The 20 Amino Acids Cheat Sheet

by [deleted] via cheatography.com/2754/cs/14124/

Introduction

The amino acids are put together into a polypeptide chain on the ribosome during protein synthesis. In this process the peptide bond, the covalent bond between two amino acid residues, is formed. There are 20 different amino acids most commonly occurring in nature. Each of them has its specific characteristics defined by the side chain, which provides it with its unique role in a protein structure.

Based on the propensity of the side chain to be in contact with polar solvent like water, it may be classified as hydrophobic (low propensity to be in contact with water), polar or charged (energetically favorable contact with water). The charged amino acid residues include lysine (+), arginine (+), aspartate (-) and glutamate (-). Polar amino acids include serine, threonine, asparagine, glutamine, histidine and tyrosine.

Source: https://proteinstructures.com/Structure/Structure/amino-acids.html

The hydrophobic amino acids

The hydrophobic amino acids include alanine, valine, leucine, isoleucine, proline, phenylalanine, tryptophane, cysteine and methionine. You probably noticed that this classification is based on the type of the amino acid side chain. However, glycine, being one of the common amino acids, does not have a side chain and for this reason it is not straightforward to assign it to one of the above classes. Generally, glycine is often found at the surface of proteins, within loop- or coil (without secondary structure) regions, providing high flexibility to the polypeptide chain at these locations. This suggests that it is rather hydrophilic. Proline, on the other hand, is generally non-polar and is mostly found buried inside the protein, although similarly to glycine, it is often found in loop regions. In contrast to glycine, proline provides rigidity to the polypeptide chain by imposing certain torsion angles on the segment of the structure. The reason for this is discussed in the section on torsion angles. Glycine and proline are often highly conserved within a protein family since they are essential for the conservation of a particular protein fold..

Charged

Arginine	Arg	R
Lysine	Lys	K
Aspartic acid	Asp	D
Glutamic acid	Glu	E

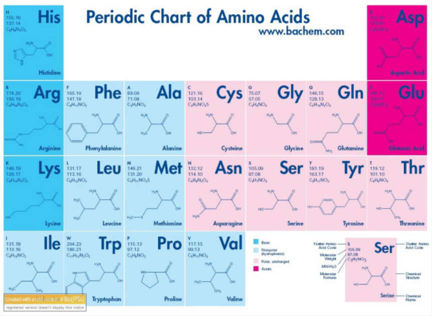
Side chains often make Salt bridges

Polar

Glutamine	Gln	Q
Asparagine	Asn	N
Histidine	His	H
Serine	Ser	S
Threonine	Thr	T
Tyrosine	Tyr	Y
Cysteine	Cys	C
Tryptophan	Trp	W

Usually participate in hydrogen bonds as proton donors or acceptors)

Periodic Chart of Amino Acids



Hydrophobic

Alanine	Ala	A
Isoleucine	Ile	I
Leucine	Leu	L
Methionine	Met	M
Phenylalanine	Phe	F
Valine	Val	V
Proline	Pro	P
Glycine	Gly	G

Normally buried inside the protein core.

Most protein molecules have a hydrophobic core

Most protein molecules have a hydrophobic core, which is not accessible to solvent and a polar surface in contact with the environment (although membrane proteins follow a different pattern). While hydrophobic amino acid residues build up the core, polar and charged amino acids preferentially cover the surface of the molecule and are in contact with solvent due to their ability to form hydrogen bonds.

Most protein molecules have a hydrophobic core (cont)

For a hydrogen bond to be formed, two electronegative atoms (for example in the case of an alpha-helix the amide N, and the carbonyl O) have to interact with the same hydrogen. The hydrogen is covalently attached to one of the atoms (called the hydrogen-bond donor), but interacts electrostatically with the other atom (the hydrogen bond acceptor, O). In proteins essentially all groups capable of forming H-bonds (both main chain and side chain, independently of whether the residues are within a secondary structure or some other type of structure) are usually H-bonded to each-other or to water molecules. Due to their electronic structure, water molecules may accept 2 hydrogen bonds, and donate 2, thus being simultaneously engaged in a total of 4 hydrogen bonds. Water molecules may also be involved in the stabilization of protein structure by making hydrogen bonds with the main chain and side chain groups in proteins and even linking different protein groups to each other. In addition, water is often found to be involved in ligand binding to proteins, mediating ligand interactions with polar or charged side chain- or main chain atoms. It is useful to remember that the energy of a hydrogen bond, depending on the distance between the donor and the acceptor and the angle between them, is in the range of 2-10 kcal/mol. A detailed atlas of hydrogen bonding for all 20 amino acids in protein structures was compiled by Ian McDonald and Janet Thornton.