



Module 5: Translation

Answer Sheet

Q1. First examine reading frame 1. Are there any stop codons in the reported exon? If there are early stop codons, do you think this is the reading frame used during translation?

Q2. Examine reading frame 2. Are there any stop codons in this reading frame within the exon?

Q3. Examine reading frame 3. Are there any stop codons in the reported exon?

Q4. Using the evidence above, which reading frame maintains an Open Reading Frame (ORF) across exon 2 of tra-RA? Is this the same reading frame as that used for exon 1?

Q5. Give the coordinates for the entire start codon for tra-RA (start codon coordinates should be three consecutive numbers, for example: nucleotides 212-214).

Q6. Which reading frame should we follow along to see the predicted amino acid sequence of tra-RA?

Q7. Zoom out to see the entire exon. Are there any stop codons in this reading frame in the first exon?

Q8. Give the coordinate for the very last base of the first exon.

Q9. Based on the evidence you see in the browser, give the coordinate for the first base of the second exon of tra-RA.

Q10. Do you observe an appropriate splice acceptor site just upstream within the intron?

Q11. Knowing that exon 1 ends with a partial codon of 1 base, what reading frame is being used in the second exon?

Q12. Give the coordinate of the base prior to the 5' splice site of intron 2.

Q13. How many bases are left in the codon before the splice site (i.e., is this phase 0, phase 1, or phase 2)?

Q14. Locate the 3' splice site of Intron 2. Give the coordinate of the first base in exon 3 for tra-RA.

Q15. Which reading frame is being translated in the final exon?

Q16. Give the coordinates for the bases in the stop codon.

Q17. Let's consolidate all the data we found above in one place:

Gene model for tra-RA:

- Coordinates for start of translation: _____
- Coordinate for last base of exon 1: _____
- Coordinate for first base of exon 2: _____
- Coordinate for last base of exon 2: _____
- Coordinate for first base of exon 3: _____
- Stop codon coordinates: _____

Take the coordinate information above to draw a map of tra-RA using rectangles to represent exons and connecting lines to represent introns. Label the ends of the exons with the appropriate coordinates and indicate the transcription start site for the tra-RA initial transcript. Below this map, provide a map of the processed mRNA after intron removal. Below this map, indicate the regions that are translated into a protein. Give precise coordinates. Color coding may be helpful.

Q18. To cement your knowledge of gene structure, you could construct a similar map of the *spd-2* gene. How many exons does this gene have? _____ How many introns? ____ How many isoforms? _____ Use the same approach to determine the coordinates for the exons, and the coordinates for the coding region (another name for the region that is translated).