

FadR regulatory binding motif and gene expression profiling

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Abstract

fadR is a transcription factor which has a Helix-turn-Helix motif, one of most common prokaryotic transcription factor. By use of cDNA microarray one can search for regulation of transcription factors using cluster analysis and sequence information¹.

By comparing wild-type W3110 strain, fadR null mutant strain and fadR overexpressed strain, and subjecting them in various conditions (i.e., different carbon sources) it is possible to identify co-regulated group of genes that is regulated by common transcription regulator, which also can reveal the functional role of fadR². Also candidate genes that could possibly be co-regulated by fadR can be predicted using various sequence information, which assist microarray data analysis.

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References

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