Decision-making mechanism for the destruction of non-functional proteins

Proteins destined for destruction and removal from the cell are also subject to specific targeting. The biological half-life of cytosolic proteins varies widely, from a few minutes to more than twenty hours. The length of existence of these proteins is determined by their N-terminal amino acid. Met, Gly, Ala, Ser, Thr, and Val is amino acid No. 1 of more stable proteins (half-life longer than 20 hours). The N-terminal with Ile or Glu signals about half an hour of peptide *survival*. Pro, Leu, Phe, Asp, Lys, and Arg provide a half-life of only a few minutes. Such a short half-life is significant for regulatory peptides, such as hormones, so that regulation changes can be fast. This signaling originated in the early stages of life, as it is known in bacteria, yeasts and mammals. The mechanism of the described targeting is not fully elucidated. **Ubiquitin** (Mr=8500), a protein which is present in all eukaryotic cells, plays an important role. The C-terminal Gly of ubiquitin is covalently bound to the ε-NH_2 group of lysine of the protein to be degraded. Interestingly, ubiquitin is first activated by ATP and three enzymes and is attached to their –SH groups. Thus, this activation resembles the activation of fatty acids or the synthesis of aa-tRNA (amino acid activation), which is one example of a general principle that we encounter more often in biochemistry.

References

Related Articles

- Translation of membrane and secretory proteins (protein sorting, targeting)
- Translation, post-translational processing of proteins in eukaryotes
- Post-translational modifications and protein targeting

Source

- ŠTÍPEK, Stanislav. *Stručná biochemie : Uchování a exprese genetické informace.* 1. edition. Medprint, 1998. ISBN 80-902036-2-0.

References

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