protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_04385	3319590	3320252	-1	hypothetical protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_04386	3320268	3321272	-1	hypothetical protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_04387	3321297	3321995	-1	hypothetical protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_04388	3322205	3322747	1	hypothetical protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_04389	3323018	3323629	1	hypothetical protein
3311061	3324214	13153	Predicted by at least one method	KALEADPK_04390	3323630	3324214	1	hypothetical protein
3337353	3343604	6251	Predicted by at least one method	KALEADPK_04404	3337353	3337886	-1	ProQ/FINO family protein
3337353	3343604	6251	Predicted by at least one method	KALEADPK_04405	3337977	3340862	-1	Bacterial extracellular solute-binding proteins, family 3
3337353	3343604	6251	Predicted by at least one method	KALEADPK_04406	3341550	3342494	-1	LysR substrate binding domain protein
3337353	3343604	6251	Predicted by at least one method	KALEADPK_04407	3342690	3343604	-1	Putative MetA-pathway of phenol degradation
3375917	3382124	6207	Predicted by at least one method	KALEADPK_04442	3375917	3376642	-1	hypothetical protein

3375917	3382124	6207	Predicted by at least one method	KALEADPK_04443	3376681	3377583	-1	hypothetical protein
3375917	3382124	6207	Predicted by at least one method	KALEADPK_04444	3377583	3378083	-1	hypothetical protein
3375917	3382124	6207	Predicted by at least one method	KALEADPK_04445	3378080	3378550	-1	hypothetical protein
3375917	3382124	6207	Predicted by at least one method	KALEADPK_04446	3378547	3379461	-1	ATPase family associated with various cellular activities (AAA)
3375917	3382124	6207	Predicted by at least one method	KALEADPK_04447	3379479	3380054	-1	PIN domain protein
3375917	3382124	6207	Predicted by at least one method	KALEADPK_04448	3380051	3380521	-1	Helix-turn-helix domain protein
3375917	3382124	6207	Predicted by at least one method	KALEADPK_04449	3380725	3381108	1	Plasmid protein of unknown function (Plasmid_RAQPRD)
3375917	3382124	6207	Predicted by at least one method	KALEADPK_04450	3381105	3381338	1	hypothetical protein
3375917	3382124	6207	Predicted by at least one method	KALEADPK_04451	3381355	3381714	1	hypothetical protein
3375917	3382124	6207	Predicted by at least one method	KALEADPK_04452	3381726	3382124	1	hypothetical protein
3375917	3382124	6207	Predicted by at least one method	KALEADPK_04453	3382121	3382813	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04447	3379479	3380054	-1	PIN domain protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04448	3380051	3380521	-1	Helix-turn-helix domain protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04449	3380725	3381108	1	Plasmid protein of unknown function (Plasmid_RAQPRD)
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04450	3381105	3381338	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04451	3381355	3381714	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04452	3381726	3382124	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04453	3382121	3382813	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04454	3382810	3383721	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04455	3383711	3385129	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04456	3385110	3385559	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04457	3385559	3388450	1	F pilus assembly Type-IV secretion system for plasmid transfer
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04458	3388475	3389242	1	Thioredoxin
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04459	3389418	3389912	1	RadC-like JAB domain protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04460	3390077	3390523	1	hypothetical protein

3380051	3422326	42275	Predicted by at least one method	KALEADPK_04461	3390520	3391470	1	TraU protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04462	3391480	3392874	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04463	3392871	3393230	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04464	3393244	3394764	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04465	3394776	3395141	-1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04466	3395226	3395858	-1	RES domain protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04467	3395871	3396497	-1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04468	3396813	3398660	1	Putative helicase
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04469	3399182	3400150	1	Barrel-sandwich domain of CusB or HlyD membrane-fusion
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04470	3400243	3400644	1	AcrB/AcrD/AcrF family protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04471	3400953	3402434	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04472	3402642	3403172	-1	Acetyltransferase (GNAT) domain protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04473	3403178	3404407	-1	Chromate transporter
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04474	3404404	3404706	-1	Transcriptional regulator PadR-like family protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04475	3404805	3405227	-1	ArsC family protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04476	3405242	3406327	-1	Sodium Bile acid symporter family protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04477	3406338	3406835	-1	Low molecular weight phosphotyrosine protein phosphatase
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04478	3406848	3407318	-1	Cadmium-induced protein CadI
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04479	3407332	3407661	-1	Helix-turn-helix domain protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04480	3408609	3409763	-1	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04481	3410017	3410709	-1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04482	3410964	3412865	1	Multicopper oxidase

3380051	3422326	42275	Predicted by at least one method	KALEADPK_04483	3412891	3413871	1	Copper resistance protein B precursor (CopB)
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04484	3413909	3414394	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04485	3414428	3414700	1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04486	3415219	3417294	1	E1-E2 ATPase
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04487	3417436	3417822	1	CopC domain protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04488	3417827	3418753	1	Copper resistance protein D
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04489	3418882	3419166	1	Copper resistance protein K
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04490	3419398	3420288	1	LysR substrate binding domain protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04491	3421183	3421425	-1	hypothetical protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04492	3421871	3422326	-1	Transposase DDE domain protein
3380051	3422326	42275	Predicted by at least one method	KALEADPK_04493	3422289	3422663	-1	hypothetical protein
3407332	3414700	7368	Predicted by at least one method	KALEADPK_04479	3407332	3407661	-1	Helix-turn-helix domain protein
3407332	3414700	7368	Predicted by at least one method	KALEADPK_04480	3408609	3409763	-1	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
3407332	3414700	7368	Predicted by at least one method	KALEADPK_04481	3410017	3410709	-1	hypothetical protein
3407332	3414700	7368	Predicted by at least one method	KALEADPK_04482	3410964	3412865	1	Multicopper oxidase
3407332	3414700	7368	Predicted by at least one method	KALEADPK_04483	3412891	3413871	1	Copper resistance protein B precursor (CopB)
3407332	3414700	7368	Predicted by at least one method	KALEADPK_04484	3413909	3414394	1	hypothetical protein
3407332	3414700	7368	Predicted by at least one method	KALEADPK_04485	3414428	3414700	1	hypothetical protein
3417436	3424177	6741	Predicted by at least one method	KALEADPK_04487	3417436	3417822	1	CopC domain protein
3417436	3424177	6741	Predicted by at least one method	KALEADPK_04488	3417827	3418753	1	Copper resistance protein D
3417436	3424177	6741	Predicted by at least one method	KALEADPK_04489	3418882	3419166	1	Copper resistance protein K
3417436	3424177	6741	Predicted by at least one method	KALEADPK_04490	3419398	3420288	1	LysR substrate binding domain protein
3417436	3424177	6741	Predicted by at least one method	KALEADPK_04491	3421183	3421425	-1	hypothetical protein
3417436	3424177	6741	Predicted by at least one method	KALEADPK_04492	3421871	3422326	-1	Transposase DDE domain protein
3417436	3424177	6741	Predicted by at least one method	KALEADPK_04493	3422289	3422663	-1	hypothetical protein

