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Shape of a chromodomain

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Histone modification represents an important mechanism of epigenetic regulation. The methylation of Lysine9 in histone H3 results in the specific binding of the HP1 (heterochromatin protein 1) factor and subsequent changes in chromatin structure and gene regulation. In an Advanced Online Publication from Nature, Peter Nielsen and researchers at the University of Cambridge, UK, present the three-dimensional structure of the chromodomain from HP1 bound to Lysine9-methylated histone H3 (20 February 2002, DOI 10.1038/nature722). They determined the structure of the Hp1β chromodomain-histone H3 peptide complex. The H3 peptide binds in an extended β-strand-like conformation in the HP1 groove using an 'induced-fit' mechanism for recognition of the modified peptide. The amino-terminal tail of the chromodomain wraps around the peptide during binding, bringing together three aromatic residues that form a pocket around the methyl group. This structure allows prediction of which HP1 residues are critical for binding and may help to predict which other chromodomains can bind peptides with methyl lysine.

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