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A Comprehensive Population Based Comparative Genomic Analysis of the Legionella Pangenome

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An abstract of a thesis submitted to the Faculty of the James T. Laney School of Graduate
Studies of Emory University in partial fulfillment of the requirement for the degree of Master of
Science in Graduate Division of Biological and Biomedial Science
Microbiology and Molecular Genetics
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Abstract

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A comparative genomic analysis of the Legionella genus' pangenome was done to elucidate the level and significance of mutation and recombination within the selected population. It was found that recombination occurred less frequently then mutation, but it had a much greater effect on the pangenome's genetic change. Additionally, a variety of phylogenetic trees were created, showing strain and clade associated genetic clustering. This was the most complete study of the Legionella genus' pangenome to date, utilizing 43 genomes with 35 strains being newly sequenced for this analysis.

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INTRODUCTION

Legionella: a Newly Emergent Pathogen

In terms of understanding and discovery, Legionella has only recently become a high profile pathogen. As such, the scientific community's knowledge and subsequently the medical and public health community's ability to best treat and prevent associated diseases is limited in scope and drastically lacking compared to many other pathogenic bacteria. Legionella is an aerobic, gram-negative, non-spore forming bacillus bacterium that is ubiquitous to freshwater environments and is considered a natural part of microbial ecosystems. To date, 56 species have been officially recognized. However, many contain serogroups, greatly expanding the pool of different strains. The two clinically relevant infections caused by Legionella are Legionnaires' disease and Pontiac fever. Legionnaires' disease manifests with a pneumonia, fever, and cough. Symptoms of Pontiac Fever include lethargy, chills, and fever as with the flu bu without any pneumonia [1]. While the symptoms of Legionnaires' disease are more severe, it has a drastically lower infection rate with only 5% of people coming into contact contrtacting the illness versus a 90% rate with Pontiac fever [1]. To cause disease, all Legionellae share common features such as: a freshwater source that has undergone amplification due to favorable conditions (often found in man-made water systems such as showers, spas, HVAC units, decorative water fountains, and cooling towers), an aerosolization step, and a susceptible host (typically immunocompromised individuals, smokers, transplant patients, and those with reduced lung function).

History

The first recognized outbreak of Legionella was in July 1976 at a bicentennial celebration by the American Legion Auxiliary. There was a total of 182 victims with 147 cases resulting in hospitalization (81%) and 29 (16%) resulting in death [2]. The outbreak was traced back to the chiller and ventilation system of the hotel that hosted the convention [2], but there was no obvious link to the etiology of any known disease at the time. The scientific community went to work identifying this unknown pathogen. The patients' tissue and serum samples were examined for a variety of pathogens and toxins with an unknown gram-negative bacillus being found and eventually cultured in guinea pigs [3].

Relevance and Recent Outbreaks

Legionella outbreaks continue to be an issue of concern, even in developed nations. Collectively, the Legionellae cause 8,000-18,000 hospitalizations per year in the United States. By far, *L. pneumophila* serogroup 1 (LP1) is the leading causative agent of Legionnaires' Disease (LD), accounting for up to 92% of clinically recognized Legionellosis in the United States and Europe [1]. Other Legionella species as well as serogroups 2-17 of L. pneumophila account for the rest of the LD cases [5]. Although LP1 predominates as the cause of LD, it is not found in disproportionately higher amounts within the environment, giving rise to the conundrum of why it causes so many of the LD cases. Other serogroups of *L. pneumophila* have been documented to cause outbreaks, but to a much lesser extent. The bacteria are ubiquitous in the environment and typically cause no harm. However, in situations involving immune compromised individuals, stagnant water systems that allow for high bacterial population multiplication, or particularly virulent strains, outbreaks can cause severe illness and death. There was a multitude of cases in 2013 from Australia and Western Europe as well as the United States. There have already been two deaths associated with Legionella during the early part of

2014 in Indiana [1,4]. The CDC's Morbidity and Mortality Weekly Report shows that between years 2000-2009 the national incidence rate of Legionellosis in the United States increased almost 200% [5].

Comparative Genomics

The ability to analyze samples at the nucleotide level allows for many insights and discoveries that would have been otherwise impossible 15 years ago. For instance, even if a particularly virulent strain of a pathogen is hard to culture, its genetic information can be sequenced to fully understand its properties and inner workings. Generation of whole genome sequences of Legionella has already played a significant role in understanding drug resistance, heavy metal secretion, disease transmission, and DNA transfer [6]. As more genomes of Legionella are sequenced they can be compared to the already existing strain population to identify clinically relevant similarities or differences. It is well known that bacteria and especially viruses are constantly going through a multitude of mutations and evolutionary events. As such, even in the process of successfully culturing a sample, important information about the actual organism or parasite that caused the original public health concern could be altered or lost. Sequencing allows for a time-specific or real time, virtually exact readout of a sample's entire genetic components at the time that it was isolated. This technology can even be used to track genetic changes as they happen in an organism as it evolves within or outside of a host [6]. Obviously, this has tremendous advantages when we sequence one strain of a bacterial species. However, the power of this system is exponentially increased when someone sequences and compares the genome sequences of several strains of the same bacterial species at the individual or community level. Once a particular species or strain has been sequenced and some or all of its gene functions assigned, it can then be used as a reference for other newly discovered organisms or even related strains [7]. This is done by ascribing orthologs: genes of common function maintained throughout diverse speciation [8]. They can be differentiated from paralogs, genes of recent common ancestor present in the same genome, by clustering gene homologs [8]. After sequencing and annotating new genomes, it is possible to look for orthologs of those genes within the same species or outside. This one to many mapping analysis within the species or outside, allows us to assign putative gene function in a newly discovered or sequenced organism. Additionally, phylogenetic reconstruction in the form of phylogenetic trees can be inferred from core sequence alignments of homologous genes across a species. This allows for an explicit mapping of evolutionary development and relationship between various organisms or strains within a species. Additionally, structure and function can be generated not only at the strain level, but across a species, genus, etc… Finally, there exists the ability to link unique phenotypic traits with particular genes or regions within a genome. This can be particularly powerful in extrapolating aspects such as disease causing characteristics, resistance abilities, and other phenotypes of interest such as CRISPR Cas9 [6]. These abilities in tandem allow researchers to paint an elaborate, detailed, and chronologically accurate evolutionary history of not just one gene at a time, but multiple strains within a species. The recent technological advancements in the field of next generation sequencing and the invention of powerful bioinformatics tools have facilitated the generation of draft whole genome sequences of thousands of strains of a species across the globe and the performance of large scale comparative analysis on a real time basis especially during disease outbreaks [9].

Pangenome

The concept of the pangenome is one that details the entirety of genes within a bacterial species or genus group [10]. While there are several schools of thought on nomenclature and how particularly to break up genes within a group; there are four fundamental classifications that are almost universal. All genes that are only found within one strain would be classified as “unique genes.” Genes that are present in only 2 to 6 strains in a species can be called as accessory genes of that species. Genes found in every strain in a species are termed as “core genes” or part of the “core genome” [10]. The genes that are not part of the core and also not unique between these two extremes of being a core or accessory gene were termed as character genes, using established terminology [10]. While the core defines the essential conserved functions of a species, the character and accessory genes potentially give insight into strain- and clade-specific attributes. Many virulence associated genes fall into these latter classes [10]. Usually the unique genes or the accessory genes indicate evidence of horizontal gene transfer. The core genome can also be used for tracking the events of mutations and recombination happening in the species. Moreover, the estimation of the pangenome of a species indicates whether the species has been receiving new genes either by horizontal gene transfer via homologous recombination or external sources and is continuing to add new genes (open pan genome as in Streptococcus and Bacillus) or has not had much gene acquisition from external sources compared to other species (closed pan genome such *Chlamydia trachomatis*) [11,12,13]. Estimating the pangenome for Legionella would allow researchers to have an approximation of where the states of new strains as well as new gene discoveries are happening in this species. It also helps to know whether Legionella has an open or closed pan genome and estimate the frequency or rate of horizontal gene transfer happening in it. That way researchers would be able to easily identify the newest gene that has been added, which might have increased the virulence of a strain especially in an event of a disease outbreak. Once the core genome for Legionella is established, researchers can focus on its crucial, preserved genes for targeting studies.

Recombination and Mutation

The factors driving bacterial evolution outside of explicit horizontal gene transfer events are mutation and recombination. Mutation is to be thought of as a seemingly random genetic change on the nucleotide level due to error or response to an external factor. Recombination on the other hand would be considered a restructuring of the genome based on the exchange of select homologous chromosomes or mobile elements within a genome. Understanding whether one or both is occurring in Legionella and at what rate this is happening would help estimate whether these evolutionary processes have made Legionella more virulent overtime. For instance, if it is discovered that mutation is the predominant factor in genetic change, then the next step would be to identify and understand the selective pressures acting to cause those changes. If on the other hand, recombination was the most paramount component of genetic change, then pertinent next questions would involve why certain strains are undergoing change over the others and does this implicate or affect relevant phenotypic exchanges. Differentiating between the two processes in the absence of information about multiple species genomes can be difficult. Methods like ClonalFrame have been developed to estimate the frequency of mutation and recombination considering the clonality of bacterial strains [14]. ClonalFrame estimates the probability that all regions of the core genome alignment have undergone recombination and generates maps that track the events of DNA exchange, which is very helpful for understanding hotspots of recombination that would eventually help in designing targets for antimicrobial drugs as well as vaccines. Tracking the genetic flow (or genetic flux) of DNA within a species will be very helpful, especially in disease outbreaks. Analysis software like ChromoPainter and fineStructure will help in understanding species specific genetic flux [14, 15].   Tracking and mapping all the putative sites of mutations and recombinations allows for directed questions to be asked based on connections identified between strains. For instance, whether recombination happening between or arising from predominantly strains linked by commonalities such as geographic location, body site where the strains are infected, clinical versus environmental isolates, or those within a phenotypic trait of interest are possible inquiries to be explored. Since recombination is obviously an important evolutionary process shaping many important bacterial pathogens like *E.coli*, *Chlamydia trachomatis*, and *Bacillus cereus*, I undertook a comparative genome analysis of Legionella in order to determine if recombination was taking place and to what extent [11,12,13].

Project Aims

In this study, a comparative whole genome analysis was performed using 43 strains of Legionella (35 newly sequenced strains + 8 publically available genomes) in order to estimate the pangenome of the Legionella species. Establishing the pangenome was done to determine whether mutations and/or homologous recombination were occurring and of those what is the major evolutionary force acting on this bacterium. Additionally, a phylogenetic tree was created to determine if the levels of mutation and recombination were associated with any particular clade or population subsets. My project seeks to show that establishing a more comprehensive pangenome of Legionella in tandem with *in silico* methods can demonstrate a more accurate picture of recombination and mutation events taking place across the entirety of strains in the population as well as each factor's influence on genetic change.

Materials and Methods

De Novo Assembly of Contigs and Genome Sequencing

Using the isolates from our CDC collaborators, the genomic DNA was extracted and sequenced in Illumina and 454 platforms. Illumina reads were trimmed for base sequence quality using FASTQC [12]. Processed reads were then assembled for optimal kmer content using Velvet [13]. Finally, the assembled Illumina contigs were chopped into 454 sized read lengths (~400 base pairs). These chopped sequences were combined with the 454 short read data generated for each strain and then again de novo assembly was performed using Newbler [14]. A BLASTP search was run for best hits with an e value cutoff of e-05 [15]. Finally, all genomes including the strains newly sequenced for this study, and the already curated genomes were annotated using Prokka [16].

Pan Genome Establishment and Inference of Phylogeny Based on Alignment of Core Clusters from Ortholog Retrieval

The results from BLASTP were transformed into a similarity matrix using normalization in OrthoMCL [17]. This algorithm incorporates an extra component of the Markov Clustering Algorithm for improved specificity and sensitivity for any identified ortholog sequences. OrthoMCL was run with a BLAST E-value cut-off of 1e-05, and an inflation parameter of 1.5. We defined the core genes as the orthologous genes that are shared by all of the 43 Legionella strains. Multiple Sequence Alignment (MSA) was used on the genes constituting the core proteome using the MUSCLE program on default settings [18]. The generated MSA was filtered for non-pertinent characters using the program GBLOCKS in its default settings [19]. All the core protein coding MSA's were concatenated in order to generate a super alignment for reconstructing the Legionella phylogeny. Phylogenetic methods implemented in this study were; UPGMA and neighbor joining (NJ) from the PHYLIP package [20], along with maximum likelihood based phylogenetic reconstruction using PhyML [21] and RAxML [22]. For both UPGMA and NJ methods, the evolutionary distances between the 43 strains were inferred using the PROTDIST function in the PHYLIP package. DAYHOFF and Jones-Taylor-Thornton (JTT) substitution models were used [23]. Internal branches of the phylogeny were estimated with 100 bootstraps.

Whole Genome Core-Nucleotide Alignment and Genome-Wide Haplotype Data

In order to generate the whole core-nucleotide alignment, all the corresponding nucleotide sequences for the 1140 protein-coding core genes, identified in the OrthoMCL step, were concatenated together. Then the whole genome core-nucleotide alignment was generated using MAUVE [24]. The single nucleotide polymorphisms (SNPs) were extracted from the MAUVE core alignment based on the reference strain, *Legionella philadelphia* and these core SNP positions were combined to prepare the genome-wide haplotype data.

Analysis of Homologous Recombination

ClonalFrame (version 1.2) was run at 40,000 iterations on the whole genome core nucleotide alignment identified by MAUVE, and the initial half was discarded as Markov Chain Monte Carlo (MCMC) burn in [24]. Three independent and parallel runs of ClonalFrame were performed. Their reconstructed phylogenies and recombination events across the 3 runs had high congruency. Additionally, for each reconstructed branch substitution event introduced by either mutation or recombination, the number of mutation events, and the number of recombination events were approximated. The relative effect of recombination and mutation on genetic change (r/m) and the relative rate of mutation and recombination (ρ/θ) were estimated.

ChromoPainter and fineSTRUCTURE Analysis

The ChromoPainter algorithm was applied to the genome-wide haplotype data using the linkage model [25]. The main purpose for this analysis was to elucidate the population structure of Legionella. A recombination map file was created by specifying a uniform recombination rate per-site per-generation using a Perl script called makeuniformrecfile.pl provided as a preprocessing tool in the ChromoPainter website (http://www.paintmychromosomes.com). The output from the ChromoPainter analysis is a co-ancestry matrix that summarizes the recombination-derived DNA imports and their donors across the 43 Legionella genomes.

The fineSTRUCTURE algorithm uses the co-ancestry matrix generated using the ChromoPainter analysis and performs model-based clustering using the Bayesian MCMC approach to explore the population structure[25]. FineSTRUCTURE was run at a total of 400,000 iterations and the first 200,000 iterations were discarded as MCMC burn in. The thin interval was specified as 100.

Results

Quality Scoring and Processing

In total, 43 strains representing *Legionella pneumophila* (17 serogroups), *longbeachae* (2 serogroups), *bozemanii* (2 serogroups), *dumoffii, micdadei, birminghamensis, brunensis, cherii, cincinnatiensis, erythra, jamestowniensis, jordanis, maceachernii, nautarum, rowbothamii, tusconensis, wadsworthii, anisa, lens, corby, philadelphia, paris, lorraine,* and *pneumophila* (subspecies Thunder Bay) were used for this analysis with 35 strains representing unpublished data/newly sequenced used for the first time in this study. For the newly sequenced strains, data was generated at the CDC from samples given by Dr. Jonas Winchell. Sequencing was performed using 454 and Illumina sequencing machines, presenting a challenge for the hybrid assembly (**Table 1**).

Table 1. List of Legionella strains sequenced in this study along with the total number of reads generated using both 454 and Illumina sequencing runs and the number of de novo assembly contigs generated for each strain.

Legionella Strains	**Total Number of Reads Generated Using Both 454 and Illumina Sequencing Runs**	**Number of De novo Assembly Contigs**
L. anisa (D5641)	12,440,367	126
L. pneumophila sg2 (D5762)	12,644,433	47
L. pneumophila sg3 (D5517)	12,539,147	35
L. pneumophila sg4 (D5739)	9,010,736	95
L. pneumophila sg5 (D5698)	13,708,986	44
L. pneumophila sg6 D5864	12,064,214	35
L. pneumophila sg7 (D5178)	12,647,927	37
L. pneumophila sg8 (D5744)	11,778,210	43
L. pneumophila sg9 (D4366)	16,329,031	37
L. pneumophila sg10 (D5602)	3,637,672	64
L. pneumophila sg11 (D797)	3,385,529	53
L. pneumophila sg12 (D4955)	14,002,235	24
L. pneumophila sg13 (D5677)	10,606,713	108
L. pneumophila sg14 (D4677)	11,255,691	100
L. pneumophila sg15 (D4613)	12,443,216	32
L. pneumophila sg16 (D5564)	2,475,679	95
L. pneumophila sg17 (D4954)	11,220,305	51
L. birminghamensis (D1407)	2,994,685	125
L. erythra (D3308)	4,650,940	89
L. jamestowniensis (D4855)	9,436,629	34
L. wadsworthii (D4735)	10,208,601	17
L. nautarum (D4144)	7,059,586	112
L. micdadei (D5727)	44,586,161	44

L. cherii (D3084)	10,677,467	21
L. bozemanii sg1 (D5751)	4,889,018	78
L. bozemanii sg2 (D4398)	4,373,003	253
L. maceachernii (D5800)	12,176,672	109
L. jordanis (D5875)	10,165,832	58
L. rowbothamii (D5054)	13,499,246	59
L. cincinnatiensis (D3325)	3,332,320	77
L. tusconensis (D1087)	8,211,209	17
L. brunensis (D1635)	6,955,499	49
L. dumoffii (D5637)	6,280,579	15

The quality of the sequence reads was assessed using the FASTQC program. This program performs a variety of analyses on raw sequence datasets that had low quality data at the end of the sequence read and were trimmed to include only regions of a certain base scoring. After trimming, the data was reexamined via FASTQC format to validate acceptable quality levels. The average sequence length was 70-75bp for Illumina reads and 395 bp for 454 reads. The GC content was 38%. Per base sequence quality control (QC) cutoffs of 20% were used to trim the reads (**Fig.1A/2B**).

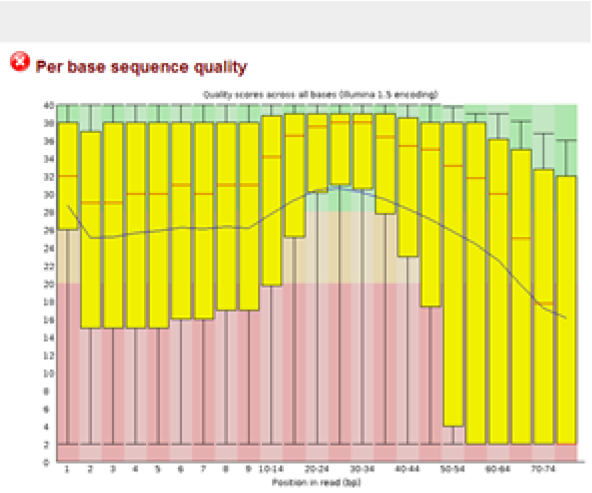


Fig. 1. **Quality control trimming at the sequence read level.** (**A**). Shows the per base sequence quality before trimming and (**B**) shows the per base sequence quality after trimming.

Hybrid Assembly and Gene Annotation

The program Velvet was used to perform the de novo assembly of the trimmed reads that passed the QC in order to generate the de novo contigs. After the de novo assembly, the contigs were chopped into short sequences of 400 bps, similar to the standard long length reads generated using 454 technology and again assembled into contigs via the Newbler program along with the 454 reads generated separately for each of the strains. The average genome size was an approximately 3.5Mb genome. All the de novo contigs were annotated using a Prokka annotation pipeline. The number of protein-coding genes for each of the strains is shown in **Table 2**.

Pseudo Contig Framing

An attempt was made to match genomic segments to a reference genome of the *Legionella pneumophila* Philadelphia subspecies strain. This was done using the ABACAS program. Ideally, this process would have used the reference genome as a foundation that the known genetic segments could be overlaid on to establish a filled out or complete genome. This would have allowed us to close gaps and accurately demonstrate where and when overlap took place. However, the persisting gaps were irreconcilable with this process and the core genome extracted out of the OrthoMCL analysis was used for subsequent whole genome inferences for the recombination analysis.

Estimating the Legionella Pangenome

OrthoMCL is a clustering technique that identifies orthologous genes across several strains. It utilizes Markov clustering algorithms to cluster or group proteins using their sequence similarities [8]. This is done using an "all-against-all" BLAST search for each species' or strain's proteome. Following this, there is an allowance for similarities or differences between species to be set as a threshold for clustering. A stricter similarity rating would result in more individual clusters, and a looser similarity rating would result in fewer individual clusters. The threshold that I used gave enough clusters to differentiate between genome groupings, but still showed a loose enough allowance that every strain was 86% or more clustered, with most in the mid to high nineties (**Table 2**).

Table 2. List of each Legionella strain with its corresponding number of protein coding genes utilized by OrthoMCL for clustering genes based on similarity values. A breakdown of the number of clustered (at or exceeding the similarity threshold with one or more other genes) and unclustered (below the similarity threshold with all other genes) protein coding genes is shown along with a percentage of the clustered protein coding genes over the total number of protein coding genes.

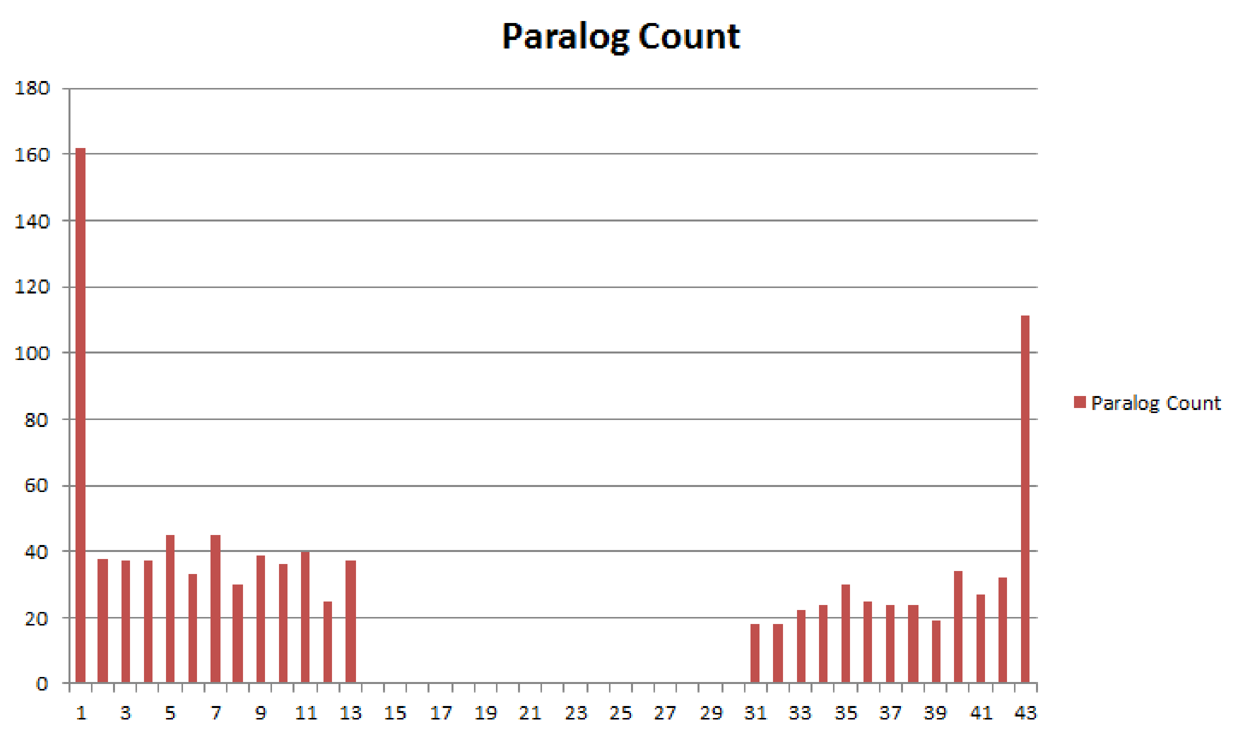
Strain	**Total Number of Protein Coding Genes**	**Number of Protein Coding Genes Clustered**	**Number of Protein Coding Genes Unclustered**	**Percentage of Protein Coding Genes Clustered**
L. alcoy	3127	3114	13	99.58%
L.anisa	3893	3622	271	93.04%
L.bozemanii 1	3628	3507	121	96.66%
L.bozemanii 2	3449	3399	50	98.55%
L.birminghamensis	3323	2874	449	86.49%

L.brunensis	3312	3060	252	92.39%
L.cherii	3223	3007	216	93.30%
L.cincinnatiensis	3501	3212	289	91.75%
L.corby	3194	3177	17	99.47%
L.dumoffii	3446	3313	133	96.14%
L.erythra	3279	2902	377	88.50%
L.jamestowniensis	3322	3017	305	90.82%
L.jordanis	2961	2764	197	93.35%
L.lorraine	3130	3096	34	98.91%
L.pneumophia (LPE509)	3055	3054	1	99.97%
L.maceachernii	3336	2939	397	88.10%
L.micdadei	2878	2752	126	95.62%
L.nautarum	3378	3044	334	90.11%
L.longbeachae	3473	3202	271	92.20%
L.pneumophia (ATCC 43290)	2993	2993	0	100.00%
L.paris	3102	3064	38	98.77%
L.philadelphia	3023	3020	3	99.90%
L.pneumophila (HL06041035)	3113	3076	37	98.81%
L.rowbothamii	3559	3052	507	85.75%

L.pneumophila10	3181	3149	32	98.99%
L.pneumophila11	3181	3118	63	98.02%
L.pneumophila12	3049	3047	2	99.93%
L.pneumophila13	3104	3044	60	98.07%
L.pneumophila14	3200	3114	86	97.31%
L.pneumophila15	3059	3000	59	98.07%
L.pneumophila16	3231	3198	33	98.98%
L.pneumophila17	3242	3167	75	97.69%
L.pneumophila2	2986	2943	43	98.56%
L.pneumophila3	3041	3021	20	99.34%
L.pneumophila4	3143	3114	29	99.08%
L.pneumophila5	3179	3149	30	99.06%
L.pneumophila6	3187	3136	51	98.40%
L.pneumophila7	3153	3085	68	97.84%
L.pneumophila8	3063	3021	42	98.63%
L.pneumophila9	3051	3016	35	98.85%
L.pneumophila (Thunder Bay)	3116	3107	9	99.71%
L.tusconensis	2999	2845	154	94.86%

L.wadsworthii	3336	3150	186	94.42%

This method was performed and then corrected for paralogs (**Fig.2A/2B**). It was found that the pangenome contained 5353 unique genes, 5311 accessory genes, and 1140 core genes (**Fig.3**). A listing of each strain's unique genes was created along with the percentage of each strain that was constituted of unique genes and that of core genes (**Appendix A**). I analyzed a total of 43 *Legionella* genomes (**Table 3**). This is the largest and most comprehensive analysis of extant *Legionella* strains to date.