3417436	3424177	6741	Predicted by at least one method	KALEADPK_04494	3422870	3424177	1	Outer membrane efflux protein
3554156	3559225	5069	Predicted by at least one method	KALEADPK_04603	3554156	3554473	-1	hypothetical protein
3554156	3559225	5069	Predicted by at least one method	KALEADPK_04604	3554717	3555301	-1	hypothetical protein
3554156	3559225	5069	Predicted by at least one method	KALEADPK_04605	3555301	3555744	-1	hypothetical protein
3554156	3559225	5069	Predicted by at least one method	KALEADPK_04606	3556331	3557410	-1	Type II secretion system (T2SS), protein K
3554156	3559225	5069	Predicted by at least one method	KALEADPK_04607	3557400	3557990	-1	hypothetical protein
3554156	3559225	5069	Predicted by at least one method	KALEADPK_04608	3557987	3558412	-1	hypothetical protein
3554156	3559225	5069	Predicted by at least one method	KALEADPK_04609	3558412	3558849	-1	hypothetical protein
3554156	3559225	5069	Predicted by at least one method	KALEADPK_04610	3558791	3559225	-1	Type II secretion system (T2SS), protein G
3633572	3647670	14098	Predicted by at least one method	KALEADPK_04677	3633572	3633925	-1	Gamma-glutamyl cyclotransferase, AIG2-like
3633572	3647670	14098	Predicted by at least one method	KALEADPK_04678	3634120	3634662	1	hypothetical protein
3633572	3647670	14098	Predicted by at least one method	KALEADPK_04679	3634751	3635695	1	Dyp-type peroxidase family protein
3633572	3647670	14098	Predicted by at least one method	KALEADPK_04680	3635938	3637767	1	AAA domain (Cdc48 subfamily)
3633572	3647670	14098	Predicted by at least one method	KALEADPK_04681	3637769	3638407	1	4Fe-4S single cluster domain protein
3633572	3647670	14098	Predicted by at least one method	KALEADPK_04682	3638422	3644718	1	AAA domain protein
3633572	3647670	14098	Predicted by at least one method	KALEADPK_04683	3644715	3646064	1	hypothetical protein
3633572	3647670	14098	Predicted by at least one method	KALEADPK_04684	3646273	3647670	-1	Helix-turn-helix domain protein
3646273	3650296	4023	Predicted by at least one method	KALEADPK_04684	3646273	3647670	-1	Helix-turn-helix domain protein
3646273	3650296	4023	Predicted by at least one method	KALEADPK_04685	3647685	3648083	-1	HTH-like domain protein
3646273	3650296	4023	Predicted by at least one method	KALEADPK_04686	3648116	3648712	-1	Transposase
3646273	3650296	4023	Predicted by at least one method	KALEADPK_04687	3649385	3650296	-1	Restriction endonuclease
3669314	3684162	14848	Predicted by at least one method	KALEADPK_04709	3669314	3669583	1	Extracellular deoxyribonuclease
3669314	3684162	14848	Predicted by at least one method	KALEADPK_04710	3669905	3670132	-1	helix-turn-helix protein
3669314	3684162	14848	Predicted by at least one method	KALEADPK_04711	3670234	3670824	1	hypothetical protein

3669314	3684162	14848	Predicted by at least one method	KALEADPK_04712	3670821	3672221	1	Type III restriction enzyme, res subunit
3669314	3684162	14848	Predicted by at least one method	KALEADPK_04713	3672311	3672619	1	hypothetical protein
3669314	3684162	14848	Predicted by at least one method	KALEADPK_04714	3673012	3673611	1	hypothetical protein
3669314	3684162	14848	Predicted by at least one method	KALEADPK_04715	3673765	3675015	-1	TerD domain protein
3669314	3684162	14848	Predicted by at least one method	KALEADPK_04716	3675262	3676467	-1	hypothetical protein
3669314	3684162	14848	Predicted by at least one method	KALEADPK_04717	3676791	3677936	-1	Glycerate kinase family protein
3669314	3684162	14848	Predicted by at least one method	KALEADPK_04718	3678064	3679149	-1	Putative sugar diacid recognition
3669314	3684162	14848	Predicted by at least one method	KALEADPK_04719	3679309	3679692	-1	Transposase IS66 family protein
3669314	3684162	14848	Predicted by at least one method	KALEADPK_02995	3681525	3682718	-1	hypothetical protein
3669314	3684162	14848	Predicted by at least one method	KALEADPK_02994	3682831	3684162	-1	hypothetical protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02994	3682831	3684162	-1	hypothetical protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02993	3684537	3685115	-1	TerD domain protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02992	3685151	3685729	-1	TerD domain protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02991	3685758	3686792	-1	Integral membrane protein TerC family protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02990	3686805	3687254	-1	Tellurite resistance protein TerB
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02989	3687302	3688483	-1	TerD domain protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02988	3688480	3689073	-1	TerD domain protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02987	3689076	3689804	-1	haloacid dehalogenase-like hydrolase
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02986	3689804	3690751	-1	C-C_Bond_Lyase of the TIM-Barrel fold protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02985	3690751	3691845	-1	Phosphoribosyl transferase (PRTase)
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02984	3691838	3692596	-1	hypothetical protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02983	3692586	3693713	-1	Phosphoribosyl transferase
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02982	3693782	3694921	-1	Trypsin-like peptidase domain protein

3682831	3704658	21827	Predicted by at least one method	KALEADPK_02981	3694997	3696244	-1	ATP-grasp in the biosynthetic pathway with Ter operon
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02980	3696473	3697579	-1	Deoxyribonuclease
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02979	3698364	3700238	-1	Phage integrase family protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02978	3700238	3701905	-1	hypothetical protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02977	3701902	3703041	-1	Phage integrase family protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02976	3703108	3703617	1	Endonuclease I
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02975	3703636	3704154	1	Staphylococcal nuclease homologue
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02974	3704129	3704359	-1	hypothetical protein
3682831	3704658	21827	Predicted by at least one method	KALEADPK_02973	3704425	3704658	-1	hypothetical protein
3692586	3703041	10455	Predicted by at least one method	KALEADPK_02984	3691838	3692596	-1	hypothetical protein
3692586	3703041	10455	Predicted by at least one method	KALEADPK_02983	3692586	3693713	-1	Phosphoribosyl transferase
3692586	3703041	10455	Predicted by at least one method	KALEADPK_02982	3693782	3694921	-1	Trypsin-like peptidase domain protein
3692586	3703041	10455	Predicted by at least one method	KALEADPK_02981	3694997	3696244	-1	ATP-grasp in the biosynthetic pathway with Ter operon
3692586	3703041	10455	Predicted by at least one method	KALEADPK_02980	3696473	3697579	-1	Deoxyribonuclease
3692586	3703041	10455	Predicted by at least one method	KALEADPK_02979	3698364	3700238	-1	Phage integrase family protein
3692586	3703041	10455	Predicted by at least one method	KALEADPK_02978	3700238	3701905	-1	hypothetical protein
3692586	3703041	10455	Predicted by at least one method	KALEADPK_02977	3701902	3703041	-1	Phage integrase family protein
4127091	4137608	10517	Predicted by at least one method	KALEADPK_00423	4127091	4128107	-1	Glycosyl transferase family 4
4127091	4137608	10517	Predicted by at least one method	KALEADPK_00422	4128107	4129060	-1	NAD dependent epimerase/dehydratase family protein
4127091	4137608	10517	Predicted by at least one method	KALEADPK_00421	4129057	4130010	-1	Glycosyl transferases group 1
4127091	4137608	10517	Predicted by at least one method	KALEADPK_00420	4130238	4131890	-1	Heparinase II/III-like protein
4127091	4137608	10517	Predicted by at least one method	KALEADPK_00419	4131899	4134043	-1	Zinc-binding dehydrogenase
4127091	4137608	10517	Predicted by at least one method	KALEADPK_00418	4134181	4135023	-1	hypothetical protein
4127091	4137608	10517	Predicted by at least one method	KALEADPK_00417	4135020	4135691	-1	hypothetical protein
4127091	4137608	10517	Predicted by at least one method	KALEADPK_00416	4135685	4136353	-1	hypothetical protein

