Identification of Essential Protein Domains From High-density Transposon Insertion Sequencing

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Identification of Essential Protein Domains from High-density Transposon Insertion Sequencing

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Abstract

A first clue to gene function can be obtained by examining whether a gene is required for life in certain standard conditions, that is, whether a gene is essential. In bacteria, essential genes are usually identified by high-density transposon mutagenesis followed by sequencing of insertion sites (Tn-seq). These studies assign the term “essential” to whole genes rather than the protein domain sequences that confer the essential functions. However, genes can code for multiple protein domains that evolve their functions independently. Therefore, when essential genes code for more than one protein domain, only one of them could be essential. In this study, we defined this subset of genes as “essential domain-containing” (EDC) genes. Using a Tn-seq data set built-in *Burkholderia cenocepacia* K56-2, we developed an *in silico* pipeline to identify EDC genes and the essential protein domains they encode. We found forty candidate EDC genes and demonstrated growth defect phenotypes using CRISPR interference (CRISPRi). This analysis included two knockdowns of genes encoding the protein domains of unknown function DUF2213 and DUF4148. These essential domains are conserved in more than two hundred bacterial species, including human and plant pathogens. Together, our study suggests that essentiality should be assigned to individual protein domains rather than genes, contributing to a first functional characterization of protein domains of unknown function.
Keywords
DUFs, Essential genes, Tn-seq, Protein Domain

Author contributions
ASMZR- performed the majority of the experiments and wrote the manuscript
LT- created the python script and contributed to manuscript editing
FG- created CRISPRi mutants and contributed to manuscript editing
STC- conceived the idea, supervised the work, provided financial support, and edited the final version of the manuscript.
**Introduction**

A first step when characterizing gene function should be asking whether a given gene encodes an essential cellular function, whether the gene is necessary for the survival of the organism. A widely accepted method to identify essential genes in bacteria is high-density transposon mutagenesis, followed by Illumina-sequencing of the transposon insertion junctions (Tn-seq). During Tn-seq, transposon mutant cells are pooled and grown in optimal conditions, allowing cells with a transposon insertion located in a non-essential element to survive. Cells with a transposon insertion in an essential element should be lost or depleted from the population. When transposon insertions are identified by Illumina sequencing, read counts per gene in the central 70-90% of the open reading frame (disruptive insertions) are normalized by gene length and used to predict essentiality. 5-15% sequences from the 3' and 5' ends are usually removed from the analysis, as insertions within the terminal regions are likely non-disruptive. While disrupted genes are regarded as “non-essential,” the method yields a list of putative essential genes as those with zero or very few mapped reads (Figure 1a and b).

Another step towards identifying gene function is the annotation of the protein domains encoded by genes. Protein domains are functional or structural units that can fold, evolve, and function independently. Homology-based protein domain prediction and function assignment are effective starting points for understanding protein function, even when diverse protein architectures add complexity to functional annotations. While domain databases such as Pfam and InterPro aim to provide maximum sequence coverage to predict protein domain identity, approximately 30% of all domains listed in these databases (Pfam 33.1 and InterPro 81.0) are ‘domains of unknown function (DUFs).’ Single DUFs are usually predicted to span through functionally uncharacterized proteins. However, studies suggest that at least some of these proteins may contain more than one domain.
While robust and comprehensive, Tn-seq studies do not consider that genes may encode for more than one protein domain. Tn-seq analysis may classify a gene as “non-essential” due to the presence of transposon insertions in a non-essential coding region, despite the gene coding for a second domain not spanning through the whole gene length that might be essential. We operationally defined this subclass of essential genes as “essential domain-containing” (EDC) genes (Figure 1c and d) and set out to identify them in a Tn-seq dataset built-in *Burkholderia cenocepacia* K56-2. By analyzing biases in transposon density in genes previously identified as “non-essential”, we found 40 genes where the encoded proteins contained putative essential and non-essential domains. Using a CRISPR Interference (CRISPRi) platform we developed for *Burkholderia*, we experimentally confirmed growth defects, representing the loss of an essential function, in 27 EDC gene knockdowns. The identified EDC genes include ten encoding known multidomain proteins and two entirely uncharacterized genes encoding different N-terminal DUFs, demonstrating the utility of the approach. This study highlights that gene essentiality depends on the function of individual protein domains rather than entire proteins.