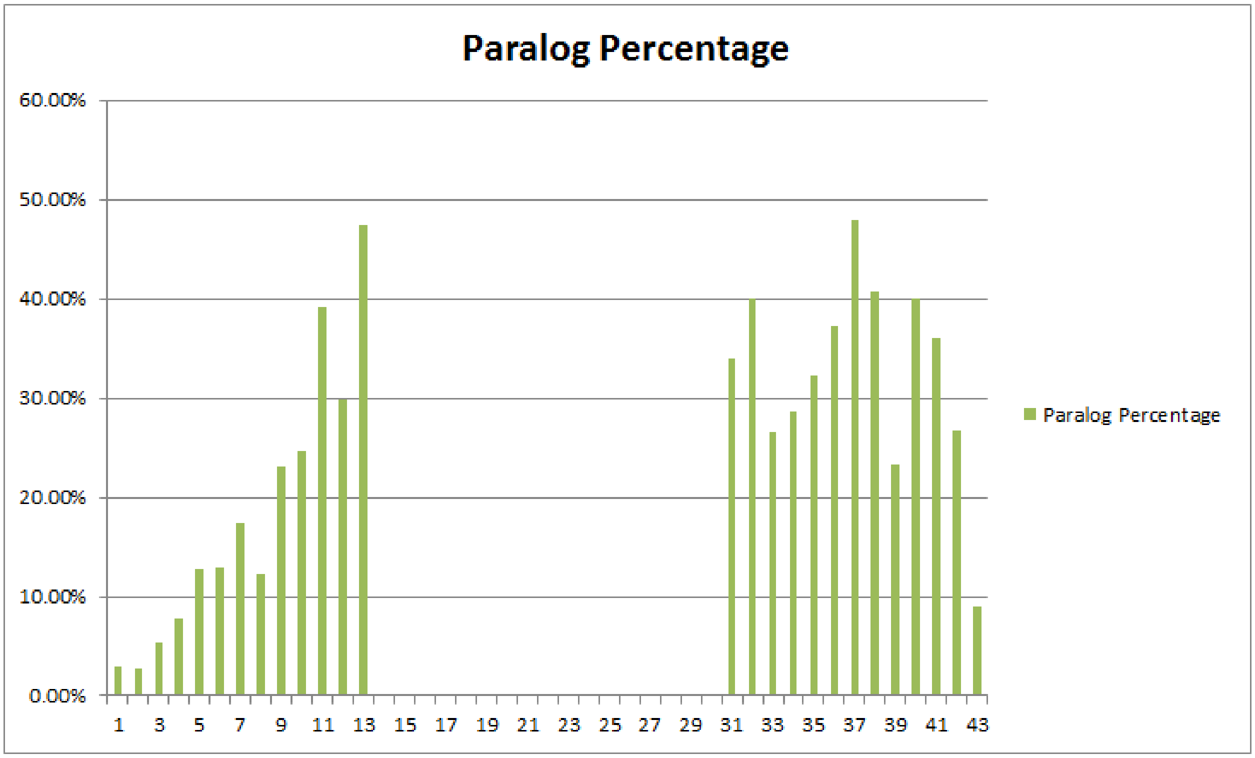


Fig.2A/B Paralogs of the Legionella Pangenome. (**A**) Paralog counts as each successive genome is added to the pangenome. (**B**) The percentages of total genes that are paralogs in each successive genome.

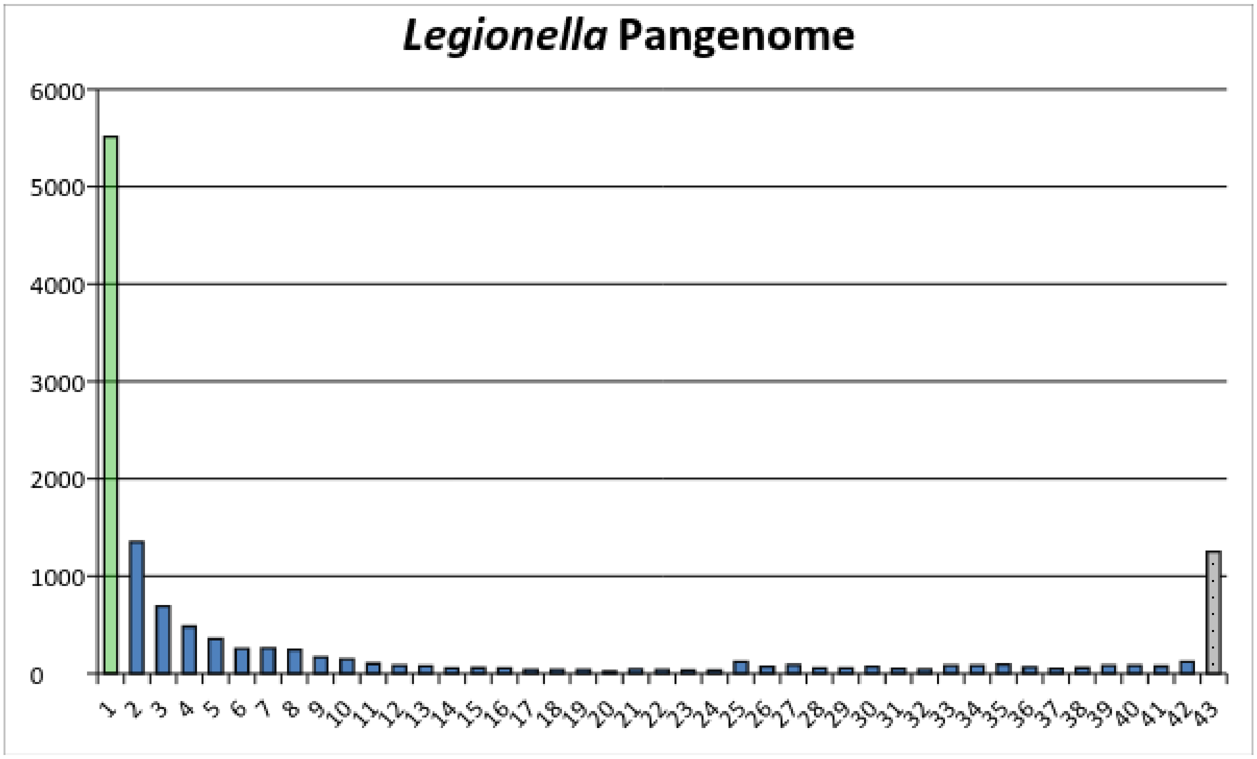


Fig.3 The Distribution of Gene Families Throughout the 43 Legionella Genomes of the Pangenome. Utilizing the Lapierre and Gogarten classification with a merged accessory and character pool of genes [10]. The X-axis shows the number of genomes, and Y-Axis shows the corresponding number of gene clusters associated with that genome value. There were 5353 unique gene clusters constituting 41.77% of of the total gene clusters (GREEN). The merged accessory and character gene region held 6323 gene clusters, making up 49.34% of the total gene clusters (BLUE). The core genome contained 1140 gene clusters that made up 8.90% of the total gene clusters (GREY with DOTS). This core genome cluster percentage was in agreement with the approximately eight percent value suggested in the literature [10].

Table 3. Grouping of the Legionella strains used in this study by clinical relevance with applicable serotypes listed

Clinically Relevant Disease Causing	**Known Serotypes**	**Rarely Disease Causing**	**Known Serotypes**
L.pneumophila	1-17	*L.anisa*	N/A
L. pneumophila (Thunder Bay)	N/A	*L. birminghamensis*	N/A
L.longbeachae	N/A	*L. brunensis*	N/A
L. bozemanii1	1,2	*L. cherii*	N/A
L. dumoffii	N/A	*L. cincinnatiensis*	N/A
L. micdadei	N/A	*L. erythra*	N/A
L.philadelphia	N/A	*L. jamestowniensis*	N/A
L.corby	N/A	*L. jordanis*	N/A
L.lens	N/A	*L. maceachernii*	N/A
L.paris	N/A	*L. nautarum*	N/A
	N/A	*L. rowbothamii*	N/A
	N/A	*L. tusconensis*	N/A
	N/A	*L. wadsworthii*	N/A

The core genome established from the 43 strains contained 1140 genes with a total length of 1.1 Mb. The core genome was ordered and arranged in reference to the *Legionella philadelphia* strain (**Appendix A**).

Phylogenetic Analysis

To best determine evolutionary pathways, descendancy, and interrelatedness for horizontal gene transfer and recombination studies, three different methods were used to establish a phylogenetic tree of the 43 strains. With minor pathways differences, the highest weighted method confirmed

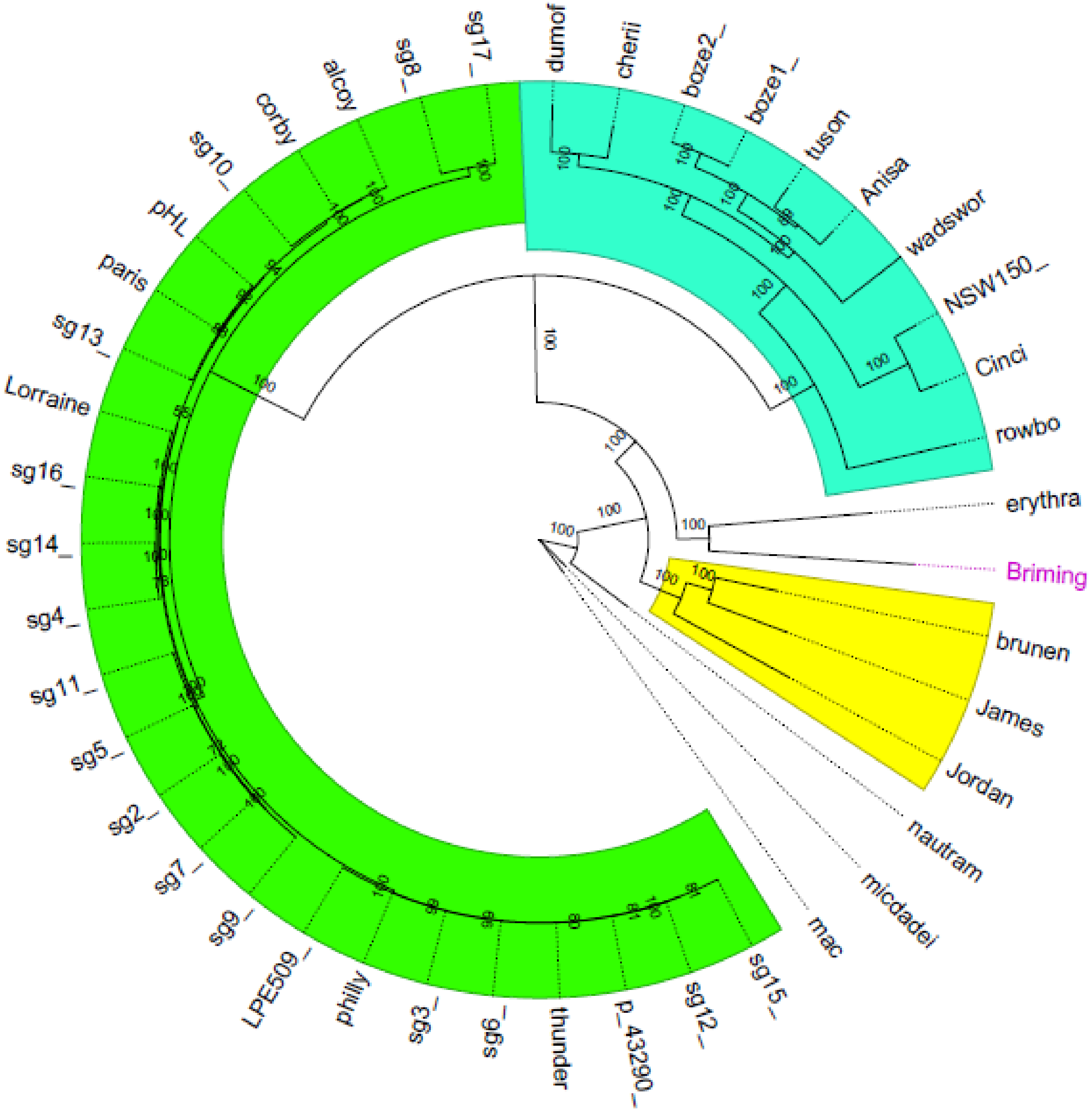


Fig.3 PhyML Phylogenetic Tree. Each major clade is shown in a highlighted color. The predominant clinically relevant strains all associate in the same clade (GREEN). The assigned root strain's name is colored in purple. The numerical values are confidence values out of 100.

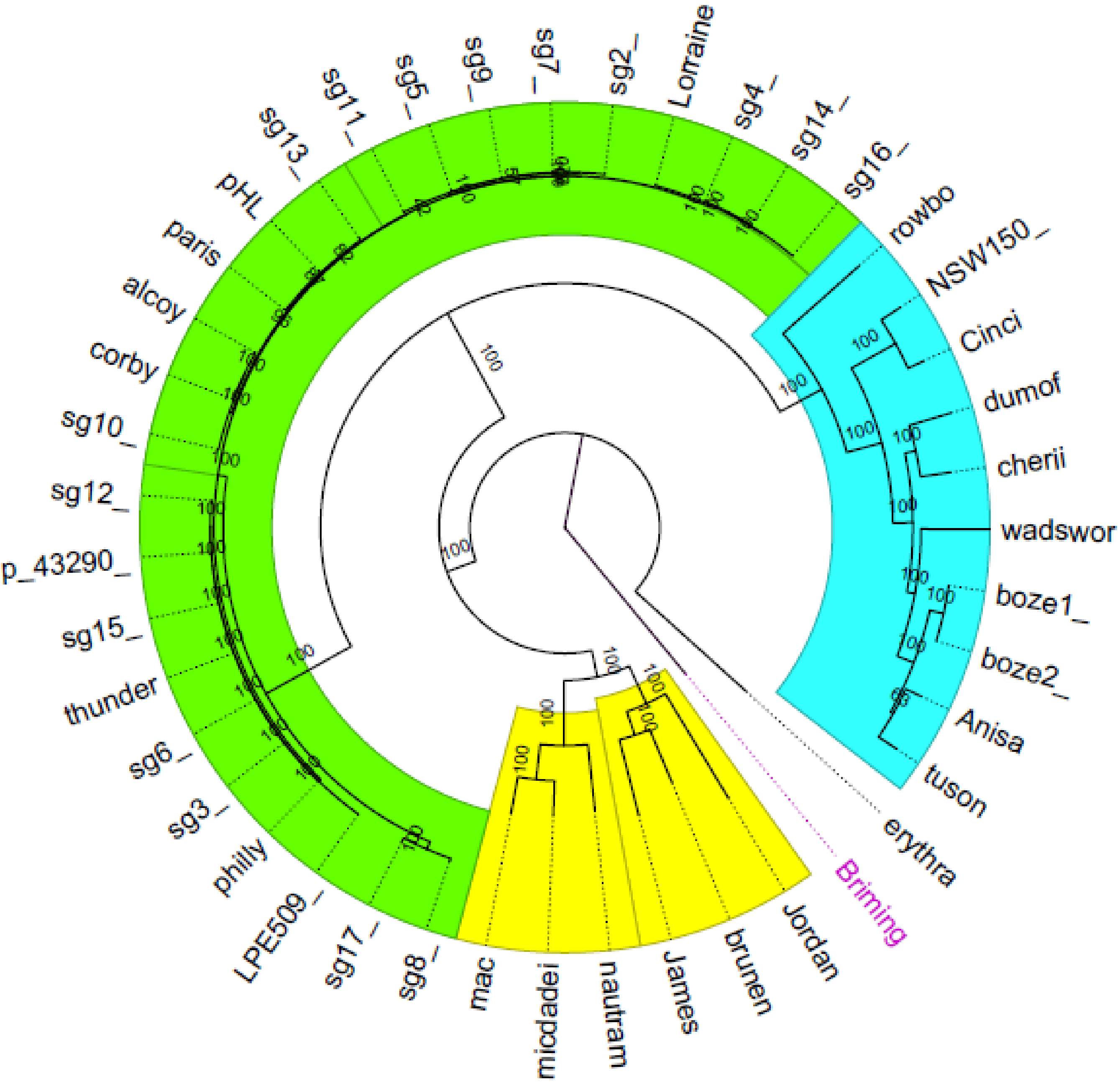


Fig.4 RAxML Phylogenetic Tree Generated with DAYHOFF Amino Acid Substitution Method. Each major clade is shown in a highlighted color. The predominant clinically relevant strains all associate in the same clade (GREEN). The assigned root strain's name is colored in purple. The numerical values are confidence values out of 100.

a similar tree and clade arrangement. I used Phylip initially to establish a tree without weighted root information [21]. Then, I ran PhyML (**Fig.4**) and RAxML (**Fig.5, Fig.6**) as validating steps.

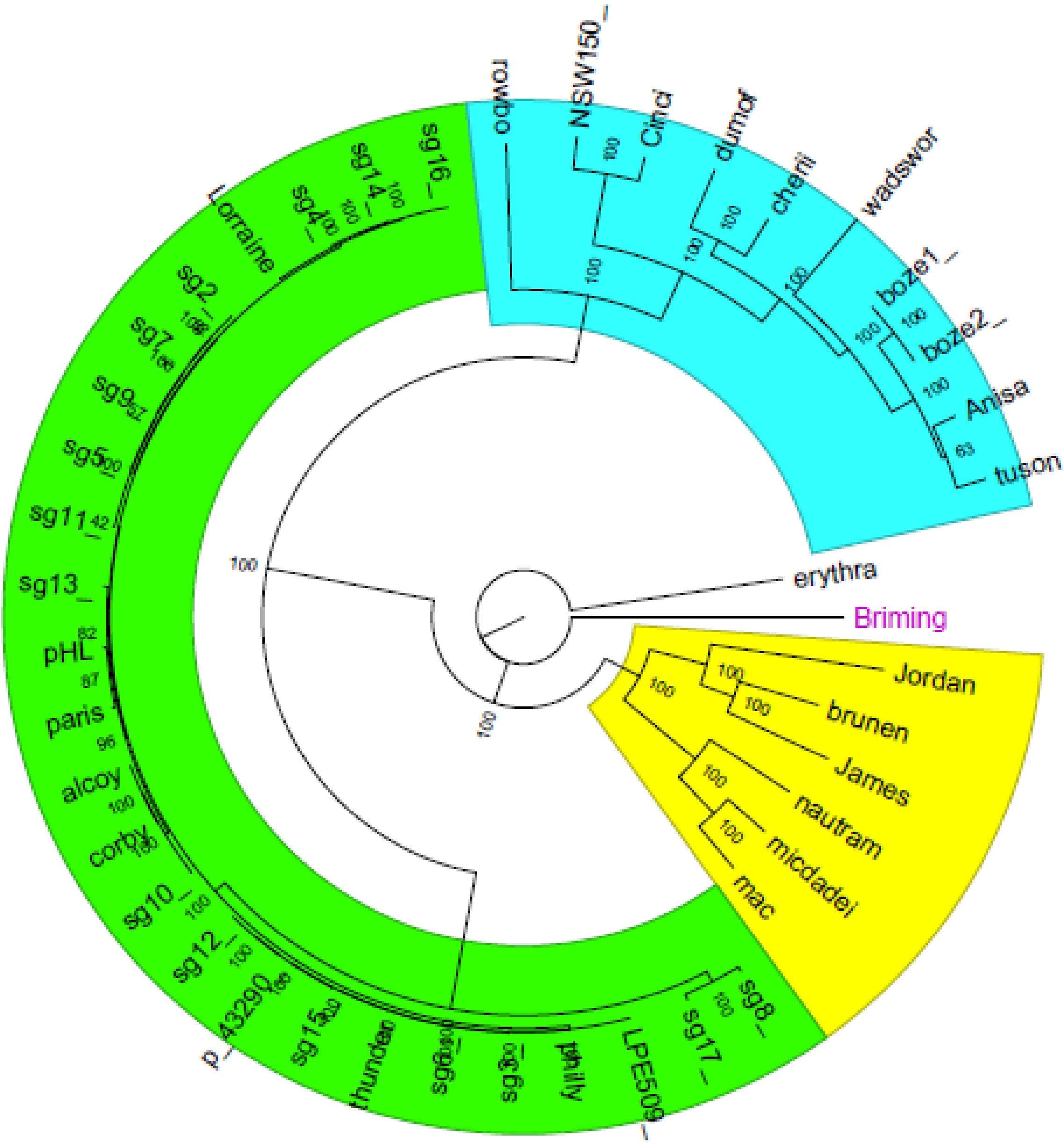


Fig.5 RAxML Phylogenetic Tree Generated with JTT Amino Acid Substitution Method. Each major clade is shown in a highlighted color. The predominant clinically relevant strains all associate in the same clade (GREEN). The assigned root strain's name is colored in purple. The numerical values are confidence values out of 100.

These approaches are much more time and processor intensive, but they utilize methods that provide results with significantly higher weight or confidence. They use bootstrapping methods to best determine the most likely tree. Bootstrapping is a process wherein a large number of phylogenetic trees are generated and then the most common connections or relatedness between strains are selected for. I ran a set of 100 trees for each program. These majority pathways were then established as the final tree. It can be seen throughout the three trees that there is identical or very similar clade agreement (**Fig.4, 5, 6**). Additionally, they were all rooted at the *Legionella birminghamensis* strain. This shows agreement between how the trees were formed and validates the strain positions and clade organization.

RAxML

As verification, two different amino acid substitution models were run with the RAxML program. The JTT (**Fig.5)** and the DAYHOFF (**Fig.6**) models were utilized, and they produced agreeing phylogenetic tree results.

Analysis of Recombination

ChromoPainter and fineSTRUCTURE analysis

To estimate the population structure of Legionella, the ChromoPainter algorithm accounting for linkage information of the 43 Legionella genomes was applied. This algorithm is based on the concept of chromosome painting that infers recombination-derived DNA imports from a donor and reconstructs haplotypes on the genome of a recipient strain as a series of DNA imports from all other donor strains in the sample. In this study, the total sample size was the 43 Legionella strains. Based on the estimation of such recombination-derived DNA imports and their donors across the 43 legionella genomes, the ChromoPainter algorithm calculates the expected number of DNA imports from a donor to a recipient genome and then summarizes these values into a matrix called co-ancestry matrix. This co-ancestry matrix is shown in the form of a heat map in (**Fig.7**). Using this co-ancestry matrix, the fineSTRUCTURE clustering algorithm assigned each

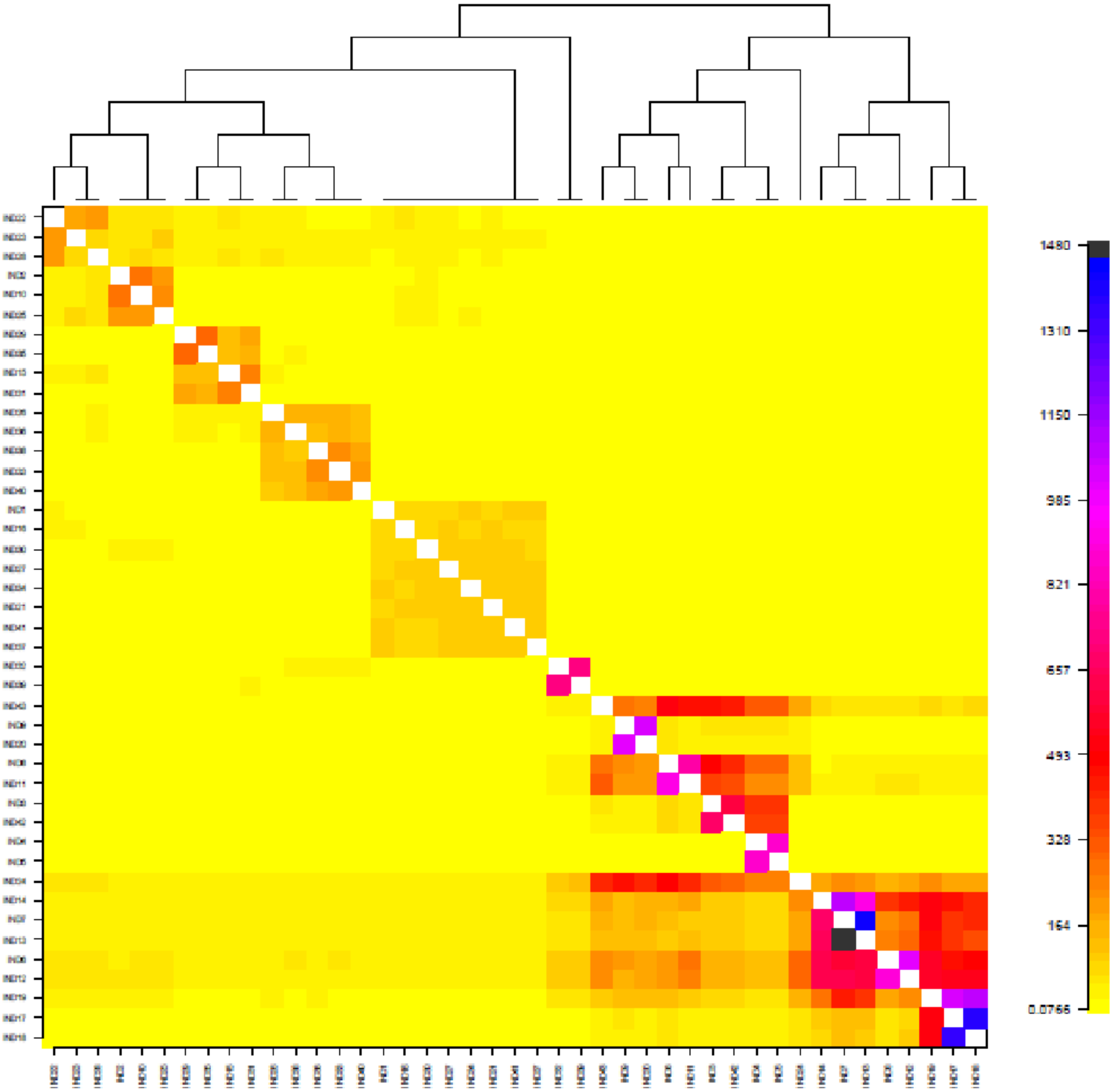


Fig. 6 FineStructure Co-Ancestry Matrix. Shown is the fineStrucutre recombination analysis heat map. This list examines within population originating genetic material only. The X and Y-axis both have the same list of strain identifiers with genetic donors being the columns and recipient genomes being the rows. The cell where a strain meets itself is shown in white. All other cells are shown with a hue from the color gradient on the right indicate little or no recombination at yellow to high recombination activity at dark blue/black coloring. At top is shown a phylogenetic tree of the examined strains. The dark cells in the bottom right quadrant correspond with the higher rates of recombination seen between and among the clinically relevant *Legionella pneumophila* serogroups 1-17. This correlates with the clade groupings seen in **Fig.4, 5, 6, 8**.

of the individual Legionella strains into subpopulations, which can also be called as ancestral populations. The results from the model based fineSTRUCTURE clustering are shown as a tree on the top of the co-ancestry matrix (**Fig.7**). A total of 21 subpopulations (ancestral populations) for Legionella were estimated in this study. The heat map also indicates evidence of admixture populations in Legionella. The term "admixture" indicates the evidence of flow of chunks of DNA (or recombination events) between the ancestral populations. Such admixture events cause interesting asymmetry in the co-ancestry matrix. Many such examples of interesting asymmetry were observed in some Legionella strains (that are not *L. pneumophila*). Such events of admixtures can be seen at the bottom right portion of the heat map (**Fig.7**) that mainly consists of non pneumophila strains. In other words, higher rates of DNA exchange across sub-populations were found in non *L. pneumophila* strains compared to *L. pneumophila* strains. A similar trend was also observed in the number of recombination events inferred using the ClonalFrame algorithm (**Fig.8**). It generated a heat map with more intense color variation for genome-wide DNA sequence segments transferred via homologous recombination associated with the clade maintaining most of the *Legionella pneumophila* serotypes [27]. Our results found recombination present between all strains to some extent (**Fig.7**). However, the greatest intensity of recombination took place between *Legionella pneumophila* serotypes as a grouping and then as non pneumophila strains as a grouping.

