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Structural Analysis of Histone Methyltransferases. Rui-Ming Xu, Jinrong Min, W.M. Keck Structural Biology Laboratory, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY 11724.

Methylation of lysine residues of core histones plays important roles in epigenetic control of gene expression. Lysine residues located at the N-terminal tails of histone H3 and H4 are methylated by SET domain histone methyltransferases, while lysine-79 of histone H3, which is located in the histone-fold core domain, is methylated by Dot1. Unlike many SET domain histone methyltransferases, Dot1 only methylates nucleosomal histone H3. We will analyze the crystal structures of SET-domain and Dot1-like histone methyltransferases to understand the catalytic mechanism and substrate specificity of histone lysine methylation.