

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Transcriptional targets

ArticleInfo		
ArticleID	:	3968
ArticleDOI	:	10.1186/gb-spotlight-20010130-01
ArticleCitationID	:	spotlight-20010130-01
ArticleSequenceNumber	:	39
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2001-01-30 OnlineDate : 2001-01-30
ArticleCopyright	:	BioMed Central Ltd2001
ArticleGrants	:	
ArticleContext	:	130592211

Jonathan B Weitzman

Email: jonathanweitzman@hotmail.com

In the January 25 *Nature*, Iyer *et al.* describe an elegant technique to identify transcriptional target genes throughout the genome (*Nature* 2001, **409**:533-538). They combined chromatin immunoprecipitation (ChIP) with **microarray** analysis (DNA chips) to probe individual protein-genome interactions. The technique involved cross-linking, immunoprecipitation, PCR amplification and fluorescent labeling, followed by hybridization to microarrays containing genomic DNA. They searched the **yeast genome** for intergenic regions that contained functional binding sites for the cell cycle transcription factors SBF (Swi6/Swi4) and MBF (Swi6/Mbp1). They identified 183 SBF-regulated genes, many of which are involved in budding or cell wall biogenesis. The 98 potential MBF target genes include those implicated in DNA replication, recombination and repair. And 43 loci appear to be targets of both factors. This is a **powerful technique** for identifying common and distinct targets of related transcription factors.

References

1. *Nature*, [<http://www.nature.com>]
2. Microarrays.org, [<http://www.microarrays.org>]
3. *Saccharomyces* genome database, [<http://genome-www.stanford.edu/Saccharomyces/>]
4. Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF, [<http://genome-www.Stanford.edu/chromatinip>]