Module 5: Translation

Answer Sheet

**Questions:**

1. 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?\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
2. Examine reading frame 2. Are there any stop codons in this reading frame within the exon? \_\_\_\_\_\_\_\_\_
3. Examine reading frame 3. Are there any stop codons in the reported exon? \_\_\_\_\_\_\_
4. 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? \_\_\_\_\_\_\_\_\_
5. Give the coordinates for the entire start codon for *tra-RA*. (start codon coordinates should be three consecutive numbers, for example: nucleotides 212-214).

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

1. Which reading frame should we follow along to see the predicted amino acid sequence of *tra-RA*? \_\_\_\_\_\_\_\_\_\_\_\_\_
2. Zoom out to see the entire exon. Are there any stop codons in this reading frame in the first exon? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
3. Give the coordinates for the very last base of the first exon. \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
4. Knowing that exon 1 ends with a partial codon of 1 base, what reading frame is being used in the second exon? \_\_\_\_\_
5. Based on the evidence you see in the browser, give the coordinates for the first base of the second exon of *tra-RA*. \_\_\_\_\_
6. Do you observe an appropriate splice acceptor site just upstream within the intron? \_\_\_\_\_\_\_\_
7. Give the coordinate of the base prior to the 5’ splice site of intron 2  **\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**
8. How many bases are left in the codon before the splice site, i.e. is this phase 0, phase 1, or phase 2? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
9. Locate the 3’ splice site of Intron 2. Give the coordinate of the first base in exon 3 for *tra-RA* \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
10. Which reading frame is being translated in the final exon? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
11. Give the coordinates for the bases in the stop codon. \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
12. 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).