Problem 2 -blastp and blastn BRCA1 against genes in different organisms

Bos taurus

blastn top scores: 5781, 5750 blastp top scores: 2592, 2587

Rattus norvegicus

blastn top scores: 3386, 3384 blastp top scores: 1854, 1849

Drosophila melanogaster

blastn top scores: 41, 41 blastp top scores: 52.4, 52.4

Mus musculus

blastn top scores: 3283, 3279 blastp top scores: 1847, 1846

Xenopus laevis

blastn top scores: 167, 167 blastp top scores: 293, 293

Problem 3

Two letters will only be included in the subsequence if they match exactly. The score of the subsequence should increase linearly with the length of the subsequence. The "unit-score" scheme, where matching letters receive a score of 1 and non-matching letters (including 2 gaps) receive a score of 0, will work for this.

Problem 4

Letters that are not amino acids: b,j,o,u,x,z

- 1) a) "cmpterscience" versus "ilgy"
 - b) "cmpterscience" has the highest score of 30.8
 - c) "cmpterscience" has a match with a longer string length
- 2) a) "prtein" versus "aminacid"
 - b) "aminacid" has a highest score 28.2
 - c) "aminacid" has a match with a longer string length
- 3) a) "dynamicprgramming" versus "divideandcnqer"
 - b) "divideandcnqer" has the highest score of 32
 - c) "dynamicprgramming" has a match with a longer string length

Problem 5

- 1) Yes. Shakespeare likely used certain phrases or constructs more frequently than expected by random chance. Aligning the books would highlight these phrases if they exist.
- 2) No. Alignment highlights similarities. A better approach would be to look for k-phrases that occur more frequently than expected in all texts.

- 3) Yes. As we saw in class with the translation of "massa" alignment against a dictionary could highlight possible translation.
- 4) No. A substitution cipher would not be helped by alignment. It's a different story for a Caesar cipher, though.
- 5) Yes. Aligning the papers could highlight phrases or larger constructs that are similar.

Problem 6

I used the NCBI COBALT tool with default settings to do multiple alignment. The results:

10001	1	TPNVSVVDLTVRLGKG	16
10002	1	LEKPAKYDDIK	11
10003	1	LDDDVTESDVNAA	13
10004	1	KGASYEDVKAA	11
10005	1	DVSVVDLTV	9
10006	1	LTCRLEKPAKY	11
10007	1	NKETTYDEIKKV	12