**Results**

**Identification of EDC Genes from Tn-seq Data**

To identify EDC genes in *B. cenocepacia* K56-2, we built a custom script that used our previous Tn-seq data to select genes that i) were not previously found to be essential in *B. cenocepacia* K56-2, and ii) had an asymmetric distribution of transposon insertions (Figure 2). The script split each gene into two equal parts and selected genes with reads in only one region to identify genes with transposon insertion biases. We worked under the assumption that (i) each half could represent one functional domain and (ii) one of the domains may be essential while the other may not. We arbitrarily set the parameters “min ratio” and “min reads” to 0 and 0.14, respectively (see Material and Methods and Supplementary Figure 1). These settings
looked for genes that had zero reads at one end, while the number of reads in the non-empty end was at least 14% of that region's length. For example, if a section of a gene was 100 bp in length, it would require at least 14 reads mapped to that section to be considered non-essential. With these settings, the script produced an extensive list of 178 candidate EDC genes (Supplementary Table 1).

**Bioinformatic Analysis of the Candidate EDC Genes**

We reasoned that if EDC genes contained essential protein domains, then the essential protein domains may be encoded by essential genes in at least some other bacteria. We then searched for essential ortholog genes of the 178 candidate EDC genes by BLASTx searches against the ‘Database of Essential Genes (DEG)’\(^{17}\) using 50% sequence alignment and 30% sequence identity as the cut-off. We found that 40 of the 178 genes had orthologs annotated as ‘essential’ in other bacterial species. We wished to interrogate the domains encoded by these 40 genes using UniProt\(^{18}\) based on InterPro domains\(^9\). InterPro predicts the domain information by matching the protein or nucleic acid sequences against the member databases (collectively known as InterPro consortium) to identify ‘signatures’ associated with known domains. Thus, the InterPro prediction relies on the availability of sequence characterization and annotation. This analysis showed that from the 40 candidate EDC genes predicted to be essential by homology with other essential genes, 10 genes encoded multidomain proteins, and 7 of them were well-characterized, such as the N-terminal domain of DnaK and NusA (Figure 3a). The remaining genes were predicted to have one single annotated domain (19 genes) that did not span the whole gene-length or encoded uncharacterized proteins (11 genes) (Supplementary Table 2). All 40 genes had transposon insertions located in one half of the gene, showing that the script was able to identify genes with biased transposon insertions (Supplementary Figure 2). Taken together, these results suggest that the identified genes
could be essential due to the presence of essential protein domains orthologues. Notably, 17 DNA regions were identified as coding for new putative essential protein domains (Table 1).

