



Figure 6. Sites of histone tail modifications. The amino-terminal tails of histones account for a quarter of the nucleosome mass. They host the vast majority of known covalent modification sites as illustrated. Modifications do occur in the globular domain (boxed), some of which are indicated. In general, active marks include acetylation (turquoise Ac flag), arginine methylation (purple Me hexagon), and some lysine methylation, such as H3K4 (green Me hexagon) and H3K36 (yellow Me hexagon). H3K79, found in globular domain, has an antisilencing function. Repressive marks include methylation at H3K9, H3K27, and H4K20 (red Me hexagon). In addition to the modifications shown here, many others exist (e.g., citrullination, ADP-ribosylation, sumoylation, O-GlcNAcylation), most of which are listed in App. 2 (Zhao and Garcia 2014).