

# Prokaryotic resistance gene search system database

Team: SYSU-Software



## 1. Background

- > Prokaryotes have been fighting against viruses for billions of years with resistance genes like CRISPR-Cas system as their weapons.
- > Interestingly, defense island, which means resistance genes that encode different defense systems are distributed in clusters like islands in oceans, hidden in their genomes.
- > The flanking region of defense island often are house-keeping genes, and at least one known resistance gene will be included.



Fig.1 Defense Island

## 3. Workflow

- All steps are based on protein sequences.
- > **Stage 1: Select Baits**  
Baits are genes that you have interest in (like bacterial's resistance genes).

The content should include locus ID, ORFStart:End, etc

- > **Stage 2: Select the neighbourhood around Baits**

Different systems have different gene retrieval lengths (like CRISPR-Cas 10~20 kbp, TA 1~2 kbp)

- > **Stage 3: Search for clusters**

With MMSeq2 and PSIBLAST running for 3~5 times, we can get high quality clusters.

- > **Stage 4: Identify Hits**

Hits are protein relative to clusters. Using PSIBLAST we can get a data set with both sensitivity and specificity

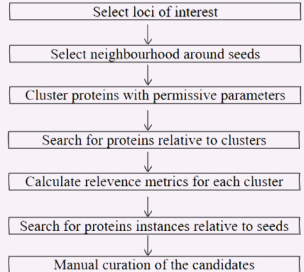
- > **Stage 5: Rank by relevance**

Using metrics like 'DS3P' to evaluate the possibility of Hits being members of defense system.

- > **Stage 6: Final Screen**

With pre-set parameters and manual curation, we can finally dig out which genes can be a new member of defense system.

## 2. Model



## 4. Meaning

- > We dig the data hidden in papers and build a platform to give existing databases a update and extension.
- > Our platform can enhance the understanding of defense system in prokaryotes and through prediction we may find new gene editing tools.
- > Forward: We want to find out whether relationships between defense system in prokaryotes and immune system in eukaryotes exist and address this question will do something on evolution.



## Reference:

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