**Table 1: Essential genes and domains identified based on biased transposon insertions.**

<table>
<thead>
<tr>
<th>K56-2 Locus Tag</th>
<th>Homolog J2315 Locus Tag</th>
<th>Product Name</th>
<th>Function</th>
<th>Reads at 5' Half</th>
<th>Reads at 3' Half</th>
<th>Identified Essential Domain</th>
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<tr>
<td>WQ49_RS0 0050</td>
<td>BCAL3469</td>
<td>cell division protein FtsL</td>
<td>Essential cell division protein</td>
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<td>Domain (FtsL)</td>
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<td>NUDIX hydrolase</td>
<td>Nucleoside-diphosphatase</td>
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<td>49</td>
<td>Domain (Nudix hydrolase)</td>
</tr>
<tr>
<td>WQ49_RS0 0885</td>
<td>BCAL3305</td>
<td>prep protein translocase subunit YajC</td>
<td>Secretase/insertase</td>
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<td>0</td>
<td>new</td>
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<td>Chaperone</td>
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<td>227</td>
<td>N-terminal Domain</td>
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<td>0</td>
<td>new</td>
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<td>WQ49_RS0 3550</td>
<td>QU43_RS6 2245</td>
<td>hypothetical protein</td>
<td>Unknown</td>
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<td>WQ49_RS0 3805</td>
<td>BCAM1624</td>
<td>MaoC family dehydratase</td>
<td>MaoC-like dehydratase</td>
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<td>0</td>
<td>new</td>
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<td>hypothetical protein</td>
<td>Unknown</td>
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<td>0</td>
<td>new</td>
</tr>
<tr>
<td>WQ49_RS0 7360</td>
<td>BCAM2338</td>
<td>glycosyl transferase family 1</td>
<td>UDP-glycosyltransferase</td>
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<td>152</td>
<td>Domain (Glyco_transf_28)</td>
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<tr>
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<td>QU43_RS6 6100</td>
<td>hypothetical protein</td>
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<td>WQ49_RS0 9185</td>
<td>BCAS0417</td>
<td>cytochrome biogenesis protein CcdA</td>
<td>electron transfer</td>
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<td>38</td>
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<td>Unknown</td>
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<td>Domain (DUF4148)</td>
</tr>
<tr>
<td>WQ49_RS1 1915</td>
<td>BCAL0324</td>
<td>TatB</td>
<td>protein transmembrane transporter</td>
<td>0</td>
<td>57</td>
<td>Domain (TatA_B_E)</td>
</tr>
<tr>
<td>WQ49_RS1 2045</td>
<td>BCAL0298</td>
<td>thiamine biosynthesis protein ThiS</td>
<td>thiamine biosynthesis protein ThiS</td>
<td>0</td>
<td>50</td>
<td>Domain (ThiS)</td>
</tr>
<tr>
<td>Accession</td>
<td>Gene ID</td>
<td>Description</td>
<td>Location</td>
<td>Domain Details</td>
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<td></td>
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<tr>
<td>-----------</td>
<td>---------</td>
<td>--------------------------------------------------</td>
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<td>WQ49_RS1</td>
<td>BCAL0250</td>
<td>50S ribosomal protein L18 structural constituent of ribosome</td>
<td>0 65</td>
<td>Domain (Ribosomal_L18p)</td>
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<tr>
<td>WQ49_RS1</td>
<td>BCAL0245</td>
<td>RplX structural constituent of ribosome</td>
<td>20 0</td>
<td>Domain (L24-Pfam)</td>
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<td></td>
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<td>WQ49_RS1</td>
<td>BCAL0243</td>
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<td></td>
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<tr>
<td>WQ49_RS1</td>
<td>BCAL0233</td>
<td>RpsJ structural constituent of ribosome</td>
<td>0 25</td>
<td>new</td>
<td></td>
<td></td>
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<td>WQ49_RS1</td>
<td>BCAM1066</td>
<td>hypothetical protein</td>
<td>0 425</td>
<td>Domain (DUF2213)</td>
<td></td>
<td></td>
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<tr>
<td>WQ49_RS1</td>
<td>BCAM0549</td>
<td>molecular chaperone GroES Chaperone</td>
<td>0 21</td>
<td>Domain (Cpn10)</td>
<td></td>
<td></td>
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<td>WQ49_RS2</td>
<td>BCAM2699</td>
<td>alpha/beta hydrolase Putative hydrolase</td>
<td>120 0</td>
<td>Domain (Abhydrolase_3)</td>
<td></td>
<td></td>
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<tr>
<td>WQ49_RS2</td>
<td>BCAL0558</td>
<td>Cca 3'-cytidine-cytidine-tRNA adenylyltransferase</td>
<td>0 79</td>
<td>Domain (PolyA Polymerase)/Domain (Binding)</td>
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<td></td>
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<td>WQ49_RS2</td>
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<td>0 23</td>
<td>new</td>
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<td></td>
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<tr>
<td>WQ49_RS2</td>
<td>BCAL0878</td>
<td>FmdB family transcriptional regulator Regulatory activity</td>
<td>0 30</td>
<td>Domain (CxxC_CXXC_SSSS)</td>
<td></td>
<td></td>
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<tr>
<td>WQ49_RS2</td>
<td>BCAL0909</td>
<td>16S rRNA maturation RNase YbeY Endoribonuclease activity</td>
<td>68 0</td>
<td>Domain (UPF0054)</td>
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<td>WQ49_RS2</td>
<td>BCAL2715</td>
<td>RpmG structural constituent of ribosome</td>
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<td>Domain (Ribosomal_L33)</td>
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<td>WQ49_RS2</td>
<td>BCAL2334</td>
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<td>0 21</td>
<td>Domain (Oxidored_q2)</td>
<td></td>
<td></td>
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<tr>
<td>WQ49_RS2</td>
<td>BCAL2199</td>
<td>Fe-S cluster assembly transcriptional regulator IscR DNA-binding transcription factor</td>
<td>39 0</td>
<td>Domain (Rrf2)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>WQ49_RS2</td>
<td>BCAL2091</td>
<td>30S ribosomal protein S2 structural constituent of ribosome</td>
<td>0 86</td>
<td>Domain (Ribosomal_S2)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
### CRISPRi Knockdowns of EDC Genes Show Growth Defects

