



Select one sequence from the list below (20 nucleotides, 5'-3' orientation). Alternatively you can select any 20 nt from the human genome or write your own (random) 20 nt DNA sequence using symbols A, C, T, G, each at least once, in 5'-3' orientation (it will be easier to check your results if you can type the sequence in your computer using any text editor):

- 1: **TTGATGATATGGAGAGCATA** 2: **CCAGCAGTGACTACATGGAA**
3: **CTGTCCACAAGAGCTTAATT** 4: **TTTGTGCTAATTTGGTGCTT**

1. **Write complementary DNA strand (working strand)**

a. in 3'-5' orientation

b. in 5'-3' orientation

2. **Write amino acid sequence which would arise by translation of your coding sequence (use genetic code table on page 4 of this protocol) for different possible reading frames starting with:**

a. first nucleotide

b. second nucleotide

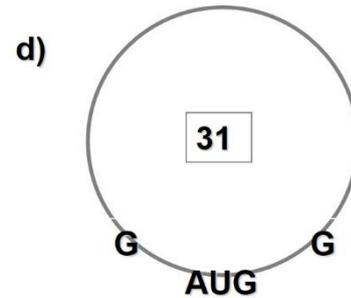
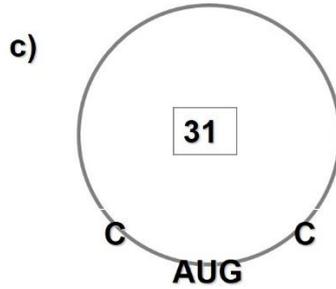
c. third nucleotide

(The result for task 2 can be checked at many places, e.g. <https://web.expasy.org/translate/> or <http://insilico.ehu.es/translate/>)

3. **What would be the amino acid sequence, if your DNA strand from task 1 was not coding (+), but working (-)? (write in the amino- to carboxy terminus orientation, in all possible reading frames)**



4. (Task 3, p. 109): Execute translation of the artificial circular mRNA.



5. In the given DNA sequence (in middle of the coding sequence of a gene, and it is unknown whether it is the coding/memory/+ or the working/- strand)

5' G G C T A G C G T C T G A T T A A G C G 3'

a. find an open reading frame (ORF, no stop codon)

1 2 3 -1 -2 -3

b. write the peptide fragment amino acid sequence from the open reading frame:

6. Determine the extent of homology at DNA and protein level in first 30 nucleotides or 10 amino acids respectively of the insulin B chain of the man, the pig, and the dog.

Homo sapiens (man)

TTT GTG AAC CAA CAC CTG TGC GGC TCA CAC

Sus scrofa (pig)

TTC GTG AAC CAG CAC CTG TGC GGC TCC CAC

Canis lupus familiaris (dog)

TTC GTT AAC CAG CAC CTG TGT GGC TCC CAC



Fill in the table:

Sequence identity H - human, P - pig, D - dog	%
of nucleotides H:P	
of nucleotides H:D	
of amino acids, H:P	
of amino acids H:D	

Task 8-11 should be solved assuming that first nucleotide at 5' end is also first nucleotide of the codon.

7. In positions 6-9 of your coding sequence from task 1, 4 nucleotides were deleted.

- a. What is the mutated DNA sequence?

- b. What is the new amino acid sequence?

- c. What is the type of mutation at the translational level?

8. At the first G nucleotide in your coding sequence a transversion changed the G to T (G>T).

- a. What is the effect in amino acid sequence?

- b. What is the type of mutation at the translational level?

SAMESENSE MISSENSE NONSENSE

c. If there is a missense mutation, is the new amino acid chemically similar to the original? (refer to the amino acid similarity chart at the end of the protocol, use the 5 point scale)

utterly dissimilar 1 2 3 4 5 very similar

9. 3 nucleotides CAT inserted between nucleotide 3 and 4 of your coding sequence. What is the effect in amino acid sequence?

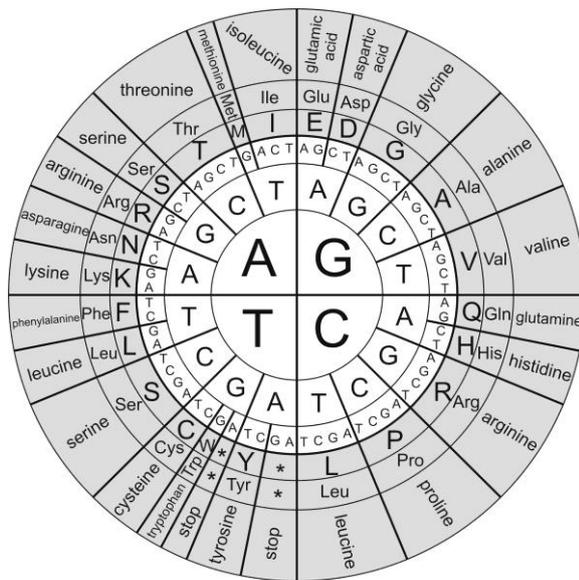
10. 3 nucleotides TAG inserted between nucleotide 3 and 4 of your coding sequence. What is the effect in amino acid sequence?



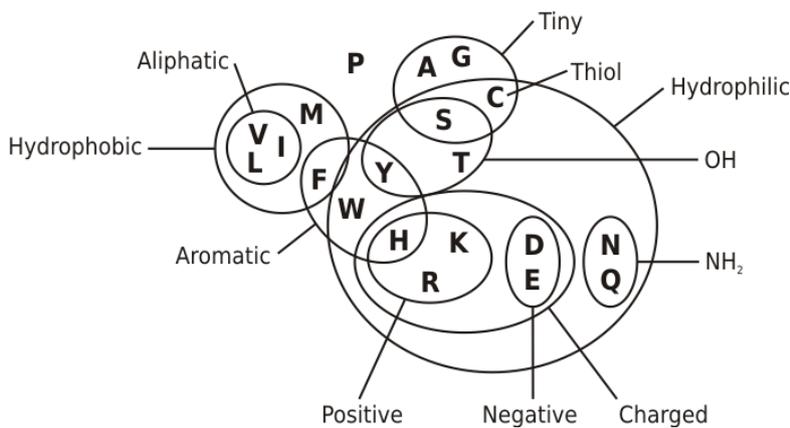
11. Task 5, p. 110

- a.
- b.
- c.

Genetic code table



Chemical similarity of amino acids (in single letter code, see the genetic code table above; OH = hydroxy-; NH₂ = amides)



source:

<http://etutorials.org/Misc/blast/Part%2BII%2BTheory/Chapter%2B4.%2BSequence%2BSimilarity/4.2%2BAmino%2BAcid%2BSimilarity/>



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