SnapShot: Histone Modifications

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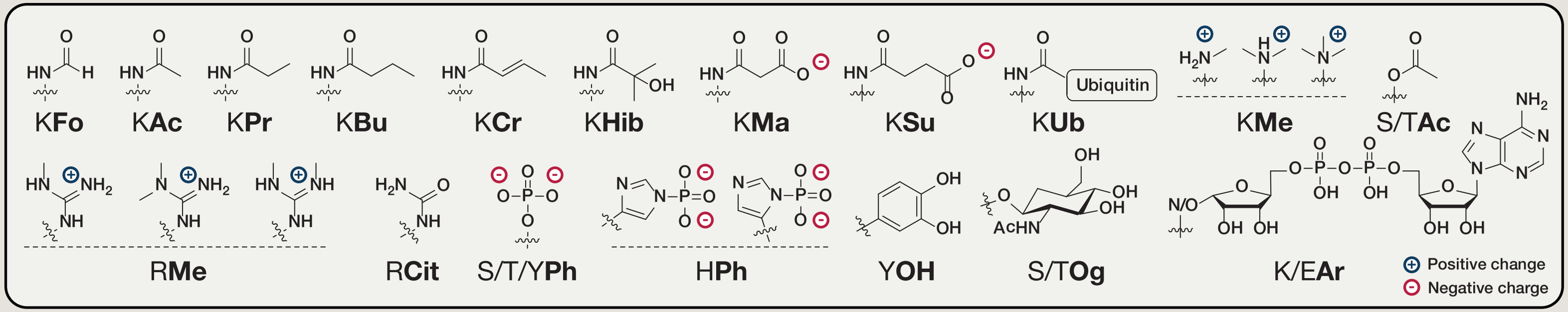
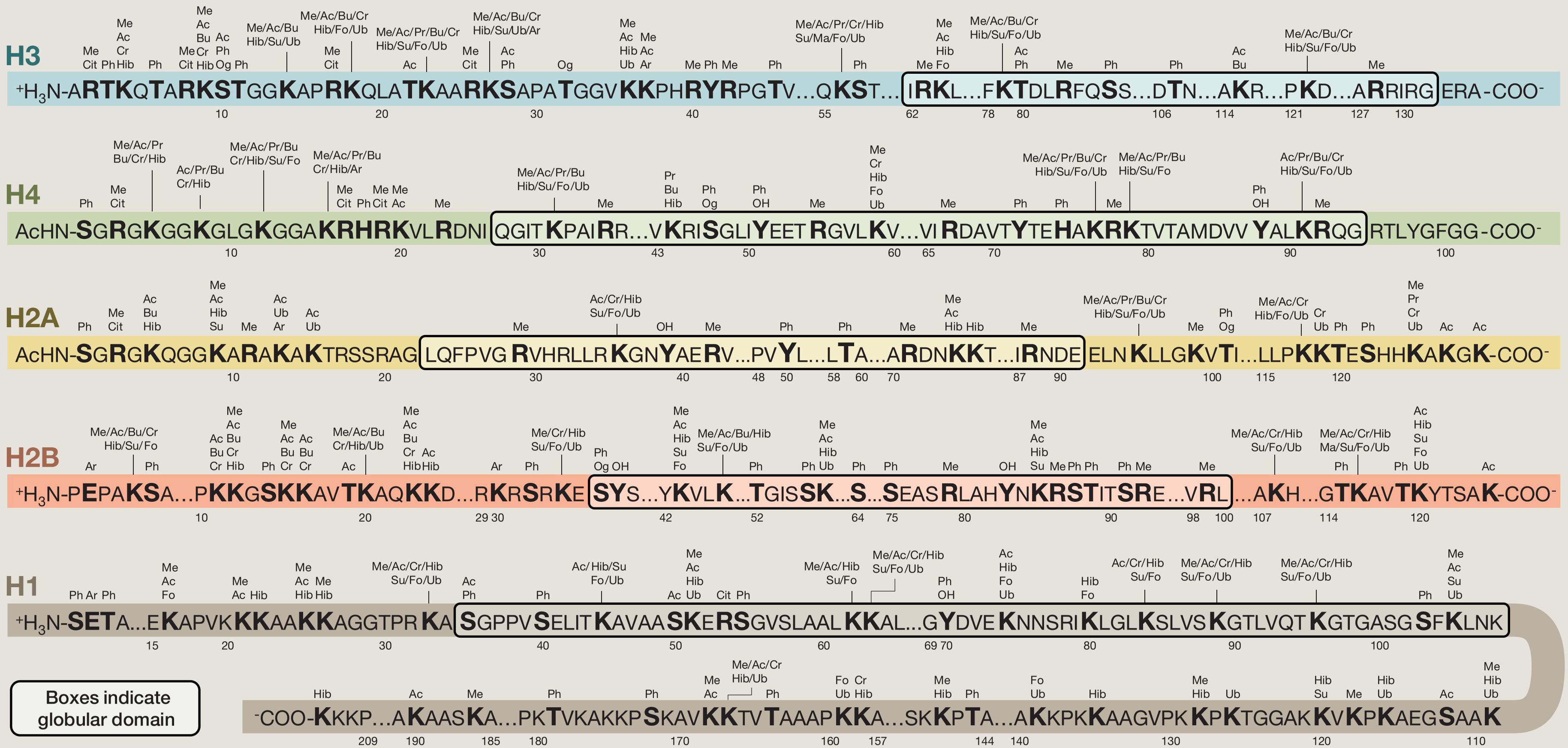


Me	Methylation (K, R)
Ac	Acetylation (K, S, T)
Pr	Propionylation (K)
Bu	Butyrylation (K)
Cr	Crotonylation (K)
Hib	2-Hydroxyisobutyrylation (K)
Ma	Malonylation (K)
Su	Succinylation (K)
Fo	Formylation (K)
Ub	Ubiquitination (K)
Cit	Citrullination (R)
Ph	Phosphorylation (S, T, Y, H)
OH	Hydroxylation (Y)
Og	O-GlcNAcylation (S, T)
Ar	ADP ribosylation (K, E)



See online version for for legend and references.

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The histone proteins are decorated by a variety of protein posttranslational modifications (also called histone marks). Histone marks are critical to dynamic modulation of chromatin structure and function, contributing to the cellular gene expression program. In addition to the well-studied acetylation and methylation modifications, recent studies have revealed several new types of histone marks, including lysine propionylation, lysine butyrylation, lysine crotonylation, lysine 2-hydroxyisobutyrylation, lysine malonylation, and lysine succinylation. Preliminary studies on some of the new histone marks (e.g., crotonylation and 2-hydroxyisobutyrylation) suggest that their effects on chromatin function are distinct from those of lysine acetylation. Given that the newly discovered lysine acylation reactions likely use the corresponding acyl-CoA molecules as cofactors, it is proposed that histone acylations provide a link between cellular metabolism and epigenetic mechanisms.

This SnapShot summarizes the reported human, mouse, and rat histone marks, including recently identified lysine acylation marks.

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