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# MODULE 5: TRANSLATION

## ANSWER SHEET

### Questions:

- 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 exon2 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 coordinates for the very last base of the first exon. \_\_\_\_\_
- Q9.** Knowing that exon 1 ends with a partial codon of 1 base, what reading frame is being used in the second exon? \_\_\_\_\_
- Q10.** Based on the evidence you see in the browser, give the coordinates for the first base of the second exon of *tra-RA*. \_\_\_\_\_

**Q11.** Do you observe an appropriate splice acceptor site just upstream within the intron?  
\_\_\_\_\_

**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*

Coordinate 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.

**Summary Question 1.** 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).