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Kinetic Of Protein Folding In Genetic Regulation on Animal Cell

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Abstract
The mammalian cells is costly than that of bacterial, yeast, plant cells and there commercial use is there limited preparation of natural product of animal cells such as hormones& virus particles for vaccines.
The science biotechnology is develop in present scenario in essential nutrient is varies the age, sex and lifestyle of the self, protein is to provide tissue repair and synthesis for energy and its effect is secondary. The quality of protein depend amino acid make up and enzyme. Amino content depend of complete proteins and incomplete proteins. Controlled a sequence of genes located one after the other on the same chromosome DNA strand and area name of DNA strand is an operon. Genes responsible for forming the respective enzymes are called structure genes.
The figure the segment on the DNA strand are called promoter. This is a group of nucleotides that has specific affinity for RNA polymerase as already discussed. The polymerase must bind with this promoter before it can begin traveling along the DNA strand to synthesize RNA. An additional band of nucleotides lying in middle the promoter. This area is called a repressor operator and the enzymatic reaction of kinetic method of the protein folding is regulatory protein bind to this operator it helps attract RNA polymerase to the promoter.
Key Word:- *lifestyle, amino acid, genes, DNA strand, protein folding.*

I. Introduction

The Protein-folding problem can be treated as a kinetic problem by analyzing the pathways of folding partially folded protein intermediates are inherently unstable. The strategy of trapping these intermediates & analyzing there structures with the aim of understanding the rules of Protein-folding has been followed using biophysical methods, Creighton's work on bovine Pancreatic Trypsin Inhibitor (BPTI) trapping structural intermediates and analyzing S-S bond formation as a way of studying folding pathways is a method that has been other groups to study folding pathways in other disulphide containing proteins.

Folding pathways can also be studied by introducing mutants and analyzing the effects of mutations on the kinetics of folding engineering mutations in BPTI & other protein supports the folding model wherein different regions of the polypeptide acquire tertiary structure in a preferred order. Mutation at different sites in a protein have distinct effects on the kinetics & equilibria of different steps in protein –folding pathways. Local sequence alternations & environment can influence the overall structure of proteins.

Transient state kinetic analysis involves the time course of a reaction to completion for two reasons (i) To determine the rate of the reaction and to use that information to establish mechanism. The term transient state usually refers to the rapid analysis of chemical or enzymatic reactions in the early phase of the reaction preceding the more commonly steady state.

(ii) Most of the kinetic analysis of biological reaction relies on transient state kinetic methods because these methods because these methods pertain to single molecular events.

For example, The binding of a ligand to a cell surface receptor and the binding of a repressor to DNA fall under the binding of transient kinetics, because both involve a single reaction proceeding to completion as opposed to the multiple turnover that characterize the conceptual framework of steady state enzyme kinetic analysis.

II. Material & Method

Protein folding rules are relatively straight forward in the case of fibrous proteins. Many of them are helical and in many cases several monomers entwine to form coil-coil helical cables. In some special cases where only a few amino acid residues form repeating units, the deduction of tertiary structures from their primary structure data become simplified. The collagen molecule is one times repeat sequence in collagen

monomers is $(Gly\text{-}X\text{-}Y)_n$ where X&Y is are generally proline &4-hydroxyproline respectively and glycin in the first position cannot be replaced by any other amino acid residue due to steric restraints. This reduces the folding problems in collagen. Essentially to a 'two amino acid residue' problems. Protein folding rules which are simpler in the case of fibrous protein cannot be a priori, extended to predict secondary structures of globular proteins from their amino acid sequence data because (i) All of the twenty amino acid can be involved in the construction of polypeptide chains (no longer a few –residue problem and no repeating units &(ii)Globular protein are not liner, the direction of backbone folding changes many times and the structure are compact & globular.

III. Results & Discussion

The role of s-s brides is both structural and functional and s-s bridges are common in protein that operate in extracellular bridge are common in proteins that operate in extracellular regions-Toxins, Hormones, Digestive enzymes, Immuno-globulins, Milk proteins, Lysozymes, etc very few intracellular proteins posses disulphide bridges and where they are found ,they have functional roles s-s bridge are found as integral parts of structural motifs in disulphide - containing proteins means lysozymes of hen egg –white contains s-s bonds . In disulphide containing proteins, s-s bridges are found as integral parts of structural motifs creating hydrophobic motifs, and also there exist a structural hierarchy of s-s Bridge in stabilizing structural motifs which could be help in improving protein –folding rules in structural prediction.

ENGINEERING OF THE PROTEIN FOLDING ;- It is a novel and powerful method which holds a great promise for addressing folding mechanisms, altering chemical behavior and improving the physical characteristics of proteins, protein engineering bring about changes in the function of the protein by altering amino acid residue at crucial position site directed mutagenesis techniques have been applied to modified functions of various protein by rational amino acid replacement and to study the effects on structural & enzymatic function of protein & enzymes A single amino acid replacement in a protein at a crucial position can have drastic effects on its function without appreciable changes in its folding site –directed mutagenesis combined with electro physiochemical experiments holds much promise in the detailed analysis of voltage dependent upon studies emphasis the fact that protein folding is remarkably stable to tike ring &the functional properties of protein are sensitive to minute changes within size & environment. A further attraction of viruses contain very strong promoters used to insure of inserted, foreign genes. virus is sv40,contain circular DNA molecule about 5.2 kb in length and which code for viral coat protein.

Table:-The coding of Protein with RNA code words

Amino acid	RNA code words	same
Alanine	CCG	UCG
Arginine	CGC	AGA
Asparagine	ACA	AUA
Aspartic acid	GUA	
Cysteine	UUG	
Glutamic acid	GAA	
Glutamine	ACA	AGA
Glycine	UGG	AGG
Histidine	ACC	
Isoleucine	UAU	UAA
Leucine	UUG	UUC
Lysine	AAA	AAG
methionnine	UGA	
Phenylalanine	UUU	
Proline	CCC	CCU
Serine	UCU	UCC
Theronine	CAC	CAA
Tryptophan	CGU	
Tyrocine	AUU	
Valine	UGU	

* Emmobilized enzyme Reactors *Protein Engineering *Biophasic Mixture *solubilization of Proteins using PEG modification

*chemical modification *Enzymes in Supercritical *Enzymes in Anhydrous organic

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