# New Regulation Data
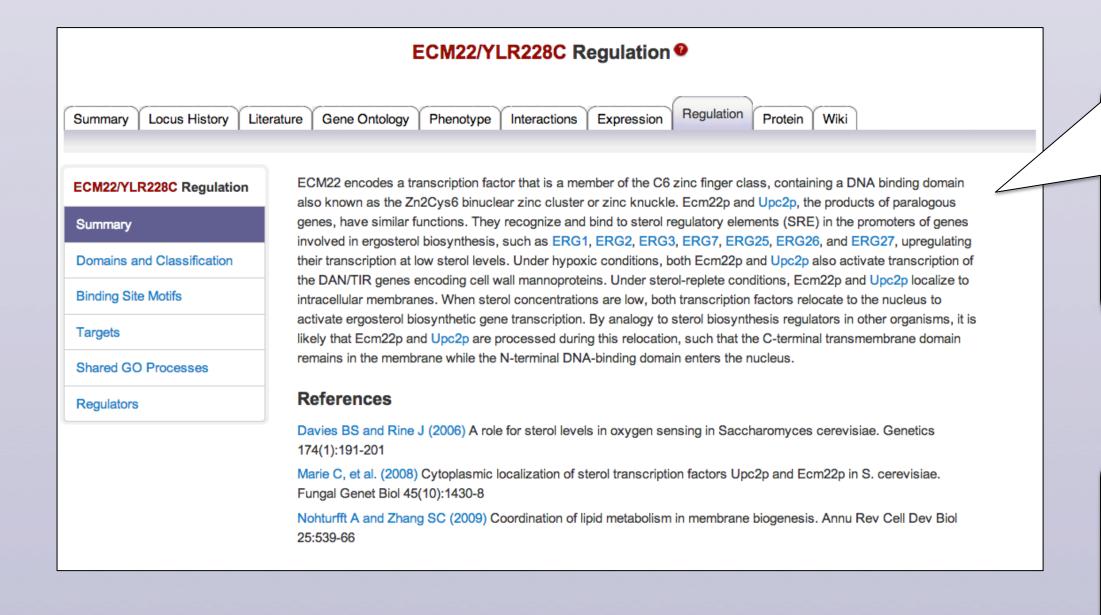# in the *Saccharomyces* Genome Database

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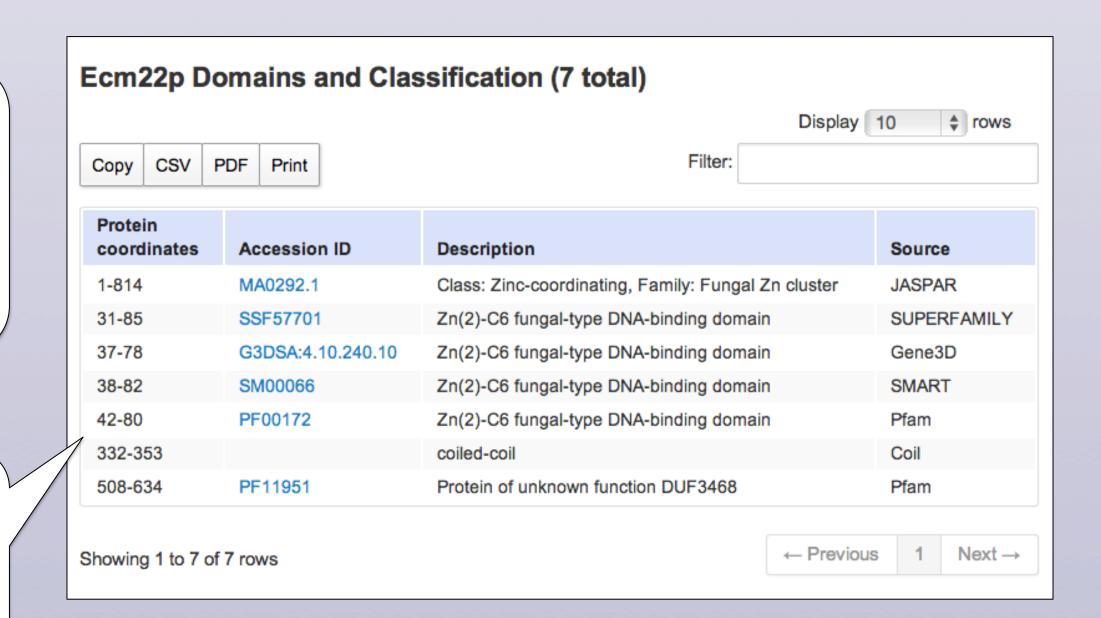Department of Genetics, School of Medicine, Stanford University, Stanford, CA, USA.

