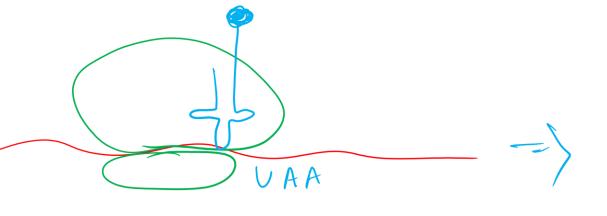
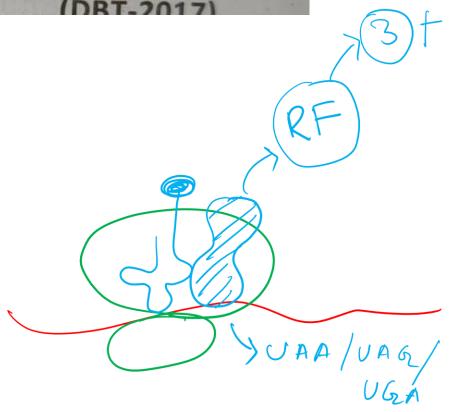
20. Protein 'A' from Pseudomonas putida contains 135 amino acids. The number of nucleotides present in the gene encoding the protein will be ----.

(1) 405

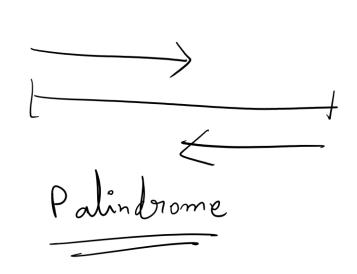
(3)411

135 x 3 = 405 +3 = 408





- 17. Which one of the following sequences is a palindrome?
 - (1) 5' ACGGATTCGC 3'
 - (3) 5' CCATT 3'



18. The molecular weight of a protein is 30 kDa. The minimal length of mRNA encoding this polypeptide will be close to

(1) 800
(2) 900
(3) 1000
(4) 300
(DBT-2016)

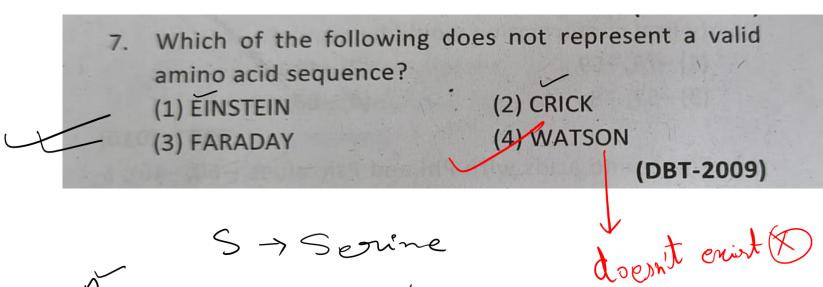
Avg. wt of any Amino acid \rightarrow 110 Da [1 a.a. = 110 Da] $30,000 \quad Da = 30,000 \quad Da = 272.$ $110 \quad 30,000 \quad Da = 272 \times 3$ $110 \quad 30,000 \quad Da = 272 \times 3$ $110 \quad 30,000 \quad Da = 272 \times 3$ $110 \quad 30,000 \quad Da = 272 \times 3$ $110 \quad 30,000 \quad Da = 272 \times 3$ $110 \quad 30,000 \quad Da = 272 \times 3$ $110 \quad 30,000 \quad Da = 272 \times 3$ $110 \quad 30,000 \quad Da = 272 \times 3$ $110 \quad 30,000 \quad Da = 272 \times 3$ $110 \quad 30,000 \quad Da = 272 \times 3$ $110 \quad 30,000 \quad Da = 272 \times 3$ $110 \quad 30,000 \quad Da = 272 \times 3$ $110 \quad 30,000 \quad Da = 272 \times 3$

 $G = C \leftarrow e$ A = T

25. Of the dsDNA sequences given below, the sequence that is expected to have a higher melting temperature is:

- (1) ATGACATTATTACATTAGTG
- (2) GCGCGTGCATGCCGATGCC
- (3) ATTATTATACGTATTTATAT X
- (4) CGCGATCGGGGATTACGAGC X

(DBT-2019)



