Pyrimidine Ratio

Uracil

demethylated form of thymine. Uracil is a common and naturally occurring pyrimidine derivative. The name "uracil" was coined in 1885 by the German chemist - Uracil () (symbol U or Ura) is one of the four nucleotide bases in the nucleic acid RNA. The others are adenine (A), cytosine (C), and guanine (G). In RNA, uracil binds to adenine via two hydrogen bonds. In DNA, the uracil nucleobase is replaced by thymine (T). Uracil is a demethylated form of thymine.

Uracil is a common and naturally occurring pyrimidine derivative. The name "uracil" was coined in 1885 by the German chemist Robert Behrend, who was attempting to synthesize derivatives of uric acid. Originally discovered in 1900 by Alberto Ascoli, it was isolated by hydrolysis of yeast nuclein; it was also found in bovine thymus and spleen, herring sperm, and wheat germ. It is a planar, unsaturated compound that has the ability to absorb light.

Uracil that was formed extraterrestrially has been detected in the Murchison meteorite, in near-Earth asteroid Ryugu, and possibly on the surface of the moon Titan. It has been synthesized under cold laboratory conditions similar to outer space, from pyrimidine embedded in water ice and exposed to ultraviolet light.

Chargaff's rules

equal to the amount of thymine. Further, a 1:1 stoichiometric ratio of purine and pyrimidine bases (i.e., A+G=T+C) should exist. This pattern is found in - Chargaff's rules (given by Erwin Chargaff) state that in the DNA of any species and any organism, the amount of guanine should be equal to the amount of cytosine and the amount of adenine should be equal to the amount of thymine. Further, a 1:1 stoichiometric ratio of purine and pyrimidine bases (i.e., A+G=T+C) should exist. This pattern is found in both strands of the DNA. They were discovered by Austrian-born chemist Erwin Chargaff in the late 1940s.

Nucleic acid metabolism

to one of two categories: purines or pyrimidines. In complex multicellular animals, both purines and pyrimidines are primarily synthesized in the liver - Nucleic acid metabolism refers to the set of chemical reactions involved in the synthesis and degradation of nucleic acids (DNA and RNA). Nucleic acids are polymers (biopolymers) composed of monomers called nucleotides.

Nucleotide synthesis is an anabolic process that typically involves the chemical reaction of a phosphate group, a pentose sugar, and a nitrogenous base. In contrast, the degradation of nucleic acids is a catabolic process in which nucleotides or nucleobases are broken down, and their components can be salvaged to form new nucleotides.

Both synthesis and degradation reactions require multiple enzymes to facilitate these processes. Defects or deficiencies in these enzymes can lead to a variety of metabolic disorders.

Orotate phosphoribosyltransferase

(OPRTase) or orotic acid phosphoribosyltransferase is an enzyme involved in pyrimidine biosynthesis. It catalyzes the formation of orotidine 5'-monophosphate - Orotate phosphoribosyltransferase

(OPRTase) or orotic acid phosphoribosyltransferase is an enzyme involved in pyrimidine biosynthesis. It catalyzes the formation of orotidine 5'-monophosphate (OMP) from orotate and phosphoribosyl pyrophosphate. In yeast and bacteria, orotate phosphoribosyltransferase is an independent enzyme with a unique gene coding for the protein, whereas in mammals and other multicellular organisms, the catalytic function is carried out by a domain of the bifunctional enzyme UMP synthase (UMPS).

Satellite DNA

one or two base pairs with A (purine) interrupting the pyrimidine-rich strand and T (pyrimidine) interrupting the purine-rich strand. These interruptions - Satellite DNA consists of very large arrays of tandemly repeating, non-coding DNA. Satellite DNA is the main component of functional centromeres, and form the main structural constituent of heterochromatin.

The name "satellite DNA" refers to the phenomenon that repetitions of a short DNA sequence tend to produce a different frequency of the bases adenine, cytosine, guanine, and thymine, and thus have a different density from bulk DNA such that they form a second or "satellite" band(s) when genomic DNA is separated along a cesium chloride density gradient using buoyant density centrifugation.

Sequences with a greater ratio of A+T display a lower density while those with a greater ratio of G+C display a higher density than the bulk of genomic DNA. Some repetitive sequences are ~50% G+C/A+T and thus have buoyant densities the same as bulk genomic DNA. These satellites are called "cryptic" satellites because they form a band hidden within the main band of genomic DNA. "Isopycnic" is another term used for cryptic satellites.

Transversion

which a single (two ring) purine (A or G) is changed for a (one ring) pyrimidine (T or C), or vice versa. A transversion can be spontaneous, or it can - Transversion, in molecular biology, refers to a point mutation in DNA in which a single (two ring) purine (A or G) is changed for a (one ring) pyrimidine (T or C), or vice versa. A transversion can be spontaneous, or it can be caused by ionizing radiation or alkylating agents. It can only be reversed by a spontaneous reversion.

Base pair

single-ringed chemical structures called pyrimidines. Purines are complementary only with pyrimidines: pyrimidine–pyrimidine pairings are energetically unfavorable - A base pair (bp) is a fundamental unit of double-stranded nucleic acids consisting of two nucleobases bound to each other by hydrogen bonds. They form the building blocks of the DNA double helix and contribute to the folded structure of both DNA and RNA. Dictated by specific hydrogen bonding patterns, "Watson–Crick" (or "Watson–Crick–Franklin") base pairs (guanine–cytosine and adenine–thymine/uracil) allow the DNA helix to maintain a regular helical structure that is subtly dependent on its nucleotide sequence. The complementary nature of this based-paired structure provides a redundant copy of the genetic information encoded within each strand of DNA. The regular structure and data redundancy provided by the DNA double helix make DNA well suited to the storage of genetic information, while base-pairing between DNA and incoming nucleotides provides the mechanism through which DNA polymerase replicates DNA and RNA polymerase transcribes DNA into RNA. Many DNA-binding proteins can recognize specific base-pairing patterns that identify particular regulatory regions of genes.

