Trans Proline Affect Secondary Structure

Proline

ending in proline; with the creation of proline-proline bonds slowest of all. The exceptional conformational rigidity of proline affects the secondary structure

Proline (symbol Pro or P) is an organic acid classed as a proteinogenic amino acid (used in the biosynthesis of proteins), although it does not contain the amino group -NH2 but is rather a secondary amine. The secondary amine nitrogen is in the protonated form (NH2+) under biological conditions, while the carboxyl group is in the deprotonated ?COO? form. The "side chain" from the ? carbon connects to the nitrogen forming a pyrrolidine loop, classifying it as a aliphatic amino acid. It is non-essential in humans, meaning the body can synthesize it from the non-essential amino acid L-glutamate. It is encoded by all the codons starting with CC (CCU, CCC, CCA, and CCG).

Proline is the only proteinogenic amino acid which is a secondary amine, as the nitrogen atom is attached both to the ?-carbon and to a chain of three carbons that together form a five-membered ring.

Protein primary structure

acids, which cannot be cleaved by most proteases. Additionally, proline can form stable trans-isomers at the peptide bond. Additionally, the protein can undergo

Protein primary structure is the linear sequence of amino acids in a peptide or protein. By convention, the primary structure of a protein is reported starting from the amino-terminal (N) end to the carboxyl-terminal (C) end. Protein biosynthesis is most commonly performed by ribosomes in cells. Peptides can also be synthesized in the laboratory. Protein primary structures can be directly sequenced, or inferred from DNA sequences.

Structure and genome of HIV

(14–15 kDa) binds to the bulged genomic RNA stem-loop secondary structure near the 5' LTR region forming the trans-activation response element (TAR). rev (regulator

The genome and proteins of HIV (human immunodeficiency virus) have been the subject of extensive research since the discovery of the virus in 1983. "In the search for the causative agent, it was initially believed that the virus was a form of the Human T-cell leukemia virus (HTLV), which was known at the time to affect the human immune system and cause certain leukemias. However, researchers at the Pasteur Institute in Paris isolated a previously unknown and genetically distinct retrovirus in patients with AIDS which was later named HIV." Each virion comprises a viral envelope and associated matrix enclosing a capsid, which itself encloses two copies of the single-stranded RNA genome and several enzymes. The discovery of the virus itself occurred two years following the report of the first major cases of AIDS-associated illnesses.

Biomolecule

and carboxylate functionalities are attached to the same carbon, plus proline which is not actually an amino acid). Modified amino acids are sometimes

A biomolecule or biological molecule is loosely defined as a molecule produced by a living organism and essential to one or more typically biological processes. Biomolecules include large macromolecules such as proteins, carbohydrates, lipids, and nucleic acids, as well as small molecules such as vitamins and hormones.

A general name for this class of material is biological materials. Biomolecules are an important element of living organisms. They are often endogenous, i.e. produced within the organism, but organisms usually also need exogenous biomolecules, for example certain nutrients, to survive.

Biomolecules and their reactions are studied in biology and its subfields of biochemistry and molecular biology. Most biomolecules are organic compounds, and just four elements—oxygen, carbon, hydrogen, and nitrogen—make up 96% of the human body's mass. But many other elements, such as the various biometals, are also present in small amounts.

The uniformity of both specific types of molecules (the biomolecules) and of certain metabolic pathways are invariant features among the wide diversity of life forms; thus these biomolecules and metabolic pathways are referred to as "biochemical universals" or "theory of material unity of the living beings", a unifying concept in biology, along with cell theory and evolution theory.

Protein folding

of the protein. Secondary structure hierarchically gives way to tertiary structure formation. Once the protein's tertiary structure is formed and stabilized

Protein folding is the physical process by which a protein, after synthesis by a ribosome as a linear chain of amino acids, changes from an unstable random coil into a more ordered three-dimensional structure. This structure permits the protein to become biologically functional or active.

The folding of many proteins begins even during the translation of the polypeptide chain. The amino acids interact with each other to produce a well-defined three-dimensional structure, known as the protein's native state. This structure is determined by the amino-acid sequence or primary structure.

The correct three-dimensional structure is essential to function, although some parts of functional proteins may remain unfolded, indicating that protein dynamics are important. Failure to fold into a native structure generally produces inactive proteins, but in some instances, misfolded proteins have modified or toxic functionality. Several neurodegenerative and other diseases are believed to result from the accumulation of amyloid fibrils formed by misfolded proteins, the infectious varieties of which are known as prions. Many allergies are caused by the incorrect folding of some proteins because the immune system does not produce the antibodies for certain protein structures.

Denaturation of proteins is a process of transition from a folded to an unfolded state. It happens in cooking, burns, proteinopathies, and other contexts. Residual structure present, if any, in the supposedly unfolded state may form a folding initiation site and guide the subsequent folding reactions.

