Abbreviations and Symbols for the Description of the Conformation of Polypeptide Chains

Rules approved 1974

http://www.chem.qmul.ac.uk/iupac/misc/ppep1.html

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Any comments should be sent to the current secretary of the Committee, or any other member of the Committee

Important Note: This version is formatted using the font symbol for Greek letters. If you cannot see a Delta (a triangle) in quotation marks next "D" click here for a version where Greek letters are created using graphic images.

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**Rule 6. Helical Segments**

A regular helix is strictly of infinite length, with all $\Phi$'s identical and all $\Psi$'s identical. A helical segment of polypeptide chain may be defined either in terms of $\Phi$ and $\Psi$ or in terms of symmetry and hydrogen-bond arrangement.

**6.1. Symbols**

In the description of helices or helical segments the following symbols should be used: $n$=number of residues per turn; $h$=unit height (translation per residue along the helix axis); $t=360^\circ/n$=unit twist (angle of rotation per residue about the helix axis).

**6.2. Definition in terms of $\Phi$ and $\Psi$.**

Under this definition a helical segment is referred to as a $(\Phi,\Psi)$ helix; thus a right-handed $\alpha$ helix would be a $(-57^\circ,-47^\circ)$ helix. The first and last residues of the helical segment are taken to be the first and last residues which have $\Phi$ and $\Psi$ values equal to those defining the helix, within limits which should be defined in the context. No account is taken of hydrogen-bonding arrangements.

**6.3. Definition in terms of symmetry and hydrogen-bond arrangement.**

A helix is referred to as an $n_r$ helix, where $n$ = number of residues per turn and $r$ = number of atoms in ring formed by a hydrogen bond and the segment of main chain connecting its extremities. Thus an $\alpha$ helix would be $3.6_{13}$. The first helical residue is taken as the first whose CO group is regularly bonded to NH along the helix (in the case of an $\alpha$ helix, to the NH of the fifth residue); the last helical residue is the last whose NH is regularly hydrogen bonded to CO along the helix (in the case of an $\alpha$ helix, to the CO of the residue last but four). Irregular hydrogen-bonding arrangements are not considered to form part of the helix.

**Notes.**

(i) A helical segment defined by Rule 6.2 may, but need not necessarily, be two residues shorter than the same segment defined by Rule 6.3.

(ii) These rules prescribe no definitions for irregular helical segments.