Intramolecular base pairs can occur within single-stranded nucleic acids. This is particularly important in RNA molecules (e.g., transfer RNA), where Watson–Crick base pairs (guanine–cytosine and adenine-uracil) permit the formation of short double-stranded helices, and a wide variety of non–Watson–Crick interactions (e.g., G–U or A–A) allow RNAs to fold into a vast range of specific three-dimensional structures. In addition,

base-pairing between transfer RNA (tRNA) and messenger RNA (mRNA) forms the basis for the molecular recognition events that result in the nucleotide sequence of mRNA becoming translated into the amino acid sequence of proteins via the genetic code.

The size of an individual gene or an organism's entire genome is often measured in base pairs because DNA is usually double-stranded. Hence, the number of total base pairs is equal to the number of nucleotides in one of the strands (with the exception of non-coding single-stranded regions of telomeres). The haploid human genome (23 chromosomes) is estimated to be about 3.2 billion base pairs long and to contain 20,000–25,000 distinct protein-coding genes. A kilobase (kb) is a unit of measurement in molecular biology equal to 1000 base pairs of DNA or RNA. The total number of DNA base pairs on Earth is estimated at 5.0×1037 with a weight of 50 billion tonnes. In comparison, the total mass of the biosphere has been estimated to be as much as 4 TtC (trillion tons of carbon).

Hoogsteen base pair

a pyrimidine base (C/T) uses its Watson–Crick (anti, N3–C4) face to bind the syn (N6–N7) face of a purine (A/G). Adenine, which is not a pyrimidine, is - A Hoogsteen base pair is a variation of base-pairing in nucleic acids such as the A•T pair. In this manner, two nucleobases, one on each strand, can be held together by hydrogen bonds in the major groove. Specifically, it happens when a pyrimidine base (C/T) uses its Watson–Crick (anti, N3–C4) face to bind the syn (N6–N7) face of a purine (A/G).

Adenine, which is not a pyrimidine, is capable of using its anti (N1–N6) face to pair with the syn face of a purine to form a Hoogsteen-like base pair. Guanine can form a similar interaction with another purine base, forming a rigid cycle called a guanine tetrad in the case of four guanines. These are also "Hoogsteen base pairs" under the expanded understanding as anti-syn interaction.

A reverse Hoogsteen base pair is when a pyrimidine's syn (N3–C2) face binds a purine's syn face. Under a systemic view of non-canonical base pairing, Hoogsteen base pairs (in the expanded sense) are called Watson-Crick/Hoogsteen, based on what faces are interacting (the syn face is called the Hoogsteen face). The reverse Hoogsteen base pair is called "Hoogsteen/Hoogsteen".

Uridine monophosphate synthase

PMID 8650301. {{cite book}}: |journal= ignored (help) Jones ME (1980). "Pyrimidine nucleotide biosynthesis in animals: genes, enzymes, and regulation of - The enzyme Uridine monophosphate synthase (EC 4.1.1.23, UMPS) (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) catalyses the formation of uridine monophosphate (UMP), an energy-carrying molecule in many important biosynthetic pathways. In humans, the gene that codes for this enzyme is located on the long arm of chromosome 3 (3q13).

Nicotinamide adenine dinucleotide

Reiss PD, Zuurendonk PF, Veech RL (1984). "Measurement of tissue purine, pyrimidine, and other nucleotides by radial compression high-performance liquid chromatography" - Nicotinamide adenine dinucleotide (NAD) is a coenzyme central to metabolism. Found in all living cells, NAD is called a dinucleotide because it consists of two nucleotides joined through their phosphate groups. One nucleotide contains an adenine nucleobase and the other, nicotinamide. NAD exists in two forms: an oxidized and reduced form, abbreviated as NAD+ and NADH (H for hydrogen), respectively.

In cellular metabolism, NAD is involved in redox reactions, carrying electrons from one reaction to another, so it is found in two forms: NAD+ is an oxidizing agent, accepting electrons from other molecules and becoming reduced; with H+, this reaction forms NADH, which can be used as a reducing agent to donate electrons. These electron transfer reactions are the main function of NAD. It is also used in other cellular processes, most notably as a substrate of enzymes in adding or removing chemical groups to or from proteins, in posttranslational modifications. Because of the importance of these functions, the enzymes involved in NAD metabolism are targets for drug discovery.

In organisms, NAD can be synthesized from simple building-blocks (de novo) from either tryptophan or aspartic acid, each a case of an amino acid. Alternatively, more complex components of the coenzymes are taken up from nutritive compounds such as nicotinic acid; similar compounds are produced by reactions that break down the structure of NAD, providing a salvage pathway that recycles them back into their respective active form.

In the name NAD+, the superscripted plus sign indicates the positive formal charge on one of its nitrogen atoms.

A biological coenzyme that acts as an electron carrier in enzymatic reactions.

Some NAD is converted into the coenzyme nicotinamide adenine dinucleotide phosphate (NADP), whose chemistry largely parallels that of NAD, though its predominant role is as a coenzyme in anabolic metabolism.

NADP is a reducing agent in anabolic reactions like the Calvin cycle and lipid and nucleic acid syntheses. NADP exists in two forms: NADP+, the oxidized form, and NADPH, the reduced form. NADP is similar to nicotinamide adenine dinucleotide (NAD), but NADP has a phosphate group at the C-2? position of the adenosyl.