



# Module 1: Introduction to the Genome Browser: What is a gene?

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## *Answer Sheet*

**Q1.** How many genes are there in contig1?

**Q2.** What are the names of these genes?

**Q3.** Which gene has the largest span (i.e., the largest distance between the start and end of the gene)?

**Q4.** What is the relationship between the bases displayed when the arrow is pointed to the left versus when it is pointed to the right?

**Q5.** Why do you think the bases are displayed in this way in the Genome Browser?

**Q6.** How many exons does tra-RA contain?

**Q7.** How many introns does tra-RA contain?

**Q8.** Why do you think it takes three lines to display the amino acid information? Hint: remember that a codon is specified by three bases, e.g., CCG = Proline (circled in Figure 12).

**Q9.** Based on the screenshot shown in **Figure 22**, which reading frame contains the amino acid sequence for the second coding exon of tra-RA?

**Q10.** Does frame +2 have an ORF in the coding region of this exon? What about frame +1 and frame +3?

**Q11.** Given that 3 of the 64 possible codons are stop codons, what is the chance of having a stop codon at any given position, assuming that the sequence is random?

**Q12.** How many exons and introns are present in this gene?

**Q13.** What is the orientation of this gene relative to contig1? How do you know? Where are the start codon and the stop codon — give the base position numbers (coordinates) of the start and the stop codon)?

**Bonus:** Take a little time to explore some of the other evidence tracks on the browser.

**Q14.** While looking at contig1 (size 11,000 bp), put the “GC Percent” track on **full**. What sort of pattern do you see, relative to the map of the genes? What can you conclude about gene structure?