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Sommario/riassunto	In his master thesis Thorsten Will proposes the substantial information content of protein complexes involving transcription factors in the context of gene regulatory networks, designs the first computational approaches to predict such complexes as well as their regulatory function and verifies the practicability using data of the well-studied yeast S.cereviseae. The novel insights offer extensive capabilities towards a better understanding of the combinatorial control driving transcriptional regulation. Contents Protein Complex Prediction Protein-Protein Interaction Networks Domain-Domain Interaction Networks Combinatorial Algorithms Algorithm Engineering Target Groups Computational biologists and biologists working with gene regulatory networks Computer scientists interested in biological

issues The Author Currently, the author is pursuing his Ph.D. at the Center for Bioinformatics in Saarbrücken, Germany. .