4127091	4137608	10517	Predicted by at least one method	KALEADPK_00415	4136346	4137608	-1	Polysaccharide biosynthesis protein
4139035	4143888	4853	Predicted by at least one method	KALEADPK_00413	4139035	4140120	-1	UDP-N-acetylglucosamine 2-epimerase
4139035	4143888	4853	Predicted by at least one method	KALEADPK_04310	4142098	4143015	-1	Chain length determinant protein
4139035	4143888	4853	Predicted by at least one method	KALEADPK_04311	4143604	4143888	-1	Bacterial DNA-binding protein
4277872	4282485	4613	Predicted by at least one method	KALEADPK_02609	4277872	4278825	-1	LysR substrate binding domain protein
4277872	4282485	4613	Predicted by at least one method	KALEADPK_02610	4278927	4279481	1	NADPH-dependent FMN reductase
4277872	4282485	4613	Predicted by at least one method	KALEADPK_02611	4279557	4280174	1	hypothetical protein
4277872	4282485	4613	Predicted by at least one method	KALEADPK_02612	4280320	4281159	1	NAD(P)H-binding protein
4277872	4282485	4613	Predicted by at least one method	KALEADPK_02613	4281271	4281657	1	Glycine cleavage H-protein
4277872	4282485	4613	Predicted by at least one method	KALEADPK_02614	4281742	4282485	1	hypothetical protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03747	4727394	4728797	1	Beta-Casp domain protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03746	4728880	4729950	1	putative lysine decarboxylase
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03745	4729972	4730433	-1	RecX family protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03744	4730439	4731062	-1	recA bacterial DNA recombination protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03743	4731134	4732882	1	hypothetical protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03742	4732875	4734764	1	hypothetical protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03741	4735302	4736588	1	hypothetical protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03740	4736765	4737124	1	hypothetical protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03739	4737125	4737421	1	hypothetical protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03738	4737506	4738084	-1	Plasmid pRiA4b ORF-3-like protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03737	4738413	4738613	-1	hypothetical protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03736	4738757	4739581	-1	hypothetical protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03735	4739993	4741198	1	Fatty acid desaturase
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03734	4742429	4743880	1	Aldehyde dehydrogenase family protein

4727394	4760080	32686	Predicted by at least one method	KALEADPK_03733	4743919	4745577	1	GMC oxidoreductase
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03732	4745654	4747048	1	AMP-binding enzyme
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03731	4747395	4748087	1	OmpW family protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03730	4749102	4750544	1	Methyl-accepting chemotaxis protein (MCP) signaling domain protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03729	4750786	4751064	-1	IstB-like ATP binding protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03728	4751162	4751500	-1	IS66 Orf2 like protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03727	4751849	4753006	-1	Pyridine nucleotide-disulfide oxidoreductase
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03726	4753056	4755704	-1	Bacterial regulatory proteins, luxR family
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03725	4755964	4756140	-1	Transposase DDE domain protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03724	4756803	4757402	-1	hypothetical protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03723	4757772	4758314	-1	recA bacterial DNA recombination protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03722	4758916	4759440	-1	recA bacterial DNA recombination protein
4727394	4760080	32686	Predicted by at least one method	KALEADPK_03721	4759574	4760080	-1	Competence-damaged protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03743	4731134	4732882	1	hypothetical protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03742	4732875	4734764	1	hypothetical protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03741	4735302	4736588	1	hypothetical protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03740	4736765	4737124	1	hypothetical protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03739	4737125	4737421	1	hypothetical protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03738	4737506	4738084	-1	Plasmid pRiA4b ORF-3-like protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03737	4738413	4738613	-1	hypothetical protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03736	4738757	4739581	-1	hypothetical protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03735	4739993	4741198	1	Fatty acid desaturase
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03734	4742429	4743880	1	Aldehyde dehydrogenase family protein

4731134	4756140	25006	Predicted by at least one method	KALEADPK_03733	4743919	4745577	1	GMC oxidoreductase
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03732	4745654	4747048	1	AMP-binding enzyme
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03731	4747395	4748087	1	OmpW family protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03730	4749102	4750544	1	Methyl-accepting chemotaxis protein (MCP) signaling domain protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03729	4750786	4751064	-1	IstB-like ATP binding protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03728	4751162	4751500	-1	IS66 Orf2 like protein
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03727	4751849	4753006	-1	Pyridine nucleotide-disulfide oxidoreductase
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03726	4753056	4755704	-1	Bacterial regulatory proteins, luxR family
4731134	4756140	25006	Predicted by at least one method	KALEADPK_03725	4755964	4756140	-1	Transposase DDE domain protein
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01726	5204561	5206642	-1	Clp protease
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01727	5206614	5208260	-1	Phage portal protein, lambda family
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01728	5208260	5208475	-1	hypothetical protein
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01729	5208466	5210445	-1	Phage terminase large subunit (GpA)
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01730	5210417	5210962	-1	Phage DNA packaging protein Nu1
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01731	5211082	5211825	-1	hypothetical protein
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01732	5211878	5212075	-1	hypothetical protein
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01733	5212289	5212528	-1	hypothetical protein
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01734	5212528	5213145	-1	hypothetical protein
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01735	5213142	5213474	-1	Phage holin family (Lysis protein S)
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01736	5213559	5214086	-1	Phage regulatory protein Rha (Phage_pRha)
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01737	5214625	5215014	-1	Phage antitermination protein Q
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01738	5215011	5215289	-1	hypothetical protein
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01739	5215286	5216683	-1	hypothetical protein

5206614	5218542	11928	Predicted by at least one method	KALEADPK_01740	5216680	5217495	-1	IstB-like ATP binding protein
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01741	5217476	5218315	-1	Helix-turn-helix domain protein
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01742	5218312	5218542	-1	hypothetical protein
5206614	5218542	11928	Predicted by at least one method	KALEADPK_01743	5218539	5219303	-1	Phage regulatory protein Rha (Phage_pRha)
5452468	5500510	48042	Predicted by at least one method	KALEADPK_04808	5451722	5452471	1	RDD family protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_04807	5452468	5453448	1	Stage II sporulation protein M
5452468	5500510	48042	Predicted by at least one method	KALEADPK_04806	5453435	5455006	1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_04805	5455003	5456286	1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_04804	5456678	5457124	1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_04803	5457397	5457759	-1	MerR family regulatory protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_04802	5457830	5458552	-1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_04801	5458948	5460093	1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_04800	5460123	5460911	1	Enoyl-CoA hydratase/isomerase
5452468	5500510	48042	Predicted by at least one method	KALEADPK_04799	5461002	5461778	1	short chain dehydrogenase
5452468	5500510	48042	Predicted by at least one method	KALEADPK_04798	5461986	5463551	1	AMP-binding enzyme
5452468	5500510	48042	Predicted by at least one method	KALEADPK_04797	5463650	5464891	1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05274	5466662	5466901	1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05275	5466894	5467226	1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05276	5468418	5468882	-1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05277	5469399	5470526	-1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05278	5470610	5471797	-1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05279	5471888	5472655	-1	short chain dehydrogenase
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05280	5472725	5473765	-1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05281	5473836	5475539	-1	AMP-binding enzyme
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05282	5475831	5477321	1	Aldehyde dehydrogenase family protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05283	5477417	5479321	-1	Sigma-54 interaction domain protein