Table 4. List of identifiers for the fineStructure results (**Fig.7**) and the ClonalFrame results (**Fig.8**) along with their corresponding Legionella strain name.

Figure	**Strain**	**Figure**	**Strain**	**Figure**	**Strain**	**Figure**	**Strain**

IND1	*L.philadelphia*	IND12	*L. erythra*	IND23	*L.pneumophila (HL06041035)*	IND34	*L.pneumophila3*
IND2	*L.alcoy*	IND13	*L. jamestowniensis*	IND24	*L. rowbothamii*	IND35	*L.pneumophila4*
IND3	*L. anisa*	IND14	*L. jordanis*	IND25	*L.pneumophila10*	IND36	*L.pneumophila5*
IND4	*L. bozemanii 1*	IND15	*L.lorraine*	IND26	*L.pneumophila11*	IND37	*L.pneumophila6*
IND5	*L. bozemanii 2*	IND16	*L.pneumophia* (LPE509)	IND27	*L.pneumophila12*	IND38	*L.pneumophila7*
IND6	*L. birminghamensis*	IND17	*L. maceachernii*	IND28	*L.pneumophila13*	IND39	*L.pneumophila8*
IND7	*L. brunensis*	IND18	*L. micdadei*	IND29	*L.pneumophila14*	IND40	*L.pneumophila9*
IND8	*L. cherii*	IND19	*L. nautarum*	IND30	*L.pneumophila15*	IND41	*L.pneumophila* (Thunder Bay)
IND9	*L. cincinnatiensis*	IND20	*L.longbeachae*	IND31	*L.pneumophila16*	IND42	*L. tusconensis*
IND10	*L.corby*	IND21	*L.pneumophia* (ATCC 43290)	IND32	*L.pneumophila17*	IND43	*L. wadsworthii*
IND11	*L. dumoffii*	IND22	*L.paris*	IND33	*L.pneumophila2*		

ClonalFrame Analysis

ClonalFrame reconstructed the clonal genealogy between the 43 Legionella strains, assuming these 43 strains represent a sample set for all of the Legionella population using a Bayesian phylogenetic framework that accounts not only for mutation events but also for recombination events. **Figure 9** shows the distribution of recombination events on the branches of the clonal genealogy inferred using the whole core-genome alignment. The clonal genealogy is shown on the left of the heat map of **figure 9**. Mutli Locus Sequence Typing (MLST) based recombination has previously been reported in *Legionella pneumophila,* and I wanted to assess the role it played in the evolution of this intracellular bacterial pathogen. [25,28]. ClonalFrame estimates two values, namely ρ/θ and r/m, where the former measures the frequency of occurrence of recombination relative to mutation, whereas the latter measures how important the effect of recombination is in genetic diversification relative to mutation [28]. ClonalFrame estimated the ρ/θ value to be 0.562 (mean of three runs) with a 95% credibility interval of 0.31 - 0.911, indicating that recombination happened less frequently than mutation. The r/m value was found to be 6.941 (mean of three runs) with a 95% credibility interval of 3.693–11.255, demonstrating that recombination, not mutation plays a larger role in genetic evolution for Legionella **(Table** 5). This is consistent with the fact that unlike mutation, recombination often affects several nucleotides at each occurrence This method utilized Whole Genome Sequencing instead of MLST so it is has much more credence. In MLST methods, 7 or 8 genes would be considered. However, with the method performed in this study, the entirety of the genome down to the nucleotide level is examined. As such, we now have a much more thorough as well as comprehensive understanding of the evolutionary factors driving genetic change in the Legionella pangenome. We are now able to see where the interplay of mutation and recombination not only in Legionella but how this fits in to the global picture of mutation and recombination driven changes in other bacteria. Results were garnered from three independent runs and established as a mean value (**Fig.9, Table 5**). The resulting estimated relative rate of mutation and recombination and the resulting estimated effect of mutation and recombination were significantly higher than the previously reported value of 0.9 with a 95% confidence of 0.2-1.9 (**Table 5**) [28]. This previous finding used Multi Locus Sequencing Typing with only 2 loci [28].

Table 5. List of the resulting ClonalFrame values from each of three runs with calculated means. The relative rate

of recombination occurring within the pangenome versus the relative rate of mutation occurring within the pangenome shown as a ratio (ρ/θ) shown with its 95% confidence interval for each run of ClonalFrame. The relative effect of recombination on genetic change within the pangenome versus the relative effect of mutation on genetic change within the pangenome shown as a ratio (r/m) with its 95% confidence interval for each of the three runs of ClonalFrame.

	Run 1	**Run 2**	**Run 3**	**Average of All Runs**
Relative Rate of Recombination Versus Mutation (ρ/θ)	0.555	0.539	0.592	0.562
95% Confidence Interval	0.31-0.818	0.385-0.752	0.363-0.911	0.352-0.827
Relative Effect of Recombination Versus Point Mutation (r/m)	6.823	6.741	7.26	6.941
95% Confidence Interval	3.693-9.894	4.384-8.838	3.833-11.255	3.97-10.000

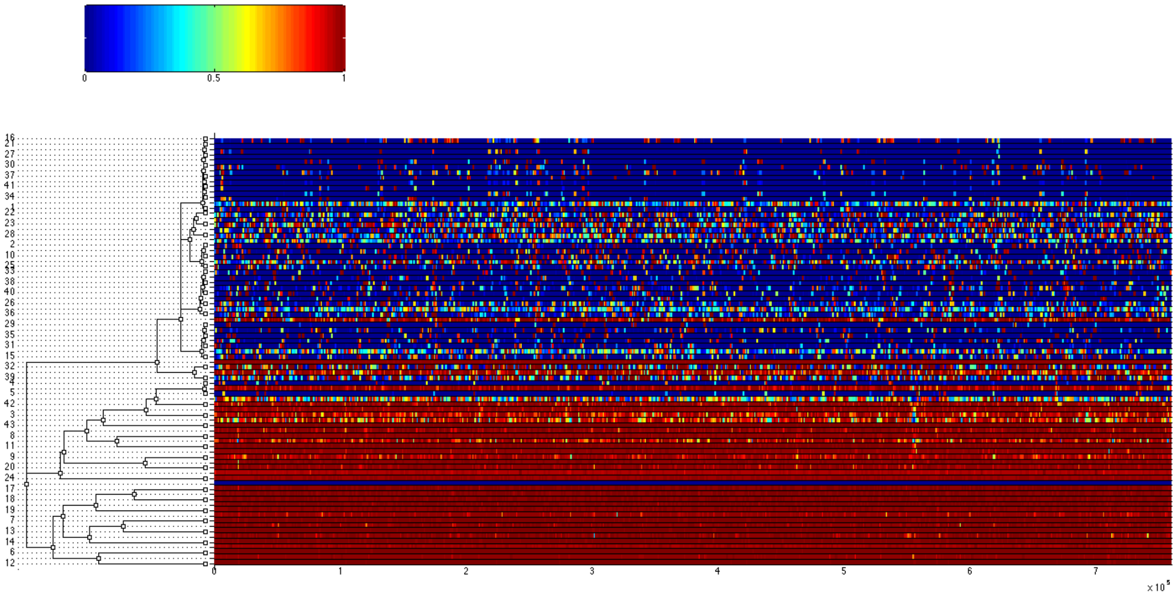


Fig. 7 Results of the ClonalFrame Analysis of the 43 Legionella Genomes. At left is shown the inferred clonal genealogy with each branch of the tree corresponding to one of the heat map rows. Within each row of the heat map is shown the probability of recombination as it was estimated by ClonalFrame corresponding to the connecting branch (strain). Along the X-axis the positions of alignment in sequence are listed (X-axis *10^5 bp). The probability values are color coded as shown on the scale at the upper left. It can be seen that there is extreme recombination (red at a majority alignment positions) associated with specific clades (branch groupings on the left).

Discussion

In this study, I have made the most comprehensive analysis to date of the basic parameters of the Legionella genus using state of the art tools and techniques. In particular, I focused on recombination, which was found to be of much greater importance in Legionella than previously realized. This study showed a drastically higher r/m value than previous published studies using a significantly smaller selection of Legionella strains [29]. This indicates that even though mutation within the pangenome is happening at a much higher rate, it is in fact recombination that is driving genetic change within this species population. It is interesting to note that studies in the past have utilized entirely or mostly environmental samples of Legionella and found the r/m rate to be drastically lower (0.9 versus our three run average of 6.941) [28,29]. This indicates that having a more robust and complete study gives a different and more accurate picture of factors driving genetic change within the pangenome. This is supported by the fact that in addition to utilizing the largest amount of Legionella strains to date for this study, it also featured Whole Genome Sequencing instead of Multi Locus Sequence Typing. The previous values for the r/m rate were calculated using only two loci so it had significantly less weight behind its conclusions [29]. However, this could also reveal a nuance of evolutionary change within vying segments of the Legionella species. This would mean essentially breaking the species into subsets of clinically relevant and environmental strains. It might indicate that genetic change in environmental samples of Legionella is more driven by mutation, whereas it is shaped by recombination in clinically relevant samples. As such, it would be easier to target either sub-population knowing that they maintained distinctly different genetic change profiles. For human health concerns, the next step after identifying recombination as the driving force in clinical isolates or across the species, would be to understand what genetic components are being exchanged and why. This is supported by the fineStructure results showing clade specific recombination [25]. This clade specific association was seen predominantly in the *Legionella pneumophila* numbered serogroups in three independently verified phylogenetic trees (**Fig.4, 5, 6**). Already, efforts have been made to create a system of rapid identification for pathogenic strains [30]. With the role of recombination in Legionella more clearly defined, it would make sense to start looking not only for pathogenic strains themselves, but for strains that contain genes or gene regions that have been identified as readily and favorably participating in recombination with pathogenic strains. This could drastically change the way that clinical isolates are analyzed and treated in the future. The effect of Legionella's recombination is significant in a variety of ways. It has been shown that recombination's role in a bacterial population's adaptation is paramount [11, 31, 32]. Homologous recombination has been detected utilizing comparative genomic methods in a variety of bacterial pathogens such as *E.coli, Chlamydia spp, Streptococcus spp*, and *Listeria monocytogenes* [31, 34-36]. Additionally, species influenced predominantly by recombination might have quicker adaptation capabilities because it has been shown that recombination can provide an evolutionary advantage over point mutations [37-39]. Finally, the r/m rate from this study changes Legionella's relationship with other pathogens. While its earlier 0.9 r/m value meant that it originally closely associate with E.coli (0.7 r/m), its 6.941 r/m value from this study now puts Legionella squarely amongst pathogens such as *Chlamydia spp, Streptococcus spp*, and *Listeria monocytogenes* (r/m 6-7) [28]. Strain dependent paralog percentages were clearly evident (**Fig.2**). As such, these strains should be examined to see causation of duplication events and any relatedness of paralogs or paralog groups within strains. It would be worthy of noting whether any relationships delineated follow any particular pattern such as phylogeny connections, geographic range, host range/preference, or phenotypes. It has been shown, that not just the presence or absence of a paralog can define phenotypes as such as secretion ability or toxicity, but the interplay of related paralogs and the number of duplicated paralogs [39]. In this project I identified the core and non-core components of the Legionella pangenome and illustrated the recombination rates and significance between strains. Each of these could be pursued separately from the view of potential future studies. The importance of this pangenome mapping is that now specific gene targets can be identified on a population wide instead of individual basis. Also, once a genetic map is established, genotyping can quickly show what differences a new or changed strain has on the sequence level, then these specifically can be examined. Furthermore, a map has been established of the common genes throughout all known Legionella strains, this provides targets for drug design. It is known that constituents of the core genome are highly conserved and therefore most likely crucial to function. If they could be disrupted, then a treatment could be developed that works against all strains of this pathogen instead of only some. If a vaccine were to target a component of unique or accessory genes, then it would be much easier for the organism to evolve past that target. However, conserved, core targets are more difficult to modify. Utilizing a pangenome study provides researchers with explicit genes or regions of interest to focus their efforts. For example, accessory genes associated with most or all of the clinically relevant strains or those strains that they most often interact with via recombination would be high impact targets. Additionally, since only some strains of Legionella are disease causing, their particular unique or shared accessory genes could be searched for virulence factors. The way to address this question would be to generate a rarefaction curve from this data. A rarefaction curve identifies the amount of genetic diversity compared to the number of samples in a population [12]. This is the tool that demonstrates whether a genome has an open or closed nature. Beyond the core genome, the unique genes of strains with phenotypes of interest should be searched to determine in potential links. Then this could be extrapolated with knock out studies. Going forward, next steps of this project would include investigating whether strains with common unknown gene function clusters shared any commonality of prominent or inexplicable phenotypic traits. Furthermore, the isolation times of samples should be factored into a tree to describe chronological descent and relatedness. Along with this, isolate locations should be mapped so that geographic dependence can be elucidated. Any strains being newly discovered could be easily inserted into the framework this project created, allowing the

Legionella pangenome to be fully illustrated. This will be invaluable in disease research and understanding past and future Legionella outbreaks. Once the framework has been established, pointed research can be done on the most clinically relevant aspects of the population. Ideally, this would allow not just for targeted treatment, but also prevention. Later collaborative work would involve confirmation of putative function in genes of interest. Additionally, an analysis could be done on point mutations to see which strains or gene families are most readily mutated and if there is a pattern of mutation that matches or conflicts with the ρ/θ and r/m patterns seen in this study (**Table 5**). Using the recombination information from this study, the gene sources could be tracked. For example, in which strain did something first appear, then how did it spread within the pangenome. Beyond that, a global search could fing an ancestral progenitor of the gene from outside of the pangenome. Identifying which genes are undergoing recombination events allows for studies of why recombination is happening between certain strains and why certain genetic components are more viable and conserved within a genus or associated with pathogenicity. As such, the established pangenome and recombination analysis for Legionella will serve as a vital tool to further understanding of this pathogen's history, dynamics, and ability to be successfully treated.

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APPENDIX

FASTA Source	CORE Philly	START	STOP	NT Length	GENE	PRODUCT	INFERENCE
594.fasta	Philly_00001	654	2012	1358.00	dnaA	Chromosomal replication initiator protein DnaA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P03004
595.fasta	Philly_00002	2026	3129	1103.00	dnaN	DNA polymerase III subunit beta	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A988
596.fasta	Philly_00003	3126	4187	1061.00	recF	DNA replication and repair protein RecF	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7H0
597.fasta	Philly_00004	4485	6902	2417.00	gyrB	DNA gyrase subunit B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AES6
598.fasta	Philly_00005	7271	8311	1040.00	aguA	Agmatine deiminase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9I6J9
599.fasta	Philly_00006	8314	10206	1892.00	speA	Biosynthetic arginine decarboxylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P21170
600.fasta	Philly_00007	10226	11071	845.00	hfq	N-carbamoyl-D-amino acid hydrolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60327
601.fasta	Philly_00009	13059	13316	257.00	hfq	Host factor-I protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6X3
602.fasta	Philly_00010	13344	14588	1244.00	hflX	GTP-binding protein HflX	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P25519
603.fasta	Philly_00011	14693	15163	470.00	resA	Thiol-disulfide oxidoreductase ResA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P35160

604.fasta	Philly_00013	17055	17894	839.00	yhhW_1	Quercetin 2,3-dioxygenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P46852
605.fasta	Philly_00022	26016	26927	911.00	yjgA	Sulfite exporter TauE/SafE	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF01925.13
606.fasta	Philly_00023	27119	27598	479.00	yjgA	x96 protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8X0
607.fasta	Philly_00024	27595	29718	2123.00	rlmL	Ribosomal RNA large subunit methyltransferase K/L	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P75864
608.fasta	Philly_00025	29788	30330	542.00	pagP	putative membrane protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG4323
609.fasta	Philly_00028	31774	33165	1391.00	yhdG_1	putative amino acid permease YhdG	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O07576
610.fasta	Philly_00029	33175	34170	995.00	pitA_1	Low-affinity inorganic phosphate transporter 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFJ7
611.fasta	Philly_00030	34187	34828	641.00	coq7	2-nonaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9I5R6
612.fasta	Philly_00056	60077	60970	893.00	prpB	Methylisocitrate lyase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77541
479.fasta	Philly_00077	77642	78820	1178.00	uvrB	Aspartate aminotransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P23034
711.fasta	Philly_00078	78867	80858	1991.00	uvrB	Excinuclease ABC subunit B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8F8
712.fasta	Philly_00081	84555	84869	314.00	zapA	Z ring-associated protein ZapA	ab initio prediction:Prodigal:2.60 similar to AA

							sequence:UniProtKB:Q9HTW3
714.fasta	Philly_00082	85025	85606	581.00	pepP	yecA family protein	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR02292
715.fasta	Philly_00083	85711	87021	1310.00	pepP	Xaa-Pro aminopeptidase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P15034
716.fasta	Philly_00084	87011	88213	1202.00	ubiH	2-octaprenyl-6-methoxyphenol hydroxylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P25534
717.fasta	Philly_00085	88210	89373	1163.00	ubiF	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P75728
718.fasta	Philly_00089	92368	93315	947.00	artJ_2	hypothetical protein	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR02291
719.fasta	Philly_00090	93312	94835	1523.00	artJ_2	hypothetical protein	ab initio prediction:Prodigal:2.60
720.fasta	Philly_00091	94825	95352	527.00	artJ_2	hypothetical protein	ab initio prediction:Prodigal:2.60
721.fasta	Philly_00092	95602	97527	1925.00	artJ_2	hypothetical protein	ab initio prediction:Prodigal:2.60
722.fasta	Philly_00093	97493	98083	590.00	artJ_2	hypothetical protein	ab initio prediction:Prodigal:2.60
723.fasta	Philly_00097	103878	104342	464.00	rnr	hypothetical protein	ab initio prediction:Prodigal:2.60
724.fasta	Philly_00098	104829	106928	2099.00	rnr	Ribonuclease R	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P21499
725.fasta	Philly_00099	106909	107670	761.00	rlmB	23S rRNA (guanosine-2'-O-)-methyltransferase RlmB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P63177
726.fasta	Philly_00105	112238	114928	2690.00	polA	DNA polymerase I	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00582
727.fasta	Philly_00106	114931	115986	1055.00	lpxD_1	UDP-3-O-acylglucosamine N-acyltransferas	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0C

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728.fasta	Philly_00108	117029	118258	1229.00	fabF_1	3-oxoacyl-[acyl-carrier-protein] synthase 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P73283
729.fasta	Philly_00109	118383	119243	860.00	msrA_1	ribosomal-protein-alanine N-acetyltransferase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK09491
730.fasta	Philly_00113	122242	123048	806.00	gcvPB	hypothetical protein	ab initio prediction:Prodigal:2.60
731.fasta	Philly_00114	123147	123416	269.00	gcvPB	hypothetical protein	ab initio prediction:Prodigal:2.60
732.fasta	Philly_00115	124044	125846	1802.00	gcvPB	branched-chain alpha-keto acid dehydrogenase subunit E2	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK11856
966.fasta	Philly_00119	132222	133676	1454.00	gcvPB	putative glycine dehydrogenase [decarboxylating] subunit 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P99168
734.fasta	Philly_00121	133978	135348	1370.00	gcvPA	putative glycine dehydrogenase [decarboxylating] subunit 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P64218
735.fasta	Philly_00122	135351	135728	377.00	gcvH	Glycine cleavage system H protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6T9
736.fasta	Philly_00123	135762	136844	1082.00	gcvT	Aminomethyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P27248
737.fasta	Philly_00124	136979	137446	467.00	opuAB	hypothetical protein	ab initio prediction:Prodigal:2.60
738.fasta	Philly_00125	137421	137951	530.00	opuAB	Macrophage killing protein with similarity to conjugation protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF11393.2
739.fasta	Philly_00126	138448	140187	1739.00	opuAB	Glycine betaine transport system permease protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P46921

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740.fasta	Philly_00127	140195	141493	1298.00	cmpD	Bicarbonate transport ATP-binding protein CmpD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q55463
741.fasta	Philly_00128	141570	142184	614.00	dsbA_1	Thiol:disulfide interchange protein DsbA precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0C2B2
742.fasta	Philly_00129	142195	142797	602.00	cc4	Cytochrome c4 precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q52369
743.fasta	Philly_00130	142872	143474	602.00	engB	putative GTP-binding protein EngB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6P7
744.fasta	Philly_00132	146993	148876	1883.00	acsA_1	Acetyl-coenzyme A synthetase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q89WV5
745.fasta	Philly_00134	149798	151297	1499.00	mmsA	Methylmalonate-semialdehyde dehydrogenase [acylating]	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P28810
746.fasta	Philly_00137	154334	155065	731.00	dapB	4-hydroxy-tetrahydrodipicolinate reductase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P63895
747.fasta	Philly_00138	155787	156479	692.00	proQ_1	ProP effector	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45577
748.fasta	Philly_00139	156480	157550	1070.00	pykA	hypothetical protein	ab initio prediction:Prodigal:2.60
1060.fasta	Philly_00142	164776	165966	1190.00	pgk	Phosphoglycerate kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A799
749.fasta	Philly_00143	165977	166969	992.00	gapA	Glyceraldehyde-3-phosphate dehydrogenase 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P09124
750.fasta	Philly_00144	167051	169057	2006.00	tktA	Transketolase 1	ab initio prediction:Prodigal:2.60 similar to AA

							sequence:UniProtKB:P27302
751.fasta	Philly_00146	170748	172763	2015.00	prlC	Oligopeptidase A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P27237
752.fasta	Philly_00172	197445	197855	410.00	prfA_1	Peptide chain release factor 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P75420
1140.fasta	Philly_00233	270123	270569	446.00	zur	Zinc uptake regulation protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AC51
1139.fasta	Philly_00242	285047	285979	932.00	glsA	Glutaminase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5KY26
1070.fasta	Philly_00262	309672	310310	638.00	copA_1	uracil-DNA glycosylase, family 4	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR00758
1163.fasta	Philly_00264	311962	312618	656.00	copA_1	lysozyme	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PHA0447
1059.fasta	Philly_00286	340430	341203	773.00	ydfG	NADP-dependent 3-hydroxy acid dehydrogenase YdfG	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P39831
1055.fasta	Philly_00288	342005	342574	569.00	efp	Elongation factor P	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83AR4
1054.fasta	Philly_00289	342646	343626	980.00	epmB	L-lysine 2,3-aminomutase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P39280
1053.fasta	Philly_00290	343695	345767	2072.00	ppk	Polyphosphate kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7B1
1052.fasta	Philly_00292	347089	347622	533.00	fadE_1	chromate transporter, chromate ion transporter (CHR) family	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR00937

1051.fasta	Philly_00293	347619	348239	620.00	fadE_1	hypothetical protein	ab initio prediction:Prodigal:2.60
1050.fasta	Philly_00294	348415	350853	2438.00	fadE_1	Acyl-coenzyme A dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8ZRJ7
1049.fasta	Philly_00295	350967	351659	692.00	rmlA_1	hypothetical protein	ab initio prediction:Prodigal:2.60
1048.fasta	Philly_00296	351696	352358	662.00	rmlA_1	Glucose-1-phosphate thymidylyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P39629
1047.fasta	Philly_00297	352355	353332	977.00	lptD	putative phosphotransferase related to Ser/Thr protein kinases	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG3178
1046.fasta	Philly_00298	353575	356094	2519.00	lptD	Organic solvent tolerance protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P31554
1045.fasta	Philly_00299	356270	357559	1289.00	surA	Peptidyl-prolyl cis-trans isomerase SurA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q4K4X7
1044.fasta	Philly_00300	357556	358530	974.00	pdxA1	4-hydroxythreonine-4-phosphate dehydrogenase 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9I5U4
1043.fasta	Philly_00301	358532	359023	491.00	dhfrIII	Dihydrofolate reductase type 3	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P12833
1042.fasta	Philly_00312	367148	367696	548.00	nusG	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFG0
1348.fasta	Philly_00313	367807	368241	434.00	rplK	50S ribosomal protein L11	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7J7
1347.fasta	Philly_00314	368251	368946	695.00	rplA	50S ribosomal protein L1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7L0

