

1. What is k (in k-mer) ?

- ☐ It is a negative integer
- ☒ It is a positive integer
- ☐ It is a long sequence
- ☐ It is a short sequence

2. What is the species for this unknown sample (run the analysis of the file using default parameters in KmerFinder) ?

unknown_sample.fasta.zip

Please note that the sequence file need to be **unzipped** prior uploading to the web tool.

- ☒ *Salmonella enterica*
- ☐ *Escherichia coli*
- ☐ *Vibrio cholera*

3. If the KmerFinder result shows *Salmonella enterica* with 25,000 score and *Staphylococcus aureus* with 15,000 score. What is the best explanation for this result ?

- ☐ An error from the tool
- ☐ Your genome data has not been uploaded completely
- ☒ Contamination
- ☐ All of above

4. If you select 'type of your reads' as Illumina – paired end reads. How many files should you upload to MLST tool ?

- ☐ 1
- ☒ 2
- ☐ 3

5. What is the ST type for the unknown sample (using default parameters from MLST tool) ?

Please use the unknown sequence as in Question 2.

☐ ST-313

☐ ST-9

☐ ST-11

☒ ST-19

6. What is the alignment quality between the unknown sample and 7 alleles in MLST tool ?

☐ Low matching quality

☐ No match found

☒ Perfect match

☐ None of above

7. What alignment tool does ResFinder use for identifying resistance genes ?

- ☐ Burrows-Wheeler Aligner (BWA)
- ☒ BLAST: Basic Local Alignment Search Tool
- ☐ ClustalW2
- ☐ All above

8. If you run ResFinder tool selecting percent identity at 99% and the result shows that your genome doesn't contain any resistance genes but you expect to find resistance genes. What is the best option you should do to confirm if your genome doesn't actually contain any resistance genes ?

- ☐ Rerun the tool without changing any parameters
- ☐ Email to tool developer
- ☒ Rerun the tool by lowering percent identity
- ☐ None of above

9. What gene is NOT found in the unknown sample using ResFinder with default parameters ?

Please use the unknown sequence as in Question 2.

- ☐ *floR*
- ☐ *aadA2*
- ☐ *tet(G)*
- ☒ *mcr-1*

10. Which following option shows that your genome contains resistance genes ?

- ☐ Percent identity is 100%
- ☐ HSP length nearly equals to resistance gene length
- ☐ Percent identity is 99%
- ☒ All of above