5452468	5500510	48042	Predicted by at least one method	KALEADPK_05284	5479577	5480485	1	Putative MetA-pathway of phenol degradation
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05285	5480534	5482621	1	PQQ enzyme repeat protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05286	5482833	5483747	1	Beta-lactamase superfamily domain protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05287	5483777	5484529	1	TENA/THI-4/PQQC family protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05288	5484526	5484804	1	Coenzyme PQQ synthesis protein D (PqqD)
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05289	5484776	5485927	1	Radical SAM superfamily protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05290	5485928	5488288	1	Insulinase (Peptidase family M16)
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05291	5488285	5489217	-1	LysR substrate binding domain protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05292	5489530	5489856	1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05293	5489853	5491502	1	Sodium:solute symporter family protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05294	5491919	5493619	1	AMP-binding enzyme
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05295	5493720	5495228	1	Aldehyde dehydrogenase family protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05296	5495275	5496048	1	Enoyl-CoA hydratase/isomerase
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05297	5496085	5496975	1	NAD binding domain of 6-phosphogluconate dehydrogenase
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05298	5496978	5498063	1	Enoyl-CoA hydratase/isomerase
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05299	5498079	5499230	1	hypothetical protein
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05300	5499434	5500057	1	Bacterial regulatory proteins, tetR family
5452468	5500510	48042	Predicted by at least one method	KALEADPK_05301	5500130	5500510	1	MerR HTH family regulatory protein
5456678	5468882	12204	Predicted by at least one method	KALEADPK_04804	5456678	5457124	1	hypothetical protein

5456678	5468882	12204	Predicted by at least one method	KALEADPK_04803	5457397	5457759	-1	MerR family regulatory protein
5456678	5468882	12204	Predicted by at least one method	KALEADPK_04802	5457830	5458552	-1	hypothetical protein
5456678	5468882	12204	Predicted by at least one method	KALEADPK_04801	5458948	5460093	1	hypothetical protein
5456678	5468882	12204	Predicted by at least one method	KALEADPK_04800	5460123	5460911	1	Enoyl-CoA hydratase/isomerase
5456678	5468882	12204	Predicted by at least one method	KALEADPK_04799	5461002	5461778	1	short chain dehydrogenase
5456678	5468882	12204	Predicted by at least one method	KALEADPK_04798	5461986	5463551	1	AMP-binding enzyme
5456678	5468882	12204	Predicted by at least one method	KALEADPK_04797	5463650	5464891	1	hypothetical protein
5456678	5468882	12204	Predicted by at least one method	KALEADPK_05274	5466662	5466901	1	hypothetical protein
5456678	5468882	12204	Predicted by at least one method	KALEADPK_05275	5466894	5467226	1	hypothetical protein
5456678	5468882	12204	Predicted by at least one method	KALEADPK_05276	5468418	5468882	-1	hypothetical protein
5749094	5756549	7455	Predicted by at least one method	KALEADPK_05536	5749094	5749459	1	hypothetical protein
5749094	5756549	7455	Predicted by at least one method	KALEADPK_05537	5749456	5750988	1	hypothetical protein
5749094	5756549	7455	Predicted by at least one method	KALEADPK_05538	5751023	5751376	-1	hypothetical protein
5749094	5756549	7455	Predicted by at least one method	KALEADPK_05539	5751701	5752615	-1	hypothetical protein
5749094	5756549	7455	Predicted by at least one method	KALEADPK_05540	5752641	5752880	-1	hypothetical protein
5749094	5756549	7455	Predicted by at least one method	KALEADPK_05541	5753323	5755212	1	Putative helicase
5749094	5756549	7455	Predicted by at least one method	KALEADPK_05542	5755209	5756549	1	Phage integrase family protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03373	5914803	5915999	1	Phage integrase family protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03374	5915977	5916675	1	hypothetical protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03375	5916698	5918320	-1	N-6 DNA Methylase
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03376	5918317	5919432	-1	AAA domain protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03377	5919429	5920691	-1	Type I restriction modification DNA specificity domain protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03378	5920688	5921851	-1	Putative DNA-binding domain protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03379	5921833	5924472	-1	hypothetical protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03380	5924469	5927441	-1	hypothetical protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03381	5927509	5927718	-1	Helix-turn-helix domain protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03382	5928306	5929043	-1	hypothetical protein

5914803	5933583	18780	Predicted by at least one method	KALEADPK_03383	5929173	5930747	1	ATPase family associated with various cellular activities (AAA)
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03384	5930728	5931009	-1	hypothetical protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03385	5930996	5931472	-1	Putative molybdenum carrier
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03386	5931469	5931885	-1	hypothetical protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03387	5931882	5932526	-1	hypothetical protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03388	5932544	5933200	-1	hypothetical protein
5914803	5933583	18780	Predicted by at least one method	KALEADPK_03389	5933344	5933583	1	helix-turn-helix protein
5915977	5924472	8495	Predicted by at least one method	KALEADPK_03373	5914803	5915999	1	Phage integrase family protein
5915977	5924472	8495	Predicted by at least one method	KALEADPK_03374	5915977	5916675	1	hypothetical protein
5915977	5924472	8495	Predicted by at least one method	KALEADPK_03375	5916698	5918320	-1	N-6 DNA Methylase
5915977	5924472	8495	Predicted by at least one method	KALEADPK_03376	5918317	5919432	-1	AAA domain protein
5915977	5924472	8495	Predicted by at least one method	KALEADPK_03377	5919429	5920691	-1	Type I restriction modification DNA specificity domain protein
5915977	5924472	8495	Predicted by at least one method	KALEADPK_03378	5920688	5921851	-1	Putative DNA-binding domain protein
5915977	5924472	8495	Predicted by at least one method	KALEADPK_03379	5921833	5924472	-1	hypothetical protein
5915977	5924472	8495	Predicted by at least one method	KALEADPK_03380	5924469	5927441	-1	hypothetical protein
5927509	5935264	7755	Predicted by at least one method	KALEADPK_03381	5927509	5927718	-1	Helix-turn-helix domain protein
5927509	5935264	7755	Predicted by at least one method	KALEADPK_03382	5928306	5929043	-1	hypothetical protein
5927509	5935264	7755	Predicted by at least one method	KALEADPK_03383	5929173	5930747	1	ATPase family associated with various cellular activities (AAA)
5927509	5935264	7755	Predicted by at least one method	KALEADPK_03384	5930728	5931009	-1	hypothetical protein
5927509	5935264	7755	Predicted by at least one method	KALEADPK_03385	5930996	5931472	-1	Putative molybdenum carrier
5927509	5935264	7755	Predicted by at least one method	KALEADPK_03386	5931469	5931885	-1	hypothetical protein
5927509	5935264	7755	Predicted by at least one method	KALEADPK_03387	5931882	5932526	-1	hypothetical protein
5927509	5935264	7755	Predicted by at least one method	KALEADPK_03388	5932544	5933200	-1	hypothetical protein
5927509	5935264	7755	Predicted by at least one method	KALEADPK_03389	5933344	5933583	1	helix-turn-helix protein
5927509	5935264	7755	Predicted by at least one method	KALEADPK_03390	5933991	5935013	-1	Plasmid encoded RepA protein