C -> Cyrtaine

> Tyroxine K > Lysine

E > Glu/ Colutamic acid

I -> Isoleucine

N > Asparagine (Asm)

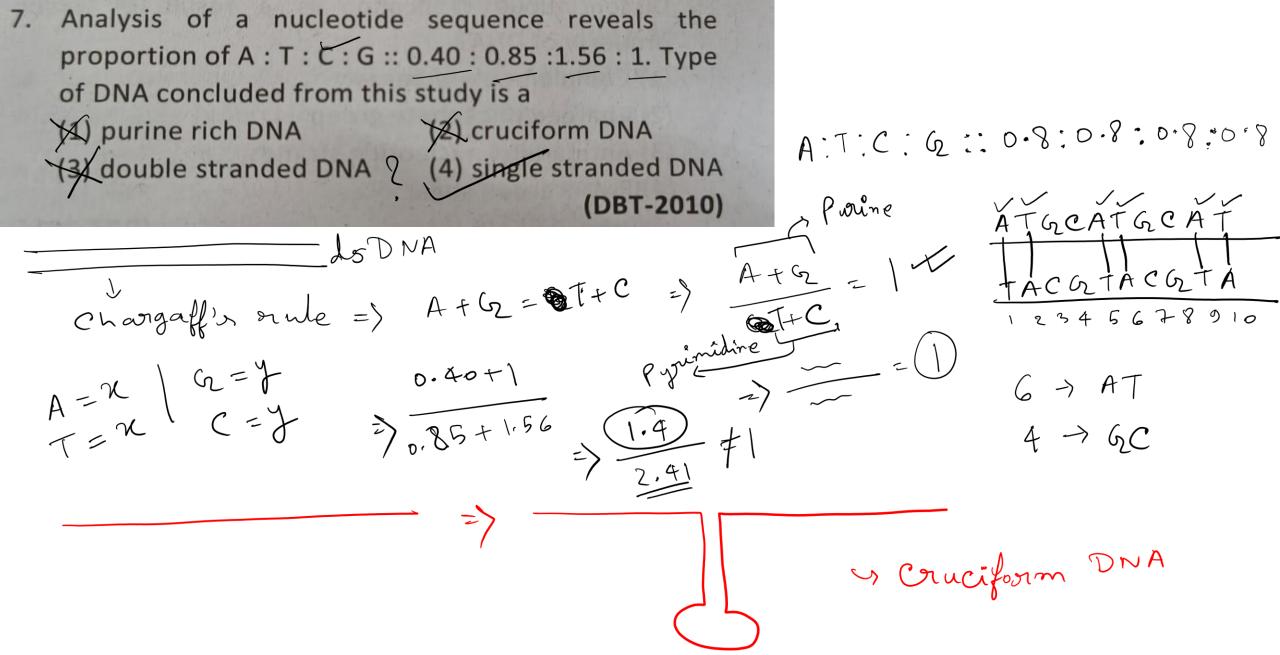
D > Aspartic acid (Asp)

F) Phenyl

R -> Arginine

- 37. The melting temperature (T_m) of DNA is higher when the content of:
 - (1) A:T base pairs is higher.
 - (2) G:C base pairs is higher.
 - (3) A:T base pairs is same as G:C base pairs.
 - (4) G:C base pairs is lower.

(DBT-2022)



18. You have obtained a sample of DNA, and you transcribe mRNA from this DNA and purify it. You then separate the two strands of the DNA and analyze the base composition (%) of each strand and of the mRNA. You obtain the data shown in table below. Which strand of the DNA is the coding strand, serving as a template for mRNA synthesis?

