Self-Quiz 1 Questions

Match the correct term with each definition or select the best answer for each question.

1. A series of codons from a single strand of DNA sequence which can be "read" in three different ways, depending on whether one starts at the first nucleotide position, the second or third

Reading Frame (RF)
Alternative Splicing
Open Reading Frame (ORF)
mRNA Processing

2. Modifications made after transcription has been completed (in eukaryote cells), including the addition of a 5'cap and 3' polyA tail and the removal of noncoding regions

Alternative Splicing
Annotation
mRNA Processing
ab initio gene prediction

3. Transcribed as part of the normal gene primary transcript, but these sequences are not found in the functional mRNA outside of the nucleus

Exon
mRNA
Intron
Reading Frame

4. A section of a sequence that begins with an initiation (methionine, ATG) codon and ends with a nonsense (stop) codon

Untranslated Region (UTR)
Open Reading Frame (ORF)
Exon
Intron

5. The portion of an mRNA from the 5' end to the position of the first codon used in translation, and also the portion of an mRNA from the 3' end of the mRNA to the position of the last codon

Exon
Intron
Open Reading Frame
Untranslated Region (UTR)

6. A region of a gene that is present in the final functional mRNA transcript; these segments of the mRNA are spliced together and translated into protein
Alternative Splicing
Exon
Intron
Untranslated Region (UTR)

7. Which of the following best describes the process of alternative splicing?
Various ways of splicing out introns in eukaryotic pre-mRNAs resulting in one gene producing several different mRNAs and protein products.
The succession of codons determined by reading nucleotides in groups of three from a specific initiation codon.
The alternation of gametophyte and sporophyte stages in the life cycle of a plant.
The reaction that removes introns and joins together exons in eukaryotic nuclear primary RNA transcripts.

8. Which of the following best explains why a genome project is not finished when the sequence has been completed?
Genomes change too fast and must constantly be updated.
Individuals within a species are so unique that having a single sequence is insufficient to characterize a species' genome.
Without knowing the number, the function, and the location of genes within a genome, the sequence is not very useful.
Many sections of a genome are too difficult to sequence and have not actually been included in 'complete' genomes.

