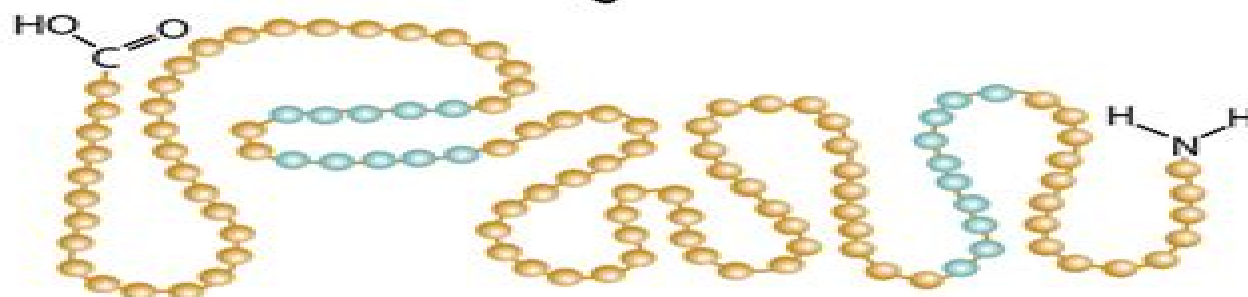
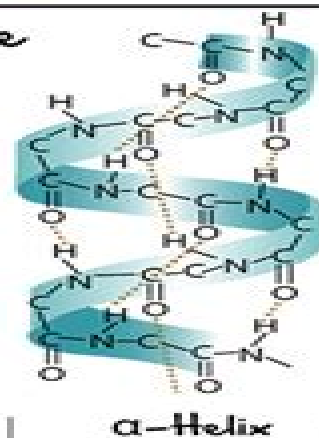
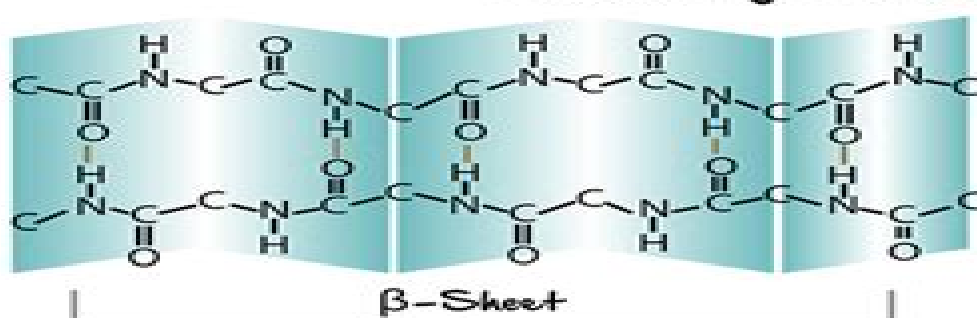


Levels of Protein Structure

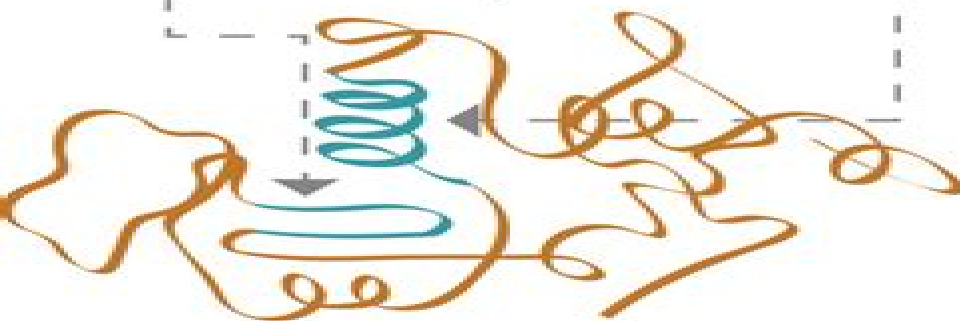
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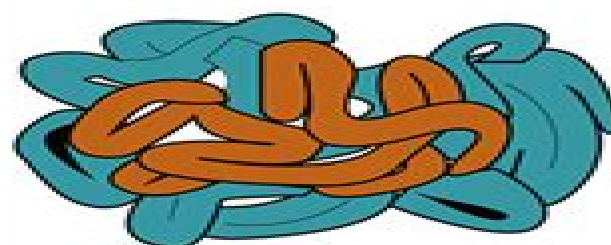
Secondary Structure



Tertiary Structure



Quaternary Structure



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Proteins: Structure, Function, and Engineering B.B. Biswas, Siddhartha Roy, 2013-06-29 Here researchers review the latest breakthroughs in protein research Their contributions explore emerging principles and techniques and survey important classes of proteins that will play key roles in the field's future Articles examine the possibility of a Boltzmann-like distribution in protein substructures the new technique of Raman spectroscopy and compact intermediate states of protein folding This well illustrated volume also features coverage of proteins that bind nucleic acids