The duration of the folding process varies dramatically depending on the protein of interest. When studied outside the cell, the slowest folding proteins require many minutes or hours to fold, primarily due to proline isomerization, and must pass through a number of intermediate states, like checkpoints, before the process is complete. On the other hand, very small single-domain proteins with lengths of up to a hundred amino acids typically fold in a single step. Time scales of milliseconds are the norm, and the fastest known protein folding reactions are complete within a few microseconds. The folding time scale of a protein depends on its size, contact order, and circuit topology.

Understanding and simulating the protein folding process has been an important challenge for computational biology since the late 1960s.

Ketimine Mannich reaction

creation of a ketimine group. Typically, this is done with a reaction with proline or another nitrogen-containing heterocycle, which control chirality with

The ketimine Mannich reaction is an asymmetric synthetic technique using differences in starting material to push a Mannich reaction to create an enantiomeric product with steric and electronic effects, through the creation of a ketimine group. Typically, this is done with a reaction with proline or another nitrogen-containing heterocycle, which control chirality with that of the catalyst. This has been theorized to be caused by the restriction of undesired (E)-isomer by preventing the ketone from accessing non-reactive tautomers. Generally, a Mannich reaction is the combination of an amine, a ketone with a ?-acidic proton and aldehyde to create a condensed product in a ?-addition to the ketone. This occurs through an attack on the ketone with a suitable catalytic-amine unto its electron-starved carbon, from which an imine is created. This then undergoes electrophilic addition with a compound containing an acidic proton (which is an enol). It is theoretically possible for either of the carbonyl-containing molecules to create diastereomers, but with the addition of catalysts which restrict addition as of the enamine creation, it is possible to extract a single product with limited purification steps and in some cases as reported by List et al.; practical one-pot syntheses are possible. The process of selecting a carbonyl-group gives the reaction a direct versus indirect distinction, wherein the latter case represents pre-formed products restricting the reaction's pathway and the other does not. Ketimines selects a reaction group, and circumvent a requirement for indirect pathways.

Protein moonlighting

1K87?; Lee YH, Nadaraia S, Gu D, Becker DF, Tanner JJ (Feb 2003). "Structure of the proline dehydrogenase domain of the multifunctional PutA flavoprotein"

Protein moonlighting is a phenomenon by which a protein can perform more than one function. It is an excellent example of gene sharing.

Ancestral moonlighting proteins originally possessed a single function but, through evolution, acquired additional functions. Many proteins that moonlight are enzymes; others are receptors, ion channels or chaperones. The most common primary function of moonlighting proteins is enzymatic catalysis, but these enzymes have acquired secondary non-enzymatic roles. Some examples of functions of moonlighting proteins secondary to catalysis include signal transduction, transcriptional regulation, apoptosis, motility, and structural.

Protein moonlighting occurs widely in nature. Protein moonlighting through gene sharing differs from the use of a single gene to generate different proteins by alternative RNA splicing, DNA rearrangement, or post-translational processing. It is also different from the multifunctionality of the protein, in which the protein has multiple domains, each serving a different function. Protein moonlighting by gene sharing means that a gene may acquire and maintain a second function without gene duplication and without loss of the primary function. Such genes are under two or more entirely different selective constraints.

Various techniques have been used to reveal moonlighting functions in proteins. The detection of a protein in unexpected locations within cells, cell types, or tissues may suggest that a protein has a moonlighting function. Furthermore, the sequence or structure homology of a protein may be used to infer both primary functions as well as secondary moonlighting functions of a protein.

The most well-studied examples of gene sharing are crystallins. These proteins, when expressed at low levels in many tissues function as enzymes, but when expressed at high levels in eye tissue, become densely packed and thus form lenses. While the recognition of gene sharing is relatively recent—the term was coined in 1988, after crystallins in chickens and ducks were found to be identical to separately identified enzymes—recent studies have found many examples throughout the living world. Joram Piatigorsky has suggested that many or all proteins exhibit gene sharing to some extent, and that gene sharing is a key aspect of molecular evolution. The genes encoding crystallins must maintain sequences for catalytic function and transparency maintenance function.

Inappropriate moonlighting is a contributing factor in some genetic diseases, and moonlighting provides a possible mechanism by which bacteria may become resistant to antibiotics.

Steroid

terminal "e" in the parent structure name should be elided before the vowel (the presence or absence of a number does not affect such elision). This means

A steroid is an organic compound with four fused rings (designated A, B, C, and D) arranged in a specific molecular configuration.