5927509	5935264	7755	Predicted by at least one method	KALEADPK_03391	5935052	5935264	-1	Prophage CP4-57 regulatory protein (AlpA)
6322474	6334250	11776	Predicted by at least one method	KALEADPK_00303	6322474	6323373	-1	Bacterial extracellular solute-binding proteins, family 3
6322474	6334250	11776	Predicted by at least one method	KALEADPK_00304	6323416	6323766	-1	Endoribonuclease L-PSP
6322474	6334250	11776	Predicted by at least one method	KALEADPK_00305	6323791	6325041	-1	FAD dependent oxidoreductase
6322474	6334250	11776	Predicted by at least one method	KALEADPK_00306	6325154	6326062	1	LysR substrate binding domain protein
6322474	6334250	11776	Predicted by at least one method	KALEADPK_00307	6326130	6327008	-1	Putative beta-lactamase HcpC
6322474	6334250	11776	Predicted by at least one method	KALEADPK_00308	6327008	6327886	-1	Sel1 repeat protein
6322474	6334250	11776	Predicted by at least one method	KALEADPK_00309	6327886	6328734	-1	Sel1 repeat protein
6322474	6334250	11776	Predicted by at least one method	KALEADPK_00310	6328765	6329586	-1	Sel1 repeat protein
6322474	6334250	11776	Predicted by at least one method	KALEADPK_00311	6329644	6331881	-1	PLD-like domain protein
6322474	6334250	11776	Predicted by at least one method	KALEADPK_00312	6331878	6334250	-1	Phage late control gene D protein (GPD)
6400927	6412329	11402	Predicted by at least one method	KALEADPK_00376	6400927	6401958	1	Phage integrase family protein
6400927	6412329	11402	Predicted by at least one method	KALEADPK_00377	6402025	6402444	-1	hypothetical protein
6400927	6412329	11402	Predicted by at least one method	KALEADPK_00378	6403142	6408100	1	AAA domain protein
6400927	6412329	11402	Predicted by at least one method	KALEADPK_00379	6408093	6409649	1	hypothetical protein
6400927	6412329	11402	Predicted by at least one method	KALEADPK_00380	6410150	6410665	-1	hypothetical protein
6400927	6412329	11402	Predicted by at least one method	KALEADPK_00381	6410662	6412329	-1	Phage integrase family protein
6466531	6470606	4075	Predicted by at least one method	KALEADPK_01217	6466531	6466701	-1	hypothetical protein
6466531	6470606	4075	Predicted by at least one method	KALEADPK_01218	6466698	6468389	-1	Phage integrase family protein
6466531	6470606	4075	Predicted by at least one method	KALEADPK_01219	6468386	6469516	-1	Phage integrase family protein
6466531	6470606	4075	Predicted by at least one method	KALEADPK_01220	6469915	6470241	1	hypothetical protein
6466531	6470606	4075	Predicted by at least one method	KALEADPK_01221	6470238	6470606	1	hypothetical protein
6471136	6476830	5694	Predicted by at least one method	KALEADPK_01223	6471136	6471651	1	Acetyltransferase (GNAT) domain protein
6471136	6476830	5694	Predicted by at least one method	KALEADPK_01224	6472168	6473208	-1	hypothetical protein
6471136	6476830	5694	Predicted by at least one method	KALEADPK_01225	6473814	6476078	-1	hypothetical protein
6471136	6476830	5694	Predicted by at least one method	KALEADPK_01226	6476666	6476830	1	hypothetical protein

6608090	6614169	6079	Predicted by at least one method	KALEADPK_01348	6608090	6608713	-1	hypothetical protein
6608090	6614169	6079	Predicted by at least one method	KALEADPK_01349	6609292	6610080	-1	hypothetical protein
6608090	6614169	6079	Predicted by at least one method	KALEADPK_02867	6611840	6612565	-1	Sulfite exporter TauE/SafE
6608090	6614169	6079	Predicted by at least one method	KALEADPK_02866	6612901	6613314	1	Low molecular weight phosphotyrosine protein phosphatase
6608090	6614169	6079	Predicted by at least one method	KALEADPK_02865	6613323	6613679	1	Bacterial regulatory protein, arsR family
6608090	6614169	6079	Predicted by at least one method	KALEADPK_02864	6613699	6614169	1	Low molecular weight phosphotyrosine protein phosphatase
6617540	6630704	13164	Predicted by at least one method	KALEADPK_02859	6617540	6618772	1	Major Facilitator Superfamily protein
6617540	6630704	13164	Predicted by at least one method	KALEADPK_02858	6618852	6619289	1	hypothetical protein
6617540	6630704	13164	Predicted by at least one method	KALEADPK_02857	6619348	6620109	1	Helix-turn-helix domain protein
6617540	6630704	13164	Predicted by at least one method	KALEADPK_02856	6620142	6620957	1	Fatty acid hydroxylase superfamily protein
6617540	6630704	13164	Predicted by at least one method	KALEADPK_02855	6621077	6622933	1	AAA domain, putative AbiEii toxin, Type IV TA system
6617540	6630704	13164	Predicted by at least one method	KALEADPK_02854	6622930	6624642	1	hypothetical protein
6617540	6630704	13164	Predicted by at least one method	KALEADPK_02853	6624708	6624845	-1	hypothetical protein
6617540	6630704	13164	Predicted by at least one method	KALEADPK_02852	6624796	6626154	-1	Phage integrase family protein
6617540	6630704	13164	Predicted by at least one method	KALEADPK_02851	6626644	6628608	-1	hypothetical protein
6617540	6630704	13164	Predicted by at least one method	KALEADPK_02850	6628608	6630704	-1	hypothetical protein
6620142	6634456	14314	Predicted by at least one method	KALEADPK_02856	6620142	6620957	1	Fatty acid hydroxylase superfamily protein
6620142	6634456	14314	Predicted by at least one method	KALEADPK_02855	6621077	6622933	1	AAA domain, putative AbiEii toxin, Type IV TA system
6620142	6634456	14314	Predicted by at least one method	KALEADPK_02854	6622930	6624642	1	hypothetical protein
6620142	6634456	14314	Predicted by at least one method	KALEADPK_02853	6624708	6624845	-1	hypothetical protein
6620142	6634456	14314	Predicted by at least one method	KALEADPK_02852	6624796	6626154	-1	Phage integrase family protein
6620142	6634456	14314	Predicted by at least one method	KALEADPK_02851	6626644	6628608	-1	hypothetical protein

6620142	6634456	14314	Predicted by at least one method	KALEADPK_02850	6628608	6630704	-1	hypothetical protein
6620142	6634456	14314	Predicted by at least one method	KALEADPK_02849	6630790	6631254	1	hypothetical protein
6620142	6634456	14314	Predicted by at least one method	KALEADPK_02848	6631379	6633364	1	BCCT, betaine/carnitine/choline family transporter
6620142	6634456	14314	Predicted by at least one method	KALEADPK_02847	6633407	6634456	-1	hypothetical protein
6910795	6918882	8087	Predicted by at least one method	KALEADPK_06446	6910795	6914166	-1	AAA domain protein
6910795	6918882	8087	Predicted by at least one method	KALEADPK_06445	6914170	6914607	-1	hypothetical protein
6910795	6918882	8087	Predicted by at least one method	KALEADPK_06444	6914610	6915140	-1	hypothetical protein
6910795	6918882	8087	Predicted by at least one method	KALEADPK_06443	6915137	6916213	-1	hypothetical protein
6910795	6918882	8087	Predicted by at least one method	KALEADPK_06442	6916364	6917755	-1	Type III restriction enzyme, res subunit
6910795	6918882	8087	Predicted by at least one method	KALEADPK_06441	6917752	6918336	-1	hypothetical protein
6910795	6918882	8087	Predicted by at least one method	KALEADPK_06440	6918440	6918667	1	helix-turn-helix protein
6910795	6918882	8087	Predicted by at least one method	KALEADPK_06439	6918664	6918882	-1	hypothetical protein
6929981	6937604	7623	Predicted by at least one method	KALEADPK_06430	6929981	6931603	-1	Transposon Tn7 transposition protein TnsE
6929981	6937604	7623	Predicted by at least one method	KALEADPK_06429	6931596	6933098	-1	TniQ
6929981	6937604	7623	Predicted by at least one method	KALEADPK_06428	6933100	6934710	-1	Bacterial TniB protein
6929981	6937604	7623	Predicted by at least one method	KALEADPK_06427	6934703	6936790	-1	Integrase core domain protein
6929981	6937604	7623	Predicted by at least one method	KALEADPK_06426	6936777	6937604	-1	hypothetical protein
7013436	7028947	15511	Predicted by at least one method	KALEADPK_04309	7013436	7013681	-1	hypothetical protein
7013436	7028947	15511	Predicted by at least one method	KALEADPK_04308	7014024	7014500	1	hypothetical protein
7013436	7028947	15511	Predicted by at least one method	KALEADPK_04307	7015787	7017139	1	hypothetical protein
7013436	7028947	15511	Predicted by at least one method	KALEADPK_04306	7017142	7017891	1	hypothetical protein
7013436	7028947	15511	Predicted by at least one method	KALEADPK_04305	7017888	7021193	1	P-loop containing region of AAA domain protein
7013436	7028947	15511	Predicted by at least one method	KALEADPK_04304	7021177	7022334	1	hypothetical protein
7013436	7028947	15511	Predicted by at least one method	KALEADPK_04303	7023730	7023912	1	hypothetical protein
7013436	7028947	15511	Predicted by at least one method	KALEADPK_04302	7024031	7024294	1	hypothetical protein
7013436	7028947	15511	Predicted by at least one method	KALEADPK_04301	7024297	7024902	1	hypothetical protein

