GENE-CENTERED PROTEIN-DNA INTERACTOME MAPPING

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Transcription regulatory networks play a pivotal role in the development, function and pathology of metazoan organisms. Such networks are comprised of protein-DNA interactions between transcription factors (TFs) and their target genes[1]. We are interested in the architecture and functionality of such networks. We developed high-throughput gene-centered methods[2] for the identification of protein-DNA interactions between large sets of regulatory gene segments and various TF resources, including novel Steiner Triple System-based TF smart pools and a TF array[3]. So far, we mapped two gene-centered networks using *C. elegans* gene promoters[4,5]. These networks already provided insights into differential gene expression at a systems level. For instance, we found that most *C. elegans* genes are controlled by a layered hierarchy of TFs that sometimes function in a modular manner. Our data can be accessed in our database, EDGEdb[6].

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