On protein structure, function and modularity from an evolutionary perspective Robert Pilstål, 2018-05-23 We are compounded entities given life by a complex molecular machinery When studying these molecules we have to make sense of a diverse set of dynamical nanostructures with vast and intricate patterns of interactions Protein polymers is one of the major groups of building blocks of such nanostructures which fold up into more or less distinct three dimensional structures Due to their shape dynamics and chemical properties proteins are able to perform a plethora of specific functions essential to all known cellular lifeforms The connection between protein sequence translated into protein structure and in the continuation into protein function is well accepted but poorly understood Malfunction in the process of protein folding is known to be implicated in natural aging cancer and degenerative diseases such as Alzheimer's Protein folds are described hierarchically by structural ontologies such as SCOP CATH and Pfam all which has yet to succeed in deciphering the natural language of protein function These paradigmatic views centered on protein structure fail to describe more mutable entities such as intrinsically disordered proteins IDPs which lack a clear defined structure As of 2012 about two thirds of cancer patients was predicted to survive past 5 years of diagnosis Despite this about a third do not survive and numerous of successfully treated patients suffer from secondary conditions due to chemotherapy surgery and the like In order to handle cancer more efficiently we have to better understand the underlying molecular mechanisms Elusive to standard methods of investigation IDPs have a central role in pathology dysfunction in IDPs are key factors in cellular system failures such as cancer as many IDPs are hub regulators for major cell functions These IDPs carry short conserved functional boxes that are not described by known ontologies which suggests the existence of a smaller entity In an investigation of a pair of such boxes of c-MYC a plausible structural model of its interacting with Pin1 emerged but such a model still leaves the observer with a puzzle of understanding the actual function of that interaction If the protein is represented as a graph and modeled as the interaction patterns instead of as a structural entity another picture emerges As a graph there is a parable from that of the boxes of IDPs to that of sectors of allosterically connected residues and the theory of foldons and folding units Such a description is also useful in deciphering the implications of specific mutations In order to render a functional description feasible for both structured and disordered proteins there is a need of a model separate from form and structure Realized as protein primes patterns of interaction which has a specific function that can be defined as prime interactions and context With function defined as interactions it might be

possible that the discussion of proteins and their mechanisms is thereby simplified to the point rendering protein structural determination merely supplementary to understanding protein function. Man kan byggs upp av celler de i sin tur består av mindre beständsdelar livets molekyler. Dessa fungerar som mekaniska byggstenar likt maskiner och robotar som sliter vid fabriken band envar utförandes en absolut nödvändig funktion för cellens och hela kroppens fortsatta överlevnad. De av livets molekyler som beskrivs centralt i den här avhandlingen är proteiner vilka i sin tur består utav en lång kedja med olika typer av länkar som likt garn lindar upp sig i ett nystan av en mer eller mindre bestämd struktur som avgör dess roll och funktion i cellen. Intrinsiskt ordnade proteiner (IDP) gör emot denna enkla skildring de är proteiner som saknar struktur och beter sig mer likt spaghetti i vatten än maskin. IDP har funktionella och bör spela centrala roller i cellens maskineri. Exempel är oncoproteinet c-Myc som agerar gaspedal för cellen. Fel i c-Mycs funktion leder till att cellerna låper amok, delar sig hejdlöst och vi får cancer. Man har upptäckt att c-Myc har en ombytlig struktur vi inte kan se. Studier av punktvisa förändringar (mutationer) i kedjan av byggstenar hos c-Myc visar att många länkar har viktiga roller i funktionen. Detta ger oss bättre förståelse om cancer men samtidigt är laboratoriearbetet både komplicerat och dyrt. Här kan evolutionen hjälpa oss och avslöja hemligheterna snabbare. Molekylär evolution studeras genom att beräkna variation i proteinkedjan mellan beslötade arter som finns lagrade i databaser. Detta visar snabbt via en tverksanalys och grafteori vilka delar av proteinet som är centrala och kopplade till varandra av nödvändighet för artens överlevnad. Påvisar evolutionen oss att förstå proteinfunktioner via modeller baserade på proteinernas interaktioner snarare än deras struktur. Samma modeller kan nyttjas för att förstå dynamiska förlopp och skillnader mellan normala och patologiska varianter av proteiner. Mutationer kan uppstå i vår arvs massa som kan leda till sjukdom. Genom analys av proteinernas kopplingsnätverk i grafmodellerna kan man bättre förstå vilka mutationer som är farligare än andra. Dessutom har det visat sig att en sådan representation kan ge bättre förståelse för den normala funktionen hos ett protein än vad en proteinstruktur kan. Här introduceras även konceptet proteinprimär vilket är en abstrakt representation av proteiner centrerad på deras interaktiva mönster snarare än på partikulär form och struktur. Det är en förhoppning att en sådan representation skall förklara diskussionen anbelangande proteinfunktioner till den grad att strukturbestämning av proteiner som är en mycket kostsam och tidskrävande process till viss mån kan anses vara sekundär i betydelse jämfört med funktionellt modellerande baserat på evolutionära data extraherade ur våra sekvensdatabaser.

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Lipids in Photosynthesis: Structure, Function and Genetics Paul-André Siegenthaler,N. Murata,2006-04-11 Lipids in Photosynthesis provides readers with a comprehensive view of the structure function and genetics of lipids in plants algae and bacteria with special emphasis on the photosynthetic apparatus in thylakoid membranes This volume includes the historical background of the field as well as a full review of our current understanding of the structure and molecular organization of lipids and their role in the functions of photosynthetic membranes The physical properties of membrane lipids in thylakoid membranes and their relationship to photosynthesis are also discussed Other topics include the biosynthesis of glycerolipids and triglycerides reconstitution of photosynthetic structures and activities with lipids lipid protein interactions in the import of proteins into chloroplasts the development of thylakoid membranes as it relates to lipids genetic engineering of the unsaturation of membrane glycerolipids with a focus on the ability of the photosynthetic machinery to tolerate temperature stress and the involvement of chloroplast lipids in the reactions of plants upon exposure to stress This book is intended for a wide audience and should be of interest to advanced undergraduate and graduate students and to researchers active in the field as well as to those scientists whose fields of specialization include the biochemistry physiology molecular biology biophysics and biotechnology of membranes Introduction to a Biological Systems Science Edward H.

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