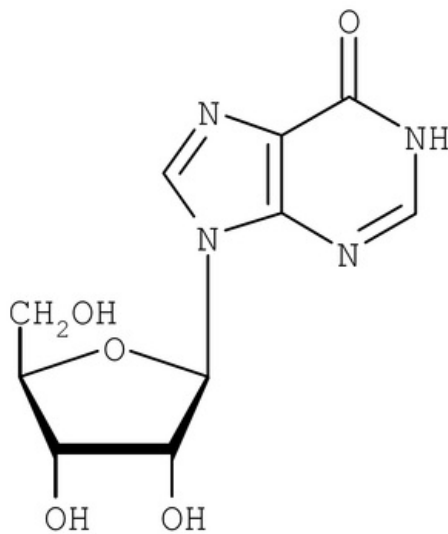


# tRNA

All **transfer RNAs** (tRNAs) share numerous **common structural features**. In general, RNAs consist of one nucleotide chain with a length of **around 80 nucleotides**. The 5'-end is usually phosphorylated while the 3'-end regularly has the sequence **-CCA**. There are several **unusual nucleotides** that can be found in tRNA. Those nucleotides include various rarely occurring (**minor**) **bases** such as dihydrouracil, methylated bases, hypoxanthine (in inosine) and also nucleotides with an atypical bond (pseudouridine). They arise from post-transcriptional modifications of tRNA. The importance of the unusual nucleotides lies in the creation of recognition sites for proteins which help create the correct conformation of the molecule and increase the possibilities of interactions with mRNA codons.

On the basis of the possible base pairings, the "clover leaf" conformation of tRNA with 4–5 arms can be deduced. The structure is comprised of an **acceptor arm** with the sequence -CCA, to whose 2' or 3'-terminal -OH an amino acid is esterified, a **dihydrouracil arm** (DHU loop), a **pseudouridyl arm** (T $\phi$ C loop) and an **anticodon arm** with a triplet (**anticodon**) pairing with the corresponding codon on the mRNA. This section usually contains the sequence PyPy-XYZ-modif.Pu (XYZ is the anticodon). Some tRNAs have an additional, variable or secondary arm.

Spatially, tRNA takes the shape of the letter L; each of the two segments of this conformation is actually one turn of a double helix (10 pb), one is formed by the anticodon and DHU arm and the other by the T $\phi$ C and acceptor arm.



Inosine

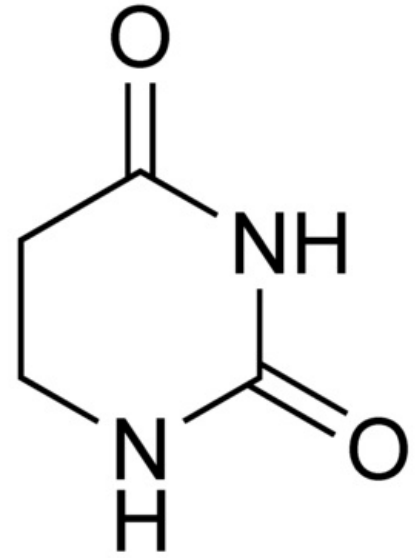
## Aminoacyl-tRNA synthesis

Peptide bond formation is an endergonic reaction. The amino acid is first activated by binding to the 3'-end of the respective tRNA (binding to the 2'-OH or 3'-OH of the last adenosine). The resulting ester, i.e. **aminoacyl-tRNA** (aa-tRNA), then contains enough energy to bind the amino acid to the growing peptide chain. In addition to this activation function, aa-tRNA

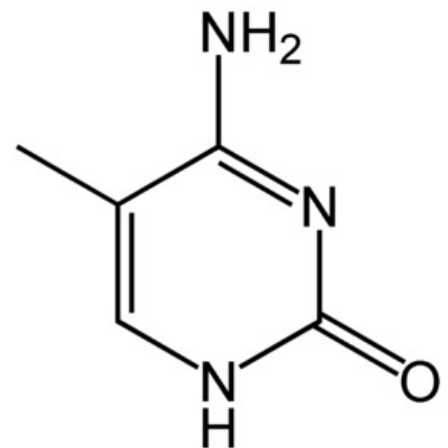
also has an adapter function. The anticodon of the specific tRNA base-pairs to the corresponding mRNA codon, thus determining the correct placement of the transferred amino acid in the amino acid sequence of the peptide chain. It follows that the enzyme that catalyzes the synthesis of aa-tRNA, called **aminoacyl-tRNA-synthetase**, must be strictly substrate-specific, since the wrong amino acid will be included in the peptide if the combination of amino acid and tRNA is wrong. The enzyme has a binding site for an amino acid, for the corresponding tRNA and for ATP. Interestingly, for a given amino acid, one synthetase can join tRNAs with different anticodons, corresponding to the anticodons for a given amino acid within the degeneracy of the genetic code (**isoacceptor tRNAs**). This is made possible by the fact that the enzyme recognizes the correct tRNA not by the sequence of nucleotides, but by the conformation of those parts of the tRNA to which it binds, i.e. the surface of the anticodon, DHU and acceptor arm.

The aa-tRNA synthetase reaction takes place in **two steps**. First, a mixed anhydride of an amino acid and AMP (**aminoacyladenylate**) is formed. In the second phase of the reaction, the **activated amino acid is transferred from AMP to the 3'-OH** or, in some cases, to the 2'-OH of the **terminal adenosine of tRNA**. Both of these reactions are reversible. Hydrolysis of pyrophosphate by the enzyme pyrophosphatase ensures the direction of synthesis thermodynamically.

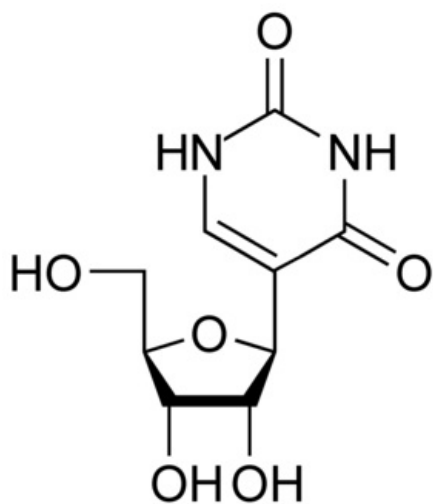
If aa-tRNA-synthetase attaches the wrong amino acid to AMP, it is able to correct its mistake. In addition to synthetase activity, it also has hydrolase activity, which cleaves aa-adenylate and releases the amino acid, instead of transferring it to a non-matching tRNA.



Dihydrouracil (DHU)



5-methylcytosine



Pseudouridine

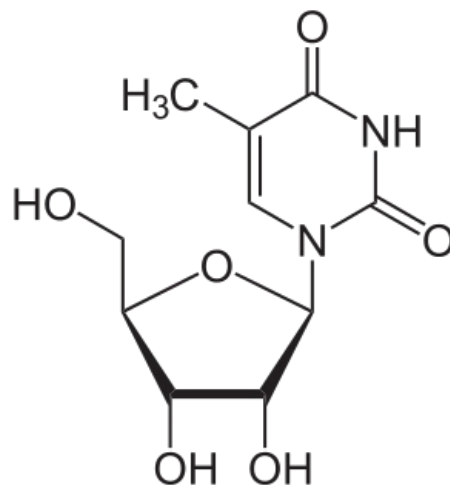
## Links

### Related articles

- Translation
- Transcription
- RNA

### References

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5-Methyluridin,also called Ribosylthimine

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