L-RNA-	A	J	G	c	v	J	A	6.	C	J
Template DNA strend	A	T	G	C	T	τ	A	G	C,	T
Codine DNA strand	τ	A	C	G	A	A	て	C	6	A

- 2) Amino acid is encoded by a set of consensive bases.

 The three-base sets in RNA are called codons. Also each I amino acid can have more than one corresponding codon but each codon has only I matching amino acid.
- 1- Primary structure is the protein sequence, the topes and order of the amino axids in the protein chain
 - 2-Secondary structure is the list level of protein folding in which parts of the chain fold to fam generic structure that are found in all proteins
 - 3- Tertions structure is formed by the further folding and packing Eosether of these elements to give the final three dimensional conformation unique to protein
 - 4-Quaternors Conformation, the subunit (protein chain) composition and arransement in such multisubunit proteins

	0	C	T	A	G	T	(A	G	A
4) 6	•				0,					L
A										
T	de d		•			•		10		
6	•			9						
G	9			4					•	
7			,	R						
c							,			
A C								1		
٥.			10	de		0.7	-			
A	_1/2			-	-			0		
			_	_	_	-	_	_		_

5) 'A filtering method is used which includes a sliding window. Meshod uses 2 parameters window size and minimum identity score (stringerey) over the window size to consider this window

6)
$$\frac{\mathcal{E}}{\mathcal{E}} = 2^{\frac{1}{2}} \binom{2}{2} \binom{8}{2}$$
 $2^{\frac{1}{2}} \binom{8}{2} = \frac{2^{\frac{1}{2}} \binom{8}{2}}{8} = \frac{2^{\frac{1}{2}} \binom{8}{2}}{8}$
 $1 + \frac{2^{\frac{1}{2}} \binom{8}{2}}{8} = \frac{1256465}{8}$

alternatives

7)		G	A		7	7	A	C
	0	-2	-4	-6	- 2	-(5	-12	-(4
6	- 2	3 4	= 5	(@	-3	-5	-7	-9
T	-4	1	2	0	12	0	- 2	- 4
G	-6	-1	0	1	0	1	-1	-3
A	- 8	-3	2	0	0	-1	4	2
Α	-10	-5	0	l	-1	-1	2	3
L	-12	-7	- 2	3	1	1-1	0	2
					-		-	-

Optimal Global Alignment

G--TGAAC

GACT-TAC