1346.fasta	Philly_00315	369119	369652	533.00	rplJ	50S ribosomal protein L8	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7J3
1345.fasta	Philly_00316	369683	370063	380.00	rplL	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7K2
1344.fasta	Philly_00317	370155	374261	4106.00	rpoB	DNA-directed RNA polymerase subunit beta	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q4K526
1343.fasta	Philly_00318	374308	378555	4247.00	rpoC	DNA-directed RNA polymerase subunit beta'	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8T7
1342.fasta	Philly_00319	378669	379049	380.00	rpsL	30S ribosomal protein S12	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7S3
1341.fasta	Philly_00320	379070	379597	527.00	rpsG	30S ribosomal protein S7	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P02359
1340.fasta	Philly_00321	379612	381696	2084.00	fusA	Elongation factor G	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6M8
1339.fasta	Philly_00323	382913	383230	317.00	rpsJ	30S ribosomal protein S10	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7R5
819.fasta	Philly_00324	383268	383915	647.00	rplC	50S ribosomal protein L3	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60438
818.fasta	Philly_00325	383915	384520	605.00	rplD	50S ribosomal protein L4	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60726
817.fasta	Philly_00326	384517	384813	296.00	rplW	50S ribosomal protein L23	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9K1I6
816.fasta	Philly_00327	384825	385652	827.00	rplB	50S ribosomal	ab initio prediction:Prodigal:2.60

						protein L2	similar to AA sequence:UniProtKB:P60422
815.fasta	Philly_00329	385959	386294	335.00	rplV	50S ribosomal protein L22	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P61175
814.fasta	Philly_00330	386297	386953	656.00	rpsC	30S ribosomal protein S3	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7V3
813.fasta	Philly_00331	386970	387383	413.00	rplP	50S ribosomal protein L16	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ADY7
812.fasta	Philly_00332	387383	387577	194.00	rpmC	50S ribosomal protein L29	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HWE3
811.fasta	Philly_00333	387579	387833	254.00	rpsQ	30S ribosomal protein S17	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q1R616
810.fasta	Philly_00334	387922	388287	365.00	rplN	50S ribosomal protein L14	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q7DDT2
809.fasta	Philly_00335	388300	388629	329.00	rplX	50S ribosomal protein L24	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60624
808.fasta	Philly_00336	388645	389196	551.00	rplE	50S ribosomal protein L5	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P62399
807.fasta	Philly_00337	389209	389511	302.00	rpsN	30S ribosomal protein S14	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AG59
806.fasta	Philly_00338	389534	389929	395.00	rpsH	30S ribosomal protein S8	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7W7
805.fasta	Philly_00339	389947	390486	539.00	rplF	50S ribosomal protein L6	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A

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804.fasta	Philly_00340	390497	390856	359.00	rplR	50S ribosomal protein L18	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:A6U875
803.fasta	Philly_00341	390866	391372	506.00	rpsE	30S ribosomal protein S5	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7W4
802.fasta	Philly_00343	391560	391994	434.00	rplO	50S ribosomal protein L15	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P02413
801.fasta	Philly_00344	391997	393325	1328.00	rpsM	preprotein translocase subunit SecY	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK09204
800.fasta	Philly_00345	393533	393889	356.00	rpsM	30S ribosomal protein S13	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7S9
799.fasta	Philly_00346	393913	394311	398.00	rpsK	30S ribosomal protein S11	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7R9
798.fasta	Philly_00347	394328	394948	620.00	rpsD	30S ribosomal protein S4	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7V8
797.fasta	Philly_00348	394967	395959	992.00	rpoA	DNA-directed RNA polymerase subunit alpha	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A0Y1
796.fasta	Philly_00349	395978	396361	383.00	rplQ	50S ribosomal protein L17	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AG44
795.fasta	Philly_00350	396429	396908	479.00	ssb_1	Helix-destabilizing protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83EP4
794.fasta	Philly_00351	396992	398359	1367.00	yajR	Inner membrane transport protein YajR	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77726

793.fasta	Philly_00352	398521	399279	758.00	fabL_1	Enoyl-[acyl-carrier-protein] reductase [NADPH] FabL	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P71079
792.fasta	Philly_00353	399350	399763	413.00	acpXL	Acyl carrier protein AcpXL	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A2W5
791.fasta	Philly_00354	399763	400659	896.00	fabF_2	(3R)-hydroxymyristoyl-ACP dehydratase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK00006
790.fasta	Philly_00355	400664	401956	1292.00	fabF_2	3-oxoacyl-[acyl-carrier-protein] synthase 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83E37
789.fasta	Philly_00356	401957	403234	1277.00	fabF_3	3-oxoacyl-[acyl-carrier-protein] synthase 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P73283
788.fasta	Philly_00357	403227	404072	845.00	htrB_1	Lipid A biosynthesis lauroyl acyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ACV0
787.fasta	Philly_00360	407663	408496	833.00	dapF	Diaminopimelate epimerase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5ZYK6
785.fasta	Philly_00362	409345	409992	647.00	estB	Carboxylesterase 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q53547
784.fasta	Philly_00363	409989	410423	434.00	ratA	Toxin RatA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AGL5
783.fasta	Philly_00364	410410	410682	272.00	bamE	hypothetical protein	ab initio prediction:Prodigal:2.60
782.fasta	Philly_00365	410771	411085	314.00	bamE	Outer membrane protein assembly factor BamE precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A937
781.fasta	Philly_00366	411313	411723	410.00	fur	Ferric uptake regulation protein	ab initio prediction:Prodigal:2.60 similar to AA

							sequence:UniProtKB:P37736
780.fasta	Philly_00375	423535	424008	473.00	osmY_1	hypothetical protein	ab initio prediction:Prodigal:2.60
778.fasta	Philly_00378	425369	428224	2855.00	uvrA	Excinuclease ABC subunit A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A698
777.fasta	Philly_00379	428407	428988	581.00	htpX_2	LemA family protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF04011.6
776.fasta	Philly_00380	428999	430018	1019.00	htpX_2	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O30795
775.fasta	Philly_00382	430808	431722	914.00	drrA_1	Daunorubicin/doxorubicin resistance ATP-binding protein DrrA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P32010
774.fasta	Philly_00384	433098	433781	683.00	ogt	putative proline hydroxylase	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG3751
773.fasta	Philly_00385	433822	434529	707.00	ogt	SprT-like family protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF10263.3
772.fasta	Philly_00386	434714	434995	281.00	ogt	hypothetical protein	ab initio prediction:Prodigal:2.60
771.fasta	Philly_00389	436579	436944	365.00	rplS	50S ribosomal protein L19	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7K6
770.fasta	Philly_00390	436971	437723	752.00	trmD	tRNA (guanine-N(1)-)-methyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A873
769.fasta	Philly_00391	437723	438232	509.00	rimM	Ribosome maturation factor RimM	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P44568
768.fasta	Philly_00392	438238	438498	260.00	rpsP	30S ribosomal protein S16	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7T3
767.fasta	Philly_00393	438585	439961	1376.00	ffh	p48	ab initio prediction:Prodigal:2.60 similar to AA

							sequence:UniProtKB:P0AGD7
766.fasta	Philly_00397	445085	446488	1403.00	gadC_1	Glutamate/gamma-aminobutyrate antiporter	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O30417
765.fasta	Philly_00398	446544	447068	524.00	ctaB	hypothetical protein	ab initio prediction:Prodigal:2.60
764.fasta	Philly_00399	447268	447609	341.00	ctaB	alkylhydroperoxidase AhpD family core domain protein	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR00778
763.fasta	Philly_00400	447822	448265	443.00	ctaB	hypothetical protein	ab initio prediction:Prodigal:2.60
762.fasta	Philly_00402	449249	449452	203.00	ctaB	hypothetical protein	ab initio prediction:Prodigal:2.60
761.fasta	Philly_00403	449520	450248	728.00	ctaB	hypothetical protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG3346
760.fasta	Philly_00405	450782	451789	1007.00	ctaB	Cytochrome oxidase assembly protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF02628.9
758.fasta	Philly_00406	451779	452663	884.00	ctaB	Protoheme IX farnesyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3J5F9
757.fasta	Philly_00407	452673	453314	641.00	lysX	SCO1/SenC	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF02630.8
756.fasta	Philly_00408	453681	454589	908.00	lysX	Alpha-aminoadipate--LysW ligase LysX	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5SH23
755.fasta	Philly_00409	454593	454838	245.00	zwf	hypothetical protein	ab initio prediction:Prodigal:2.60
754.fasta	Philly_00419	464892	465887	995.00	hemH	Ferrochelatase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P23871
753.fasta	Philly_00420	465998	466231	233.00	cspD	Cold shock-like protein CspD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A968
1323.fasta	Philly_00434	479014	479274	260.00	yiaD_1	hypothetical protein	ab initio prediction:Prodigal:2.60
1322.fasta	Philly_00435	479275	479619	344.00	yiaD_1	hypothetical protein	ab initio prediction:Prodigal:2.60

1321.fasta	Philly_00437	480172	480747	575.00	yiaD_1	Dot/Icm secretion system protein IcmQ	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR02527
1320.fasta	Philly_00438	480934	482064	1130.00	yiaD_1	hypothetical protein	ab initio prediction:Prodigal:2.60
1319.fasta	Philly_00439	482061	484412	2351.00	yiaD_1	conjugative coupling factor TraD, SXT/TOL subfamily	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR03743
1318.fasta	Philly_00440	484816	485385	569.00	yiaD_1	Inner membrane lipoprotein YiaD precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P37665
1317.fasta	Philly_00441	485397	485681	284.00	proP_1	hypothetical protein	ab initio prediction:Prodigal:2.60
1316.fasta	Philly_00442	485697	486335	638.00	proP_1	Macrophage killing protein with similarity to conjugation protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF11393.2
1315.fasta	Philly_00443	486335	487420	1085.00	proP_1	hypothetical protein	ab initio prediction:Prodigal:2.60
1314.fasta	Philly_00445	490589	491395	806.00	proP_1	hypothetical protein	ab initio prediction:Prodigal:2.60
1313.fasta	Philly_00446	491403	491987	584.00	proP_1	hypothetical protein	ab initio prediction:Prodigal:2.60
1312.fasta	Philly_00447	492013	492411	398.00	proP_1	hypothetical protein	ab initio prediction:Prodigal:2.60
1311.fasta	Philly_00448	492609	493235	626.00	proP_1	hypothetical protein	ab initio prediction:Prodigal:2.60
1310.fasta	Philly_00449	493271	496300	3029.00	proP_1	Type IV secretory pathway, VirB4 components	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG3451
1309.fasta	Philly_00451	497705	500626	2921.00	purH	type VI secretion protein IcmF	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR03348
1285.fasta	Philly_00452	500626	501411	785.00	purH	type IV/VI secretion system protein, DotU family	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR03349
1284.fasta	Philly_00454	503312	504181	869.00	prmA	Ribosomal protein L11 methyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8T1
679.fasta	Philly_0	505539	506021	482.00	accB	Biotin	ab initio

	0456					carboxyl carrier protein of acetyl-CoA carboxylase	prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABD8
678.fasta	Philly_00457	506035	506472	437.00	aroQ	3-dehydroquinate dehydratase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P43877
677.fasta	Philly_00459	509030	510661	1631.00	fda	Zinc metalloproteinase precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P21347
676.fasta	Philly_00460	510663	511511	848.00	fda	Tropinesterase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P07383
675.fasta	Philly_00461	511979	512734	755.00	fda	Endonuclease/Exonuclease/phosphatase family protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF03372.17
674.fasta	Philly_00462	512912	513922	1010.00	fda	Fructose-bisphosphate aldolase class 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P99117
673.fasta	Philly_00463	514072	514764	692.00	dmpP	Phenol hydroxylase P5 protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P19734
672.fasta	Philly_00464	514890	515432	542.00	ptsH	hypothetical protein	ab initio prediction:Prodigal:2.60
671.fasta	Philly_00467	516090	516827	737.00	ptsH	CDP-diacylglycerol-serine O-phosphatidyltransferase	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR00473
670.fasta	Philly_00469	517528	517827	299.00	hpf	Ribosome hibernation promoting factor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFX0
669.fasta	Philly_00470	517854	519248	1394.00	rpoN1	RNA polymerase sigma-54 factor 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P30332
668.fasta	Philly_00471	519458	519622	164.00	rpmG	50S ribosomal protein L33	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9RSS4

667.fasta	Philly_00472	519637	519873	236.00	rpmB	50S ribosomal protein L28	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7M2
666.fasta	Philly_00473	520142	520819	677.00	trmB	tRNA (guanine-N(7)-)-methyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P44648
665.fasta	Philly_00475	522033	523520	1487.00	hflK_1	Ankyrin repeats (3 copies)	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF12796.1
664.fasta	Philly_00476	523728	524870	1142.00	hflK_1	Modulator of FtsH protease HflK	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABC7
663.fasta	Philly_00477	524873	525787	914.00	hflC	Modulator of FtsH protease HflC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABC3
662.fasta	Philly_00478	525922	527217	1295.00	purA	Adenylosuccinate synthetase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3KIY4
661.fasta	Philly_00482	529250	529708	458.00	argR	Arginine repressor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O31408
561.fasta	Philly_00484	530569	531216	647.00	artQ	Arginine transport system permease protein ArtQ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P54536
562.fasta	Philly_00485	531200	531868	668.00	glnQ	Glutamine transport ATP-binding protein GlnQ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P10346
563.fasta	Philly_00486	531865	533082	1217.00	argG	Argininosuccinate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P59846
564.fasta	Philly_00487	533075	534310	1235.00	argH1	Argininosuccinate lyase 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q92MH1
565.fasta	Philly_00491	538358	539695	1337.00	ctpB	Carboxy-terminal processing	ab initio prediction:Prodigal:2.60 similar to AA

						protease CtpB precursor	sequence:UniProtKB:O35002
660.fasta	Philly_00492	539776	540918	1142.00	envC	Septal ring factor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P37690
659.fasta	Philly_00497	544546	545262	716.00	ispU	Ditrans,polycis-undecaprenyl-diphosphate synthase ((2E,6E)-farnesyl-diphosphate specific)	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60472
658.fasta	Philly_00498	545273	546070	797.00	cdsA	Phosphatidate cytidylyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABG1
657.fasta	Philly_00499	546103	547455	1352.00	rseP_1	Regulator of sigma E protease	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AEH1
656.fasta	Philly_00500	547578	549938	2360.00	bamA	Outer membrane protein assembly factor BamA precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A943
655.fasta	Philly_00501	550052	550552	500.00	skp	Cationic 19 kDa outer membrane protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P31519
654.fasta	Philly_00502	550566	551585	1019.00	lpxD_2	UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P21645
653.fasta	Philly_00503	551703	552155	452.00	fabZ	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6Q6
652.fasta	Philly_00504	552152	552922	770.00	lpxA_1	Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferas	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A722

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651.fasta	Philly_00505	552926	553330	404.00	serS	camphor resistance protein CrcB	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK14217
1232.fasta	Philly_00506	553352	554632	1280.00	serS	Serine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3KA84
650.fasta	Philly_00522	566512	567138	626.00	sdhC	hypothetical protein	ab initio prediction:Prodigal:2.60
834.fasta	Philly_00525	569158	569532	374.00	sdhC	Succinate dehydrogenase cytochrome b556 subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P69054
833.fasta	Philly_00526	569526	569873	347.00	sdhD	Succinate dehydrogenase hydrophobic membrane anchor subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P51057
832.fasta	Philly_00527	569875	571644	1769.00	sdhA	Succinate dehydrogenase flavoprotein subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AC41
831.fasta	Philly_00528	571657	572379	722.00	sdhB	Succinate dehydrogenase iron-sulfur subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P07014
830.fasta	Philly_00531	576576	577739	1163.00	sucC	Succinyl-CoA ligase [ADP-forming] subunit beta	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A836
829.fasta	Philly_00532	577814	578689	875.00	sucD	Succinyl-CoA ligase [ADP-forming] subunit alpha	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AGE9
828.fasta	Philly_00534	580363	580734	371.00	sauU_1	hypothetical protein	ab initio prediction:Prodigal:2.60
827.fasta	Philly_00535	580805	581194	389.00	sauU_1	hypothetical protein	ab initio prediction:Prodigal:2.60
826.fasta	Philly_00536	581844	583127	1283.00	sauU_1	putative sulfoacetate transporter SauU	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q0K843
825.fasta	Philly_00537	583357	584814	1457.00	fis_1	hypothetical protein	ab initio prediction:Prodigal:2.60

824.fasta	Philly_00538	585004	585285	281.00	fis_1	Hin recombinational enhancer-binding protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6R3
823.fasta	Philly_00539	585347	586294	947.00	prs_1	Ribose-phosphate pyrophosphokinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A717
822.fasta	Philly_00542	587338	587850	512.00	coaD	Phosphopantetheine adenylyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3JW91
821.fasta	Philly_00543	587834	589558	1724.00	ggt	Gamma-glutamyltranspeptidase precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P36267
820.fasta	Philly_00545	592083	592814	731.00	plsC	1-acyl-sn-glycerol-3-phosphate acyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P26647
1295.fasta	Philly_00551	596672	597496	824.00	mutM	Formamidopyrimidine-DNA glycosylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P05523
1294.fasta	Philly_00556	600719	601465	746.00	fabG_2	3-oxoacyl-[acyl-carrier-protein] reductase FabG	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9KQH7
1293.fasta	Philly_00557	601595	601993	398.00	spmA	polyhydroxyalkanoate synthesis repressor PhaR	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR01848
1292.fasta	Philly_00559	602739	603809	1070.00	spmA	hypothetical protein	ab initio prediction:Prodigal:2.60
1258.fasta	Philly_00560	603879	604484	605.00	spmA	Spore maturation protein A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P35157
1257.fasta	Philly_00561	604481	605014	533.00	spmB	Spore maturation protein B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P35158
1256.fasta	Philly_00562	605145	606578	1433.00	tyrS	Glycyl-glycine endopeptidase ALE-1 precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O05156

1255.fasta	Philly_00563	606769	608040	1271.00	tyrS	Tyrosine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q4K517
1254.fasta	Philly_00566	613387	613923	536.00	gor	carnitine operon protein CaiE	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK13627
1176.fasta	Philly_00567	613930	615288	1358.00	gor	Glutathione reductase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P06715
1175.fasta	Philly_00568	615519	616499	980.00	pitA_2	Adenine deaminase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9I6Y4
693.fasta	Philly_00569	616597	616782	185.00	pitA_2	hypothetical protein	ab initio prediction:Prodigal:2.60
692.fasta	Philly_00571	617366	618619	1253.00	pitA_2	Low-affinity inorganic phosphate transporter 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFJ7
691.fasta	Philly_00572	618629	619300	671.00	yqgF	hypothetical protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG1392
690.fasta	Philly_00574	620555	621118	563.00	yqgF	hypothetical protein	ab initio prediction:Prodigal:2.60
689.fasta	Philly_00575	621102	621530	428.00	yqgF	Putative Holliday junction resolvase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8I1
688.fasta	Philly_00576	621580	622473	893.00	pyrB	Aspartate carbamoyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P56585
687.fasta	Philly_00578	623078	624589	1511.00	comM	Competence protein ComM	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45049
686.fasta	Philly_00579	624654	624914	260.00	glnB	Membrane fusogenic activity	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF04380.7
685.fasta	Philly_00580	625023	625397	374.00	glnB	Nitrogen regulatory protein P-II 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A

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684.fasta	Philly_00581	625407	625988	581.00	pabC	putative 5-formyltetrahydrofolate cyclo-ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P75430
683.fasta	Philly_00582	626235	626420	185.00	pabC	hypothetical protein	ab initio prediction:Prodigal:2.60
682.fasta	Philly_00583	626434	627249	815.00	pabC	Aminodeoxychorismate lyase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P28305
681.fasta	Philly_00588	631254	632996	1742.00	phbC_1	Poly-beta-hydroxybutyrate polymerase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P23608
680.fasta	Philly_00589	633437	633898	461.00	cymR	Cysteine metabolism repressor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O34527
1283.fasta	Philly_00590	633891	635339	1448.00	sufB	FeS cluster assembly protein SufB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77522
1282.fasta	Philly_00591	635341	636093	752.00	sufC	putative ATP-dependent transporter SufC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77499
1281.fasta	Philly_00592	636090	637376	1286.00	sufD	FeS cluster assembly protein SufD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77689
1280.fasta	Philly_00593	637366	638610	1244.00	sufS	Cysteine desulfurase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77444
1279.fasta	Philly_00594	638607	639056	449.00	nifU_1	NifU-like protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O32163
1278.fasta	Philly_00595	639128	639463	335.00	epmA	FeS assembly SUF system protein	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR02945
1277.fasta	Philly_00596	639466	640419	953.00	epmA	Elongation factor P--(R)-beta-lysine	ab initio prediction:Prodigal:2.60 similar to AA

						ligase	sequence:UniProtKB:Q9ZJ12
1276.fasta	Philly_00597	640492	641406	914.00	rlmM	Ribosomal RNA large subunit methyltransferase M	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ADR6
485.fasta	Philly_00601	645622	646668	1046.00	adhC2	NADP-dependent alcohol dehydrogenase C 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0CH37
232.fasta	Philly_00607	651687	652259	572.00	tag	DNA-3-methyladenine glycosylase 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P05100
1155.fasta	Philly_00616	662485	662934	449.00	arnT	putative major pilin subunit	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10574
526.fasta	Philly_00622	669522	670382	860.00	arnT	polysaccharide deacetylase family sporulation protein PdaB	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR02764
525.fasta	Philly_00626	674548	675816	1268.00	gudP_1	D-glucarate permease	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q46916
524.fasta	Philly_00628	677109	678332	1223.00	deoB	Phosphopentomutase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6K6
523.fasta	Philly_00629	678519	679067	548.00	hslV	ATP-dependent protease subunit HslV	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7B8
522.fasta	Philly_00630	679069	680394	1325.00	hslU	Unfoldase HslU	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6H5
521.fasta	Philly_00635	693107	693706	599.00	tnpA_2	NAD(P)H dehydrogenase (quinone)	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9I509
520.fasta	Philly_00638	696023	696805	782.00	exoA	Exodeoxyribonuclease	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P37454

519.fasta	Philly_00639	696798	697568	770.00	xthA	Exodeoxyribonuclease III	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P09030
518.fasta	Philly_00640	697705	697932	227.00	rpmE	50S ribosomal protein L31	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HUD0
517.fasta	Philly_00641	698059	699294	1235.00	maeB	NADP-dependent malic enzyme	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P76558
516.fasta	Philly_00642	699505	700797	1292.00	sauU_2	putative sulfoacetate transporter SauU	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q0K843
515.fasta	Philly_00643	700799	702055	1256.00	garP_1	D-galactarate permease	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AA80
514.fasta	Philly_00644	702084	702902	818.00	dam_1	DNA adenine methylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AEE8
513.fasta	Philly_00645	703073	704269	1196.00	tyrP_1	Tyrosine permease	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AAD4
512.fasta	Philly_00646	704468	705658	1190.00	tyrP_2	Tyrosine permease	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AAD4
511.fasta	Philly_00647	705669	706361	692.00	yiaD_2	Inner membrane lipoprotein YiaD precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P37665
510.fasta	Philly_00653	713454	715235	1781.00	slt	Soluble lytic murein transglycosylase precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AGC3
216.fasta	Philly_00654	715277	715930	653.00	rpe	Ribulose-phosphate 3-epimerase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AG07
215.fasta	Philly_00666	726557	726823	266.00	artJ_4	hypothetical protein	ab initio prediction:Prodigal:2.60

214.fasta	Philly_00674	736392	737699	1307.00	rimO	Ribosomal protein S12 methylthiotransferase RimO	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AEI4
213.fasta	Philly_00675	737789	739579	1790.00	dsbD_1	Thiol:disulfide interchange protein DsbD precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P36655
212.fasta	Philly_00676	739735	740025	290.00	groL	co-chaperonin GroES	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK00364
211.fasta	Philly_00677	740053	741699	1646.00	groL	Stress protein H5	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P28598
210.fasta	Philly_00680	744892	746772	1880.00	parE	DNA topoisomerase 4 subunit B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P20083
1068.fasta	Philly_00681	746906	748714	1808.00	gsiA	Glutathione import ATP-binding protein GsiA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P75796
1067.fasta	Philly_00686	759971	762277	2306.00	mtcA2_1	Carbonic anhydrase 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O53573
1185.fasta	Philly_00687	762468	763319	851.00	ttcA	tRNA 2-thiocytidine biosynthesis protein TtcA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8ZP88
1186.fasta	Philly_00688	763337	764704	1367.00	tolC	Outer membrane protein TolC precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P02930
1187.fasta	Philly_00689	764716	765390	674.00	pcm	Protein-L-isoaspartate O-methyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7A5
1188.fasta	Philly_00690	765547	766731	1184.00	kbl	2-amino-3-ketobutyrate coenzyme A ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AB77
1189.fasta	Philly_00691	766819	767841	1022.00	tdh	L-threonine 3-	ab initio prediction:Prodigal:2.60

						dehydrogenase	similar to AA sequence:UniProtKB:P07913
1190.fasta	Philly_00692	767884	769557	1673.00	hutG	putative ABC transporter ATP-binding protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45127
1191.fasta	Philly_00693	769599	770210	611.00	hutG	L,D-transpeptidase catalytic domain	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF03734.8
1192.fasta	Philly_00697	772451	773413	962.00	hutG	Macrophage killing protein with similarity to conjugation protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF11393.2
1193.fasta	Philly_00699	774672	775481	809.00	yueD_1	Benzil reductase ((S)-benzoin forming)	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8RJB2
1194.fasta	Philly_00700	775481	776692	1211.00	hutI	Imidazolone propionase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8U8Z6
1195.fasta	Philly_00701	776719	777414	695.00	cusS	hypothetical protein	ab initio prediction:Prodigal:2.60
1196.fasta	Philly_00702	777414	779414	2000.00	cusS	oligopeptide transporter, OPT family	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR00733
1197.fasta	Philly_00707	783098	784345	1247.00	gltT	Glutamate-aspartate carrier protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P24943
710.fasta	Philly_00708	784467	787232	2765.00	valS	Valine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P07118
1198.fasta	Philly_00709	787491	790538	3047.00	bepE_1	Efflux pump membrane transporter BepE	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8G2M6
1106.fasta	Philly_00710	790655	791917	1262.00	mdtA	Multidrug transporter MdtA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P76397
1105.fasta	Philly_0	792158	792562	404.00	osmY_2	hypothetical	ab initio

