

Protein folding

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Protein folding

The newly formed primary structure has to acquire:

Secondary structure

Tertiary structure

Sometimes quaternary structure

This requires extensive folding of the polypeptide chain

If a correct primary structure has been formed:

The nascent protein will fold by itself

It will attain higher orders of structure

It will attain the correct conformation

However, spontaneous folding is a slow process

Rapid and correct folding of newly-synthesized proteins is ensured by:

Some
enzymes

Some protein
factors:

Chaperone
proteins

Chaperonins

Enzymes involved in protein folding

Protein
disulphide
isomerase

It ensures that the disulphide bonds are formed between the correct cysteine residues

Peptidyl prolyl
cis-trans
isomerase

It ensures that the bonds involving proline residues are *cis* or *trans* as required

The chaperone proteins are:

Heat shock proteins 40 and 70
(HSP 40 and HSP 70) in cytosol

Heat shock proteins 10 and 60
(HSP 10 and HSP 60) in mitochondria

Calnexin and calreticulin
in endoplasmic reticulum

The chaperonins include:

Binding immunoglobulin
Protein (BiP)

TCP-1 Ring Complex
(TRiC)

Thank you

The background is a solid dark blue. In the bottom right quadrant, there are several thin, white, wavy lines that create a sense of motion or a decorative flourish.