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...

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...

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...

Phlotoxin 1

Notably, the inclusion of three proline residues (Pro11, Pro18, and Pro27) introduces the potential for Cis–trans isomerism. This dynamic property can

Phlotoxin (PhlTx1, ?-TRTX-Pspp-1) is a neurotoxin from the venom of the tarantula Phlogiellus that targets mostly voltage-sensitive sodium channels and mainly Nav1.7. The only non-sodium voltage-sensitive channel that is inhibited by Phlotoxin is Kv3.4. Nav1.4 and Nav1.6 seem to be Phlotoxin-1-sensitive to some extent as well.

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,...

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...

Emily Balskus

prominent glycyl radical enzyme in human gut microbiomes metabolizes trans-4-hydroxy-L-proline outlines an important research approach utilized by Balskus and

Emily P. Balskus is an American chemical biologist, enzymologist, microbiologist, and biochemist born in Cincinnati, Ohio in 1980. She has been on the faculty of the Chemistry and Chemical Biology department of Harvard University since 2011 and is currently the Morris Kahn Professor. She has published more than 80 peer-reviewed papers and three book chapters. Since 2012 she has been invited to give over 170 lectures, has held positions on various editorial boards, and served as a reviewer for ACS and Nature journals among others. Balskus also currently serves as a consultant for Novartis, Kintai Therapeutics, and Merck & Co.

Protein folding

folding proteins require many minutes or hours to fold, primarily due to proline isomerization, and must pass through a number of intermediate states, like

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...

Missense mutation

in a region of the protein which does not significantly affect the protein secondary structure or function. Lastly, when more than one codon codes for

In genetics, a missense mutation is a point mutation in which a single nucleotide change results in a codon that codes for a different amino acid. It is a type of nonsynonymous substitution. Missense mutations change amino acids, which in turn alter proteins and may alter a protein's function or structure. These mutations may arise spontaneously from mutagens like UV radiation, tobacco smoke, an error in DNA replication, and other factors. Screening for missense mutations can be done by sequencing the genome of an organism and comparing the sequence to a reference genome to analyze for differences. Missense mutations can be repaired by the cell when there are errors in DNA replication by using mechanisms such as DNA proofreading and mismatch repair. They can also be repaired by using genetic...