	Α	G	C	T	U
DNA strand 1	39.1	26.0	31.0	14.9	0
DNA strand 2	14.2	30.8	25.7	38.3	0
mRNA	39.0	25.9	30.8	0	14.6

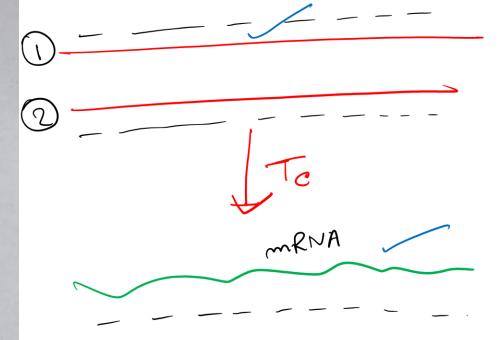
(1) Strand 1

(2) Strand 2

(3) Both strands 1 and 2

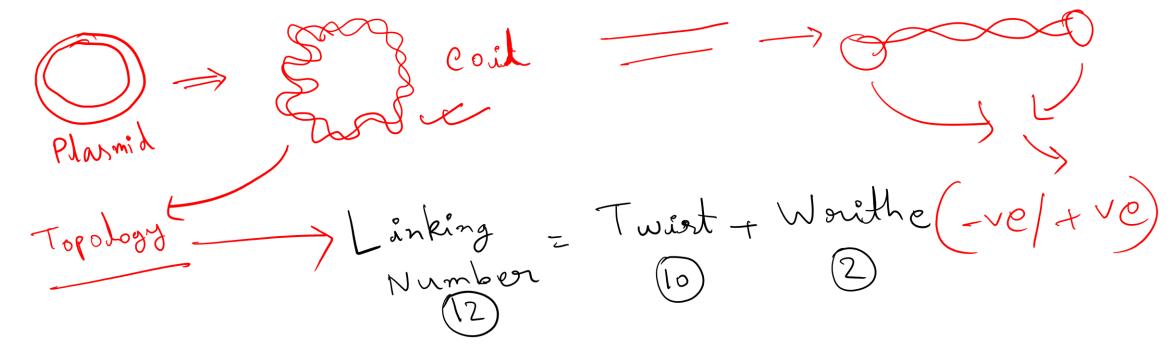
(4) Neither strand 1 nor 2

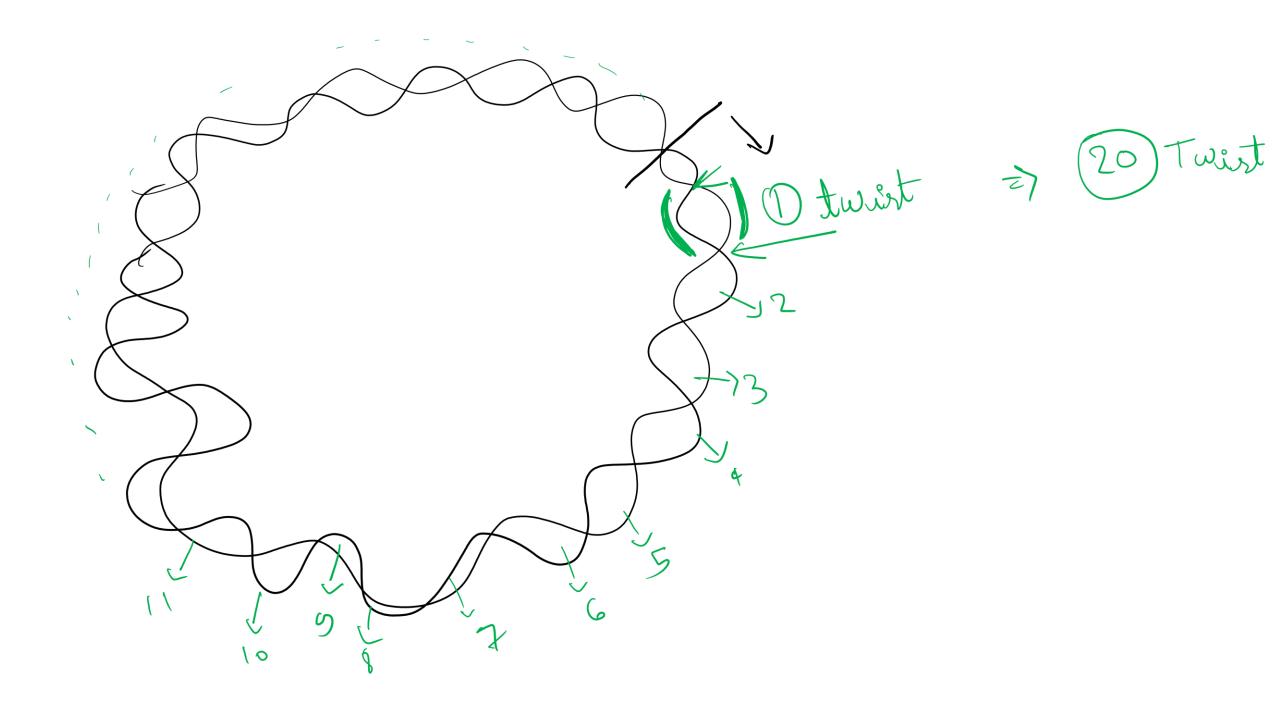
(DBT-2013)

