

THE PROTEASOME POST-TRANSLATIONAL MODIFICATIONS AND THEIR FUNCTIONAL SIGNIFICANCE

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The proteasome degrades most intracellular proteins in a ubiquitin-dependent manner and is considered a convenient and important eukaryotic model protein complex to study post-translational modifications. It is known that proteasome post-translational modifications regulate its proteolytic activity, substrate specificity, cell localization, assembly and maintenance of the complex stability. Phosphorylation and acetylation account for the largest number of the proteasome post-translational modifications, however, the functional significance for most of the known sites remains unexplored. It should be noted that no study of specific post-translational modifications of proteasome subpopulations, including immunoproteasomes and extracellular proteasomes, has yet been carried out. This review describes the proteasome post-translational modifications with known functional significance.

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