To phenotypically characterize the effect of knocking down EDC genes, we used CRISPR interference or CRISPRi\(^\text{16}\) to create knockdown mutants of the genes of interest. CRISPRi comprises a chromosomally integrated dCas9 under the control of a rhamnose-inducible promoter and plasmid-borne sgRNA driven by a constitutively active synthetic promoter, \(P_{\text{J23119}}\)\(^\text{16}\). Simultaneous expression of dCas9 and a target-specific sgRNA allows the dCas9 to bind the target DNA region and, thus, sterically interfere with transcription by RNA polymerase\(^\text{15,16}\). To inhibit the expression of the candidate genes, we designed two sgRNAs against each of the candidate genes targeting the start codon and adjacent region on the non-template strand (Supplementary Figure 3a and c). For phenotypic characterization, we grew...
the cells in LB with and without rhamnose. Upon induction of dCas9 with rhamnose, 27 out of
the 40 candidate genes showed at least 25% growth inhibition relative to the uninduced
condition (Supplementary Figure 3b-d).

**DUF2213 and DUF4148 Appear to be Essential Domains**

The presence of DUFs is a common feature of hypothetical or uncharacterized proteins.

To initiate functional characterization of DUFs, we focused on two genes containing DUF-
coding sequences, which their respective CRISPRi mutants demonstrated a conditional growth
defect (Figure 3b). WQ49_RS16145 (BCAM1066) and WQ49_RS10495 (BCAS0158) contain DUF2213 (Pfam accession PF09979) and DUF4148 (Pfam accession PF13663), respectively at the N-terminal end of the proteins (Figure 3b). BLAST searches of BCAM1066 and BCAS0158 genes as a query against the DEG showed that BCAM1066 (WQ49_RS16145) had 30% sequence similarity with lysK (B8GXH3) from Caulobacter crescentus, and BCAS0158 (WQ49_RS10495) had a 52% sequence identity with a predicted amino acid permease (BPSS1112) from Burkholderia pseudomallei K96243 (data not shown).

Mining of the Pfam database (https://pfam.xfam.org/) showed that these DUFs are well conserved across the bacterial species: DUF2213 is present in 209 bacterial species, including bacterial pathogens (Acinetobacter baumannii, Enterobacter cloacae, Haemophilus influenzae, Burkholderia cepacia, Shigella flexneri), plant pathogens (Agrobacterium tumefaciens), and biotechnologically relevant species (Pseudomonas putida) (Figure 4a and Supplementary Table 5). DUF4148 is found in 204 bacterial species, primarily in Burkholderia species (i.e., Burkholderia cepacia, Burkholderia mallei, Burkholderia vietnamiensis) and plant pathogens such as Ralstonia solanacearum (Figure 4b and Supplementary Table 5). DUF2213 is also present in many phage-related proteins (Figure 4a). Eight unique domain architectures were observed for proteins containing DUF2213 and five for DUF4148 (Figure 4c-d). DUF2213 is associated with another essential domain PF00293, a NUDIX hydrolase (Figure 4c). In other
proteins, DUF2213 is associated with the LPD3 domain (PF18798) and DUF1073 (PF06381) which is also conserved across bacterial species \(^\text{11}\) (Figure 4c). On the other hand, Pfam analysis of DUF4148 shows that DUF4148 differs in domain length among species and is associated with the Pfam domain PF00144, known to confer resistance against $\beta$-lactams (Figure 4d) \(^\text{19}\). Nonetheless, the N-terminus was highly conserved, suggesting it is functionally significant. The Pfam-based analysis of species distribution also revealed that DUF2213 is present in six eukaryotic species (five metazoans and one fungal species), whereas DUF4148 is present in five eukaryotic species (three viridiplantae species and two metazoan species). The widespread distribution of these DUFs indicates the functional importance of these essential domains, creating an impetus for further characterization.

