

3010BBS Molecular & Applied Microbiology (Assignment 1)

Background:

E. coli 16S rRNA sequence is 1548 nucleotide in length and is numbered from position 1 to 1548. In a cell, the 16S rRNA exists as secondary, tertiary and quaternary structures and is involved in protein synthesis. *E. coli* 16S rRNA secondary structure together with the numbering scheme is used as a template against which all other bacterial 16S rRNA sequences are compared and aligned.

You have been provided with secondary structures of the 16S rRNA of *E. coli*. You have to complete the following tasks for the assignment.

Task 1

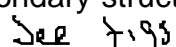
The following are short sequences from the 16S rRNA molecules of five members of domain Bacteria.

- | | |
|----------------------------------|-------------------------|
| (i) <i>Escherichia coli</i> | CUGCCAGUGAUAAACUGGAGGAA |
| (ii) <i>Thermus aquaticus</i> | CUGCCUGCGAAAGCAGGAGGAA |
| (iii) <i>Bacillus cereus</i> | CUGCCGGUGACAAACCGGAGGAA |
| (iv) <i>Campylobacter jejuni</i> | CUGCCUUCGUAAGGAGGAGGAA |
| (v) <i>Neisseria gonorrhoeae</i> | CUGCCGGUGACAAGCCGGAGGAA |

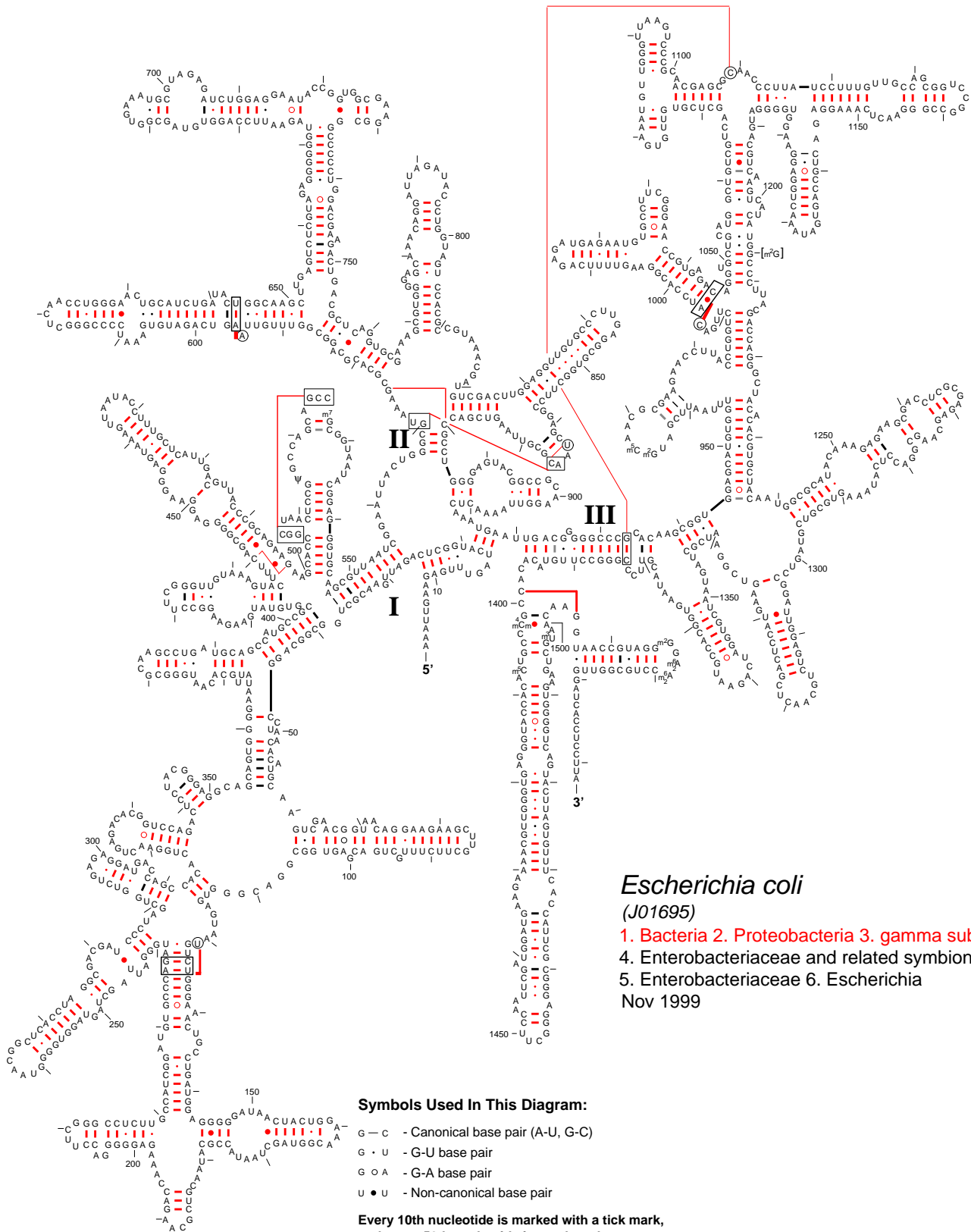
- For *E. coli* the sequence begins at position 1161. Identify and write the position at which the sequence ends.
- You now have identified the sequence start and end positions which relates to the 16S rRNA secondary structure of *E. coli*. Using this information as a guide, draw the corresponding secondary structures for each of the remaining sequences (ii to v).
- Align the sequences shown in (a) by introducing gaps (-) using the secondary structures as a guideline. This type of alignment is known as “aligning sequences using secondary structure constraints”
- Align the sequences without the constraint, that is introduce gaps (-) randomly so that the nucleotides of all the sequence match.
- Can you see the difference between the alignment in (c) and (d).
- The following sequence is from *Bacteroides fragilis* and is the same region as for the sequences shown in (a). Draw the secondary structure and modify your alignment to accommodate this new sequence.