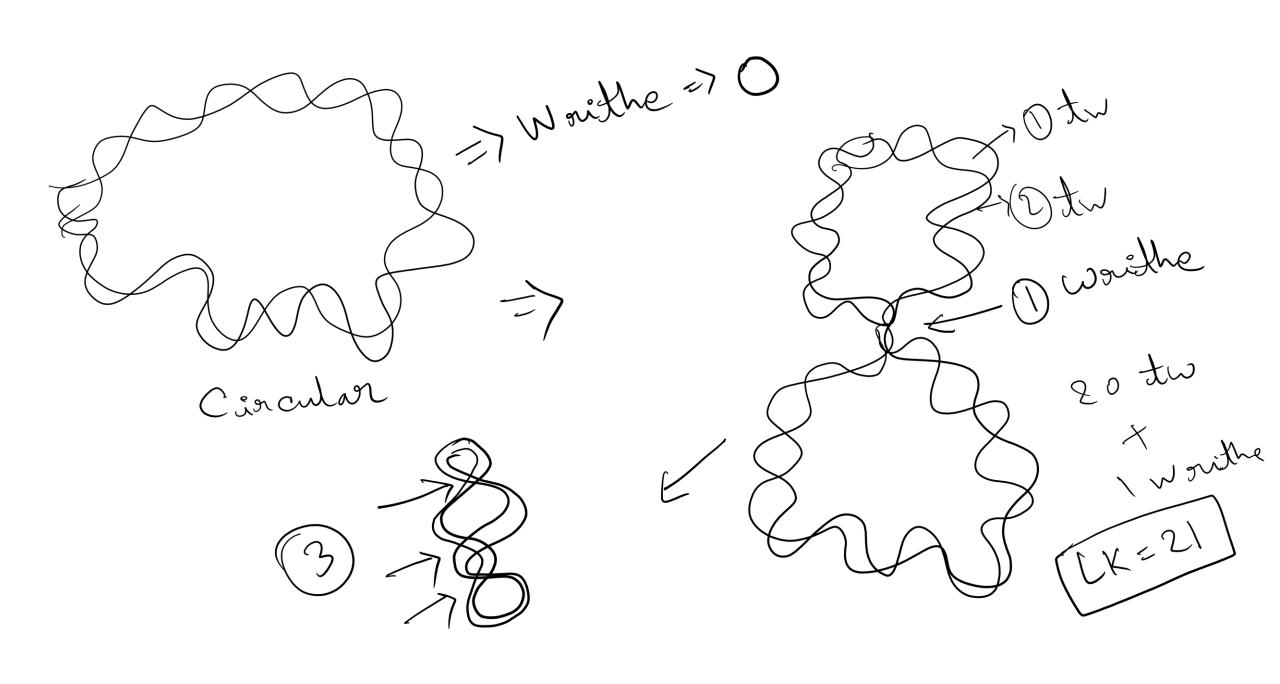


- 14. A 300 bp long B- form of plasmid DNA has 20 complete turns. This DNA molecule is:
 - (1) Positively supercoiled
 - (2) Negatively supercoiled
 - (3) Relaxed
 - (4) Cannot be predicted

(DBT-2014)







- (1) nicked circular plasmid
- (2) positively supercoiled plasmid
- (3) negatively supercoiled plasmid
- (4) relaxed circular plasmid

(DBT-2011)

Twist = total no. of Bare pain

[expected]

nolaxed DNA

Tw = 440

Vn = 440

420 (actual) = 429 bp (Tw)

Cenpected

Lex 400 (confected)

Lex 400 (actual)

Lex 400 (confected)

t on motorola edge 50 ne