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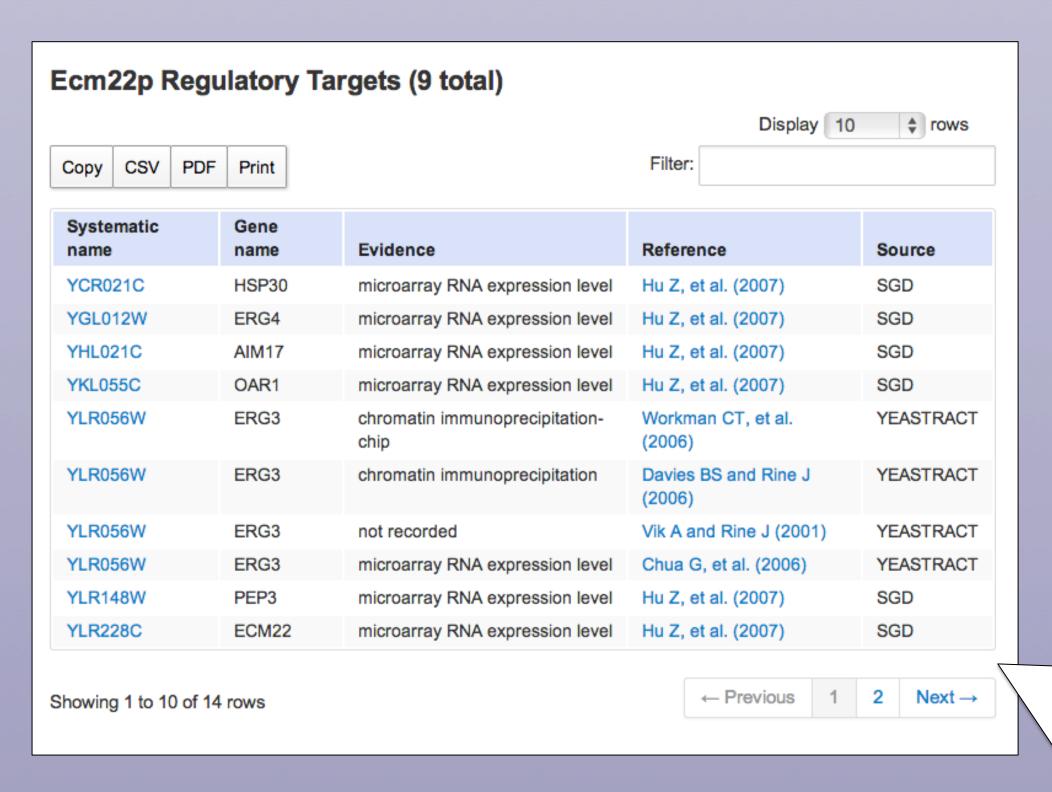
We thank the YEASTRACT group for permission to display their curated regulatory relationships in SGD. This work is supported by a grant from the US National Human Genome Research Institute (NHGRI) (P41 HG001315).

