

S2Q1 What is your favourite bacterium?

093



S2Q2 Why does LREFinder require FASTQ files as input?

1 0 4

Because if we were using FASTA files (draft assembly sequences), we would fail to detect mutations in the 23S rRNA gene, when these mutations are constituting only a minority of the bases in the given position



 82 %

Because that is the only file format that the tool accepts

 5 %

I don't know

 13 %

1 0 8

S2Q3 Why are trimethoprim and chloramphenicol not listed in the Pathogenwatch output for E. faecium?

Because the curators of Pathogenwatch database failed to include them

 6 %

Because Pathogenwatch focuses on clinical applications of WGS and these antimicrobials are not relevant for treatment of E. faecium infections



 86 %

I don't know

 7 %

S2Q4 Why is it important to record the version number of the tool(s) used?

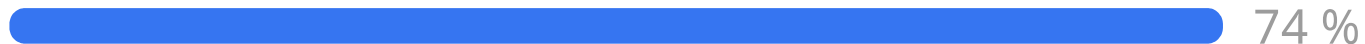
1 1 4

Because different versions may use different databases ✓



92 %

Because different versions may have different scripts ✓



74 %

Because that's just the way to do it

1 %

S2Q5 Should mcr-mediated colistin resistance be reported for this E. coli strain?

088

Yes ☒



No



I don't know



S2Q6 What could the reasons for phenotype-genotype discordance be?

0 8 4

(1/2)

Something went wrong in the phenotypic susceptibility test (either in the test itself or in the reading/reporting of the results)



88 %

Loss of plasmid (during culture or DNA extraction) ✓

85 %

Switch of strain (the phenotypic data belong to one strain and the WGS data belong to another)



74 %

Poor sequence quality ✓

92 %

No info regarding species was selected in the bioinformatics tool ✓

75 %

S2Q6 What could the reasons for phenotype-genotype discordance be?

(2/2)

084

The user forgot to select all relevant options in a tool ✓



Incomplete knowledge of genetic determinants of resistance ✓



Incomplete database ✓



Genetic determinants of resistance outside the scope of the database