Steroids have two principal biological functions: as important components of cell membranes that alter membrane fluidity; and as signaling molecules. Examples include the lipid cholesterol, sex hormones estradiol and testosterone, anabolic steroids, and the anti-inflammatory corticosteroid drug dexamethasone. Hundreds of steroids are found in fungi, plants, and animals. All steroids are manufactured in cells from a sterol: cholesterol (animals), lanosterol (opisthokonts), or cycloartenol (plants). All three of these molecules are produced via cyclization of the triterpene squalene.

HIV

the introduction of an intersubunit disulphide bond and an isoleucine to proline mutation (radical replacement of an amino acid) in gp41. The so-called

The human immunodeficiency viruses (HIV) are two species of Lentivirus (a subgroup of retrovirus) that infect humans. Over time, they cause acquired immunodeficiency syndrome (AIDS), a condition in which progressive failure of the immune system allows life-threatening opportunistic infections and cancers to thrive. Without treatment, the average survival time after infection with HIV is estimated to be 9 to 11 years, depending on the HIV subtype.

In most cases, HIV is a sexually transmitted infection and occurs by contact with or transfer of blood, pre-ejaculate, semen, and vaginal fluids. Non-sexual transmission can occur from an infected mother to her infant during pregnancy, during childbirth by exposure to her blood or vaginal fluid, and through breast milk. Within these bodily fluids, HIV is present as both free virus particles and virus within infected immune cells.

Research has shown (for both same-sex and opposite-sex couples) that HIV is not contagious during sexual intercourse without a condom if the HIV-positive partner has a consistently undetectable viral load.

HIV infects vital cells in the human immune system, such as helper T cells (specifically CD4+ T cells), macrophages, and dendritic cells. HIV infection leads to low levels of CD4+ T cells through a number of mechanisms, including pyroptosis of abortively infected T cells, apoptosis of uninfected bystander cells, direct viral killing of infected cells, and killing of infected CD4+ T cells by CD8+ cytotoxic lymphocytes that recognize infected cells. When CD4+ T cell numbers decline below a critical level, cell-mediated immunity is lost, and the body becomes progressively more susceptible to opportunistic infections, leading to the development of AIDS.

Mutation

produced is. (For example, the code CCU GAC UAC CUA codes for the amino acids proline, aspartic acid, tyrosine, and leucine. If the U in CCU was deleted, the

In biology, a mutation is an alteration in the nucleic acid sequence of the genome of an organism, virus, or extrachromosomal DNA. Viral genomes contain either DNA or RNA. Mutations result from errors during DNA or viral replication, mitosis, or meiosis or other types of damage to DNA (such as pyrimidine dimers caused by exposure to ultraviolet radiation), which then may undergo error-prone repair (especially

microhomology-mediated end joining), cause an error during other forms of repair, or cause an error during replication (translesion synthesis). Mutations may also result from substitution, insertion or deletion of segments of DNA due to mobile genetic elements.

Mutations may or may not produce detectable changes in the observable characteristics (phenotype) of an organism. Mutations play a part in both normal and abnormal biological processes including: evolution, cancer, and the development of the immune system, including junctional diversity. Mutation is the ultimate source of all genetic variation, providing the raw material on which evolutionary forces such as natural selection can act.

Mutation can result in many different types of change in sequences. Mutations in genes can have no effect, alter the product of a gene, or prevent the gene from functioning properly or completely. Mutations can also occur in non-genic regions. A 2007 study on genetic variations between different species of Drosophila suggested that, if a mutation changes a protein produced by a gene, the result is likely to be harmful, with an estimated 70% of amino acid polymorphisms that have damaging effects, and the remainder being either neutral or marginally beneficial.

Mutation and DNA damage are the two major types of errors that occur in DNA, but they are fundamentally different. DNA damage is a physical alteration in the DNA structure, such as a single or double strand break, a modified guanosine residue in DNA such as 8-hydroxydeoxyguanosine, or a polycyclic aromatic hydrocarbon adduct. DNA damages can be recognized by enzymes, and therefore can be correctly repaired using the complementary undamaged strand in DNA as a template or an undamaged sequence in a homologous chromosome if it is available. If DNA damage remains in a cell, transcription of a gene may be prevented and thus translation into a protein may also be blocked. DNA replication may also be blocked and/or the cell may die. In contrast to a DNA damage, a mutation is an alteration of the base sequence of the DNA. Ordinarily, a mutation cannot be recognized by enzymes once the base change is present in both DNA strands, and thus a mutation is not ordinarily repaired. At the cellular level, mutations can alter protein function and regulation. Unlike DNA damages, mutations are replicated when the cell replicates. At the level of cell populations, cells with mutations will increase or decrease in frequency according to the effects of the mutations on the ability of the cell to survive and reproduce. Although distinctly different from each other, DNA damages and mutations are related because DNA damages often cause errors of DNA synthesis during replication or repair and these errors are a major source of mutation.