	0711					protein	prediction:Prodigal:2.60
1104.fasta	Philly_00714	793529	794782	1253.00	glyA2	Serine hydroxymethyltransferase 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q88Q27
1103.fasta	Philly_00715	794785	795252	467.00	nrdR	Transcriptional repressor NrdR	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8D0
1102.fasta	Philly_00716	795310	795753	443.00	nusB	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3K652
1101.fasta	Philly_00717	795746	796702	956.00	thiL	Thiamine-monophosphate kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AGG0
1100.fasta	Philly_00718	796792	797274	482.00	pgpA	Phosphatidylglycerophosphatase A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P18200
1099.fasta	Philly_00719	797274	798326	1052.00	nadE	putative inner membrane protein	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10983
1098.fasta	Philly_00720	798318	799055	737.00	nadE	hypothetical protein	ab initio prediction:Prodigal:2.60
649.fasta	Philly_00724	803263	806529	3266.00	dnaB	Hef nuclease	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK13766
1097.fasta	Philly_00725	806788	807222	434.00	dnaB	hypothetical protein	ab initio prediction:Prodigal:2.60
1096.fasta	Philly_00726	807400	808782	1382.00	dnaB	Replicative DNA helicase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ACB0
1095.fasta	Philly_00727	808784	809857	1073.00	alr	Alanine racemase, biosynthetic	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HUN4
1094.fasta	Philly_00728	809930	810379	449.00	pleD	Surface antigen	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG4520
1093.fasta	Philly_00729	810687	811121	434.00	pleD	putative manganese-	ab initio prediction:Prodigal:2.60

						dependent inorganic pyrophosphatase	protein motif:CLUSTERS:PRK14869
1210.fasta	Philly_00733	814524	815513	989.00	lipA	Lipoyl synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O32129
1209.fasta	Philly_00735	816831	818339	1508.00	dtpA_1	Dipeptide and tripeptide permease A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77304
1208.fasta	Philly_00736	818378	819196	818.00	hisF_1	trans-aconitate 2-methyltransferase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK01683
1207.fasta	Philly_00748	829727	831226	1499.00	pgi	Glucose-6-phosphate isomerase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5NFC4
1018.fasta	Philly_00770	854816	855010	194.00	csrA_1	Carbon storage regulator	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P69913
1206.fasta	Philly_00772	857281	858276	995.00	birA	Bifunctional protein BirA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P06709
1205.fasta	Philly_00773	858280	859017	737.00	psf-1	4'-phosphopantetheinyl transferase psf-1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P55810
1204.fasta	Philly_00774	859099	860052	953.00	accA	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q886M7
1203.fasta	Philly_00775	860045	861340	1295.00	tilS	tRNA(Ile)-lysidine synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P52097
1202.fasta	Philly_00779	865269	866645	1376.00	tdcG	L-serine dehydratase TdcG	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P42630
1201.fasta	Philly_00780	866850	867551	701.00	mip	Outer membrane	ab initio prediction:Prodigal:2.60

						protein MIP precursor	similar to AA sequence:UniProtKB:Q5ZXE0
1200.fasta	Philly_00781	867717	868976	1259.00	nadA	muropeptide transporter	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK11010
1199.fasta	Philly_00787	871761	872147	386.00	nadA	hypothetical protein	ab initio prediction:Prodigal:2.60
369.fasta	Philly_00788	872251	873594	1343.00	nadA	Quinolinate synthase A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P11458
370.fasta	Philly_00789	873669	875318	1649.00	nadB	L-aspartate oxidase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P10902
371.fasta	Philly_00790	875315	876685	1370.00	purB	Adenylosuccinate lyase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5ZXD1
372.fasta	Philly_00791	876838	878541	1703.00	dauA_1	Dicarboxylic acid uptake system A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFR2
373.fasta	Philly_00794	881900	884287	2387.00	ppsA	Phosphoenolpyruvate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P23538
374.fasta	Philly_00795	884529	885968	1439.00	yhaU	K(+)/H(+) antiporter YhaU	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O07536
375.fasta	Philly_00796	885965	886807	842.00	nadC	Nicotinate-nucleotide pyrophosphorylase [carboxylating]	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P30012
376.fasta	Philly_00797	886804	887895	1091.00	murG	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P65482

						acetylglucosamine transferase	
377.fasta	Philly_00798	887870	889285	1415.00	comEA	diaminopimelate aminotransferase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK13983
378.fasta	Philly_00799	889377	889694	317.00	comEA	ComE operon protein 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P39694
379.fasta	Philly_00800	889890	890927	1037.00	mreB	Rod shape-determining protein MreB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A9X4
380.fasta	Philly_00801	890905	891813	908.00	mreC	Rod shape-determining protein MreC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P16926
381.fasta	Philly_00802	891810	892289	479.00	mreD	Rod shape-determining protein MreD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABH4
382.fasta	Philly_00803	892225	892827	602.00	rluE	Ribosomal large subunit pseudouridine synthase E	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P75966
383.fasta	Philly_00804	893088	893786	698.00	icd	hypothetical protein	ab initio prediction:Prodigal:2.60
384.fasta	Philly_00805	893896	895152	1256.00	icd	Isocitrate dehydrogenase [NADP]	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P08200
385.fasta	Philly_00806	895554	895889	335.00	clpS	ATP-dependent Clp protease adapter protein ClpS	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8Q6
386.fasta	Philly_00807	895921	898188	2267.00	clpA	ATP-dependent Clp protease ATP-binding subunit ClpA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABH9
387.fasta	Philly_00810	900049	900828	779.00	epsH	Putative glycosyltransferase EpsH	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P71057
388.fasta	Philly_0	902082	902417	335.00	xseA	hypothetical	ab initio

	0812					protein	prediction:Prodigal:2.60
389.fasta	Philly_00813	902587	903186	599.00	xseA	Rhomboid family protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF01694.16
390.fasta	Philly_00815	904094	905425	1331.00	xseA	Exodeoxyribonuclease 7 large subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P04994
391.fasta	Philly_00821	912191	913039	848.00	ptlF	1-deoxy-11-beta-hydroxypentalenate dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q82IY9
392.fasta	Philly_00822	913515	914291	776.00	trpC	Indole-3-glycerol phosphate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q2YRR4
393.fasta	Philly_00823	914284	915318	1034.00	trpD	Anthranilate phosphoribosyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8PD71
394.fasta	Philly_00824	915296	915874	578.00	pabA	Para-aminobenzoate synthase glutamine amidotransferase component II	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00903
395.fasta	Philly_00825	915908	916633	725.00	lptB	Lipopolysaccharide export system ATP-binding protein LptB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45073
396.fasta	Philly_00826	916630	917139	509.00	lptA	Lipopolysaccharide export system protein LptA precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ADV1
397.fasta	Philly_00827	917120	917689	569.00	kdsC	lipopolysaccharide exporter periplasmic protein	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10893
398.fasta	Philly_00828	917686	918213	527.00	kdsC	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase KdsC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8ZB47

399.fasta	Philly_00829	918227	919189	962.00	kdsD	Arabinose 5-phosphate isomerase KdsD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HVW0
400.fasta	Philly_00831	920347	921129	782.00	mlaE_1	putative phospholipid ABC transporter permease protein MlaE	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P64606
401.fasta	Philly_00832	921130	921606	476.00	mlaD	putative phospholipid ABC transporter-binding protein MlaD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P64604
402.fasta	Philly_00833	921614	922222	608.00	mlaC	putative phospholipid-binding protein MlaC precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ADV7
403.fasta	Philly_00834	922225	922506	281.00	rsbV	Anti-anti-sigma-B factor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P66838
404.fasta	Philly_00835	922896	923141	245.00	murA	putative transcriptional regulator, BolA superfamily	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG5007
405.fasta	Philly_00836	923134	924402	1268.00	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3KHZ4
406.fasta	Philly_00837	924399	925157	758.00	lolD_1	metal-binding protein	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10799
407.fasta	Philly_00841	928676	929269	593.00	ntrC	hypothetical protein	ab initio prediction:Prodigal:2.60
408.fasta	Philly_00843	930924	931205	281.00	sohB	hypothetical protein	ab initio prediction:Prodigal:2.60
409.fasta	Philly_00845	932394	933113	719.00	ccmA	Cytochrome c biogenesis ATP-binding export protein CcmA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P33931
410.fasta	Philly_00846	933110	933790	680.00	ccmB	Cytochrome c-type biogenesis protein CcmB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABL8

411.fasta	Philly_00847	934004	934759	755.00	ccmC	Cytochrome c-type biogenesis protein CcmC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABM1
412.fasta	Philly_00849	934907	935338	431.00	ccmE	Heme chaperone CcmE	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8EK44
413.fasta	Philly_00850	935335	937287	1952.00	ccmF	Cytochrome c-type biogenesis protein CcmF	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P33927
414.fasta	Philly_00851	937284	937817	533.00	dsbE	Cytochrome c biogenesis protein CcmG	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9I3N1
415.fasta	Philly_00852	937817	938218	401.00	ccmH_1	Cytochrome c-type biogenesis protein CcmH precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9I3N0
416.fasta	Philly_00857	940306	942132	1826.00	recQ	ATP-dependent DNA helicase RecQ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P15043
1019.fasta	Philly_00858	942246	943400	1154.00	mmgC	Acyl-CoA dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45857
1020.fasta	Philly_00859	943417	944193	776.00	echA8_1	putative enoyl-CoA hydratase echA8	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P64016
1021.fasta	Philly_00860	944196	945254	1058.00	echA8_2	putative enoyl-CoA hydratase echA8	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P64016
1022.fasta	Philly_00862	946510	948090	1580.00	prfC	Peptide chain release factor 3	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83DC7
1156.fasta	Philly_00863	948156	948539	383.00	pntB	hypothetical protein	ab initio prediction:Prodigal:2.60
1157.fasta	Philly_00865	950095	950391	296.00	pntA	NAD(P) transhydrogenase subunit alpha	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P070

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1158.fasta	Philly_0 0866	950384	951517	1133.00	pntAA	NAD(P) transhydrogenase subunit alpha part 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q2R SB2
1159.fasta	Philly_0 0867	951911	952465	554.00	cph2_2	Cysteine-rich secretory protein family protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF00188.20
1160.fasta	Philly_0 0874	956780	957817	1037.00	gltP	Beta-hexosaminidase A precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P488 23
1161.fasta	Philly_0 0875	958332	959612	1280.00	gltP	Glutamate-aspartate carrier protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P213 45
1162.fasta	Philly_0 0876	959936	961069	1133.00	dapE_2	Succinyl-diaminopimelate desuccinylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8Z N75
1092.fasta	Philly_0 0877	961062	961892	830.00	dapD	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P562 20
1091.fasta	Philly_0 0879	962856	964007	1151.00	metC	Cystathionine beta-lyase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83 A83
1090.fasta	Philly_0 0881	966773	968122	1349.00	kmo	Kynurenine 3-monooxygenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q11 PP7
1063.fasta	Philly_0 0882	968340	969092	752.00	fas5	hypothetical protein	ab initio prediction:Prodigal:2.60
1062.fasta	Philly_0 0883	969049	970419	1370.00	fas5	putative oxidoreductase ORF5 in fasciation locus	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P463 77
1061.fasta	Philly_0 0884	970769	971278	509.00	yrbG	type II secretion system protein C	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR0 1713

1089.fasta	Philly_00885	971284	971661	377.00	yrbG	Sel1 repeat	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF08238.6
1088.fasta	Philly_00890	976937	977593	656.00	htrA	hypothetical protein	ab initio prediction:Prodigal:2.60
1087.fasta	Philly_00895	980240	980785	545.00	fabG_3	Isochorismatase family protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF00857.14
1086.fasta	Philly_00896	980995	981738	743.00	fabG_3	3-oxoacyl-[acyl-carrier-protein] reductase FabG	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9KQH7
1085.fasta	Philly_00900	983508	983915	407.00	coaX	Cytochrome c5	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P11732
1084.fasta	Philly_00902	984836	985606	770.00	coaX	Type III pantothenate kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5ZX22
1083.fasta	Philly_00903	986224	986682	458.00	rsmH	cell division protein MraZ	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK00326
1082.fasta	Philly_00904	986694	987620	926.00	rsmH	Ribosomal RNA small subunit methyltransferase H	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60390
1081.fasta	Philly_00905	987617	987955	338.00	ftsI	cell division protein FtsL	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10772
1080.fasta	Philly_00906	988336	989997	1661.00	ftsI	Peptidoglycan synthase FtsI precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AD68
1079.fasta	Philly_00907	990018	991469	1451.00	murE	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P22188
1078.fasta	Philly_00908	991514	992566	1052.00	pdxB	Erythronate-4-phosphate dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60802

1077.fasta	Philly_00909	992563	993222	659.00	etfB	Zn-dependent proteases	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG1994
1076.fasta	Philly_00910	993480	994118	638.00	etfB	PAP2 superfamily protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF01569.15
1075.fasta	Philly_00912	995810	996559	749.00	etfB	Electron transfer flavoprotein small subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P38975
1074.fasta	Philly_00913	996573	997511	938.00	etfA	Electron transfer flavoprotein large subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P38974
1073.fasta	Philly_00914	997523	998644	1121.00	ald	Alanine dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8KY18
1072.fasta	Philly_00915	998716	1001100	2384.00	mrcA	Penicillin-binding protein 1A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P02918
1010.fasta	Philly_00917	1002679	1003743	1064.00	pilQ	ethanolamine utilization protein EutJ	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK15080
1011.fasta	Philly_00919	1004309	1004908	599.00	pilQ	Pilus assembly protein, PilO	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF04350.7
1012.fasta	Philly_00920	1004905	1005492	587.00	pilQ	Pilus assembly protein, PilP	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF04351.7
1013.fasta	Philly_00921	1005496	1007592	2096.00	pilQ	Type IV pilus biogenesis and competence protein PilQ precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q70M91
1014.fasta	Philly_00922	1008038	1008565	527.00	aroK	Shikimate kinase 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6D7
1015.fasta	Philly_00923	1008552	1009661	1109.00	aroB	3-dehydroquinate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9KNV2

1016.fasta	Philly_00924	1009658	1011109	1451.00	uspA2_1	putative secretion ATPase, PEP-CTERM locus subfamily	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR03015
1017.fasta	Philly_00925	1011218	1011649	431.00	uspA2_1	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45680
417.fasta	Philly_00926	1011773	1012759	986.00	ribF	Riboflavin biosynthesis protein RibF	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AG40
418.fasta	Philly_00927	1012872	1015667	2795.00	ileS	Isoleucine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00956
419.fasta	Philly_00928	1015664	1016128	464.00	lspA	Lipoprotein signal peptidase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00804
420.fasta	Philly_00929	1016427	1016990	563.00	kdgA	KHG/KDPG aldolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P50846
421.fasta	Philly_00931	1019601	1022726	3125.00	era	hypothetical protein	ab initio prediction:Prodigal:2.60
422.fasta	Philly_00932	1022988	1023875	887.00	era	GTPase Era	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P51836
423.fasta	Philly_00933	1023865	1024554	689.00	recO	Recombination protein O	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7H3
424.fasta	Philly_00936	1027127	1027873	746.00	pdxJ	Pyridoxine 5'-phosphate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A794
425.fasta	Philly_00939	1030958	1031632	674.00	yccA	Modulator of FtsH protease YccA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AAC6
426.fasta	Philly_00940	1031851	1032657	806.00	ramA	(R)-stereoselective amidase	ab initio prediction:Prodigal:2.60 similar to AA

							sequence:UniProtKB:Q75SP7
427.fasta	Philly_00941	1032669	1034111	1442.00	rssA	protease TldD	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10735
428.fasta	Philly_00949	1045932	1048115	2183.00	hbpA	Hemin-binding lipoprotein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P33950
429.fasta	Philly_00951	1049113	1050459	1346.00	dppC	Dipeptide transport system permease protein DppC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P26904
430.fasta	Philly_00952	1050534	1053980	3446.00	dnaE	DNA polymerase III subunit alpha	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P10443
431.fasta	Philly_00954	1055637	1056521	884.00	pglF	Decaprenyl-phosphate phosphoribosyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O53583
1039.fasta	Philly_00956	1058084	1059961	1877.00	pglF	UDP-N-acetyl-alpha-D-glucosamine C6 dehydratase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q0P9D4
1040.fasta	Philly_00960	1064069	1065532	1463.00	rocC	Amino-acid permease RocC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P39636
1041.fasta	Philly_01163	1280985	1281635	650.00	proP_3	Putative phosphoribosyl transferasec/MT0597	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O53768
1056.fasta	Philly_01169	1288522	1289007	485.00	cph2_5	putative nucleotide-binding protein	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK05412
1006.fasta	Philly_01180	1301488	1302924	1436.00	yfgC	TPR repeat-containing protein YfgC precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P66948
1005.fasta	Philly_01182	1304045	1304659	614.00	ribE	Riboflavin synthase	ab initio prediction:Prodigal:2.60 similar to AA

							sequence:UniProtKB:P16440
1107.fasta	Philly_01183	1304656	1305864	1208.00	ribBA	Riboflavin biosynthesis protein RibBA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:A5U2B7
1004.fasta	Philly_01185	1306465	1308102	1637.00	pyrG	CTP synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q886M5
1003.fasta	Philly_01186	1308099	1308923	824.00	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:B4EDA2
1002.fasta	Philly_01190	1313851	1314624	773.00	bamD	Competence lipoprotein ComL	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9K0B1
1350.fasta	Philly_01191	1314772	1315710	938.00	rdgC	Recombination-associated protein RdgC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P36767
1351.fasta	Philly_01192	1315828	1317723	1895.00	rlmI	potassium transport protein Kup	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10745
1352.fasta	Philly_01195	1320088	1321236	1148.00	inhA	Beta-hexosaminidase A precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P48823
1008.fasta	Philly_01197	1322190	1322813	623.00	hisE	Phosphoribosyl-ATP pyrophosphatase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q81G00
1353.fasta	Philly_01198	1322810	1323577	767.00	hisF_2	Imidazole glycerol phosphate synthase subunit HisF	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60664
1354.fasta	Philly_01199	1323571	1324290	719.00	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P10371

1355.fasta	Philly_01200	1324284	1324883	599.00	hisH2	Imidazole glycerol phosphate synthase subunit HisH 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9PM75
1356.fasta	Philly_01201	1324880	1325938	1058.00	hisB	Histidine biosynthesis bifunctional protein HisB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9S5G5
1357.fasta	Philly_01202	1325916	1327010	1094.00	hisC	Histidinol-phosphate aminotransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P06986
1358.fasta	Philly_01203	1327011	1328306	1295.00	hisD	Histidinol dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P10370
1359.fasta	Philly_01204	1328312	1329193	881.00	hisG	ATP phosphoribosyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00499
1360.fasta	Philly_01205	1329190	1329486	296.00	cydA_2	Trp operon repressor	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK01381
1361.fasta	Philly_01210	1332772	1333404	632.00	pyrE	Orotate phosphoribosyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P08870
1324.fasta	Philly_01221	1341674	1342609	935.00	hemF	Coproporphyrinogen-III oxidase, aerobic	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3KKE0
1325.fasta	Philly_01224	1343653	1344330	677.00	flgD	Basal-body rod modification protein FlgD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A1I9
1326.fasta	Philly_01287	1403689	1405320	1631.00	maeA_1	Electron transfer flavoprotein-ubiquinone oxidoreductase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HZP5
950.fasta	Philly_01290	1407804	1408175	371.00	maeA_1	putative secreted protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG5513

951.fasta	Philly_01291	1408223	1409947	1724.00	maeA_1	NAD-dependent malic enzyme	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P26616
952.fasta	Philly_01292	1410027	1410410	383.00	surE	hypothetical protein	ab initio prediction:Prodigal:2.60
953.fasta	Philly_01293	1410413	1411168	755.00	surE	5'-nucleotidase SurE	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9KI21
954.fasta	Philly_01295	1412016	1413041	1025.00	rpoS	RNA polymerase sigma factor RpoS	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9KI19
955.fasta	Philly_01296	1413144	1414394	1250.00	hmgA	Homogentisate 1,2-dioxygenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9X4F5
956.fasta	Philly_01297	1414540	1415283	743.00	ruvC	putative transcriptional regulatory protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83BE4
957.fasta	Philly_01298	1415283	1415807	524.00	ruvC	Crossover junction endodeoxyribonuclease RuvC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A814
958.fasta	Philly_01299	1415804	1416403	599.00	ruvA	Holliday junction ATP-dependent DNA helicase RuvA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A809
959.fasta	Philly_01302	1418676	1420091	1415.00	qseC	Sensor protein QseC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P40719
960.fasta	Philly_01303	1420088	1420765	677.00	qseB	Transcriptional regulatory protein QseB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8XBS3
961.fasta	Philly_01304	1420826	1421371	545.00	yciB	Intracellular septation protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P95745
962.fasta	Philly_01305	1421614	1423053	1439.00	mltD_2	Membrane-bound lytic murein	ab initio prediction:Prodigal:2.60 similar to AA

						transglycosylase D precursor	sequence:UniProtKB:P0AEZ7
963.fasta	Philly_01306	1423168	1423932	764.00	gloB	Hydroxyacylglutathione hydrolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AC84
964.fasta	Philly_01309	1425272	1426126	854.00	folD	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P51696
965.fasta	Philly_01314	1431186	1431974	788.00	truA	tRNA pseudouridine synthase A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P07649
968.fasta	Philly_01315	1432011	1432598	587.00	trpF	N-(5'-phosphoribosyl)anthranilate isomerase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q56320
969.fasta	Philly_01316	1432600	1433799	1199.00	trpB	Tryptophan synthase beta chain	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:A6UEI1
970.fasta	Philly_01318	1434640	1436295	1655.00	glnS	Glutamine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00962
971.fasta	Philly_01319	1436305	1437675	1370.00	cysS	Cysteine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3KA28
972.fasta	Philly_01329	1450911	1452395	1484.00	epsE_1	Type II traffic warden ATPase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P37093
973.fasta	Philly_01330	1452399	1454774	2375.00	gspD	Putative general secretion pathway protein D	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45758
974.fasta	Philly_01341	1468603	1469979	1376.00	degP	Periplasmic serine endoprotease DegP precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0C0V0
527.fasta	Philly_01343	1470711	1471676	965.00	rluD	Ribosomal large subunit pseudouridine synthase D	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P336

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528.fasta	Philly_01344	1471676	1473019	1343.00	miaB	(Dimethylallyl)adenosine tRNA methylthiotransferase MiaB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AEI1
529.fasta	Philly_01345	1473056	1474354	1298.00	sauU_3	putative sulfoacetate transporter SauU	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q0K843
530.fasta	Philly_01346	1474594	1475268	674.00	fliS	L,D-transpeptidase catalytic domain	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF03734.8
531.fasta	Philly_01351	1479974	1480858	884.00	accD	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HZA7
532.fasta	Philly_01352	1480839	1482125	1286.00	folC	Bifunctional protein FolC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P08192
533.fasta	Philly_01353	1482122	1482892	770.00	cvpA	cell division protein DedD	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK11633
534.fasta	Philly_01354	1482895	1483428	533.00	cvpA	Pur regulon 18 kDa protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P08550
535.fasta	Philly_01355	1483403	1484038	635.00	nadD	Nicotinate-nucleotide adenylyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A752
536.fasta	Philly_01356	1484026	1485051	1025.00	holA	DNA polymerase III subunit delta	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P28630
537.fasta	Philly_01357	1485053	1485544	491.00	lptE	Rare lipoprotein B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ADC1
538.fasta	Philly_01358	1485646	1488117	2471.00	leuS	Leucine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P078

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539.fasta	Philly_01360	1489873	1490961	1088.00	lysDH	Lysine 6-dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9AJC6
540.fasta	Philly_01361	1490971	1492491	1520.00	gabD	Succinate-semialdehyde dehydrogenase [NADP(+)] GabD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P25526
541.fasta	Philly_01366	1501020	1502150	1130.00	hcpC_2	Putative beta-lactamase HcpC precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O25728
1249.fasta	Philly_01368	1504982	1505950	968.00	xcpW	Type II secretory pathway, component PulK	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG3156
1248.fasta	Philly_01369	1505937	1506554	617.00	xcpW	PilD-dependent protein PddD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q00517
1247.fasta	Philly_01370	1506551	1506928	377.00	gspH	type II secretion system protein I	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR01707
1246.fasta	Philly_01371	1506925	1507431	506.00	gspH	Putative general secretion pathway protein H	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P41443
1245.fasta	Philly_01372	1507397	1507819	422.00	epsG	General secretion pathway protein G	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45773
1244.fasta	Philly_01373	1507923	1509122	1199.00	epsF_1	General secretion pathway protein F	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45780
1243.fasta	Philly_01374	1509219	1510628	1409.00	glnA_1	Glutamine synthetase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A9C5
1242.fasta	Philly_01379	1514897	1516768	1871.00	htpG	High temperature protein G	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A

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1241.fasta	Philly_01380	1516880	1517176	296.00	fis_2	Hin recombinational enhancer-binding protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6R3
1240.fasta	Philly_01381	1517292	1518446	1154.00	lpxB_1	Lipid-A-disaccharide synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P10441
1239.fasta	Philly_01382	1518433	1519395	962.00	ydgJ	putative oxidoreductase YdgJ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77376
1238.fasta	Philly_01383	1519616	1520191	575.00	rnhB	Ribonuclease HII	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P10442
1237.fasta	Philly_01384	1520302	1521420	1118.00	mrdB	Rod shape-determining protein RodA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABG7
1236.fasta	Philly_01385	1521417	1523270	1853.00	spoVD	Sporulation-specific penicillin-binding protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q03524
1235.fasta	Philly_01386	1523437	1523907	470.00	rlmH	Ribosomal RNA large subunit methyltransferase H	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8I8
1234.fasta	Philly_01387	1523916	1524254	338.00	rsfS	Ribosomal silencing factor RsfS	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5NLX3
1233.fasta	Philly_01389	1526024	1527688	1664.00	hutU	Urocanate hydratase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HU83
368.fasta	Philly_01390	1527702	1529222	1520.00	hutH	Histidine ammonia-lyase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P21310
367.fasta	Philly_01393	1531442	1531873	431.00	rnhA	Ribonuclease HI	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7Y4

