

Commentary on Homology Modeling

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ABOUT THE STUDY

Homology Modeling:

Homology modeling is popularly known as comparative modeling of protein. It is the method that is used to generate reasonable models of the proteins.

Homology proteins are the portion of 2 portions with the amino acids which have a similar protein with the basic function.

Evolutionarily related proteins are almost like parallel sequences. They're present homologous proteins that are analogous to protein structure. The three-dimensional protein structure is evolutionarily more conserved than would be expected on the premise of sequence conservation alone.

The target and the template should be closely related so that the homology modeling can produce structurally high-quality models that are inspired by the genomics formation.

The Homology modeling is:

- 1) It is atomic modeling for the protein from the amino acid sequencing.
- 2) They provide an experimental three-dimensional structure of a related homologous protein. It is also called template-based modeling. The template modeling results in the 3D structure by the homologous protein which is known as the template.

Proteins:

Biomolecules, or macromolecules, consist of one or more long chains of amino acids of the proteins. Proteins help in the regulation of cells, tissues, and organs. Proteins act as neurotransmitters in the body. Haemoglobin in the blood is also known as protein. Amino acids are the building blocks of protein.

Amino acids:

It has 20 amino acids which there are essential and non-essential. The amino acids which grow and function properly. The 11 non-essential are Arginine, Serine, Proline, Cysteine,

Aspartic acid, Alanine, Tyrosine, Asparagine, Glutamic acid, Glycine and Glutamine.

They are 9 essential amino acids they are Histidine, Threonine, Lysine, Leucine, Tryptophan, Phenylalanine, Methionine, Valine, Isoleucine.

Steps Involved In Homology Modeling:

The template recognition and initial alignment

Alignment correction

Backbone generation

Loop Modeling

Side chain modeling

Model optimization

Model validation

Uses of Homology modeling:

Protein modeling is given useful information:

The homology modeling could give useful information for the structural models; this generates the thesis of a protein's function and directing further experimental work.

The protein analysis function and antigenic behavior.

The protein design is rational, with increased stability.

The drug design is based on the structure.

It is a time consuming and so difficult to acquire the experiments from methods such as NMR and X-ray crystallography.

CONCLUSION:

Homology modeling provides the most reliable results. Homology modeling is the computational structure prediction methods that are used to determine protein 3D structure from its amino acid sequence. It is considered to be the most accurate of the computational structure prediction methods. It consists of multiple steps that are straightforward and easy to apply. Homology modeling has many tools. Homology modeling has

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many applications in the drug discovery process. The drugs which can interact with the receptors; they mainly consist of the proteins, protein 3D structure. In the drug discovery, homology

modeling plays a crucial role. Homology modeling plays a vital role in drug discovery.