**ANALYSIS OF TRANSCRIPTIONAL FACTORS IN E. COLI.**

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Most of the transcriptional regulatory proteins have a modular architecture with distinct domains for various functions such as DNA-binding, dimerization, and ligand binding (Kaptein, 1993). The most thoroughly DNA-binding motif studied contains a helix-turn-helix (HTH) structure, with two a-helices linked by a turn. The first a-helix contacts with the DNA backbone and the second a-helix contacts atoms exposed in the major groove of the operator, thereby determining the specificity of binding (Wharton, 1984). This motif (around 20 amino acids) has first been identified in many activator and repressor gene-regulatory proteins of prokaryotes (Ohlendorf, 1983). In E. coli not all transcriptional factors have an obvious hth or another dna-binding motif. We are interesting in detecting and predicting putative dna-binding motifs in an exhaustive set of regulatory proteins in E. coli. Using sequence and structure information, and the Gibbs sampler algorithm we detected the dna-binding motif in a set of 297 transcriptional factors. In most of these proteins the hth is located in the protein terminus. Taking into account this criteria as well as additional propertie, we detected putatives hth's in all regulatory transcriptional factors so far described. This information adjunt to sequence comparisons will be important in analyzing genomic information related to regulatory process.