**Discussion**

A first step in the functional characterization of proteins is performed through protein depletion and growth phenotype characterization. As multidomain proteins can perform multiple functions driven by the activity of their individual domains \(^\text{20}\), the function assigned to a gene product could indeed correspond to one of its domains and not to the whole protein. That is the case of essential genes identified by Tn-seq \(^\text{1}\). In standard Tn-seq analysis the condition of essentiality is assigned to genes and not to domains, resulting in incorrect classification of many essential genes as non-essential. Rather, essentiality assignment pipeline should be revised to analyze the essentiality of individual protein domains \(^\text{21}\). Indeed, essentiality can be assigned to individual domains of a multidomain protein rather than the entire protein \(^\text{12,13}\). In this work, we defined as essential-domain-containing (EDC) genes those genes that encode more than one protein domain, with one of the domains coding for an essential function. By analyzing a Tn-seq dataset \(^\text{14}\) for transposon insertion biases, we show that standard Tn-seq analysis pipelines may miss EDC genes, whose detection often requires either manual curation or additional considerations \(^\text{22}\).
We validated our approach by identifying previously characterized multidomain essential proteins in which the essential function is assigned to one single domain. For instance, our analysis of biases in the Tn-seq dataset showed that the N-terminal domain of NusA \(^{23}\) is sufficient to mediate the essential function, in agreement with previous work \(^{24}\). Similarly, the \(B. \) cenocepacia K56-2 \(dnaK\) gene was previously defined as non-essential \(^{14}\); however, we found that the Tn-seq reads mapped onto \(dnaK\) were biased toward the C-terminal domain (CTD), suggesting that only the NTD is necessary for its essential function. (Figure 3b, Supplementary Figure 2). DnaK is a multidomain protein and a master regulator of the chaperone network \(^{25}\). DnaK comprises an N-terminal ATPase domain (NTD) and a C-terminal substrate-binding domain (CTD) \(^{25}\). Perturbations either within the NTD that leads to the abrogation of the ATPase activity or within the conserved linker peptide that impairs the interdomain mechanistic interaction abrogate the \textit{in vivo} activity of DnaK \(^{26,27}\).

While 14 EDC genes that demonstrated a growth defect when knocked down code for proteins annotated to have a single domain, none of these domains span the entire gene, and transposon insertions are only mapped to the annotated domain (Supplementary Figure 2). Thus, it is possible that the remaining regions code for novel domains that perform the essential biological functions independently of the adjacent sequences. Indeed, multidomain proteins that are involved in direct protein-protein interactions are more often detected as essential than proteins with a single domain \(^{12}\), hinting towards the functional contribution of individual domains within a protein complex.

We demonstrated a conditional growth defect in 27 out of 40 CRISPRi mutants of EDC genes. It remains a possibility that the sgRNAs designed for CRISPRi-mediated gene silencing of the remaining 13 genes were not efficient in target binding, thus yielding no growth defect. CRISPRi is more effective in blocking transcription initiation than elongation, and is the most efficient in silencing gene expression when promoter regions are targeted with gRNAs \(^{15,28-30}\).
However, as promoter regions for *B. cenocepacia* genomes remained largely unannotated we targeted translation start sites. It remains to be investigated whether targeting the promoter region to block the transcription initiation rather than elongation might yield conditional a growth phenotype in the remaining 13 genes.

A large portion of the protein domains that lack functional assignment can be grouped within the DUF category. DUFs are members of ever-increasing uncharacterized protein families; they are the object of experimental and computational efforts towards their functional characterization \(^{10,31-33}\). Determining if a DUF is essential is among the first steps in functional characterization. In this study, we focused on two EDC genes that encode putative essential DUFs: DUF2213 and DUF4148. Both domains have a high degree of conservation across diverse phyla, which highlights their biological relevance. DUF2213, a phage-associated domain (PF09979), is well distributed across bacteria and phages. Interestingly, we found that DUF4148 (PF13663) is putatively essential and associated with \(\beta\)-lactamase (PF00144) (Figure 4).

In summary, our study identified 27 EDC genes whose knockdown produced a growth defect, highlighting the essential nature of one of their protein domains. By leveraging a Tn-Seq dataset in *B. cenocepacia* K56-2 \(^{14}\), we demonstrate that the essential nature of protein-coding genes is a function of the individual protein domains they encode. We propose that determining essentiality of a domain of unknown function should be the first step in the process to define their function.

**Methods**

*Bacterial Strains and Growth Conditions*

The list of bacterial strains and plasmids used in this study is provided in **Supplementary Table 3**. Bacterial strains were grown in LB-Lennox medium (Difco) at 37\(^\circ\)C. *E. coli* strain MM290 carrying the helper plasmid pRK2013 was selected in kanamycin
40µg/mL (Fisher Scientific). Donor strains of *E. coli* DH5α and *B. cenocepacia* K56-2 carrying the sgRNA plasmids were selected in trimethoprim 50µg/mL and 100µg/mL (Sigma), respectively.