<i>Bacteroides fragilis</i>	CUGCCGUCGUAAGAUGUGAGGAA
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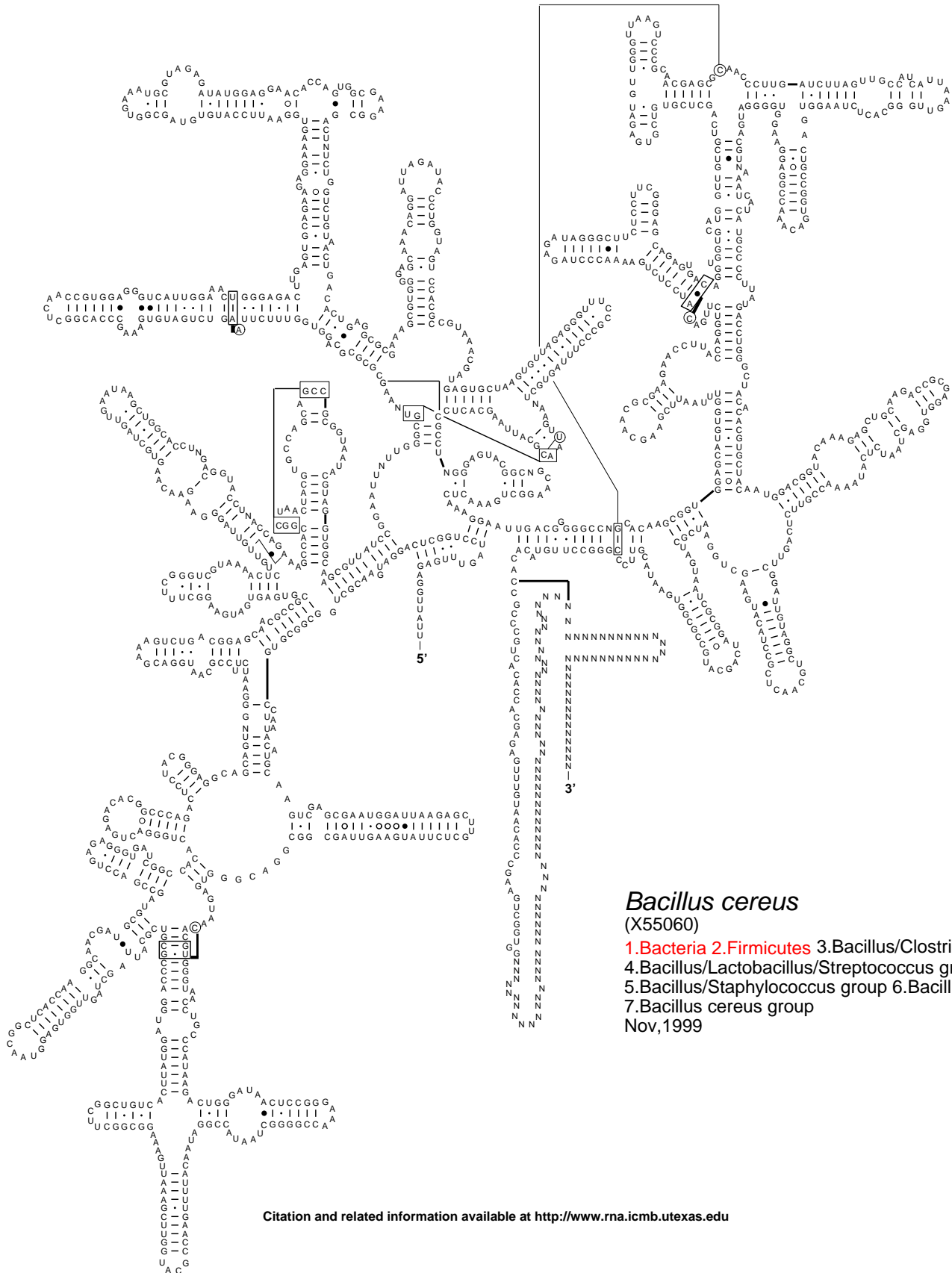
Task 2

From the *E. coli* secondary structure, extract the sequence from positions 826 to 860. Extract the sequence for the same secondary structure region for the 5 other organisms and align all six sequences. 

Secondary Structure: small subunit ribosomal RNA



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Citation and related information available at <http://www.rna.icmb.utexas.edu>

