



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 have added a new category, regulatory information. In the first phase of this project, we are focusing on 147 gene products identified as DNA-binding transcription factors (TFs). The Locus Summary page for each of these regulators has a new tabbed section, Regulation, that provides several different types of information about the regulatory role of each TF. A short free-text Regulation Summary Paragraph gives an overview of the biological context in which the TF acts. The consensus binding site motif sequences and logos are displayed, with a link to view predicted sites in the Genome Browser. A table of targets of each regulator along with references and evidence, compiled from information curated at SGD and at the YEASTRACT database, is displayed along with a summary of the biological processes in which the target genes are involved. The Regulation tab also shows the structural classification of each TF, the protein domains that it contains, and information regarding its regulation by other TFs. All of these data are 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).

ECM22/YLR228C Regulation

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

ECM22/YLR228C Regulation

Summary

Domains and Classification

Binding Site Motifs

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. 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

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

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

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

TF structural
classifications and
domains

Ecm22p Domains and Classification (7 total)

Display 10 rows

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Filter:

Protein coordinates	Accession ID	Description	Source
1-814	MA0292.1	Class: Zinc-coordinating, Family: Fungal Zn cluster	JASPAR
31-85	SSF57701	Zn(2)-C6 fungal-type DNA-binding domain	SUPERFAMILY
37-78	G3DSA:4.10.240.10	Zn(2)-C6 fungal-type DNA-binding domain	Gene3D
38-82	SM00066	Zn(2)-C6 fungal-type DNA-binding domain	SMART
42-80	PF00172	Zn(2)-C6 fungal-type DNA-binding domain	Pfam
332-353		coiled-coil	Coil
508-634	PF11951	Protein of unknown function DUF3468	Pfam

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

Ecm22p Binding Site Motifs

Click on a motif to view YeTFaSCo record

bits

bits

5' 3' 5' 3'

View predicted binding sites in the [Genome Browser](#).

Ecm22p Regulatory Targets (9 total)

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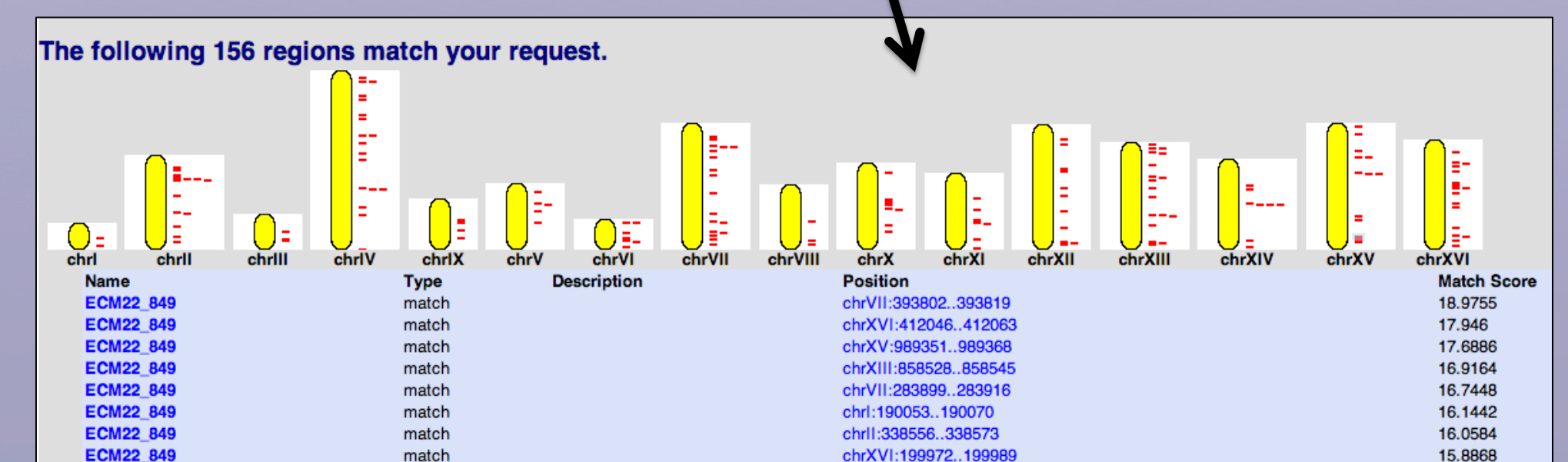
Systematic name	Gene name	Evidence	Reference	Source
YCR021C	HSP30	microarray RNA expression level	Hu Z, et al. (2007)	SGD
YGL012W	ERG4	microarray RNA expression level	Hu Z, et al. (2007)	SGD
YHL021C	AIM17	microarray RNA expression level	Hu Z, et al. (2007)	SGD
YKL055C	OAR1	microarray RNA expression level	Hu Z, et al. (2007)	SGD
YLR056W	ERG3	chromatin immunoprecipitation-chip	Workman CT, et al. (2006)	YEASTRACT
YLR056W	ERG3	chromatin immunoprecipitation	Davies BS and Rine J (2006)	YEASTRACT
YLR056W	ERG3	not recorded	Vik A and Rine J (2001)	YEASTRACT
YLR056W	ERG3	microarray RNA expression level	Chua G, et al. (2006)	YEASTRACT
YLR148W	PEP3	microarray RNA expression level	Hu Z, et al. (2007)	SGD
YLR228C	ECM22	microarray RNA expression level	Hu Z, et al. (2007)	SGD

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Regulatory targets of
the TF:

- pre-2011 data curated by YEASTRACT (www.yeasttract.com)
- HTP data curated by SGD



GO Process enrichment
of TF targets

Shared GO Processes Among Ecm22p Regulatory Targets (9 total)

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Filter:

GO Term	P-value	Number of genes
ergosterol biosynthetic process	0.00013	4
phytosteroid biosynthetic process	0.00013	4
cellular alcohol biosynthetic process	0.00013	4
ergosterol metabolic process	0.00022	4
phytosteroid metabolic process	0.00022	4
cellular alcohol metabolic process	0.00033	4
steroid biosynthetic process	0.00051	4
sterol biosynthetic process	0.00051	4
steroid metabolic process	0.00162	4
sterol metabolic process	0.00162	4

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Regulators whose
target is this TF

Regulators of ECM22/YLR228C (40 total)

Display 10 rows

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Filter:

Systematic name	Gene name	Evidence	Reference	Source
YBR112C	CYC8	chromatin immunoprecipitation-chip	Venters BJ, et al. (2011)	SGD
YBR198C	TAF5	chromatin immunoprecipitation-chip	Venters BJ, et al. (2011)	SGD
YBR289W	SNF5	chromatin immunoprecipitation-chip	Venters BJ, et al. (2011)	SGD
YCR084C	TUP1	chromatin immunoprecipitation-chip	Venters BJ, et al. (2011)	SGD
YER159C	BUR6	chromatin immunoprecipitation-chip	Venters BJ, et al. (2011)	SGD
YHL027W	RIM101	chromatin immunoprecipitation-chip	Macisaac KD, et al. (2006)	SGD
YHR084W	STE12	chromatin immunoprecipitation-chip	Borneman AR, et al. (2007)	YEASTRACT
YHR084W	STE12	chromatin immunoprecipitation	Lefrancois P, et al. (2009)	YEASTRACT
YHR084W	STE12	chromatin immunoprecipitation	Zheng W, et al. (2010)	YEASTRACT
YIL038C	NOT3	chromatin immunoprecipitation-chip	Venters BJ, et al. (2011)	SGD

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