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which contains all of the
information to build the new
protein (house). The working copy

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of the master blueprint is called messenger RNA (mRNA), which is copied from DNA. The construction site is either the cytoplasm in a prokaryote or the endoplasmic reticulum (ER) in a eukaryote. The building materials are amino acids.

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Experiments. The protein modeling community has been a pioneer in the concept of “blinded” challenges. The basic idea is very

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simple: structural biology
laboratories make available to the
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information on proteins that are in
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modeling groups generate 3D
structural prediction(s) for these
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structure is published and compared to the predictions; a ...

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This protein structure lays to rest
previous debate about the number
of active sites needed for glucan
polymerization ; one is evidently
sufficient. Prior to publication of

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the Rhodobacter structure,
Sethaphong et al. developed a
computational model of the
catalytic domain of a plant CESA
(Figure 2a). Despite low sequence
similarity, the two ...

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for the construction of proteins,
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Ribosomal Ribonucleic acid,
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bonds between amino acids when
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The copying of information from the template strand of DNA onto mRNA by forming matching base pairs between the two nucleic acids.

Key: Yell onent Modeling Protein Synthe sis

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Proteins are biomolecules composed of amino acids that participate in nearly all cellular activities.; Occurring in the cytoplasm, translation is the process through which proteins are synthesized. The typical protein is constructed from a

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single set of amino acids. Every
protein is specially equipped for its
function.

The Structure and Function of
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comparative modeling of protein,

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refers to constructing an atomic-

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protein from its amino acid

sequence and an experimental

three-dimensional structure of a

related homologous protein.

Homology modeling relies on the

identification of one or more

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known protein structures likely to resemble the structure of the query sequence, and on the production of an alignment that maps residues in the query sequence to residues in the template

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Homology modeling - Wikipedia
To obtain PDB coordinates for a protein of your interest, go to the Protein Data Bank or Molecules to Go or NCBI. PHYRE2 - Protein Homology/analogY Recognition Engine - this is my favourite site for the prediction of the 3D

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structure of proteins. In each case
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