

What can 16S rRNA from the gut tell us about one's health?

The **National Center for Biotechnology Information (NCBI)** has a lot of bioinformatics resources, including the **Basic Local Alignment Search Tool (BLAST)**. This program lets you very quickly compare a DNA or protein sequence to many (millions) known DNA or protein sequences. The top hit has the highest similarity to the input sequence.

After profiling the guts of Romeo and Juliet by amplifying and sequencing 16S rRNA marker genes, we got lots of different sequences but chose one very common one in each sample. One of them is healthy but the other has lots of abdominal pain. Who might need to see a doctor?

1 - To start, go to the NCBI page: <https://www.ncbi.nlm.nih.gov/>

2 - Under "Popular Resources" (top right), click on "BLAST".

3 - Since we will be comparing DNA sequences to DNA sequences, click on the "Nucleotide BLAST" box.

4 - In the box under "Enter accession number(s), gi(s), or FASTA sequence(s)", copy and paste all lines in the file "16S_rRNA_sequences.txt". Note that we have two sequences, one for 16S rRNA from ROMEO's gut and one for 16S_rRNA from JULIET's gut.

5 - Next to "Database", note that we're going to compare Romeo and Juliet's RNA to a "Nucleotide collection" of many genes in many species.

6 - Click on the BLAST button at the bottom left and wait 15-60 seconds.

7 - When the results page appears, next to "Results for", select Romeo (if not already selected).

8 - Scroll below the Graphic Summary and look at the first entry in the Descriptions table. What species is the first sequence from?

9 - What do you know about that species? Search the Web to find out more.

10- Does Romeo appear to be healthy?

11- Go back to "Results for" at the top of the page and select Juliet.

12- Does Juliet appear to be healthy?