7013436	7028947	15511	Predicted by at least one method	KALEADPK_04300	7025276	7026313	1	DDE superfamily endonuclease
7013436	7028947	15511	Predicted by at least one method	KALEADPK_04299	7026373	7027959	-1	Gamma-glutamyltranspeptidase
7013436	7028947	15511	Predicted by at least one method	KALEADPK_04298	7027952	7028947	-1	D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04306	7017142	7017891	1	hypothetical protein
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04305	7017888	7021193	1	P-loop containing region of AAA domain protein
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04304	7021177	7022334	1	hypothetical protein
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04303	7023730	7023912	1	hypothetical protein
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04302	7024031	7024294	1	hypothetical protein
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04301	7024297	7024902	1	hypothetical protein
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04300	7025276	7026313	1	DDE superfamily endonuclease
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04299	7026373	7027959	-1	Gamma-glutamyltranspeptidase
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04298	7027952	7028947	-1	D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04297	7028950	7030077	-1	Ring hydroxylating alpha subunit (catalytic domain)
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04296	7030077	7030820	-1	ABC transporter
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04295	7030817	7031602	-1	ABC transporter
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04294	7031599	7033584	-1	Branched-chain amino acid transport system / permease component
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04293	7033660	7034769	-1	Periplasmic binding protein
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04292	7034954	7035721	1	FCD domain protein
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04291	7035727	7037169	1	Aldehyde dehydrogenase family protein
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04290	7037204	7038019	-1	Transposase IS66 family protein

7017888	7042898	25010	Predicted by at least one method	KALEADPK_04289	7038148	7038969	1	hypothetical protein
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04288	7038906	7040036	-1	Integrase core domain protein
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04287	7040385	7042898	1	hypothetical protein
7017888	7042898	25010	Predicted by at least one method	KALEADPK_04286	7042895	7043599	1	hypothetical protein
7040385	7050130	9745	Predicted by at least one method	KALEADPK_04287	7040385	7042898	1	hypothetical protein
7040385	7050130	9745	Predicted by at least one method	KALEADPK_04286	7042895	7043599	1	hypothetical protein
7040385	7050130	9745	Predicted by at least one method	KALEADPK_04285	7043640	7043918	1	Transposase
7040385	7050130	9745	Predicted by at least one method	KALEADPK_05238	7045940	7048003	-1	Patatin-like phospholipase
7040385	7050130	9745	Predicted by at least one method	KALEADPK_05239	7048128	7048601	-1	Integrase core domain protein
7040385	7050130	9745	Predicted by at least one method	KALEADPK_05240	7048836	7049111	1	hypothetical protein
7040385	7050130	9745	Predicted by at least one method	KALEADPK_05241	7049179	7049433	1	hypothetical protein
7040385	7050130	9745	Predicted by at least one method	KALEADPK_05242	7049525	7050130	1	hypothetical protein
7055191	7087778	32587	Predicted by at least one method	KALEADPK_05644	7055191	7056078	-1	hypothetical protein
7055191	7087778	32587	Predicted by at least one method	KALEADPK_05643	7056085	7056348	-1	helix-turn-helix protein
7055191	7087778	32587	Predicted by at least one method	KALEADPK_05642	7056545	7057648	1	Prokaryotic E2 family E
7055191	7087778	32587	Predicted by at least one method	KALEADPK_05641	7057645	7059045	1	ThiF family protein
7055191	7087778	32587	Predicted by at least one method	KALEADPK_04337	7065785	7066549	-1	Transposase, Mutator family
7055191	7087778	32587	Predicted by at least one method	KALEADPK_04338	7066717	7075710	-1	hemolysin-type calcium-binding repeat (2 copies)
7055191	7087778	32587	Predicted by at least one method	KALEADPK_04339	7077022	7077648	-1	hypothetical protein
7055191	7087778	32587	Predicted by at least one method	KALEADPK_04340	7077822	7078682	-1	hypothetical protein
7055191	7087778	32587	Predicted by at least one method	KALEADPK_04341	7078709	7079335	-1	hypothetical protein
7055191	7087778	32587	Predicted by at least one method	KALEADPK_04342	7079842	7081053	-1	Gkycosyl transferase family 4 group
7055191	7087778	32587	Predicted by at least one method	KALEADPK_04343	7081079	7082494	-1	HlyD family secretion protein
7055191	7087778	32587	Predicted by at least one method	KALEADPK_04344	7082497	7084644	-1	ABC transporter transmembrane region
7055191	7087778	32587	Predicted by at least one method	KALEADPK_04345	7084982	7085671	1	hypothetical protein
7055191	7087778	32587	Predicted by at least one method	KALEADPK_04346	7085682	7086437	1	hypothetical protein
7055191	7087778	32587	Predicted by at least one method	KALEADPK_04347	7086422	7087003	1	hypothetical protein
7055191	7087778	32587	Predicted by at least one method	KALEADPK_04348	7087000	7087500	1	hypothetical protein

7055191	7087778	32587	Predicted by at least one method	KALEADPK_04349	7087509	7087778	1	hypothetical protein
7056085	7082494	26409	Predicted by at least one method	KALEADPK_05643	7056085	7056348	-1	helix-turn-helix protein
7056085	7082494	26409	Predicted by at least one method	KALEADPK_05642	7056545	7057648	1	Prokaryotic E2 family E
7056085	7082494	26409	Predicted by at least one method	KALEADPK_05641	7057645	7059045	1	ThiF family protein
7056085	7082494	26409	Predicted by at least one method	KALEADPK_04337	7065785	7066549	-1	Transposase, Mutator family
7056085	7082494	26409	Predicted by at least one method	KALEADPK_04338	7066717	7075710	-1	hemolysin-type calcium-binding repeat (2 copies)
7056085	7082494	26409	Predicted by at least one method	KALEADPK_04339	7077022	7077648	-1	hypothetical protein
7056085	7082494	26409	Predicted by at least one method	KALEADPK_04340	7077822	7078682	-1	hypothetical protein
7056085	7082494	26409	Predicted by at least one method	KALEADPK_04341	7078709	7079335	-1	hypothetical protein
7056085	7082494	26409	Predicted by at least one method	KALEADPK_04342	7079842	7081053	-1	Gkycosyl transferase family 4 group
7056085	7082494	26409	Predicted by at least one method	KALEADPK_04343	7081079	7082494	-1	HlyD family secretion protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04352	7091385	7092083	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04353	7092581	7092889	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04354	7092983	7093321	1	Plasmid protein of unknown function (Plasmid_RAQPRD)
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04355	7093318	7093557	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04356	7093575	7093931	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04357	7093942	7094328	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04358	7094325	7094984	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04359	7094981	7095865	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05230	7097270	7097926	-1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05231	7097927	7099126	-1	Phage integrase family protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05232	7099712	7100308	-1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05233	7100730	7101068	-1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05234	7101862	7103085	1	Phage integrase family protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05235	7103085	7104629	1	Phage integrase family protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05236	7104622	7106928	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05237	7107516	7111151	1	AAA domain protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_06129	7112521	7112844	1	hypothetical protein

