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## TUBULIN POSTTRANSLATIONAL MODIFICATIONS

### Summary

Both, free tubulin and tubulin incorporated into microtubules can be extensively posttranslationally modified. Among numerous identified modifications of  $\alpha$ - and  $\beta$ -tubulin, at least some modifications such as acetylation, deetyrosination or glutamylation are highly evolutionarily conserved from protists to man. The posttranslational modifications of tubulin form a specific pattern on the microtubule surface, called a tubulin code, that is recognized and interpreted by microtubule interacting proteins. Thus, tubulin posttranslational modifications can affect the microtubule properties, both directly and indirectly, by regulating the interactions with microtubule associated proteins. The level of the tubulin posttranslational modifications vary on different types of microtubules and depends upon the type of the microtubular structures and the cell type. Additionally, the levels of tubulin modifications can change during the cell cycle and cell differentiation. The extensive studies carried out during the last years resulted in a discovery of some of the key enzymes that modify  $\alpha$ - and  $\beta$ -tubulin as well as partial understanding of the mechanisms of their action. However, despite all the efforts we are still far from the full understanding of the significance of the microtubule posttranslational modifications in the regulation of cellular processes.

Key words: acetylation, deetyrosination, polyamination, glutamylation, glycylation