


# Recap Exercise 4

## RUCS 1.0

### Rapid Identification of PCR Primers Pairs for Unique Core Sequences

Service Information: [Show](#)

#### Entry point:



Choose the entry point you want to use. (See instructions for more information)

#### Reference\*:

No file chosen

The reference file to which the k-mers should be mapped.

\*Optional: if left blank, the algorithm uses one of the positive samples as reference.

#### k-mer size:

The k-mer size defines the size of the oligo nucleotides. Small values decrease specificity, and large values increase specificity. A balance is needed for optimal results.

#### Read length:

This option helps the program ignore insignificant contigs which can cause noise. Default is 250, which corresponds to all contigs below 500 bp are ignored as noise.


#### Upload Instructions:

1. Create 2 folders called "positives" and "negatives" (No caps allowed, names must be exact!)
2. Add the draft genomes you wish to target in the "positives" folder (FASTA only)
3. Add the draft genomes you do NOT wish to target in the "negatives" folder (FASTA only!)
4. Zip the two directories, and upload them

Notice: The name(s) of the zip file(s) are irrelevant as long as the extension is '.zip'.

For more help and examples, see the instruction page.

**WARNING:** To avoid exceeding the maximum runtime, our recommendation is to keep below 50 genomes per submission.

 Isolate File

Name

Size

Progress

Status

 Upload

 Remove

## **Prepare the data for RUCS:**

Create a directory/folder called "positives" and add all positive draft genomes in fasta format (not zipped)

Create a directory/folder called "negatives" and add all negative draft genomes in fasta format (not zipped)

Select both folders and create a zip file (on Mac you right click and select "Compress 2 items")

The zipped file is what you upload as "Isolate File"

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## Sequence Analysis

	Sequences	Size in bases	Seqs >200	Size >200
Reference	187	5701668	186	5701516
Core Sequences	53487	2737882	933	282228
Unique Core Sequences	2	1894	1	1754

## Downloads:

UCS Dissected Scaffolds

UCS Contigs

CS Contigs

Statistics

## CITATION

For publication of results, please cite:

- Martin Christen Frølund Thomsen, Henrik Hasman, Henrik Westh, Hülya Kaya, Ole Lund; RUCS: rapid identification of PCR primers for unique core sequences, *Bioinformatics*, 2017, btx526, <https://doi.org/10.1093/bioinformatics/btx526>

## ResFinder-3.0 Server - Results

Input Files: *unique\_core\_sequences.contigs.fa*

Show Acquired antimicrobial resistance results

### Acquired antimicrobial resistance gene - Results

#### Aminoglycoside

No resistance genes found.

#### Beta-lactam

No resistance genes found.

#### Colistin

Resistance gene	Identity	Query/HSP	Contig	Position in contig	Phenotype	Accession no.
mcr-1	100.00	1626/1626	71_0_0	85..1710	Colistin resistance	<a href="#">KP347127</a>

#### Fluoroquinolone

No resistance genes found.

#### Fosfomycin

No resistance genes found.

#### Fusidic Acid

No resistance genes found.

#### Glycopeptide

No resistance genes found.

#### MLS - Macrolide, Lincosamide and Streptogramin B

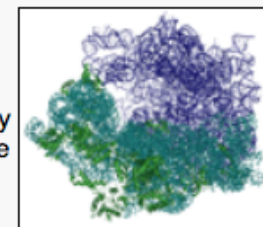
No resistance genes found.

# Searching for Open Reading Frames

## Virtual Ribosome - version 2.0

The Virtual Ribosome is a comprehensive tool for translating DNA sequences to the corresponding peptide sequences.

Besides being a strong translation tool in its own right (with an integrated ORF finder, support for all translation tables defined by the NCBI taxonomy group, and a number of options regarding START and STOP codons), the Virtual Ribosome can work directly on files containing annotation of gene structure. This makes it easy to map various aspect of Intron/Exon structure onto the translated sequence.

[Instructions](#)[Output format](#)[Software download](#)[Article abstract](#)

Paste in DNA sequences in FASTA, GenBank or TAB format

Upload DNA sequences in FASTA, GenBank or TAB format

Choose File

View [example DNA files](#)

*Instructions: Basic usage - Paste in or upload one or more DNA sequences in FASTA (sequence only), GenBank (CDS sections are processed) or TAB (sequence and intron/exon annotation) format and hit submit. The Virtual Ribosome will then translate the DNA sequences using the standard genetic code (by default). **Options can be customized in the section below.***

# The longest peptide sequence hits to known colistin resistance genes

```
>71_0_0 position=37652_rframe-3_ORF
MMQHTSVWYRRSVSPFVLVASVAVFLTATANLTFFDKISQTYPIADNLGFVLTIAVVLF
GAMLLITLLSSYRYVLKPVLILLIMGAVTSYFTDTYGTVYDTTMLQNALQTDQAETKDL
LNAAFIMRIIGLGVLPSELLVAFVKVDYPTWGKGLMRRLGLIVASLALILLPVVAFSSH
YASFFRVHKPLRSYVNPIMPIYSVGKLASIEYKKASAPKDTIYHAKDAVQATKPD
MRKPRLVVFVGETARADHVSFNGYERDTFPQLAKIDGVTNFSNVTSCGTSTAYS
VPCMF SYLGADEYDVDTAKYQENVLDTLDR LGVSILWRDNNSDSKGVMDKLPKAQ
FADYKSATNNAICNTNPYNECRDVGMLVGLDDFVAANNGKDMLIMLHQMGNHGPAY
FKRYDEKFAKFTPVCEGNE LAKCEHQSLINAYDNALLATDDFIAQS IQWLQTHS
NAYDVSM LYVSDHGESLGENGVYLHGM PNAFAPKEQRSVPAFFWTDKQTGIT
PMATDTVLTHDAITPTLLKLF
DVTADKVKDR TAFIR
```

## Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/>	<a href="#">MULTISPECIES: phosphoethanolamine--lipid A transferase MCR-1.1 [Gammaproteobacteria]</a>	1122	1122	100%	0.0	100%	<a href="#">WP_049589868.1</a>
<input type="checkbox"/>	<a href="#">phosphoethanolamine--lipid A transferase [Escherichia coli]</a>	1121	1121	100%	0.0	99%	<a href="#">SPQ84451.1</a>
<input type="checkbox"/>	<a href="#">MCR-1 family phosphoethanolamine--lipid A transferase [Escherichia coli]</a>	1121	1121	100%	0.0	99%	<a href="#">WP_104717510.1</a>
<input type="checkbox"/>	<a href="#">phosphoethanolamine--lipid A transferase MCR-1.7 [Escherichia coli]</a>	1121	1121	100%	0.0	99%	<a href="#">WP_085562392.1</a>
<input type="checkbox"/>	<a href="#">phosphoethanolamine--lipid A transferase MCR-1.3 [Escherichia coli]</a>	1121	1121	100%	0.0	99%	<a href="#">WP_077064885.1</a>
<input type="checkbox"/>	<a href="#">MCR-1 family phosphoethanolamine--lipid A transferase [Escherichia coli]</a>	1120	1120	100%	0.0	99%	<a href="#">WP_113446596.1</a>
<input type="checkbox"/>	<a href="#">phosphoethanolamine--lipid A transferase MCR-1.9 [Escherichia coli]</a>	1120	1120	100%	0.0	99%	<a href="#">WP_099982800.1</a>
<input type="checkbox"/>	<a href="#">phosphoethanolamine--lipid A transferase MCR-1.4 [Escherichia coli]</a>	1120	1120	100%	0.0	99%	<a href="#">WP_076611062.1</a>