9.Which of the following best defines gene annotation?
Shorthand method of documenting a genes function
Describing different regions of the code and identifying which regions can be called genes
Determining the sequence of nucleotide bases for a gene
Identifying which regions of cDNA are separate exons

```
GAATGAATGT TATACTAACC AAGAAGAACC CAGCAGGTTA TCTTATCCCC AAGGGGTGGA
                                          |||| |||||||||| ||||||||||
...........................................GTTA TCTTATCCCC AAGGGGTGGA

AGGTTCAGCT GTGGTACAGA AGTGTGCACA TGGATGACCA AGTTTATCCT GACCCCAAAA
|||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
AGGTTCAGCT GTGGTACAGA AGTGTGCACA TGGATGACCA AGTTTATCCT GACCCCAAAA

TGTTCAACCC TTCAAGATGG GAGGTAAATT AAATTCAATC CATTCTTCTG CAGTTTTTGT
|||||||||| |||||||||| |||
TGTTCAACCC TTCAAGATGG GAG....... .......... ......................

TTCTTCATCA AACTAGATTA AGCTCCATCG ATTCTCTGCC TTTTTCAGTG TGTTTCAATG

.......... .......... .......... .......... .......... ..........

GTCGATGTAA TTTTTTTTGT TCTTTCAGGG ACCCCCTCCG AAAGCCGGAA CATTCCTTCC
                                || |||||||||| |||||||||| ||||||||||
...........................................GG ACCCCCTCCG AAAGCCGGAA CATTCCTTCC

ATTTGGACTG GGAGCAAGAC TGTGCCCTGG AAATGATCTT GCAAAGCTGG AGATCTCTGT
|||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
ATTTGGACTG GGAGCAAGAC TGTGCCCTGG AAATGATCTT GCAAAGCTGG AGATCTCTGT

CTTCCTCCAT CATTTTCTCC TGGGTTACAA GTAAACCTCC TCTCAACATA TTTATGACAA
|||||||||| |||||||||| ||||||||||
CTTCCTCCAT CATTTTCTCC TGGGTTACAA .......... ......................
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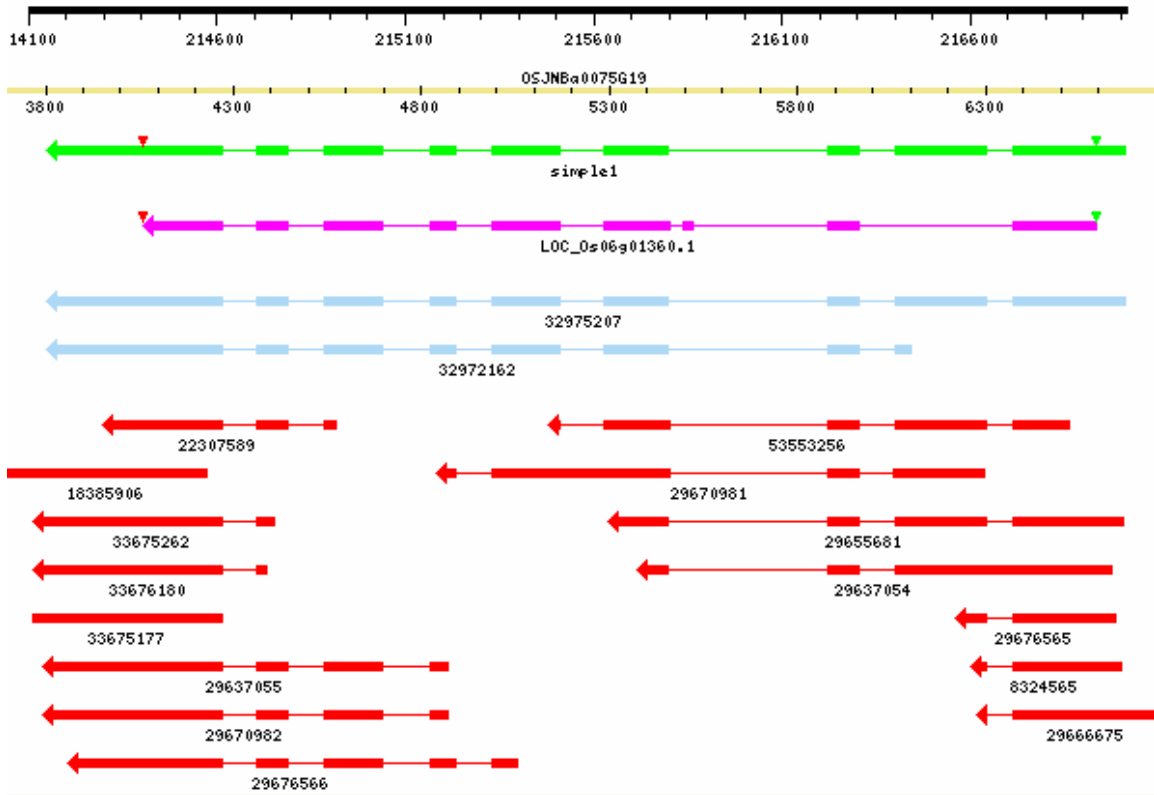
Image Name: similaritydata

10. From the above GeneSeqer output identify which colored section indicates an exon.
Yellow
Green
Blue
Pink

11. From the above GeneSeqer output identify which of the two sequences is the cDNA (or EST)?
The top row
The bottom row

File Name: contextview2

12. Refer to the above context view from the OsGDB. Which color indicates EST sequences?
