

Mitochondria are organelles of endosymbiotic origin responsible for many cellular functions, including bioenergetics, biosynthesis and apoptosis. Regulated protein turnover is crucial for proper mitochondrial function. It is controlled by cellular proteolytic system, especially by its mitochondrial part. This mitochondrial proteolytic system is comprised of several groups of proteases. The best characterized AAA⁺ proteases constitute hollow oligomeric complexes, in which the proteolytic domains are localized. Access to these domains is dependent on unfolding – an energy-consuming process driven by ATP hydrolysis mediated by ATPase domains of AAA⁺ protein. The main function of AAA proteases is proteolytic degradation of proteins, a part of quality control system of mitochondrial proteins. AAA proteases are localized freely in mitochondrial matrix (Lon and ClpXP), or anchored in the inner membrane (i-AAA and m-AA). Processing peptidases cleave off the mitochondrial targeting sequences of nuclear encoded mitochondrial proteins. Oligopeptidases cleave peptides produced by processing and proteolytical degradation to single amino acids. Incorrect function of various components of mitochondrial proteolytical system is implicated in several diseases, including certain forms of hereditary spastic paraplegia (HSP), spinocerebellar ataxia (SCA28), Perrault syndrome, and possibly Parkinson's disease and Alzheimer's disease as well.