7091385	7186340	94955	Predicted by at least one method	KALEADPK_06123	7114224	7115288	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_06124	7115285	7115569	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_06125	7115566	7116009	1	Thioredoxin
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05211	7118066	7118437	-1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05212	7119595	7120578	-1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05213	7121630	7122703	-1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05214	7122734	7123924	-1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05215	7124175	7124609	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05216	7124827	7125486	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05217	7125506	7126582	-1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05218	7126600	7127178	-1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05219	7127297	7127719	-1	Prokaryotic dksA/traR C4-type zinc finger
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05220	7127872	7128219	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04818	7129751	7130782	-1	Integrase core domain protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04819	7131473	7133251	-1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04820	7133309	7133992	-1	Bacterial regulatory proteins, tetR family
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04821	7134047	7134898	-1	3-hydroxyacyl-CoA dehydrogenase, NAD binding domain
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04822	7134919	7136103	-1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04823	7136310	7137341	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04824	7137400	7138143	-1	Integrase core domain protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04825	7138300	7139550	-1	Transposase IS116/IS110/IS902 family protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04826	7139724	7140038	-1	Transposase
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04827	7140752	7141876	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04828	7141893	7143263	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04829	7143824	7144873	1	Metallo-beta-lactamase superfamily protein

7091385	7186340	94955	Predicted by at least one method	KALEADPK_04830	7145248	7147683	1	Bacterial regulatory proteins, luxR family
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04831	7147708	7148883	-1	CoA-transferase family III
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04832	7149394	7149588	1	Transposase
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04833	7149570	7150091	-1	IstB-like ATP binding protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05645	7151535	7151765	1	Integrase core domain protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04720	7157163	7157483	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04721	7157634	7157906	1	Bacterial DNA-binding protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04722	7158013	7158498	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04723	7158495	7160711	1	Helix-hairpin-helix containing domain protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04724	7161082	7162497	1	TraM recognition site of TraD and TraG
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04725	7162534	7162875	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04726	7162980	7163330	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04727	7163334	7163729	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04728	7163732	7164109	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04729	7164111	7164737	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04730	7164740	7165534	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04731	7165531	7167054	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04732	7167064	7167387	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04733	7167447	7167848	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04734	7167848	7170796	1	AAA-like domain protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04735	7170762	7171154	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04736	7171158	7172435	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04737	7172416	7173075	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04738	7173072	7173776	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04739	7173748	7174551	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04740	7174561	7175454	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04741	7175451	7176875	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04742	7176868	7178916	1	hypothetical protein

7091385	7186340	94955	Predicted by at least one method	KALEADPK_04743	7179019	7179957	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04744	7180290	7180502	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_04745	7180560	7180997	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_06126	7182628	7183176	-1	Sigma-70, region 4
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05247	7185859	7186155	1	hypothetical protein
7091385	7186340	94955	Predicted by at least one method	KALEADPK_05248	7186137	7186340	1	hypothetical protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_04352	7091385	7092083	1	hypothetical protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_04353	7092581	7092889	1	hypothetical protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_04354	7092983	7093321	1	Plasmid protein of unknown function (Plasmid_RAQPRD)
7091385	7112844	21459	Predicted by at least one method	KALEADPK_04355	7093318	7093557	1	hypothetical protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_04356	7093575	7093931	1	hypothetical protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_04357	7093942	7094328	1	hypothetical protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_04358	7094325	7094984	1	hypothetical protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_04359	7094981	7095865	1	hypothetical protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_05230	7097270	7097926	-1	hypothetical protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_05231	7097927	7099126	-1	Phage integrase family protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_05232	7099712	7100308	-1	hypothetical protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_05233	7100730	7101068	-1	hypothetical protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_05234	7101862	7103085	1	Phage integrase family protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_05235	7103085	7104629	1	Phage integrase family protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_05236	7104622	7106928	1	hypothetical protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_05237	7107516	7111151	1	AAA domain protein
7091385	7112844	21459	Predicted by at least one method	KALEADPK_06129	7112521	7112844	1	hypothetical protein
7115285	7130782	15497	Predicted by at least one method	KALEADPK_06123	7114224	7115288	1	hypothetical protein
7115285	7130782	15497	Predicted by at least one method	KALEADPK_06124	7115285	7115569	1	hypothetical protein
7115285	7130782	15497	Predicted by at least one method	KALEADPK_06125	7115566	7116009	1	Thioredoxin
7115285	7130782	15497	Predicted by at least one method	KALEADPK_05211	7118066	7118437	-1	hypothetical protein
7115285	7130782	15497	Predicted by at least one method	KALEADPK_05212	7119595	7120578	-1	hypothetical protein
7115285	7130782	15497	Predicted by at least one method	KALEADPK_05213	7121630	7122703	-1	hypothetical protein
7115285	7130782	15497	Predicted by at least one method	KALEADPK_05214	7122734	7123924	-1	hypothetical protein

7115285	7130782	15497	Predicted by at least one method	KALEADPK_05215	7124175	7124609	1	hypothetical protein
7115285	7130782	15497	Predicted by at least one method	KALEADPK_05216	7124827	7125486	1	hypothetical protein
7115285	7130782	15497	Predicted by at least one method	KALEADPK_05217	7125506	7126582	-1	hypothetical protein
7115285	7130782	15497	Predicted by at least one method	KALEADPK_05218	7126600	7127178	-1	hypothetical protein
7115285	7130782	15497	Predicted by at least one method	KALEADPK_05219	7127297	7127719	-1	Prokaryotic dksA/traR C4-type zinc finger
7115285	7130782	15497	Predicted by at least one method	KALEADPK_05220	7127872	7128219	1	hypothetical protein
7115285	7130782	15497	Predicted by at least one method	KALEADPK_04818	7129751	7130782	-1	Integrase core domain protein
7136310	7157483	21173	Predicted by at least one method	KALEADPK_04823	7136310	7137341	1	hypothetical protein
7136310	7157483	21173	Predicted by at least one method	KALEADPK_04824	7137400	7138143	-1	Integrase core domain protein
7136310	7157483	21173	Predicted by at least one method	KALEADPK_04825	7138300	7139550	-1	Transposase IS116/IS110/IS902 family protein
7136310	7157483	21173	Predicted by at least one method	KALEADPK_04826	7139724	7140038	-1	Transposase
7136310	7157483	21173	Predicted by at least one method	KALEADPK_04827	7140752	7141876	1	hypothetical protein
7136310	7157483	21173	Predicted by at least one method	KALEADPK_04828	7141893	7143263	1	hypothetical protein
7136310	7157483	21173	Predicted by at least one method	KALEADPK_04829	7143824	7144873	1	Metallo-beta-lactamase superfamily protein
7136310	7157483	21173	Predicted by at least one method	KALEADPK_04830	7145248	7147683	1	Bacterial regulatory proteins, luxR family
7136310	7157483	21173	Predicted by at least one method	KALEADPK_04831	7147708	7148883	-1	CoA-transferase family III
7136310	7157483	21173	Predicted by at least one method	KALEADPK_04832	7149394	7149588	1	Transposase
7136310	7157483	21173	Predicted by at least one method	KALEADPK_04833	7149570	7150091	-1	IstB-like ATP binding protein
7136310	7157483	21173	Predicted by at least one method	KALEADPK_05645	7151535	7151765	1	Integrase core domain protein
7136310	7157483	21173	Predicted by at least one method	KALEADPK_04720	7157163	7157483	1	hypothetical protein
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04722	7158013	7158498	1	hypothetical protein
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04723	7158495	7160711	1	Helix-hairpin-helix containing domain protein
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04724	7161082	7162497	1	TraM recognition site of TraD and TraG
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04725	7162534	7162875	1	hypothetical protein
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04726	7162980	7163330	1	hypothetical protein

