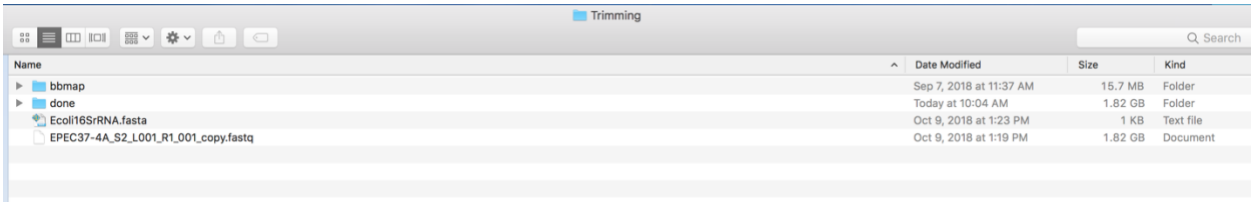
Example for *E. coli* but can be applied to any with reference sequence in NCBI

Escherichia coli 16S rRNA downloaded from NCBI:
https://www.ncbi.nlm.nih.gov/nuccore/NR_024570.1/?report=fasta

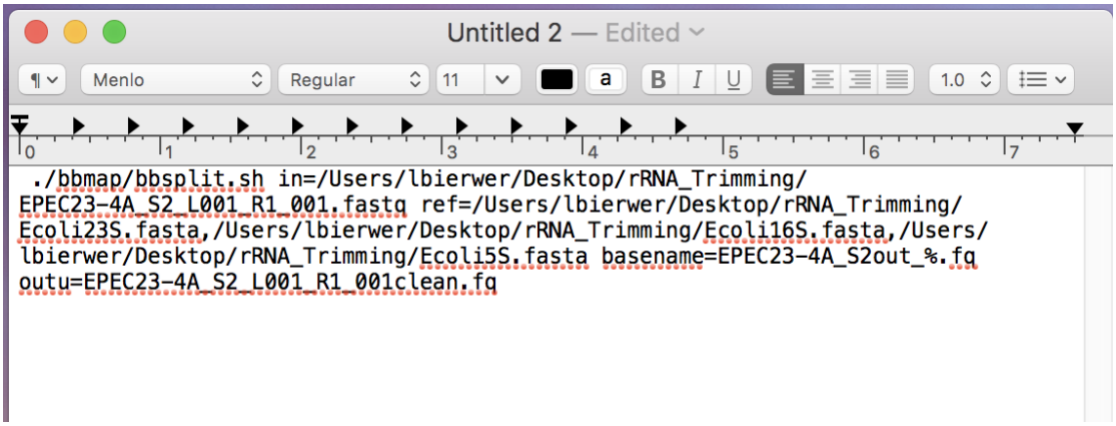
in the folder you store your reads file, e.g. Trimming:
download bbmap tool, unzip it and put the bbmap folder in the Trimming folder.

Also put *E. coli* rRNA fasta in the same folder. Cd into that folder.



Run the following command line in the terminal:
./bbmap/bbsplit.sh in=EPEC37-4A_S2_L001_R1_001_copy.fastq ref=Ecoli16SrRNA.fasta basename=out_%.fq outu=clean.fq

* I did it like this so that both output files would have the input file label on it:



clean.fq should be your reads that are free from *E. coli* rRNA sequences.
out_Ecoli16Sr/rRNA.fq should be the reads that mapped to *E. coli* rRNA

To check out first several lines for the fastq file:
head -n 40 out_Ecoli16SrDNA.fq > first40lines.fasta