

Evidence for a 200 gene Ribosome and rRNA Biosynthesis (*rrb*) Regulon in Fungi

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Two challenges of the post genomic era are 1) the need to assign functions to as yet uncharacterized gene products, and 2) the requirement to understand how the expression profiles of large sets of genes are regulated in response to changing environments. Towards these aims, we have used transcriptional profiling analysis to identify and characterize a large set (over 200 genes) of transcriptionally co-regulated genes whose products are involved in rRNA and ribosome biosynthesis. Many of the genes within this set were previously unknown with regards to their function. This RRB regulon is distinct from the ribosomal protein (RP) regulon, and is characterized by a unique pair of conserved promoter motifs. The organization of the RRB regulon appears to be evolutionarily conserved at least from *S. cerevisiae* to *S. pombe*. The strategies used to identify and characterize this gene set can be widely used in other organisms to help fulfill the two needs outlined above.