7158013	7171154	13141	Predicted by at least one method	KALEADPK_04727	7163334	7163729	1	hypothetical protein
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04728	7163732	7164109	1	hypothetical protein
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04729	7164111	7164737	1	hypothetical protein
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04730	7164740	7165534	1	hypothetical protein
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04731	7165531	7167054	1	hypothetical protein
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04732	7167064	7167387	1	hypothetical protein
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04733	7167447	7167848	1	hypothetical protein
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04734	7167848	7170796	1	AAA-like domain protein
7158013	7171154	13141	Predicted by at least one method	KALEADPK_04735	7170762	7171154	1	hypothetical protein
7172416	7180502	8086	Predicted by at least one method	KALEADPK_04736	7171158	7172435	1	hypothetical protein
7172416	7180502	8086	Predicted by at least one method	KALEADPK_04737	7172416	7173075	1	hypothetical protein
7172416	7180502	8086	Predicted by at least one method	KALEADPK_04738	7173072	7173776	1	hypothetical protein
7172416	7180502	8086	Predicted by at least one method	KALEADPK_04739	7173748	7174551	1	hypothetical protein
7172416	7180502	8086	Predicted by at least one method	KALEADPK_04740	7174561	7175454	1	hypothetical protein
7172416	7180502	8086	Predicted by at least one method	KALEADPK_04741	7175451	7176875	1	hypothetical protein
7172416	7180502	8086	Predicted by at least one method	KALEADPK_04742	7176868	7178916	1	hypothetical protein
7172416	7180502	8086	Predicted by at least one method	KALEADPK_04743	7179019	7179957	1	hypothetical protein
7172416	7180502	8086	Predicted by at least one method	KALEADPK_04744	7180290	7180502	1	hypothetical protein
7182628	7188449	5821	Predicted by at least one method	KALEADPK_06126	7182628	7183176	-1	Sigma-70, region 4
7182628	7188449	5821	Predicted by at least one method	KALEADPK_05247	7185859	7186155	1	hypothetical protein
7182628	7188449	5821	Predicted by at least one method	KALEADPK_05248	7186137	7186340	1	hypothetical protein
7182628	7188449	5821	Predicted by at least one method	KALEADPK_05249	7186359	7187180	-1	Integrase core domain protein
7182628	7188449	5821	Predicted by at least one method	KALEADPK_05250	7187213	7187521	-1	Transposase
7182628	7188449	5821	Predicted by at least one method	KALEADPK_05251	7187757	7188449	1	hypothetical protein
7196838	7207739	10901	Predicted by at least one method	KALEADPK_05263	7196838	7196987	1	hypothetical protein
7196838	7207739	10901	Predicted by at least one method	KALEADPK_05264	7197005	7197361	1	hypothetical protein
7196838	7207739	10901	Predicted by at least one method	KALEADPK_05265	7197372	7197758	1	hypothetical protein
7196838	7207739	10901	Predicted by at least one method	KALEADPK_05266	7197755	7198414	1	hypothetical protein
7196838	7207739	10901	Predicted by at least one method	KALEADPK_05221	7200698	7202455	-1	Anion-transporting ATPase
7196838	7207739	10901	Predicted by at least one method	KALEADPK_05222	7202958	7204322	-1	Pyridine nucleotide-disulfide oxidoreductase

7196838	7207739	10901	Predicted by at least one method	KALEADPK_05223	7204319	7204834	-1	Acetyltransferase (GNAT) domain protein
7196838	7207739	10901	Predicted by at least one method	KALEADPK_05224	7204896	7205393	-1	MarR family protein
7196838	7207739	10901	Predicted by at least one method	KALEADPK_05225	7205530	7206726	1	Major Facilitator Superfamily protein
7196838	7207739	10901	Predicted by at least one method	KALEADPK_05226	7207452	7207739	1	hypothetical protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_05228	7208159	7208803	1	hypothetical protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_05229	7209605	7209760	-1	hypothetical protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_06127	7212135	7213136	1	hypothetical protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04865	7216889	7217437	1	hypothetical protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04866	7217449	7217739	1	hypothetical protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04868	7218615	7219622	1	GDP-mannose 4,6 dehydratase
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04869	7219660	7220478	1	ABC-2 type transporter
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04870	7220468	7221865	1	ABC transporter
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04871	7222444	7224216	1	Methyltransferase domain protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04872	7224216	7225493	1	hypothetical protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04873	7225505	7226734	1	Glycosyl transferases group 1
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04874	7226734	7228788	1	hypothetical protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04875	7228775	7229686	1	Glycosyl transferase family 2
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04876	7229679	7230557	1	NAD dependent epimerase/dehydratase family protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04877	7230554	7231636	1	Glycosyl transferase family 4
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04878	7231640	7233616	1	Polysaccharide biosynthesis protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04879	7233613	7234206	1	hypothetical protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04880	7235225	7236175	-1	hypothetical protein
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04881	7236319	7236675	1	Sulfite exporter TauE/SafE
7208159	7236972	28813	Predicted by at least one method	KALEADPK_04882	7236772	7236972	-1	hypothetical protein

ANEXO I

Artigo 1

Type of the Paper (Article, Review, Communication, etc.)

Genomic and Phenotypic insights of surface active compounds producing *Pseudomonas aeruginosa* PSA39 isolated from magrove sediment

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Abstract: Mangroves are zones of sediment transitions, favoring the cycling of materials, associated with a high concentration of microorganisms, presenting vulnerability to anthropogenic actions. This study aimed to evaluate the microbiota capacity in mangrove sediments of the Anil River, in the city of São Luís - MA for the production of surface-active compounds (SACs). The samples were inoculated in the Bushnell Haas medium, containing carbon sources 2% (v/v). In this study, about 32 bacterial isolates were obtained from the mangrove sediment samples, and of these microorganisms, nine showed emulsifying activity (E_{24}), with E_{24} values ranged from 13% to 57.30%. The PSA39 isolate showed the best emulsifying activity and was selected for SACs stability tests against physical chemical parameters and its genome was characterized for a better understanding of its biosurfactant production pathways, and heavy metal resistance. The tests for emulsifying activity and stability with the biosurfactant recovered from *Pseudomonas aeruginosa* PSA39 with ethyl acetate showed E_{24} values ranging from 57% to 69.2% yield, with an increase in stability at basic pHs, reaching 79%, in addition to resisting the pressure and temperature autoclaving. The comparative genome of PSA39 showed genetic characteristics linked to rhamnolipid producing pathways, and heavy metal resistance similarity with, CR1, aL10 PA0-1 strains. This study demonstrated the feasibility of using regional microorganisms present in mangroves for the production of active surface compounds with emulsifying activity, from different carbon sources, due to their good emulsification and stability indexes due to the diversity of environmental factors.

Keywords: Biosurfactants, *Pseudomonas aeruginosa*, genomic analysis, resistance to heavy metals

Keywords: Biosurfactant; *Pseudomonas aeruginosa* ; Emulsifying activity; genome

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ANEXO II

Artigo 2

Detecting microorganisms producing surface active compounds in mangrove sediments in São Luís, Maranhão

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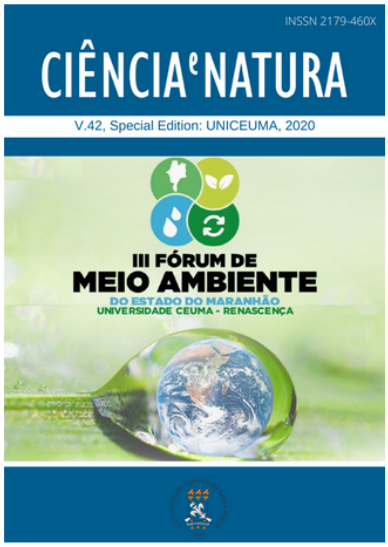

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