366.fasta	Philly_01394	1531878	1532579	701.00	dnaQ	DNA polymerase III subunit epsilon	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P03007
365.fasta	Philly_01396	1533360	1533833	473.00	erpA	L,D-transpeptidase catalytic domain	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF03734.8
364.fasta	Philly_01398	1535420	1535812	392.00	erpA	Iron-sulfur cluster insertion protein ErpA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ACC3
363.fasta	Philly_01399	1535948	1537033	1085.00	mnmA	tRNA-specific 2-thiouridylase MnmA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P25745
362.fasta	Philly_01400	1537306	1537734	428.00	rpmF	hypothetical protein	ab initio prediction:Prodigal:2.60
361.fasta	Philly_01401	1537820	1538011	191.00	rpmF	50S ribosomal protein L32	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HZN4
360.fasta	Philly_01402	1538017	1539045	1028.00	plsX	Phosphate acyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P27247
359.fasta	Philly_01403	1539042	1539995	953.00	fabH_1	3-oxoacyl-[acyl-carrier-protein] synthase 3	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6R0
358.fasta	Philly_01404	1540022	1540969	947.00	fabD	Malonyl CoA-acyl carrier protein transacylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AAI9
357.fasta	Philly_01405	1540981	1541727	746.00	fabG_5	3-oxoacyl-[acyl-carrier-protein] reductase FabG	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O54438
356.fasta	Philly_01406	1541812	1542060	248.00	acpP_1	Acyl carrier protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P80922
355.fasta	Philly_01407	1542080	1543318	1238.00	fabF_4	3-oxoacyl-[acyl-carrier-protein] synthase 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9KQH9

354.fasta	Philly_01408	1543319	1544317	998.00	tmk	putative aminodeoxychorismate lyase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10270
353.fasta	Philly_01409	1544317	1544955	638.00	tmk	Thymidylate kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9KQI2
352.fasta	Philly_01410	1544952	1545857	905.00	dnaX_1	DNA polymerase III subunit gamma/tau	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P09122
351.fasta	Philly_01412	1546381	1547169	788.00	ycfH	putative deoxyribonuclease YcfH	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFQ7
350.fasta	Philly_01413	1547281	1548381	1100.00	anmK	Anhydro-N-acetylmuramic acid kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77570
349.fasta	Philly_01414	1548437	1549729	1292.00	gudP_2	D-glucarate permease	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q46916
348.fasta	Philly_01415	1549805	1551085	1280.00	mdfA	Chloramphenicol resistance pump Cmr	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AEY8
347.fasta	Philly_01419	1555198	1555968	770.00	adk	putative 3'-5' exonuclease related to the exonuclease domain of PolB	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG3298
346.fasta	Philly_01420	1556214	1556810	596.00	adk	hypothetical protein	ab initio prediction:Prodigal:2.60
345.fasta	Philly_01421	1557205	1557861	656.00	adk	Adenylate kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:J7RC67
344.fasta	Philly_01422	1557870	1558232	362.00	trxC	Thioredoxin-2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AGG4
343.fasta	Philly_01423	1558192	1559712	1520.00	glpD	Aerobic glycerol-3-phosphate dehydrogena	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P130

						se	35
342.fasta	Philly_01424	1559774	1561249	1475.00	glpK	Glycerol kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5HGD2
341.fasta	Philly_01425	1561343	1562614	1271.00	gltA	Citrate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O33915
340.fasta	Philly_01427	1563805	1566396	2591.00	gyrA	DNA gyrase subunit A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AES5
339.fasta	Philly_01429	1567483	1568784	1301.00	aroA	3-phosphoshikimate 1-carboxyvinyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83E11
338.fasta	Philly_01430	1568784	1569476	692.00	cmk	Cytidylate kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6I0
337.fasta	Philly_01431	1569542	1571218	1676.00	rpsA	30S ribosomal protein S1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AG67
336.fasta	Philly_01432	1571331	1571621	290.00	wbpE	putative membrane protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG3771
335.fasta	Philly_01433	1571668	1572837	1169.00	wbpE	tetratricopeptide repeat protein	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK11788
334.fasta	Philly_01434	1573101	1574216	1115.00	wbpE	UDP-2-acetamido-2-deoxy-3-oxo-D-glucuronate aminotransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HZ76
333.fasta	Philly_01435	1574217	1574906	689.00	pyrF	Orotidine 5'-phosphate decarboxylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9KQT7
332.fasta	Philly_01439	1579078	1579614	536.00	ubiA	4-hydroxybenzoate synthetase	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG3161

						(chorismate lyase)	
331.fasta	Philly_01440	1579611	1580459	848.00	ubiA	4-hydroxybenzoate octaprenyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AGK1
330.fasta	Philly_01441	1580593	1580991	398.00	deoC	hypothetical protein	ab initio prediction:Prodigal:2.60
329.fasta	Philly_01443	1582897	1583661	764.00	deoC	Deoxyribose-phosphate aldolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6L0
328.fasta	Philly_01444	1583658	1584497	839.00	xapA	Purine nucleoside phosphorylase 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45563
327.fasta	Philly_01447	1585925	1587163	1238.00	cpxA	Sensor protein CpxA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AE82
326.fasta	Philly_01448	1587285	1587965	680.00	ompR_1	Transcriptional regulatory protein OmpR	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AA16
325.fasta	Philly_01449	1587973	1588836	863.00	corC	Magnesium and cobalt efflux protein CorC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AE78
324.fasta	Philly_01450	1588823	1589299	476.00	ybeY	Endoribonuclease YbeY	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P71335
323.fasta	Philly_01451	1589296	1590102	806.00	ybeZ	PhoH-like protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A9K3
322.fasta	Philly_01452	1590525	1591364	839.00	dnaE2	Error-prone DNA polymerase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O50399
321.fasta	Philly_01453	1591316	1591981	665.00	rimN_1	t(6)A37 threonylcarbamoyladenosine biosynthesis protein RimN	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45748

320.fasta	Philly_01454	1592227	1593441	1214.00	trpS	Tryptophan--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9WYW2
319.fasta	Philly_01455	1593441	1594232	791.00	scpA	Segregation and condensation protein A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P35154
318.fasta	Philly_01456	1594234	1594815	581.00	scpB	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83CP9
317.fasta	Philly_01457	1594805	1595551	746.00	rluB	Ribosomal large subunit pseudouridine synthase B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P37765
316.fasta	Philly_01467	1607223	1609427	2204.00	relA	GTP pyrophosphokinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AG20
304.fasta	Philly_01468	1609468	1609833	365.00	alaC	hypothetical protein	ab initio prediction:Prodigal:2.60
303.fasta	Philly_01469	1609892	1611085	1193.00	alaC	Glutamate-pyruvate aminotransferase AlaC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77434
302.fasta	Philly_01470	1611090	1611899	809.00	recJ	hypothetical protein	ab initio prediction:Prodigal:2.60
301.fasta	Philly_01471	1611889	1613628	1739.00	recJ	Single-stranded-DNA-specific exonuclease RecJ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P21893
300.fasta	Philly_01472	1613748	1614701	953.00	dus_1	putative tRNA-dihydrouridine synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P67717
299.fasta	Philly_01473	1614802	1617492	2690.00	mutT	preprotein translocase subunit SecA	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK13104
298.fasta	Philly_01474	1617489	1617893	404.00	mutT	8-oxo-dGTP diphosphatase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P08337
297.fasta	Philly_0	1619956	162056	605.00	coaE	Dephospho-	ab initio

	1477		1			CoA kinase	prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P44920
296.fasta	Philly_01481	1624710	1626044	1334.00	bioA	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P22805
295.fasta	Philly_01482	1626117	1627064	947.00	bioB	Biotin synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P12996
294.fasta	Philly_01483	1627065	1628210	1145.00	bioF	8-amino-7-oxononanoate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P22806
293.fasta	Philly_01484	1628191	1628910	719.00	bioH	Pimelyl-[acyl-carrier protein] methyl ester esterase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P13001
292.fasta	Philly_01485	1628907	1629545	638.00	bioD	ATP-dependent dethiobiotin synthetase BioD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5NGB5
291.fasta	Philly_01486	1629680	1629994	314.00	aspS	putative regulatory protein, FmdB family	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR02605
272.fasta	Philly_01488	1630639	1632420	1781.00	aspS	Aspartate--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P21889
271.fasta	Philly_01489	1632395	1635343	2948.00	mutH	putative MscS family protein.1 precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q57362
270.fasta	Philly_01490	1635309	1635980	671.00	mutH	Methyl-directed mismatch repair protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P06722
269.fasta	Philly_01510	1659724	1660188	464.00	lpdA	ribosomal-protein-alanine N-acetyltransferase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK09491

305.fasta	Philly_01511	1660524	1661948	1424.00	lpdA	Dihydrolipoyl dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A9P0
306.fasta	Philly_01512	1662037	1663671	1634.00	aceF	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P06959
307.fasta	Philly_01514	1666420	1666809	389.00	kefC_1	hypothetical protein	ab initio prediction:Prodigal:2.60
308.fasta	Philly_01516	1667605	1668777	1172.00	kefC_1	K(+)/H(+) antiporter	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P03819
309.fasta	Philly_01517	1669097	1669918	821.00	dacC	RlpA-like protein precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q57092
310.fasta	Philly_01518	1670114	1671337	1223.00	dacC	D-alanyl-D-alanine carboxypeptidase DacC precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P08506
311.fasta	Philly_01520	1672190	1672453	263.00	lipB	hypothetical protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG2921
312.fasta	Philly_01521	1672453	1673052	599.00	lipB	Octanoyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60720
313.fasta	Philly_01523	1675224	1675829	605.00	apxIB	hypothetical protein	ab initio prediction:Prodigal:2.60
314.fasta	Philly_01524	1675884	1676615	731.00	apxIB	hypothetical protein	ab initio prediction:Prodigal:2.60
315.fasta	Philly_01529	1682632	1683201	569.00	hpt	Hypoxanthine-guanine phosphoribosyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P99085
490.fasta	Philly_01530	1683244	1683570	326.00	epsE_2	hypothetical protein	ab initio prediction:Prodigal:2.60
489.fasta	Philly_01531	1683753	1684496	743.00	epsE_2	hypothetical protein	ab initio prediction:Prodigal:2.60
488.fasta	Philly_01532	1684755	1686479	1724.00	epsE_2	Type II traffic warden	ab initio prediction:Prodigal:2.60 similar to AA

						ATPase	sequence:UniProtKB:P37093
487.fasta	Philly_01533	1686485	1687705	1220.00	epsF_2	General secretion pathway protein F	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45780
486.fasta	Philly_01536	1689941	1690534	593.00	ppsR	hypothetical protein	ab initio prediction:Prodigal:2.60
483.fasta	Philly_01538	1691139	1691954	815.00	ppsR	Phosphoenolpyruvate synthase regulatory protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8A4
482.fasta	Philly_01539	1692079	1693527	1448.00	prpD	2-methylcitrate dehydratase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77243
481.fasta	Philly_01540	1693529	1694647	1118.00	prpC	2-methylcitrate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q56063
480.fasta	Philly_01544	1699656	1700945	1289.00	hemL	Glutamate-1-semialdehyde 2,1-aminomutase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8ZBL9
477.fasta	Philly_01545	1701368	1701544	176.00	rubA1	Rubredoxin-1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HTK7
476.fasta	Philly_01546	1701541	1701963	422.00	pcnB	putative membrane protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG1981
475.fasta	Philly_01547	1701966	1702697	731.00	pcnB	integral membrane protein, YkoY family	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR03716
474.fasta	Philly_01548	1703004	1704275	1271.00	pcnB	Poly(A) polymerase I precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABF1
473.fasta	Philly_01549	1704272	1704697	425.00	folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P43777
472.fasta	Philly_0	1704752	170517	422.00	uspA2_	hypothetical	ab initio

	1550		4		2	protein	prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45680
471.fasta	Philly_01551	1705239	1706627	1388.00	der	GTP-binding protein EngA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9XCI8
470.fasta	Philly_01552	1706632	1707786	1154.00	bamB	Outer membrane protein assembly factor BamB precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77774
469.fasta	Philly_01553	1707811	1708485	674.00	hisS	hypothetical protein	ab initio prediction:Prodigal:2.60
468.fasta	Philly_01554	1708503	1709783	1280.00	hisS	Histidine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O52765
467.fasta	Philly_01555	1709773	1710342	569.00	rlmN	cytoskeletal protein RodZ	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10856
466.fasta	Philly_01556	1710317	1711099	782.00	rlmN	tetratricopeptide repeat protein	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK11788
465.fasta	Philly_01557	1711279	1712427	1148.00	rlmN	Dual-specificity RNA methyltransferase RlmN	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P36979
464.fasta	Philly_01558	1712448	1712873	425.00	ndk	Nucleoside diphosphate kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q48LZ8
463.fasta	Philly_01559	1713008	1713892	884.00	lpxH	hypothetical protein	ab initio prediction:Prodigal:2.60
462.fasta	Philly_01560	1713966	1714589	623.00	lpxH	tRNA-(MS[2]IO[6]A)-hydroxylase (MiaE)	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF06175.5
461.fasta	Philly_01562	1715421	1716149	728.00	lpxH	UDP-2,3-diacylglucosamine hydrolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P43341
460.fasta	Philly_01563	1716146	1716841	695.00	minC	Septum site-determining	ab initio prediction:Prodigal:2.60

						protein MinC	similar to AA sequence:UniProtKB:P65359
459.fasta	Philly_01564	1716913	1718622	1709.00	fadD	Long-chain-fatty-acid--CoA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P69451
458.fasta	Philly_01566	1719561	1720112	551.00	pabB	putative NUDIX hydrolase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10707
457.fasta	Philly_01568	1721559	1722632	1073.00	pdhA	Pyruvate dehydrogenase E1 component subunit alpha	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q820A6
456.fasta	Philly_01569	1722625	1723599	974.00	pdhB_1	Pyruvate dehydrogenase E1 component subunit beta	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P21874
455.fasta	Philly_01570	1723602	1724714	1112.00	pdhC	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P65636
454.fasta	Philly_01581	1736886	1737719	833.00	exbD	S1/P1 Nuclease	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF02265.10
453.fasta	Philly_01582	1737722	1738981	1259.00	exbD	translocation protein TolB	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK04922
452.fasta	Philly_01584	1739982	1740437	455.00	exbD	Biopolymer transport protein ExbD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABV2
451.fasta	Philly_01585	1740446	1741123	677.00	exbB	Biopolymer transport protein ExbB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABU7
450.fasta	Philly_01586	1741148	1741543	395.00	ybgC	Acyl-CoA thioester hydrolase YbgC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8Z3

449.fasta	Philly_01587	1741547	1742578	1031.00	ruvB	Holliday junction ATP-dependent DNA helicase RuvB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A812
448.fasta	Philly_01591	1744048	1745106	1058.00	yceJ_1	putative global regulator	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK09559
447.fasta	Philly_01595	1751110	1752498	1388.00	sad	Succinate semialdehyde dehydrogenase [NAD(P)+] Sad	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P76149
446.fasta	Philly_01596	1752829	1753596	767.00	pcs	Phosphatidylcholine synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9KJY8
445.fasta	Philly_01597	1753919	1754407	488.00	rplI	hypothetical protein	ab initio prediction:Prodigal:2.60
444.fasta	Philly_01599	1754935	1755492	557.00	rplI	AhpC/TSA family protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF00578.15
713.fasta	Philly_01601	1757827	1758276	449.00	rplI	50S ribosomal protein L9	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7R1
443.fasta	Philly_01602	1758289	1759200	911.00	rpsR	hypothetical protein	ab initio prediction:Prodigal:2.60
442.fasta	Philly_01603	1759202	1759429	227.00	rpsR	30S ribosomal protein S18	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7T7
441.fasta	Philly_01604	1759443	1759781	338.00	rpsF	30S ribosomal protein S6	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P02358
440.fasta	Philly_01608	1762019	1764037	2018.00	fadJ	Fatty acid oxidation complex subunit alpha	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77399
439.fasta	Philly_01609	1764030	1765349	1319.00	pcaF	Beta-ketoadipyl-CoA thiolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8VPF1

438.fasta	Philly_01673	1838135	1839253	1118.00	pbpF	hypothetical protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG4299
273.fasta	Philly_01676	1840733	1843039	2306.00	pbpF	Penicillin-binding protein F	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P38050
493.fasta	Philly_01677	1843217	1848982	5765.00	purN	hypothetical protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF07703.8
492.fasta	Philly_01696	1872119	1872970	851.00	actIII	Putative ketoacyl reductase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P16544
274.fasta	Philly_01705	1884118	1885512	1394.00	gadC_3	Extreme acid sensitivity protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P63235
275.fasta	Philly_01708	1888202	1891354	3152.00	putA	Bifunctional protein PutA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P09546
276.fasta	Philly_01709	1891911	1892588	677.00	proQ_2	hypothetical protein	ab initio prediction:Prodigal:2.60
277.fasta	Philly_01710	1893020	1893385	365.00	proQ_2	ProP effector	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45577
278.fasta	Philly_01711	1893413	1894105	692.00	ubiG	3-demethylubiquinone-9 3-methyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q4K8M4
279.fasta	Philly_01712	1894092	1894811	719.00	lexA_2	uracil-DNA glycosylase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK05254
280.fasta	Philly_01718	1901787	1902830	1043.00	aruG	Arginine N-succinyltransferase subunit beta	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P80358
281.fasta	Philly_01719	1902844	1904331	1487.00	astD	N-succinylglutamate 5-semialdehyde dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P76217

282.fasta	Philly_01721	1905695	1906420	725.00	frr	spermidine synthase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK04457
283.fasta	Philly_01723	1907241	1907798	557.00	frr	Ribosome-releasing factor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P44307
284.fasta	Philly_01724	1907788	1908531	743.00	pyrH	Uridylate kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3KHB0
285.fasta	Philly_01725	1908528	1909406	878.00	tsf	Elongation factor Ts	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9X5U9
286.fasta	Philly_01726	1909472	1910236	764.00	rpsB	30S ribosomal protein S2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P66540
287.fasta	Philly_01731	1915872	1916636	764.00	map_2	Methionine aminopeptidase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A1X6
576.fasta	Philly_01733	1919230	1919673	443.00	tadA	tRNA-specific adenosine deaminase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P68398
575.fasta	Philly_01734	1919670	1921247	1577.00	guaA	GMP synthase [glutamine-hydrolyzing]	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P04079
574.fasta	Philly_01735	1921250	1922722	1472.00	guaB	Inosine-5'-monophosphate dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ADG7
573.fasta	Philly_01736	1922931	1923761	830.00	minD	Cell division inhibitor MinD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AEZ3
572.fasta	Philly_01737	1923758	1924027	269.00	minE	Cell division topological specificity factor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P58152
571.fasta	Philly_01738	1924342	1926828	2486.00	fadE_2	Acyl-coenzyme A	ab initio prediction:Prodigal:2.60

						dehydrogenase	similar to AA sequence:UniProtKB:Q47146
570.fasta	Philly_01739	1926921	1927706	785.00	ugpC	monoglyceride lipase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PHA2857
569.fasta	Philly_01740	1927703	1928611	908.00	ugpC	hypothetical protein	ab initio prediction:Prodigal:2.60
568.fasta	Philly_01742	1929662	1930489	827.00	lacG	Lactose transport system permease protein LacG	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P29824
567.fasta	Philly_01743	1930486	1931364	878.00	ugpA	sn-glycerol-3-phosphate transport system permease protein UgpA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P10905
566.fasta	Philly_01747	1936356	1936652	296.00	gatA_1	aspartyl/glutamyl-tRNA amidotransferase subunit C	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK00034
560.fasta	Philly_01748	1936655	1938106	1451.00	gatA_1	Glutamyl-tRNA(Gln) amidotransferase subunit A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q4ZNS7
559.fasta	Philly_01749	1938110	1939543	1433.00	gatB	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3KI28
558.fasta	Philly_01755	1945064	1945351	287.00	fis_3	Hin recombinational enhancer-binding protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6R3
557.fasta	Philly_01756	1945747	1946115	368.00	iscA	Iron-sulfur cluster assembly protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AAC8
556.fasta	Philly_01757	1946120	1946503	383.00	nifU_2	NifU-like protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q57074
555.fasta	Philly_01758	1946500	1947663	1163.00	iscS	Cysteine desulfurase	ab initio prediction:Prodigal:2.60 similar to AA

							sequence:UniProtKB:P0A6B7
554.fasta	Philly_01759	1947638	1948411	773.00	trmJ	tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmJ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AE01
553.fasta	Philly_01760	1948527	1949312	785.00	suhB	Inositol-1-monophosphatase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ADG4
552.fasta	Philly_01761	1949425	1950381	956.00	sppA	Putative signal peptide peptidase SppA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O34525
551.fasta	Philly_01765	1955401	1956768	1367.00	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P37773
550.fasta	Philly_01774	1966965	1968278	1313.00	qseF	Quorum-sensing regulator protein F	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFU5
548.fasta	Philly_01775	1968302	1969324	1022.00	zraS_2	Sensor protein ZraS	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P14377
547.fasta	Philly_01777	1970952	1971560	608.00	lolA	Outer-membrane lipoprotein carrier protein precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9I0M4
546.fasta	Philly_01778	1971563	1973947	2384.00	ftsK	DNA translocase FtsK	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9I0M3
545.fasta	Philly_01779	1974020	1974970	950.00	aat	Glucosaminate ammonia-lyase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q93HX6
544.fasta	Philly_01780	1974973	1975641	668.00	aat	Leucyl/phenylalanyl-tRNA--protein transferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8P1

543.fasta	Philly_01782	1976198	1976419	221.00	infA	Translation initiation factor IF-1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P69222
542.fasta	Philly_01783	1976586	1977944	1358.00	nrdA	peptidase PmbA	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK11040
1250.fasta	Philly_01784	1977990	1978766	776.00	nrdA	Exopolysaccharide biosynthesis protein related to N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG4632
1251.fasta	Philly_01786	1980237	1983065	2828.00	nrdA	Ribonucleoside-diphosphate reductase 1 subunit alpha	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00452
1252.fasta	Philly_01787	1983079	1984182	1103.00	nrdB	Ribonucleoside-diphosphate reductase subunit beta	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O84835
1253.fasta	Philly_01789	1985069	1986559	1490.00	lysU	Lysine--tRNA ligase, heat inducible	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8N5
949.fasta	Philly_01790	1986556	1987527	971.00	prfB	Peptide chain release factor 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P07012
948.fasta	Philly_01794	1989682	1990398	716.00	fliA	Sigma-F factor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AEM6
947.fasta	Philly_01795	1990495	1991364	869.00	ylxH_1	Flagellum site-determining protein YlxH	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P40742
946.fasta	Philly_01806	2000166	2001461	1295.00	dprE1	putative decaprenylphosphoryl-beta-D-ribose oxidase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P72056

944.fasta	Philly_01807	2001458	2002180	722.00	cynR_3	short chain dehydrogenase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK07102
943.fasta	Philly_01813	2007376	2009958	2582.00	alaS	Alanine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00957
942.fasta	Philly_01814	2009976	2010428	452.00	recX	Regulatory protein RecX	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8P9X1
941.fasta	Philly_01815	2010421	2011467	1046.00	recA	Recombinase A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7G6
940.fasta	Philly_01817	2012997	2013491	494.00	pncC	Nicotinamide-nucleotide amidohydrolase PncC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6G3
939.fasta	Philly_01819	2014110	2016650	2540.00	mutS	DNA mismatch repair protein MutS	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A1Y0
938.fasta	Philly_01820	2016663	2018351	1688.00	tamA	Autotransporter assembly factor TamA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:D2TN56
937.fasta	Philly_01822	2020922	2021917	995.00	hemB	Delta-aminolevulinic acid dehydratase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P64334
936.fasta	Philly_01824	2022744	2024222	1478.00	lysC	47 kDa outer membrane protein precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P80603
1177.fasta	Philly_01825	2024526	2027087	2561.00	lysC	Lysine-sensitive aspartokinase 3	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P08660
1178.fasta	Philly_01827	2030529	2031602	1073.00	ylxH_2	Flagellum site-determining protein YlxH	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P40742
1179.fasta	Philly_01829	2032320	2033210	890.00	oxyR_2	Morphology and auto-	ab initio prediction:Prodigal:2.60

						aggregation control protein	similar to AA sequence:UniProtKB:P0ACQ4
1308.fasta	Philly_01831	2034644	2035594	950.00	lpxK	hypothetical protein	ab initio prediction:Prodigal:2.60
1180.fasta	Philly_01832	2035596	2036567	971.00	lpxK	Tetraacyldisaccharide 4'-kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P27300
1181.fasta	Philly_01833	2036567	2038333	1766.00	msbA_1	Lipid A export ATP-binding/permease protein MsbA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60752
1182.fasta	Philly_01835	2039223	2040224	1001.00	pyrD	Dihydroorotate dehydrogenase (quinone)	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7E1
1183.fasta	Philly_01837	2041557	2042243	686.00	acdA_1	hypothetical protein	ab initio prediction:Prodigal:2.60
1184.fasta	Philly_01838	2042578	2043738	1160.00	acdA_1	Acyl-CoA dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45867
976.fasta	Philly_01839	2043750	2044934	1184.00	thlA	Acetyl-CoA acetyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45359
977.fasta	Philly_01840	2045072	2045386	314.00	paaF	hypothetical protein	ab initio prediction:Prodigal:2.60
978.fasta	Philly_01841	2045396	2047003	1607.00	paaF	Methylmalonyl-CoA carboxyltransferase 12S subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8GBW6
979.fasta	Philly_01842	2047023	2047817	794.00	paaF	2,3-dehydroadipyl-CoA hydratase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P76082
980.fasta	Philly_01843	2047810	2049774	1964.00	accA1	Acetyl-/propionyl-coenzyme A carboxylase alpha chain	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A508
981.fasta	Philly_01844	2049785	2050693	908.00	yngG	Hydroxymethylglutaryl-CoA lyase YngG	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O34873
982.fasta	Philly_0	2050850	205279	1940.00	acsA_2	Acetyl-	ab initio

