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Commentary

A Commentary on Post-Translational Modification

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DESCRIPTION

Post-Translational Modification (PTM) of proteins refers to the chemical changes that occur after a protein has been produced. Following protein production, post-translational modification (PTM) refers to the covalent and, in most cases, enzymatic alteration of proteins. Ribosomes convert mRNA into polypeptide chains, which may later proceed through PTM to generate the mature protein product. When prohormones are transformed to hormones, PTMs are crucial components in cell signalling. Post-translational modifications can occur on the side chains of amino acids or at the C- or N-termini of proteins. They can alter an existing functional group or introduce a new one, such as phosphate, to expand the chemical repertory of the 20 conventional amino acids. Phosphorylation is the most prevalent post-translational modification and is a typical technique for modulating enzyme activity. Many eukaryotic and prokaryotic proteins have carbohydrate molecules linked to them, a process known as glycosylation, which can help increase protein folding and stability while also having regulatory functions. Lipidation is the process of attaching lipid molecules to a protein or part of a protein that is linked to the cell membrane.

Cleaving peptide bonds, as in converting a propeptide to a mature form or deleting the initiator methionine residue, are two further types of post-translational modification. Disulfide bond production from cysteine residues is referred to be a post-translational modification. For example, once disulfide links are created, the peptide hormone insulin is cut twice and a propeptide is removed from the middle of the chain; the resulting protein is made up of two polypeptide chains joined by disulfide bonds. Oxidative stress causes some types of post-translational modifications. Carbonylation is one example of a modification that causes the changed protein to be targeted for breakdown, which can lead to the creation of protein aggregates. Specific amino acid changes can be employed as oxidative damage indicators.

Sites with a functional group that can act as a nucleophile in the reaction, such as the hydroxyl groups of serine, threonine, and tyrosine; the amine forms of lysine, arginine, and histidine; the thiolate anion of cysteine; the carboxylates of aspartate and glutamate; and the N- and C-termini, are frequently modified post-transnationally. Furthermore, while being a poor nucleophile, asparagine's amide can function as a glycan attachment site. Rarer changes can be found in oxidised methionine's and some side chain methylene's. A range of techniques, including mass spectrometry, Eastern blotting, and Western blotting, can be used to detect post-translational modifications of proteins in the lab. The external links sections provide other methods.

Databases and tools

Protein sequences contain sequence motifs that are recognised by modifying enzymes and can be found in PTM databases, which can be recorded. The vast number of various alterations being identified necessitates the use of databases to store this information. PTM data can be gathered through experiments or predicted from personally picked, high-quality data. Several databases have been constructed, many of which focus on certain taxonomic groups or other characteristics.

Addiction

Addiction's persistence is one of its most prominent characteristics. Drug seeking and relapse can persist even after decades of sobriety, indicating that the addictive phenotype is life-long. The biological foundation of addictions appears to be dependent on post-translational modifications, such as epigenetic alterations of histone protein tails in certain brain areas. When specific post-translational epigenetic alterations occur, they appear to leave long-lasting "molecular scars," which could explain why addictions persist. Nicotine addiction is common among cigarette smokers. The post-translational changes consisting of acetylation of both histones H3 and histone H4 were elevated at the FosB promoter in the nucleus accumbens of mice after 7 days of nicotine treatment, resulting in a 61% increase in FosB expression. This also boosts the expression of the Delta FosB splice variant. Delta FosB is a "sustained molecular switch" and "master control protein" in the development of addiction in the nucleus accumbens of the brain. There was an increase in post-translational modification

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of histone 3 lysine 9 acetylation, H3K9ac, in the pronociceptin promoter in the cerebral amygdala complex in rats exposed to alcohol for up to 5 days, hence this acetylation is a pronociceptin activating mark.