**Identification of EDC Genes from Tn-Seq Dataset**

Candidate EDC genes were identified with a custom python script using the Tn-seq dataset. The script analyzed every gene previously classified as “non-essential” by splitting it into two equal halves and counting the number of reads mapped to each half-gene. The script then used the “min ratio” and “min reads” as filtering criteria to call EDC genes. “Min ratio” was defined as the desired ratio of reads between the halves of the gene. “Min reads” was defined as the minimum number of reads in the non-empty end that is equal to a 14% of that half’s length. Min reads was set to 0.14, while min ratio was set as 0. For each gene, 10% from each end of the gene was discarded from the analysis. The parameters can be changed to yield either more stringent or more general results. The script is available at https://github.com/cardonalab/EssentialDomains

**Bioinformatic Analysis**

Orthologous essential genes were identified using BLASTx against DEG 15. Multidomain information was fetched from the UniProt database based on Pfam and InterPro domain features. DUF containing genes were characterized using the Pfam tool available on the Pfam website (https://pfam.xfam.org/). Domain sequences were retrieved in FASTA format from the Pfam database and aligned by Clustal Ω. Maximum-likelihood phylogenetic trees were generated with MEGA-X using a Jones-Taylor-Thornton (JTT)-based model applying 100 bootstrap values. Phylogenetic trees were visualized, edited and taxonomic labels were assigned using Interactive Tree Of Life (i-TOL). Bootstrap values are represented on a scale of 0 to 1. Taxonomic annotations were labelled based on the NCBI taxonomy database using UniProt identifiers.
Creating Knockdown Mutants of the Candidate EDC Genes with CRISPRi

CRISPRi mutants were of the EDC genes were created as previously described \(^1^6\). Briefly, pSCB2-sgRNAv2, a modified plasmid from pSCB2-sgRNA \(^1^6\), was used as the template for inverse PCR to insert 20bp target-specific sgRNA sequence. Inverse PCR was performed using Q5 high-fidelity polymerase (NEB), forward primers with individual sgRNAs as 5’ tail, and 1092 as the reverse primer. The resultant fragments were ligated to create circular plasmids by incubating 0.5µL of the respective PCR products with quick ligation buffer (NEB), 0.25 µL DpnI, 0.25 µL T4 polynucleotide kinase (NEB), and 0.25 µL T4 ligase (NEB) for 30 minutes at 37°C. Resultant plasmids were transformed into E. coli DH5α, recovered for 2h and selected in LB supplemented with trimethoprim 50µg/mL (Sigma). The transformants were further confirmed by colony PCR using primers 1409 and 848. E. coli strains carrying the sgRNA plasmids were used as donors, and E. coli MM290/pRK2013 as the helper for triparental mating to introduce the sgRNA plasmids into B. cenocepacia K56-2 containing the chromosomally integrated dCas9 under the control of a rhamnose inducible promoter, as described previously \(^3^8\). Trimethoprim resistant colonies (100µg/mL) were selected and screened by colony PCR using the primers 1409 and 848. The list of all the primers used in this study is provided in Supplementary Table 4.

Conditional Growth Phenotype Analysis of the CRISPRi Mutants

To determine the conditional growth phenotype of the candidate genes, overnight cultures of the CRISPRi mutants were back diluted to OD\(_{600nm}\) 0.01. The cultures were grown at 37°C for 20-24 hours with continuous shaking in a 384-well plate containing LB broth supplemented with trimethoprim 100µg/mL and with/without 1% rhamnose. OD\(_{600nm}\) readings were taken at 1 hour intervals using BioTek Synergy 2 microplate reader.

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Conflict of Interest Statement

The authors declare no conflict of interest.

References


While disrupted genes are regarded as “non-essential,” the method yields a list of putative essential genes as those with zero or very few mapped reads (1a and 1b). We operationally defined this subclass of essential genes as “essential domain-containing” (EDC) genes (1c and 1d).

**Figure 1**

**Essential Domain-containing (EDC) Gene**
Figure 2

Asymmetric distribution of transposon insertions
Figure 3

DUF2213 and DUF4148 Appear to be Essential Domains
DUF2213 is also present in many phage-related proteins (4a). DUF4148 is found in 204 bacterial species, primarily in Burkholderia species (4b). Eight unique domain architectures were observed for proteins containing DUF2213 and five for DUF4148 (4c-d).

Supplementary Files
This is a list of supplementary files associated with this preprint. Click to download.

- SupplementalFiles.pdf
- SupplementaryTable1.csv
- SupplementaryTable2.xlsx
- SupplementaryTable5.xlsx