

DNA phosphate crowding correlates with protein cationic side chain density and helical curvature in protein/DNA crystal structures

March 28, 2013

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Protein binding to DNA are complicated, multidimensional processes that are categorized into two groups. The first is direct (base pair) readout where the Protein binds to the DNA groove. The second is indirect (shape readout) where the protein is attracted to the DNA via helical confirmation. 58 crystal structure of DNA-protein bonding were chosen to be a subset to quantify the relationship between cationic residue density (Cpc) and DNA phosphate crowding (Cpp). It was found that DNA-protein structures that had a high Cpp/Cpc correlation had DNA curvature in concave and convex confirmations in relation to the protein.