Green
Pink
Light Blue
Red

13. Refer to the above context view from the OsGDB. Which is the ORF?
The tan colored map
The sequence between green and red triangles
The thin lines between the thicker portions of the maps
Those maps with the arrow heads on the ends

14. Refer to the above context view from the OsGDB. Determine how many exons are in cDNA 32975207?
Seven
Eight
Nine
Zero

15. Challenge Question: Refer to the above context view from the OsGDB. What is wrong with the predicted gene structure from TIGR TU?

The UTR's are too long

The UTR's need to be extended

There is a small exon that needs to be removed and a larger exon that needs to be added

Both A and C

Both B and C

Self-Quiz Questions & Answers

<u>Activity 1: When is a Genome Project Finished?</u>
Match the correct term with each definition or select the best answer for each question.

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Intron
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AGGTTCAGCT GTGGTACAGA AGTGTGCACA TGGATGACCA AGTTTATCCT GACCCCAAAA

TGTTCAACCC TTCAAGATGG GAGGTAAATT AAATTCAATC CATTCTTCTG CAGTTTTTGT
|||||||||| |||||||||| |||
TGTTCAACCC TTCAAGATGG GAG....... .......... ......................

TTCTTCATCA AACTAGATTA AGCTCCATCG ATTCTCTGCC TTTTTCAGTG TGTTTCAATG

.......... .......... .......... .......... .......... ..........

GTCGATGTAA TTTTTTTTGT TCTTTCAGGG ACCCCCTCCG AAAGCCGGAA CATTCCTTCC
                              || |||||||||| |||||||||| ||||||||||
.........................GG ACCCCCTCCG AAAGCCGGAA CATTCCTTCC

ATTTGGACTG GGAGCAAGAC TGTGCCCTGG AAATGATCTT GCAAAGCTGG AGATCTCTGT
|||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
ATTTGGACTG GGAGCAAGAC TGTGCCCTGG AAATGATCTT GCAAAGCTGG AGATCTCTGT

CTTCCTCCAT CATTTTCTCC TGGGTTACAA GTAAACCTCC TCTCAACATA TTTATGACAA
|||||||||| |||||||||| ||||||||||
CTTCCTCCAT CATTTTCTCC TGGGTTACAA .......... ......................
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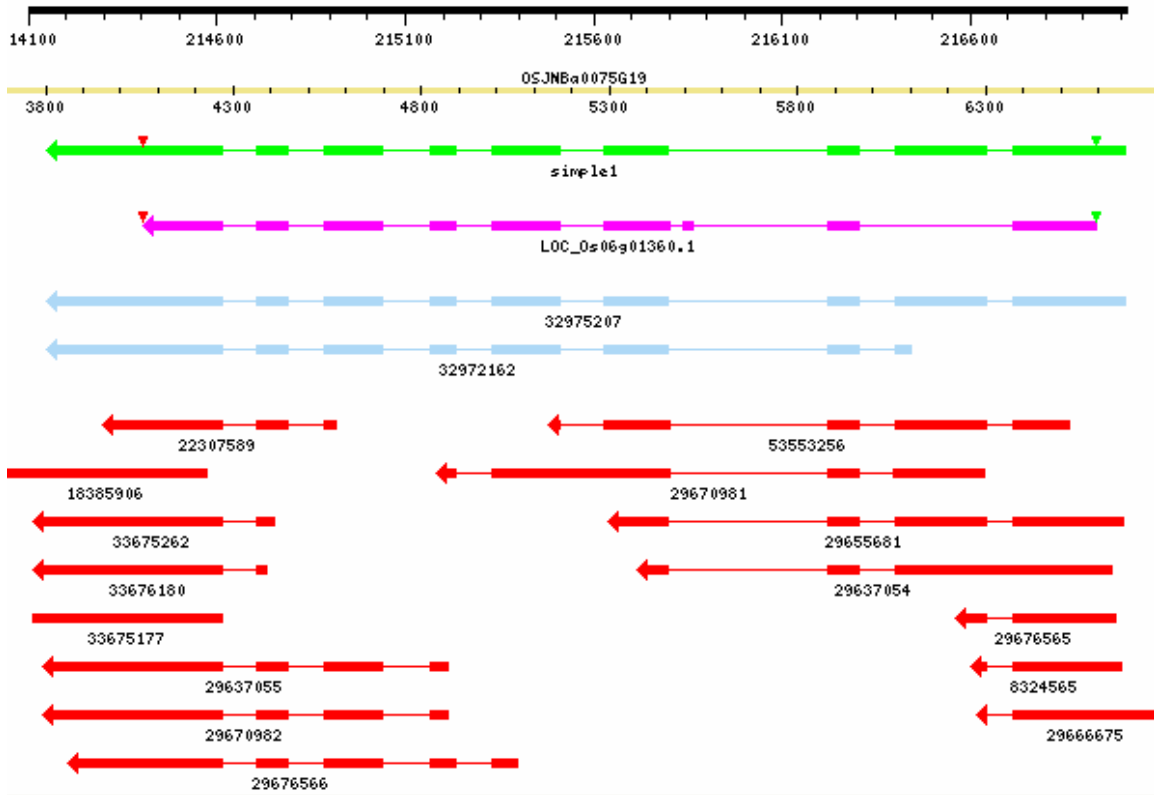
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