Deciphering genomic sequences is a challenge of the 21st century, and one of our activities focuses on the computational identification of transcription factor binding sites. While tremendous progress has been made along these lines, existing algorithms are often prone to over-fitting, and their accuracies are not yet satisfactory. In an attempt to circumvent the over-fitting problem, we combine Variable Order Markov models with Bayesian networks, and we demonstrate how the resulting Variable Order Bayesian networks can be applied to the identification of prokaryotic and eukaryotic transcription factor binding sites.