

A protein-DNA recognition code for α -helical transcription factors - (session: Structural Genomics)

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The existence of a correspondence code between DNA bases and transcription factor aminoacids is still a matter of debate. A systematic analysis of Zn-fingers-DNA 3D interfaces identified DNA-aminoacid non-bonded contacts and defined a set of rules for peptide-DNA binding. Key to a clear-cut definition of this binding code, have been the selection of specific (bases) vs non-specific (ribose, phosphate) bonds, the structural validation of identified non-bonded contacts and the analysis of a statistically meaningful sample population. Comparison with leucine-zippers and helix-turn-helix indicates that these rules extend to other classes of α -helix transcription factors. These rules were validated by a meta-analysis of systematic Zn-finger mutagenesis programs.