	1845		0			coenzyme A synthetase	prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9PMD2
983.fasta	Philly_01847	2053827	2054852	1025.00	metN	Methionine import ATP-binding protein MetN	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q87RS1
984.fasta	Philly_01848	2054830	2055477	647.00	metI	D-methionine transport system permease protein MetI	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P31547
985.fasta	Philly_01849	2055490	2056269	779.00	metQ	D-methionine-binding lipoprotein MetQ precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P28635
986.fasta	Philly_01850	2056349	2057767	1418.00	rsmJ	hypothetical protein	ab initio prediction:Prodigal:2.60
987.fasta	Philly_01852	2058256	2058987	731.00	rsmJ	Ribosomal RNA small subunit methyltransferase J	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9X6G2
988.fasta	Philly_01854	2059526	2061592	2066.00	glyS	Glycine--tRNA ligase beta subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00961
989.fasta	Philly_01855	2061582	2062487	905.00	glyQ	Glycine--tRNA ligase alpha subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00960
990.fasta	Philly_01856	2062722	2063507	785.00	dsbA_2	Thiol:disulfide interchange protein DsbA precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q7W2Q0
991.fasta	Philly_01858	2066101	2067060	959.00	pip	Proline iminopeptidase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P52279
992.fasta	Philly_01859	2067054	2067491	437.00	dtd	D-tyrosyl-tRNA(Tyr) deacylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P44814
993.fasta	Philly_01860	2067723	2068490	767.00	mlaA	putative phospholipid-binding lipoprotein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P432

						MlaA precursor	62
994.fasta	Philly_01861	2068599	2069558	959.00	gshB	Glutathione synthetase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P04425
995.fasta	Philly_01862	2069558	2070853	1295.00	moeZ_3	glutamate--cysteine ligase	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR02049
996.fasta	Philly_01864	2072131	2072412	281.00	moeZ_3	hypothetical protein	ab initio prediction:Prodigal:2.60
997.fasta	Philly_01865	2072399	2072749	350.00	moeZ_3	putative adenylyltransferase/sulfurtransferase MoeZ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q7D5X9
998.fasta	Philly_01867	2073790	2075442	1652.00	phoK	Alkaline phosphatase precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:A1YYW7
999.fasta	Philly_01868	2075435	2076133	698.00	udk_3	Uridine kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5SKR5
1000.fasta	Philly_01869	2076247	2077035	788.00	fabI	Enoyl-[acyl-carrier-protein] reductase [NADH] FabI	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P16657
1001.fasta	Philly_01873	2079705	2080007	302.00	hupB	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ACF4
1306.fasta	Philly_01874	2080112	2082562	2450.00	lon	Lon protease	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P46067
1305.fasta	Philly_01875	2082800	2084074	1274.00	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6H1
1304.fasta	Philly_01882	2087055	2088281	1226.00	yheS_2	site-specific tyrosine recombinase XerC	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK00236
1303.fasta	Philly_0	2090282	209095	674.00	rnc	Ribonuclease	ab initio

	1884		6			3	prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7Y0
1302.fasta	Philly_01886	2091350	2092105	755.00	lepB	Signal peptidase I	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00803
1301.fasta	Philly_01887	2092213	2094045	1832.00	lepA	Elongation factor 4	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60785
1300.fasta	Philly_01888	2094240	2095256	1016.00	mltB_1	Membrane-bound lytic murein transglycosylase B precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P41052
1299.fasta	Philly_01889	2095331	2096470	1139.00	dgt_2	GspL-like protein	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK09662
1298.fasta	Philly_01890	2096467	2096937	470.00	dgt_2	putative general secretion pathway protein YghD	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK09731
1297.fasta	Philly_01891	2097042	2097572	530.00	dgt_2	hypothetical protein	ab initio prediction:Prodigal:2.60
1296.fasta	Philly_01898	2101695	2102222	527.00	acyP	putative membrane protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG2862
491.fasta	Philly_01911	2114494	2114973	479.00	kefC_2	preprotein translocase subunit SecA	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK13107
1154.fasta	Philly_01921	2124889	2126070	1181.00	epmC	Golgi nucleoside diphosphatase	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG5371
1153.fasta	Philly_01925	2129542	2130537	995.00	gltX	hypothetical protein	ab initio prediction:Prodigal:2.60
1152.fasta	Philly_01927	2132087	2133499	1412.00	gltX	Glutamate--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P04805
1151.fasta	Philly_01928	2133601	2136330	2729.00	barA	Signal transduction histidine-	ab initio prediction:Prodigal:2.60 similar to AA

						protein kinase BarA	sequence:UniProtKB:P0AEC5
1150.fasta	Philly_01929	2136427	2137671	1244.00	pfp	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q59126
1149.fasta	Philly_01932	2138991	2139308	317.00	gadC_4	transcriptional regulator BolA	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK11628
1148.fasta	Philly_01935	2142611	2143363	752.00	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9KQX2
733.fasta	Philly_01936	2143360	2143539	179.00	gcp_1	Trm112p-like protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF03966.10
1147.fasta	Philly_01937	2143532	2144203	671.00	gcp_1	t(6)A37 threonylcarbamoyladenosine biosynthesis protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q7A4H8
1146.fasta	Philly_01938	2144181	2146139	1958.00	dinG	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q7A5K4
1145.fasta	Philly_01939	2146127	2146462	335.00	psuG	Ferredoxin 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P08811
1144.fasta	Philly_01942	2152575	2153132	557.00	psuG	putative glycosyltransferase	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG5581
1143.fasta	Philly_01943	2153208	2153477	269.00	psuG	putative Fe(2+)-trafficking protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HU36
1142.fasta	Philly_02014	2234514	2235707	1193.00	mltA_1	Membrane-bound lytic murein transglycosylase A precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A935
436.fasta	Philly_02015	2235817	2236374	557.00	hisC2	hypothetical protein	ab initio prediction:Prodigal:2.60
435.fasta	Philly_0	2236371	223717	806.00	hisC2	Tfp pilus	ab initio

	2016		7			assembly protein PilW	prediction:Prodigal:2.60 protein motif:Cdd:COG4966
434.fasta	Philly_02018	2237590	2238699	1109.00	hisC2	Histidinol-phosphate aminotransferase 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3K8U2
433.fasta	Philly_02019	2238736	2239077	341.00	queA	Putative pterin-4-alpha-carbinolamine dehydratase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3KG65
432.fasta	Philly_02020	2239250	2240167	917.00	queA	preprotein translocase subunit SecF	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK13022
1038.fasta	Philly_02021	2240180	2242036	1856.00	queA	preprotein translocase subunit SecD	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK05812
1037.fasta	Philly_02022	2242058	2242393	335.00	queA	preprotein translocase subunit YajC	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK05585
1036.fasta	Philly_02023	2242539	2243372	833.00	queA	queuine tRNA-ribosyltransferase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK01008
1035.fasta	Philly_02024	2243419	2244432	1013.00	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7F9
1034.fasta	Philly_02026	2245044	2246897	1853.00	uup	ABC transporter ATP-binding protein uup	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P43672
1033.fasta	Philly_02028	2247452	2247838	386.00	yabJ	Enamine/imine deaminase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P37552
1032.fasta	Philly_02029	2247838	2249961	2123.00	spoT	Bifunctional (p)ppGpp synthase/hydrolase SpoT	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AG24
1031.fasta	Philly_02030	2250129	2250332	203.00	rpoZ	DNA-directed	ab initio prediction:Prodigal:2.60

						RNA polymerase subunit omega	similar to AA sequence:UniProtKB:P0A800
1030.fasta	Philly_02031	2250383	2251012	629.00	gmk	Guanylate kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83EL7
1029.fasta	Philly_02032	2251018	2251884	866.00	rph	hypothetical protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF03755.7
1028.fasta	Philly_02033	2252185	2252892	707.00	rph	Ribonuclease PH	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P50597
1027.fasta	Philly_02035	2254420	2255115	695.00	proC	pyridoxal phosphate enzyme, YggS family	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR00044
1026.fasta	Philly_02037	2256245	2256820	575.00	bprV	YGGT family protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF02325.11
1025.fasta	Philly_02038	2256880	2257482	602.00	bprV	hypothetical protein	ab initio prediction:Prodigal:2.60
1024.fasta	Philly_02039	2257496	2257777	281.00	bprV	hypothetical protein	ab initio prediction:Prodigal:2.60
1023.fasta	Philly_02042	2260881	2262206	1325.00	ahcY_1	Adenosylhomocysteinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3JY79
494.fasta	Philly_02043	2262225	2263373	1148.00	metK	S-adenosylmethionine synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A817
495.fasta	Philly_02044	2263582	2264694	1112.00	carA	Carbamoyl-phosphate synthase small chain	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6F1
496.fasta	Philly_02045	2264790	2265929	1139.00	dnaJ	Heat shock protein J	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P08622
497.fasta	Philly_02046	2266119	2268053	1934.00	dnaK	Heat shock protein 70	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O87712

498.fasta	Philly_02047	2268198	2268797	599.00	grpE	HSP-70 cofactor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q4KIH2
499.fasta	Philly_02048	2269077	2270414	1337.00	aroH_2	Phospho-2-dehydro-3-deoxyheptonate aldolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P80574
500.fasta	Philly_02049	2270563	2271624	1061.00	hemE	Uroporphyrinogen decarboxylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83PB7
501.fasta	Philly_02050	2271861	2272199	338.00	folB	Dihydroneopterin aldolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AC16
502.fasta	Philly_02052	2272934	2274694	1760.00	argS	Arginine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q99W05
503.fasta	Philly_02053	2274807	2275865	1058.00	tqsA	Transport of quorum-sensing signal protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFS5
1065.fasta	Philly_02054	2276012	2278084	2072.00	recG	ATP-dependent DNA helicase RecG	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P24230
504.fasta	Philly_02056	2279856	2280614	758.00	yceF	ZIP zinc/iron transport family protein	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR00820
505.fasta	Philly_02057	2280607	2281209	602.00	yceF	Maf-like protein YceF	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A729
506.fasta	Philly_02058	2281241	2282509	1268.00	eno	Enolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P37869
507.fasta	Philly_02059	2282734	2283003	269.00	ftsB	Cell division protein FtsB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6S5
1213.fasta	Philly_02060	2283016	2283894	878.00	queE	mevalonate kinase	ab initio prediction:Prodigal:2.60

							protein motif:CLUSTERS:PRK03926
1214.fasta	Philly_02061	2283884	2284831	947.00	queE	diphosphomevalonate decarboxylase	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR01240
1215.fasta	Philly_02063	2285499	2286467	968.00	pal	tol-pal system protein YbgF	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10803
1216.fasta	Philly_02064	2286464	2286994	530.00	pal	Peptidoglycan-associated lipoprotein precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A912
1217.fasta	Philly_02065	2287092	2287694	602.00	mlaE_2	ABC-type uncharacterized transport system, auxiliary component	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG3218
1218.fasta	Philly_02066	2287698	2288621	923.00	mlaE_2	virulence factor Mce family protein	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR00996
1219.fasta	Philly_02067	2288651	2289388	737.00	mlaE_2	putative ABC transporter ATP-binding protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45031
1220.fasta	Philly_02068	2289389	2290513	1124.00	mlaE_2	putative phospholipid ABC transporter permease protein MlaE	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P64606
1221.fasta	Philly_02072	2293248	2294276	1028.00	fni	Isopentenyl-diphosphate delta-isomerase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P99172
935.fasta	Philly_02073	2294267	2295565	1298.00	mvaA	3-hydroxy-3-methylglutaryl-coenzyme A reductase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P13702
1222.fasta	Philly_02231	2490497	2491720	1223.00	chiA	hypothetical protein	ab initio prediction:Prodigal:2.60
1170.fasta	Philly_02232	2492063	2493076	1013.00	chiA	Zinc-type alcohol dehydrogenase-like protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P99173

1064.fasta	Philly_02238	2497935	2498858	923.00	chiA	Epimerase family protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q7A6Q5
1225.fasta	Philly_02290	2566215	2567105	890.00	cbpA	Curved DNA-binding protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P36659
1211.fasta	Philly_02291	2567108	2567422	314.00	ugpB	chaperone-modulator protein CbpM	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10265
1212.fasta	Philly_02295	2570271	2570831	560.00	ugpB	hypothetical protein	ab initio prediction:Prodigal:2.60
508.fasta	Philly_02296	2570809	2573355	2546.00	ugpB	putative DNA repair protein	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR03623
509.fasta	Philly_02300	2575835	2577148	1313.00	ugpB	sn-glycerol-3-phosphate-binding periplasmic protein UgpB precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AG80
217.fasta	Philly_02301	2577145	2577864	719.00	ugpQ	Glycerophosphoryl diester phosphodiesterase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P10908
218.fasta	Philly_02302	2577869	2578564	695.00	ldh	hypothetical protein	ab initio prediction:Prodigal:2.60
219.fasta	Philly_02303	2578877	2579950	1073.00	ldh	Leucine dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P13154
220.fasta	Philly_02304	2579965	2580621	656.00	lly	Putative O-methyltransferase/MSMEI_4947	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:A0R2D5
221.fasta	Philly_02305	2580688	2581734	1046.00	lly	4-hydroxyphenylpyruvate dioxygenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5ZT84
222.fasta	Philly_02306	2581790	2582788	998.00	nagL	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG0179

						hydratase (catechol pathway)	
223.fasta	Philly_02307	2582785	2583423	638.00	nagL	Maleylpyruvate isomerase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O86043
224.fasta	Philly_02308	2583420	2583980	560.00	asnS	hypothetical protein	ab initio prediction:Prodigal:2.60
225.fasta	Philly_02309	2584128	2585531	1403.00	asnS	Asparagine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8M0
226.fasta	Philly_02311	2585950	2586633	683.00	lolD_2	Lipoprotein-releasing system ATP-binding protein LolD	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P75957
227.fasta	Philly_02312	2586626	2587873	1247.00	lolE	Lipoprotein-releasing system transmembrane protein LolE	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P75958
228.fasta	Philly_02320	2591661	2592320	659.00	gph	Phosphoglycolate phosphatase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O67359
229.fasta	Philly_02321	2592313	2593260	947.00	rluC	Ribosomal large subunit pseudouridine synthase C	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AA39
230.fasta	Philly_02322	2594148	2596151	2003.00	rne	Ribonuclease E	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P21513
231.fasta	Philly_02325	2601375	2602778	1403.00	smrA_1	ankyrin repeat protein	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PHA3100
233.fasta	Philly_02326	2602779	2603552	773.00	smrA_1	putative DNA endonuclease SmrA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P76053
234.fasta	Philly_02327	2603700	2604722	1022.00	asd2	Aspartate-semialdehyde dehydrogenase 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P23247

235.fasta	Philly_02328	2604832	2605890	1058.00	aroC	Chorismate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P12008
236.fasta	Philly_02329	2605902	2606834	932.00	prmB	50S ribosomal protein L3 glutamine methyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P39199
237.fasta	Philly_02330	2606999	2607568	569.00	smrA_2	putative DNA endonuclease SmrA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P76053
238.fasta	Philly_02331	2607641	2608060	419.00	glpE	Thiosulfate sulfurtransferase GlpE	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6V5
239.fasta	Philly_02332	2608065	2608319	254.00	grxC	Glutaredoxin-3	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AC62
240.fasta	Philly_02333	2608329	2608817	488.00	secB	Protein-export protein SecB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q93TF4
241.fasta	Philly_02334	2608819	2609808	989.00	gpsA	Glycerol-3-phosphate dehydrogenase [NAD(P)+]	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83BJ0
242.fasta	Philly_02335	2609894	2610733	839.00	murI	Glutamate racemase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P56868
243.fasta	Philly_02338	2614736	2616028	1292.00	dapA	hypothetical protein	ab initio prediction:Prodigal:2.60
206.fasta	Philly_02339	2616038	2616268	230.00	dapA	hypothetical protein	ab initio prediction:Prodigal:2.60
207.fasta	Philly_02340	2616283	2617155	872.00	dapA	4-hydroxy-tetrahydrodipicolinate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9I4W3
208.fasta	Philly_02341	2617367	2617618	251.00	bdhA	hypothetical protein	ab initio prediction:Prodigal:2.60
209.fasta	Philly_02348	2622512	2623807	1295.00	sdaC	Serine transporter	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A

							AD6
1172.fasta	Philly_02353	2630172	2631524	1352.00	lon2	Lon protease 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P42425
244.fasta	Philly_02356	2633493	2633723	230.00	xseB	Exodeoxyribonuclease 7 small subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8G9
245.fasta	Philly_02357	2633704	2634600	896.00	bioC_1	Farnesyl diphosphate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q08291
246.fasta	Philly_02358	2634644	2635648	1004.00	bioC_1	Malonyl-CoA O-methyltransferase BioC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P12999
247.fasta	Philly_02359	2635656	2636246	590.00	rseP_2	DNA utilization protein GntX	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK11595
248.fasta	Philly_02360	2636275	2637348	1073.00	rseP_2	Regulator of sigma E protease	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AEH1
249.fasta	Philly_02361	2637405	2637683	278.00	hemA	hypothetical protein	ab initio prediction:Prodigal:2.60
250.fasta	Philly_02363	2637950	2639275	1325.00	hemA	Glutamyl-tRNA reductase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6X1
251.fasta	Philly_02364	2639259	2640347	1088.00	prfA_2	Peptide chain release factor 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7I0
252.fasta	Philly_02365	2640340	2641203	863.00	prmC	Release factor glutamine methyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ACC1
253.fasta	Philly_02366	2641302	2641778	476.00	dksA	DnaK suppressor protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABS1
254.fasta	Philly_02368	2642686	2643945	1259.00	waaA	3-deoxy-D-manno-octulosonic	ab initio prediction:Prodigal:2.60 similar to AA

						acid transferase	sequence:UniProtKB:P0AC75
255.fasta	Philly_02369	2644100	2644990	890.00	djlA	DnaJ-like protein DjlA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P31680
256.fasta	Philly_02371	2645922	2646851	929.00	deaD	Phosphatidylcholine-sterol acyltransferase precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P10480
257.fasta	Philly_02374	2648364	2650133	1769.00	deaD	Cold-shock DEAD box protein A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A9P6
258.fasta	Philly_02376	2651415	2653439	2024.00	fadH	2,4-dienoyl-CoA reductase [NADPH]	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P42593
259.fasta	Philly_02379	2654814	2655353	539.00	mdh	Alkyl hydroperoxide reductase subunit C	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:A0R1V9
1307.fasta	Philly_02381	2656503	2657495	992.00	mdh	Malate dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P10584
260.fasta	Philly_02383	2658127	2659254	1127.00	hemN	Oxygen-independent coproporphyrinogen-III oxidase 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P54304
261.fasta	Philly_02385	2661049	2661882	833.00	plsY	G3P acyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60782
262.fasta	Philly_02386	2662056	2663057	1001.00	gcp_2	t(6)A37 threonylcarbamoyladenosine biosynthesis protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P05852
263.fasta	Philly_02387	2663262	2663501	239.00	rpsU	30S ribosomal protein S21	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P68679
264.fasta	Philly_02388	2663704	2664147	443.00	dnaG	hypothetical protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG1610

265.fasta	Philly_02389	2664156	2665889	1733.00	dnaG	DNA primase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABS5
266.fasta	Philly_02390	2665976	2667841	1865.00	rpoD	Sigma-70	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00579
267.fasta	Philly_02519	2794324	2795214	890.00	eamA	putative amino-acid metabolite efflux pump	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P31125
1231.fasta	Philly_02522	2797458	2798042	584.00	rdgB	dITP/XTP pyrophosphatase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P52061
1230.fasta	Philly_02523	2798044	2799759	1715.00	yrrB	TPR repeat-containing protein YrrB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O34452
1229.fasta	Philly_02525	2801466	2801924	458.00	dut	Deoxyuridine 5'-triphosphate nucleotidohydrolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P06968
1364.fasta	Philly_02526	2801951	2803147	1196.00	coaBC	DNA/pantothenate metabolism flavoprotein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABQ0
1365.fasta	Philly_02531	2809091	2810077	986.00	adhT	Alcohol dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P12311
484.fasta	Philly_02535	2813641	2814090	449.00	trmL	tRNA (cytidine(34)-2'-O)-methyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q74Y93
1141.fasta	Philly_02554	2837380	2840532	3152.00	bepE_3	Efflux pump membrane transporter BepE	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8G2M6
1228.fasta	Philly_02558	2843865	2845097	1232.00	lrp_2	D-galactonate transporter	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR00893
1165.fasta	Philly_02627	2907822	2908979	1157.00	acdA_3	Acyl-CoA dehydrogena	ab initio prediction:Prodigal:2.60

						se	similar to AA sequence:UniProtKB:P45867
198.fasta	Philly_02628	2908957	2911194	2237.00	pdhB_2	Pyruvate dehydrogenase E1 component subunit beta	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P35488
199.fasta	Philly_02637	2921870	2923663	1793.00	dacB	D-alanyl-D-alanine carboxypeptidase DacB precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P24228
1174.fasta	Philly_02638	2923755	2924546	791.00	parB_1	putative chromosome-partitioning protein ParB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83AH2
1173.fasta	Philly_02641	2926079	2927362	1283.00	rsmB	Ribosomal RNA small subunit methyltransferase B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P36929
205.fasta	Philly_02642	2927359	2928303	944.00	fmt	Methionyl-tRNA formyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9KVU4
204.fasta	Philly_02643	2928300	2928812	512.00	def_3	Peptide deformylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6K3
203.fasta	Philly_02645	2929940	2931025	1085.00	topA	DNA protecting protein DprA	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR00732
202.fasta	Philly_02646	2931015	2931452	437.00	topA	hypothetical protein	ab initio prediction:Prodigal:2.60
201.fasta	Philly_02647	2931531	2933810	2279.00	topA	DNA topoisomerase 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q7A5Y5
200.fasta	Philly_02649	2936021	2936461	440.00	drrA_4	Bacterial membrane flanked domain protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF03703.8
694.fasta	Philly_02650	2936592	2937014	422.00	drrA_4	hypothetical protein	ab initio prediction:Prodigal:2.60
695.fasta	Philly_02652	2938637	2939434	797.00	egtC	Esterase/lipase	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG1647

1349.fasta	Philly_02655	2941026	2943062	2036.00	pepO	Neutral endopeptidase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q07744
696.fasta	Philly_02656	2943206	2944120	914.00	lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P47205
697.fasta	Philly_02657	2944368	2945564	1196.00	ftsZ	Cell division protein FtsZ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83F12
698.fasta	Philly_02658	2945759	2946997	1238.00	ftsA	Cell division protein FtsA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9K0X8
699.fasta	Philly_02659	2946997	2947716	719.00	ftsQ	Cell division protein FtsQ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P06136
700.fasta	Philly_02660	2947732	2948826	1094.00	ddlA	D-alanine--D-alanine ligase A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A1F0
701.fasta	Philly_02661	2948810	2949736	926.00	murB	UDP-N-acetylenolpyruvoylglucosamine reductase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8Y776
702.fasta	Philly_02662	2949745	2951121	1376.00	murC	UDP-N-acetylmuramate--L-alanine ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3K745
703.fasta	Philly_02663	2951164	2952339	1175.00	ftsW	Cell division protein FtsW	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABG4
704.fasta	Philly_02664	2952345	2953688	1343.00	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HVZ9
705.fasta	Philly_02665	2953702	2954787	1085.00	mraY	Phospho-N-acetylmuramoyl-pentapeptide-transferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6W3

706.fasta	Philly_02666	2954902	2956239	1337.00	murF	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P11880
707.fasta	Philly_02667	2956480	2957259	779.00	zipA	Cell division protein ZipA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77173
708.fasta	Philly_02669	2960933	2961613	680.00	greA	plant acid phosphatase	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR01675
709.fasta	Philly_02671	2963086	2963898	812.00	greA	Tim44-like domain protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF04280.9
1286.fasta	Philly_02672	2963973	2964455	482.00	greA	Transcript cleavage factor GreA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6W5
1287.fasta	Philly_02673	2964464	2967667	3203.00	carB	Carbamoyl-phosphate synthase large chain	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00968
1288.fasta	Philly_02675	2968179	2969360	1181.00	lptG	tricarballylate dehydrogenase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK08274
1289.fasta	Philly_02677	2970147	2971217	1070.00	lptG	Lipopolysaccharide export system permease protein LptG	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ADC6
1290.fasta	Philly_02678	2971214	2972293	1079.00	lptF	Lipopolysaccharide export system permease protein LptF	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AF98
1291.fasta	Philly_02679	2972496	2973947	1451.00	pepA_1	Cytosol aminopeptidase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O86436
1259.fasta	Philly_02680	2973928	2974362	434.00	holC	DNA polymerase III subunit chi	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P28905
1260.fasta	Philly_02681	2974501	2974818	317.00	pepA_2	hypothetical protein	ab initio prediction:Prodigal:2.60

1261.fasta	Philly_02682	2974841	2976205	1364.00	pepA_2	Cytosol aminopeptidase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O86436
1262.fasta	Philly_02683	2976210	2977781	1571.00	murJ_2	putative peptidoglycan biosynthesis protein MurJ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AF16
1263.fasta	Philly_02684	2978139	2978405	266.00	rpsT	30S ribosomal protein S20	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HVM1
1264.fasta	Philly_02688	2985447	2986013	566.00	gmr_5	hypothetical protein	ab initio prediction:Prodigal:2.60
1265.fasta	Philly_02689	2986010	2986732	722.00	gmr_5	L,D-transpeptidase catalytic domain	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF03734.8
1266.fasta	Philly_02693	2991885	2993741	1856.00	uvrC	Excinuclease ABC subunit C	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8G0
1267.fasta	Philly_02694	2993753	2994412	659.00	uvrY	Response regulator UvrY	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AED5
1268.fasta	Philly_02695	2994537	2995355	818.00	phhA	Phenylalanine-4-hydroxylase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P30967
1269.fasta	Philly_02697	2996850	2997875	1025.00	obgE	GTP-binding protein Obg	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P42641
1270.fasta	Philly_02699	2998381	2998692	311.00	rplU	50S ribosomal protein L21	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AG48
1271.fasta	Philly_02700	2998935	2999594	659.00	rplY	General stress protein CTC	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3K6W3
1272.fasta	Philly_02701	2999713	3000282	569.00	pth	Peptidyl-tRNA hydrolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5NGZ6

