New Regulation Data in the *Saccharomyces* Genome Database

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The *Saccharomyces* Genome Database (SGD; http://www.yeastgenome.org) is the community resource for genomic, gene, and protein information about the budding yeast *Saccharomyces cerevisiae*. SGD biocurators extract from the published literature a variety of functional information about each yeast gene and gene product. In addition to the Gene Descriptions, Gene Ontology annotations, mutant phenotype annotations, and other gene-specific data currently in SGD, we are now preparing to add a new category, regulatory information. In the first phase of this project, we are focusing on 144 gene products identified as DNA-binding transcription factors (TFs). The Locus Summary page for each of these regulators will have a new tabbed section, Regulation, that will provide several different types of information about the regulatory role of each TF. A short free-text Regulation Summary Paragraph will give an overview of the biological context in which the TF acts. The consensus binding site motif sequences and logos will be displayed, and the numbers of predicted and experimental binding sites will be summarized. The genomic distribution of binding sites will be displayed in a Circos genome visualization map. A table of targets of each regulator along with references and evidence, compiled from information curated at SGD and at the YEASTRACT database, will be displayed along with a summary of the biological processes in which the target genes are involved. The Regulation tab will also display the structural classification of each TF, as well as information regarding its regulation by other TFs. All of these data will be available for querying, analysis, and download via YeastMine, the Intermine-based data warehouse system in use at SGD. In the future, we plan to expand this information to include more types of regulation in addition to transcriptional regulation.

We thank the YEASTRACT group for permission to display their curated regulatory relationships in SGD. This work is supported by a grant from the US National Human Genome Research Institute (NHGRI) (P41 HG001315).

What types of regulation data would YOU like to see in SGD?

ECM22/YLR228C Regulation

Summary | Locus History | Literature | Gene Ontology | Phenotype | Interactions | Expression | Regulation | Protein | Wiki

ECM22/YLR228C

- Summary
- Binding Site Sequence Logo
- Predicted Binding Sites
- Experimental Binding Sites
- Regulatory Targets
- Shared GO Processes
- Regulators

ECM22 encodes a transcription factor that is a member of the C6 zinc finger class, containing a DNA binding domain also known as the Zn2Cys6 binuclear zinc cluster or zinc knuckle. Ecm22p and Upc2p, the products of paralogous genes, have similar functions. They recognize and bind to sterol regulatory elements (SRE) in the promoters of genes involved in ergosterol biosynthesis, such as ERG1, ERG2, ERG3, ERG7, ERG25, ERG26, and ERG27, upregulating their transcription at low sterol levels. Under hypoxic conditions, both Ecm22p and Upc2p also activate transcription of the DAN/TIR genes encoding cell wall mannoproteins. Under sterol-replete conditions, Ecm22p and Upc2p localize to intracellular membranes. When sterol concentrations are low, both transcription factors relocate to the nucleus to activate ergosterol biosynthetic gene transcription. By analogy to sterol biosynthesis regulators in other organisms, it is likely that Ecm22p and Upc2p are processed during this relocation, such that the C-terminal transmembrane domain remains in the membrane while the N-terminal DNA-binding domain enters the nucleus.

References

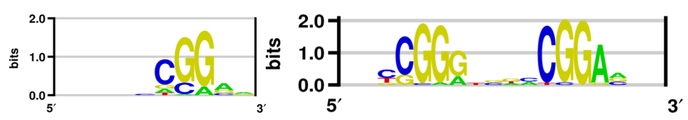
Davies BS and Rine J (2006) A role for sterol levels in oxygen sensing in Saccharomyces cerevisiae. Genetics 174(1):191-201; PMID:16783004

Marie C, et al. (2008) Cytoplasmic localization of sterol transcription factors Upc2p and Ecm22p in S. cerevisiae. Fungal Genet Biol 45(10):1430-8; PMID:18675371

Nohturfft A and Zhang SC (2009) Coordination of lipid metabolism in membrane biogenesis. Annu Rev Cell Dev Biol 25:539-66; PMID:19575637

Free-text, referenced summary of the regulatory context of each TF

Ecm22p Binding Site Sequence Logo



Binding site motifs from YeTFaSCo (the Yeast Transcription Factor Specificity Compendium, yetfasco.ccbr.utoronto.ca)

Ecm22p Regulatory Targets (15 total)

Show 10 entries Search:

Systematic name	Gene name	Evidence	Reference	Source
YBR260C	RGD1	chromatin immunoprecipitation-chip	Harbison CT, et al. (2004); PMID: 15343339	SGD
YCR021C	HSP30	microarray RNA expression level	Hu Z, et al. (2007); PMID: 17417638	SGD
YGL012W	ERG4	microarray RNA expression level	Hu Z, et al. (2007); PMID: 17417638	SGD
YHL021C	AIM17	microarray RNA expression level	Hu Z, et al. (2007); PMID: 17417638	SGD
YKL055C	OAR1	microarray RNA expression level	Hu Z, et al. (2007); PMID: 17417638	SGD
YLR056W	ERG3	chromatin immunoprecipitation-chip	Workman CT, et al. (2006); PMID: 16709784	YEASTRACT
YLR056W	ERG3	chromatin immunoprecipitation	Davies BS and Rine J (2006); PMID: 16783004	YEASTRACT
YLR056W	ERG3	not recorded	Vik A and Rine J (2001); PMID: 11533229	YEASTRACT
YLR056W	ERG3	microarray RNA expression level	Chua G, et al. (2006); PMID: 16880382	YEASTRACT
YLR148W	PEP3	microarray RNA expression level	Hu Z, et al. (2007); PMID: 17417638	SGD

Showing 1 to 10 of 15 entries Previous Next

Interactive table listing TF targets:

- Pre-2011 data curated by YEASTRACT (www.yeastract.com)
- HTP data curated by SGD

TF structural classifications and domains will also be displayed

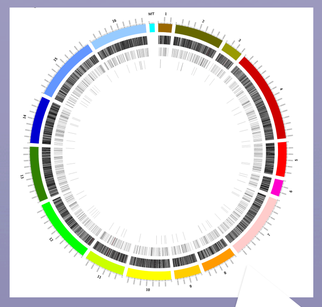
Shared GO Processes Among Ecm22p Regulatory Targets

Show 10 entries Search:

GO Term	P-value	Number of genes
cellular alcohol biosynthetic process	0.00029	4
ergosterol biosynthetic process	0.00029	4
phytosteroid biosynthetic process	0.00029	4
ergosterol metabolic process	0.00037	4
phytosteroid metabolic process	0.00037	4
cellular alcohol metabolic process	0.00051	4
steroid biosynthetic process	0.00096	4
sterol biosynthetic process	0.00096	4
steroid metabolic process	0.00266	4
sterol metabolic process	0.00266	4

Showing 1 to 10 of 13 entries Previous Next

GO Process enrichment of TF targets



TF binding site distribution in the genome will be displayed using Circos circular data visualization

Questions? Contact us! sgd-helpdesk@lists.stanford.edu Find us on: facebook @yeastgenome