1273.fasta	Philly_02702	3000301	3001392	1091.00	ychF	Ribosome-binding ATPase YchF	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P44681
1274.fasta	Philly_02704	3003002	3003970	968.00	ispB	Octaprenyl-diphosphate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AD57
1275.fasta	Philly_02705	3003997	3004212	215.00	feoB	FeoC like transcriptional regulator	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF09012.4
835.fasta	Philly_02706	3004193	3006448	2255.00	feoB	Ferrous iron transport protein B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8GNS3
836.fasta	Philly_02707	3006445	3006672	227.00	feoA	Ferrous iron transport protein A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AEL3
837.fasta	Philly_02708	3006761	3007843	1082.00	panB	DnaA regulatory inactivator Hda	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR03420
838.fasta	Philly_02709	3007840	3008502	662.00	panB	Alpha/beta hydrolase family protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF12695.1
839.fasta	Philly_02710	3008739	3009527	788.00	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P31057
840.fasta	Philly_02711	3009539	3010297	758.00	panC	Pantothenate synthetase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q5NF57
841.fasta	Philly_02714	3012238	3012954	716.00	rpoH	putative esterase	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG0400
842.fasta	Philly_02715	3013236	3014102	866.00	rpoH	acetoin dehydrogenase E2 subunit dihydrolipoyllysine-residue acetyltransferase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK14875
843.fasta	Philly_02716	3014236	3015090	854.00	rpoH	Heat shock regulatory protein F33.4	ab initio prediction:Prodigal:2.60 similar to AA

							sequence:UniProtKB:P0AGB3
844.fasta	Philly_02717	3015387	3016316	929.00	ftsX	Cell division protein FtsX	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AC30
845.fasta	Philly_02718	3016310	3016996	686.00	ftsE	Cell division ATP-binding protein FtsE	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A9R7
846.fasta	Philly_02719	3016947	3018053	1106.00	ftsY	Signal recognition particle receptor FtsY	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P10121
847.fasta	Philly_02721	3019399	3020703	1304.00	rsmD	Peptidase M16 inactive domain protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF05193.15
848.fasta	Philly_02722	3020700	3021245	545.00	rsmD	Ribosomal RNA small subunit methyltransferase D	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P44869
849.fasta	Philly_02723	3021344	3021811	467.00	pilT_3	hypothetical protein	ab initio prediction:Prodigal:2.60
850.fasta	Philly_02724	3021792	3022703	911.00	pilT_3	hypothetical protein	ab initio prediction:Prodigal:2.60
851.fasta	Philly_02725	3022703	3023836	1133.00	pilT_3	Twitching mobility protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P24559
852.fasta	Philly_02735	3034433	3037579	3146.00	pacS_2	Phagosome trafficking protein DotA	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF11388.2
853.fasta	Philly_02736	3037576	3038031	455.00	pacS_2	hypothetical protein	ab initio prediction:Prodigal:2.60
854.fasta	Philly_02737	3038144	3038599	455.00	pacS_2	hypothetical protein	ab initio prediction:Prodigal:2.60
855.fasta	Philly_02738	3038599	3039999	1400.00	pacS_2	hypothetical protein	ab initio prediction:Prodigal:2.60
856.fasta	Philly_02744	3047264	3048250	986.00	rfaQ	Lipopolysaccharide core heptosyltransferase RfaQ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P25742
857.fasta	Philly_02746	3048511	3049452	941.00	miaA	tRNA dimethylallyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P16384
858.fasta	Philly_0	3049445	305117	1730.00	mutL	DNA	ab initio

	2747		5			mismatch repair protein MutL	prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P23367
859.fasta	Philly_02748	3051166	3052593	1427.00	amiC	N-acetylmuramoyl-L-alanine amidase AmiC precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P63883
860.fasta	Philly_02749	3052593	3053075	482.00	nnr_1	ADP-binding protein	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10646
861.fasta	Philly_02750	3053201	3054682	1481.00	nnr_1	Nicotinamide nucleotide repair protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P31806
862.fasta	Philly_02751	3054810	3055205	395.00	sspB	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45206
863.fasta	Philly_02752	3055208	3055828	620.00	sspA	Stringent starvation protein A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ACA3
864.fasta	Philly_02753	3056079	3056819	740.00	petB	Cytochrome C1 family protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF02167.9
865.fasta	Philly_02754	3056816	3058030	1214.00	petB	Cytochrome b	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P23134
866.fasta	Philly_02755	3058041	3058667	626.00	petA	Ubiquinol-cytochrome c reductase iron-sulfur subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P23136
867.fasta	Philly_02756	3058832	3059263	431.00	rpsI	30S ribosomal protein S9	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7X3
868.fasta	Philly_02757	3059269	3059703	434.00	rplM	50S ribosomal protein L13	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q1R6A9
869.fasta	Philly_02759	3060361	3060654	293.00	ihfA	Integration host factor subunit alpha	ab initio prediction:Prodigal:2.60 similar to AA

							sequence:UniProtKB:P0A6X7
870.fasta	Philly_02760	3060657	3063038	2381.00	pheT	Phenylalanine--tRNA ligase beta subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P07395
871.fasta	Philly_02761	3063296	3064312	1016.00	pheS	Phenylalanine--tRNA ligase alpha subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P08312
872.fasta	Philly_02762	3064449	3064808	359.00	rplT	50S ribosomal protein L20	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7L3
873.fasta	Philly_02763	3064824	3065024	200.00	rpmI	Ribosomal protein A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7Q1
874.fasta	Philly_02764	3065045	3065425	380.00	infC	Translation initiation factor IF-3	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A707
875.fasta	Philly_02765	3065606	3067519	1913.00	thrS	Threonine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8M3
876.fasta	Philly_02767	3068032	3068319	287.00	ybdK	hypothetical protein	ab initio prediction:Prodigal:2.60
1066.fasta	Philly_02779	3077034	3077663	629.00	ppiB	putative membrane protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG2860
877.fasta	Philly_02780	3077871	3078365	494.00	ppiB	Peptidyl-prolyl cis-trans isomerase B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P23869
878.fasta	Philly_02781	3078392	3079543	1151.00	tgt	Queuine tRNA-ribosyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P66905
879.fasta	Philly_02782	3079605	3080096	491.00	dsbB	Disulfide oxidoreductase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6M2
880.fasta	Philly_02783	3080093	3080521	428.00	cqsA	Cytochrome c5	ab initio prediction:Prodigal:2.60 similar to AA

							sequence:UniProtKB:P11732
881.fasta	Philly_02789	3086607	3087359	752.00	hemD	Uroporphyrinogen-III synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P48246
882.fasta	Philly_02790	3087363	3088487	1124.00	hemX	Putative uroporphyrinogen-III C-methyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P09127
883.fasta	Philly_02791	3088490	3089677	1187.00	czcD	putative protoheme IX biogenesis protein	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK10747
884.fasta	Philly_02792	3089813	3090736	923.00	czcD	Cadmium, cobalt and zinc/H(+)-K(+) antiporter	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O07084
885.fasta	Philly_02793	3090733	3091395	662.00	orn	hypothetical protein	ab initio prediction:Prodigal:2.60
886.fasta	Philly_02794	3091385	3091948	563.00	orn	Oligoribonuclease	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A784
887.fasta	Philly_02796	3093233	3094210	977.00	rsgA	Putative ribosome biogenesis GTPase RsgA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8ZKB0
888.fasta	Philly_02802	3105110	3105448	338.00	ybaB	Nucleoid-associated protein YbaB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8B5
889.fasta	Philly_02803	3105457	3106050	593.00	recR	Recombination protein RecR	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8RDI4
890.fasta	Philly_02804	3106043	3106903	860.00	ompR_2	hypothetical protein	ab initio prediction:Prodigal:2.60
891.fasta	Philly_02807	3110823	3111548	725.00	ompR_2	Transcriptional regulatory protein OmpR	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AA16
892.fasta	Philly_02810	3113646	3114911	1265.00	tlyC_2	Hemolysin C	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O05961

893.fasta	Philly_02811	3115061	3115597	536.00	ppa	Inorganic pyrophosphatase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A7A9
894.fasta	Philly_02812	3115727	3116068	341.00	folE	HIT-like protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P44956
895.fasta	Philly_02813	3116080	3116619	539.00	folE	GTP cyclohydrolase 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P19465
896.fasta	Philly_02815	3117904	3120093	2189.00	pnp	Polyribonucleotide nucleotidyltransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q8ZLT3
897.fasta	Philly_02816	3120208	3120483	275.00	rpsO	30S ribosomal protein S15	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q2KDZ9
898.fasta	Philly_02818	3120631	3121542	911.00	truB	tRNA pseudouridine synthase B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60340
899.fasta	Philly_02819	3121529	3121900	371.00	rbfA	Ribosome-binding factor A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45141
900.fasta	Philly_02820	3121904	3124510	2606.00	infB	Translation initiation factor IF-2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A705
901.fasta	Philly_02821	3124599	3126077	1478.00	nusA	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFF6
902.fasta	Philly_02822	3126089	3126532	443.00	rimP	Ribosome maturation factor RimP	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8A8
903.fasta	Philly_02825	3128284	3129789	1505.00	nuoM	NADH-quinone oxidoreductase subunit M	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFE8
904.fasta	Philly_02826	3129805	3131778	1973.00	nuoL_2	NADH-quinone	ab initio prediction:Prodigal:2.60

						oxidoreductase subunit L	similar to AA sequence:UniProtKB:P33607
905.fasta	Philly_02827	3131783	3132088	305.00	nuoK	NADH-quinone oxidoreductase subunit K	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:A1B482
906.fasta	Philly_02828	3132106	3132765	659.00	nuoJ	NADH-quinone oxidoreductase subunit J	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFE0
907.fasta	Philly_02829	3132777	3133277	500.00	nuoI	NADH-quinone oxidoreductase subunit I	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:A1B486
908.fasta	Philly_02830	3133296	3134318	1022.00	nuoH	NADH-quinone oxidoreductase subunit H	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P42032
909.fasta	Philly_02831	3134331	3136682	2351.00	nqo3	NADH-quinone oxidoreductase chain 3	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P29915
910.fasta	Philly_02832	3136699	3137976	1277.00	nuoF	NADH-quinone oxidoreductase subunit F	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:A8GQT6
911.fasta	Philly_02833	3137995	3138498	503.00	nuoE	NADH-quinone oxidoreductase subunit E	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFD1
912.fasta	Philly_02834	3138559	3139812	1253.00	nuoD	NADH-quinone oxidoreductase subunit D	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:A1B495
913.fasta	Philly_02836	3140511	3140987	476.00	nuoB	NADH-quinone oxidoreductase subunit B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:A1B497
914.fasta	Philly_02837	3141237	3141593	356.00	ndhC	NAD(P)H-quinone oxidoreductase subunit 3	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P19045
915.fasta	Philly_02839	3141773	3142096	323.00	secG	Preprotein translocase band 1 subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A

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916.fasta	Philly_02840	3142084	3142833	749.00	tpiA	Triosephosphate isomerase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A858
917.fasta	Philly_02843	3148032	3148907	875.00	folP	Dihydropteroate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AC13
918.fasta	Philly_02844	3148940	3150850	1910.00	ftsH	ATP-dependent zinc metalloprotease FtsH	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AAI3
919.fasta	Philly_02845	3150972	3151592	620.00	rlmE	Ribosomal RNA large subunit methyltransferase E	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0C0R7
920.fasta	Philly_02846	3151695	3151961	266.00	oatA_3	RNA-binding protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P71376
921.fasta	Philly_02849	3156161	3156715	554.00	pgsA2	Putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl-transferase 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O33288
922.fasta	Philly_02850	3156718	3157410	692.00	hda	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P69931
923.fasta	Philly_02853	3159890	3161392	1502.00	dtpB	Dipeptide and tripeptide permease B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P36837
924.fasta	Philly_02855	3162983	3164092	1109.00	aroE	Patatin	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG3621
925.fasta	Philly_02856	3164142	3164939	797.00	aroE	Shikimate dehydrogenase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9KVT3
926.fasta	Philly_02857	3165149	3167740	2591.00	pepN_2	Aminopeptidase N	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P048

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927.fasta	Philly_02858	3167913	3169844	1931.00	yhbH	PrkA family serine protein kinase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK15455
928.fasta	Philly_02859	3169998	3171263	1265.00	yhbH	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45742
929.fasta	Philly_02863	3175334	3177385	2051.00	rep	hypothetical protein	ab initio prediction:Prodigal:2.60
930.fasta	Philly_02866	3179882	3180727	845.00	hslO	Heat shock protein 33	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6Y5
934.fasta	Philly_02871	3184685	3186511	1826.00	typA	Tyrosine phosphorylated protein A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P32132
933.fasta	Philly_02872	3186518	3187405	887.00	ppnK	putative inorganic polyphosphate/ATP-NAD kinase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P65774
932.fasta	Philly_02873	3187409	3189076	1667.00	recN	Recombination protein N	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P05824
931.fasta	Philly_02882	3205662	3206042	380.00	ypfD	putative acyl-CoA thioester hydrolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P44886
1108.fasta	Philly_02883	3206045	3208414	2369.00	ypfD	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P38494
1109.fasta	Philly_02885	3209200	3211014	1814.00	glmS	Glutamine--fructose-6-phosphate aminotransferase [isomerizing]	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P17169
1110.fasta	Philly_02887	3212932	3213696	764.00	smpB	putative rhodanese-related sulfurtransferase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK00142
1111.fasta	Philly_02888	3213808	3214278	470.00	smpB	Small protein B	ab initio prediction:Prodigal:2.60

							similar to AA sequence:UniProtKB:P0A832
1112.fasta	Philly_02889	3214290	3214754	464.00	bcp	Putative peroxiredoxin bcp	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83CY8
1113.fasta	Philly_02891	3216234	3217640	1406.00	phoH	Phosphate starvation-inducible protein PsiH	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A9K1
1114.fasta	Philly_02892	3217663	3218676	1013.00	guaC	GMP reductase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60560
1115.fasta	Philly_02894	3220404	3221213	809.00	rna	Thermostable monoacylglycerol lipase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P82597
1116.fasta	Philly_02896	3221661	3222623	962.00	rna	hypothetical protein	ab initio prediction:Prodigal:2.60
1117.fasta	Philly_02897	3222761	3223741	980.00	rna	Ribonuclease I precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P21338
1118.fasta	Philly_02902	3229121	3230770	1649.00	dus_2	hypothetical protein	ab initio prediction:Prodigal:2.60
1329.fasta	Philly_02904	3231690	3232622	932.00	dus_2	hypothetical protein	ab initio prediction:Prodigal:2.60
1138.fasta	Philly_02905	3232612	3233670	1058.00	dus_2	VWFA-related Acidobacterial domain protein	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR03436
1137.fasta	Philly_02906	3233634	3234119	485.00	dus_2	hypothetical protein	ab initio prediction:Prodigal:2.60
1136.fasta	Philly_02907	3234112	3235023	911.00	dus_2	hypothetical protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG1721
1135.fasta	Philly_02908	3235033	3236028	995.00	dus_2	magnesium chelatase ATPase subunit D	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR02031
1134.fasta	Philly_02909	3236205	3236648	443.00	dus_2	hypothetical protein	ab initio prediction:Prodigal:2.60
1133.fasta	Philly_02910	3236730	3237716	986.00	dus_2	putative tRNA-dihydrouridine synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P677

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1132.fasta	Philly_02912	3239928	3240683	755.00	ycdF_2	Glucose 1-dehydrogenase 2	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P80869
1131.fasta	Philly_02913	3240860	3241972	1112.00	priA	hypothetical protein	ab initio prediction:Prodigal:2.60
1130.fasta	Philly_02914	3241975	3242469	494.00	priA	queuosine biosynthesis protein QueD	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR03367
1129.fasta	Philly_02916	3244644	3245036	392.00	fadM	Long-chain acyl-CoA thioesterase FadM	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77712
1128.fasta	Philly_02918	3245498	3246292	794.00	thyA	Thymidylate synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A884
1127.fasta	Philly_02919	3246289	3247059	770.00	lgt	Prolipoprotein diacylglyceryl transferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P60955
1126.fasta	Philly_02922	3250175	3250702	527.00	rppH	RNA pyrophosphohydrolase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A776
1124.fasta	Philly_02923	3251055	3252065	1010.00	ansA	L-asparaginase 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A962
1123.fasta	Philly_02925	3253169	3254554	1385.00	glmU	Bifunctional protein GlmU	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:A4TSJ5
1122.fasta	Philly_02930	3260567	3261202	635.00	nth	Endonuclease III	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AB83
1121.fasta	Philly_02932	3261809	3263821	2012.00	metG	Methionine--tRNA ligase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P00959
1120.fasta	Philly_02933	3264100	3264669	569.00	bsdB	Phenolic acid decarboxylase subunit B	ab initio prediction:Prodigal:2.60 similar to AA

							sequence:UniProtKB:P94404
1071.fasta	Philly_02936	3266369	3267055	686.00	queC	7-cyano-7-deazaguanine synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P77756
1119.fasta	Philly_02939	3270853	3272727	1874.00	mnmG	Glucose-inhibited division protein A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6U3
1330.fasta	Philly_02940	3272724	3273350	626.00	rsmG	Ribosomal RNA small subunit methyltransferase G	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6U5
1331.fasta	Philly_02941	3273353	3274123	770.00	soj	Sporulation initiation inhibitor protein soj	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P37522
1332.fasta	Philly_02942	3274137	3275006	869.00	parB_2	putative chromosome-partitioning protein ParB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83AH2
1333.fasta	Philly_02945	3276056	3276925	869.00	ctaE	Cytochrome c oxidase subunit 3	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P06030
1334.fasta	Philly_02947	3277639	3279255	1616.00	ctaD	Cytochrome c oxidase subunit 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P31833
1335.fasta	Philly_02948	3279252	3280457	1205.00	ctaC	Cytochrome c oxidase subunit 2 precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P08306
1336.fasta	Philly_02949	3280539	3282152	1613.00	nicB	Nicotinate dehydrogenase subunit B	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q88FX8
1337.fasta	Philly_02953	3284867	3285292	425.00	ubiE_4	hypothetical protein	ab initio prediction:Prodigal:2.60
1338.fasta	Philly_02954	3285417	3286169	752.00	ubiE_4	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A887
648.fasta	Philly_02955	3286177	3286794	617.00	ubiB	Putative lipid carrier	ab initio prediction:Prodigal:2.60

						protein	protein motif:Cdd:COG3154
647.fasta	Philly_02957	3286884	3288533	1649.00	ubiB	putative ubiquinone biosynthesis protein UbiB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6A0
646.fasta	Philly_02958	3288535	3288720	185.00	tatA	Sec-independent protein translocase protein TatA	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P69428
645.fasta	Philly_02959	3288717	3288986	269.00	msrA1	twin arginine translocase protein A	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK14858
644.fasta	Philly_02962	3290460	3291329	869.00	msrA1	Peptide methionine sulfoxide reductase MsrA 1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A082
643.fasta	Philly_02973	3303692	3304654	962.00	mltB_2	Membrane-bound lytic murein transglycosylase B precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P41052
642.fasta	Philly_02978	3308597	3309286	689.00	macB_2	Macrolide export ATP-binding/permease protein MacB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q2EHL8
640.fasta	Philly_02979	3309279	3310424	1145.00	czcB_4	Cation efflux system protein CzcB	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P13510
639.fasta	Philly_02981	3312093	3312923	830.00	apaH	Bis(5'-nucleosyl)-tetraphosphatase, symmetrical	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q83SQ2
638.fasta	Philly_02982	3312916	3314253	1337.00	rsmA	integrating conjugative element relaxase, PFGI-1 class	ab initio prediction:Prodigal:2.60 protein motif:TIGRFAMs:TIGR03760
637.fasta	Philly_02983	3314290	3315060	770.00	rsmA	Ribosomal RNA small subunit methyltransferase A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P06992
636.fasta	Philly_02985	3315912	3316628	716.00	tatC	Sec-independent protein	ab initio prediction:Prodigal:2.60 similar to AA

						translocase protein TatC	sequence:UniProtKB:P69423
635.fasta	Philly_02986	3316690	3317001	311.00	hspQ	Heat shock protein HspQ	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AB20
634.fasta	Philly_02987	3317039	3317233	194.00	ascD	hypothetical protein	ab initio prediction:Prodigal:2.60
633.fasta	Philly_02988	3317252	3317965	713.00	ascD	CDP-6-deoxy-L-threo-D-glycero-4-hexulose-3-dehydrase reductase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q66DP5
632.fasta	Philly_02989	3317965	3319431	1466.00	ubiD	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AAB4
631.fasta	Philly_02990	3319576	3320838	1262.00	rho	hypothetical protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AG30
630.fasta	Philly_02991	3321161	3321487	326.00	trxA	Thioredoxin-1	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AA25
629.fasta	Philly_02992	3321700	3322428	728.00	rsmE	Ribosomal RNA small subunit methyltransferase E	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AGL7
628.fasta	Philly_02993	3322598	3323992	1394.00	fumC	Fumarate hydratase class II	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P05042
627.fasta	Philly_03012	3340034	3340984	950.00	cbs	Putative cystathionine beta-synthase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q7D8W0
626.fasta	Philly_03013	3341079	3342122	1043.00	ihfB	hypothetical protein	ab initio prediction:Prodigal:2.60
625.fasta	Philly_03015	3343437	3344153	716.00	ihfB	Histone methylation protein DOT1	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF08123.7
624.fasta	Philly_03016	3344406	3344717	311.00	ihfB	Integration host factor subunit beta	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A

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623.fasta	Philly_03017	3344733	3345299	566.00	dcd	Deoxycytidine triphosphate deaminase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HYC9
622.fasta	Philly_03018	3345538	3346293	755.00	hflK_2	Modulator of FtsH protease HflK	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABC7
621.fasta	Philly_03019	3346336	3347841	1505.00	arfA	hypothetical protein	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF01957.12
620.fasta	Philly_03021	3349937	3350908	971.00	arfA	Legionella pneumophila major outer membrane protein precursor	ab initio prediction:Prodigal:2.60 protein motif:Pfam:PF05150.6
619.fasta	Philly_03024	3353112	3354149	1037.00	pyrC	Dihydroorotase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P05020
618.fasta	Philly_03025	3354133	3354756	623.00	rnt	Ribonuclease T	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HY82
617.fasta	Philly_03026	3354883	3355488	605.00	tsaA	putative peroxiredoxin	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P21762
616.fasta	Philly_03027	3355541	3355858	317.00	grxD	Monothiol glutaredoxin	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AC69
615.fasta	Philly_03028	3356189	3356767	578.00	sodB	Superoxide dismutase [Fe]	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AGD3
614.fasta	Philly_03029	3356827	3357996	1169.00	argD	Acetylornithine aminotransferase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:O66442
613.fasta	Philly_03031	3359048	3359830	782.00	maeA_2	cytoplasmic glycerophosphodiester phosphodiesterase	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK09454

1223.fasta	Philly_03032	3360082	3361752	1670.00	maeA_2	NAD-dependent malic enzyme	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P26616
1057.fasta	Philly_03033	3361982	3362950	968.00	rimN_2	t(6)A37 threonylcarbamoyladenosine biosynthesis protein RimN	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45748
1224.fasta	Philly_03035	3363124	3363975	851.00	psd	Phosphatidylserine decarboxylase proenzyme	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A8K1
1226.fasta	Philly_03041	3370964	3371818	854.00	parC	hypothetical protein	ab initio prediction:Prodigal:2.60 protein motif:Cdd:COG5495
1227.fasta	Philly_03042	3371925	3374162	2237.00	parC	DNA topoisomerase 4 subunit A	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AFI2
1363.fasta	Philly_03043	3374808	3375230	422.00	atpC	F-ATPase epsilon subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0A6E6
577.fasta	Philly_03044	3375242	3376618	1376.00	atpD_2	ATP synthase subunit beta	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABB4
578.fasta	Philly_03045	3376631	3377497	866.00	atpG	F-ATPase gamma subunit	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABA6
579.fasta	Philly_03046	3377587	3379140	1553.00	atpA_2	ATP synthase subunit alpha	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q0SYU2
580.fasta	Philly_03047	3379158	3379700	542.00	atpH	F-type ATPase subunit delta	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q3K438
581.fasta	Philly_03048	3379702	3380172	470.00	atpF_2	F-type ATPase subunit b	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0ABA0

582.fasta	Philly_03049	3380224	3380499	275.00	atpE_2	Lipid-binding protein	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P68699
583.fasta	Philly_03050	3380540	3381376	836.00	atpB_2	F-ATPase subunit 6	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P0AB98
584.fasta	Philly_03052	3381918	3382163	245.00	gmhA	hypothetical protein	ab initio prediction:Prodigal:2.60
585.fasta	Philly_03053	3382233	3382820	587.00	gmhA	outer membrane lipoprotein	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK11023
586.fasta	Philly_03054	3382822	3383394	572.00	gmhA	outer membrane lipoprotein	ab initio prediction:Prodigal:2.60 protein motif:CLUSTERS:PRK11023
587.fasta	Philly_03055	3383398	3383997	599.00	gmhA	Phosphoheptose isomerase	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:Q9HVZ0
588.fasta	Philly_03056	3384024	3384380	356.00	lpoA	hypothetical protein	ab initio prediction:Prodigal:2.60
589.fasta	Philly_03057	3384402	3386213	1811.00	lpoA	Penicillin-binding protein activator LpoA precursor	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P45299
590.fasta	Philly_03058	3386253	3387104	851.00	rsmI	Ribosomal RNA small subunit methyltransferase I	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P67087
591.fasta	Philly_03062	3391800	3393638	1838.00	mnmE	hypothetical protein	ab initio prediction:Prodigal:2.60
592.fasta	Philly_03063	3393934	3395274	1340.00	mnmE	tRNA modification GTPase MnmE	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P25522
593.fasta	Philly_03064	3395275	3396945	1670.00	yidC	Oxa1Ec	ab initio prediction:Prodigal:2.60 similar to AA sequence:UniProtKB:P25714
1140 genes				**SUM NT Length**			

				1.11E+06			
				1.11 Mega Bases			