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



TF structural classifications and domains

**Ecm2p Domains and Classification (7 total)**

| 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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**Ecm2p Regulatory Targets (9 total)**

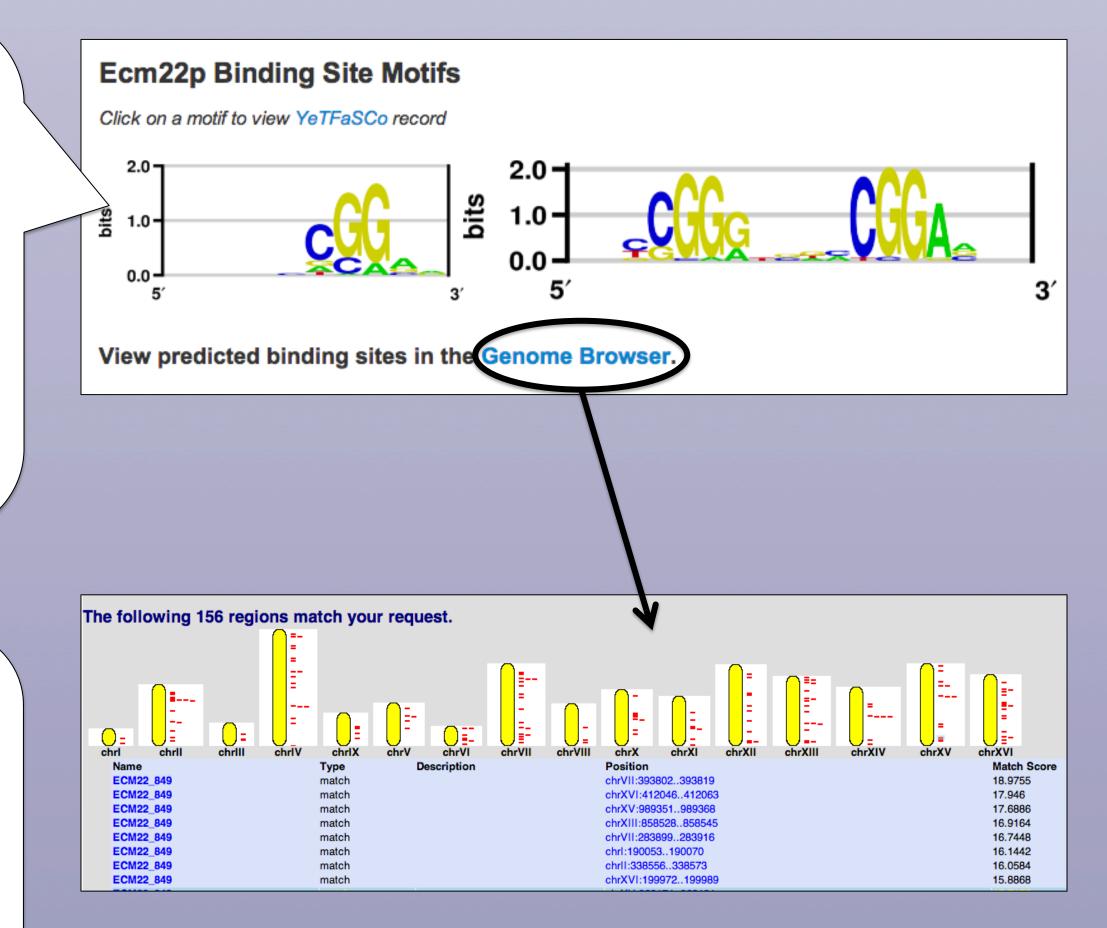| Systematic name | Gene name | Evidence | Reference | Source |
|---|---|---|---|---|
| YCR021C | HSP30 | microarray RNA expression level | Hu Z, et al. (2007) | SGD |
| YGL012W | ERG4 | microarray RNA expression level | Hu Z, et al. (2007) | SGD |
| YHL021C | AIM17 | microarray RNA expression level | 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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Binding site motifs from the Yeast Transcription Factor Specificity Compendium (YeTFaSCo; yetfasco.ccbr.utoronto.ca)



Regulatory targets of the TF:
- pre-2011 data curated by YEASTRACT (www.yeastract.com)
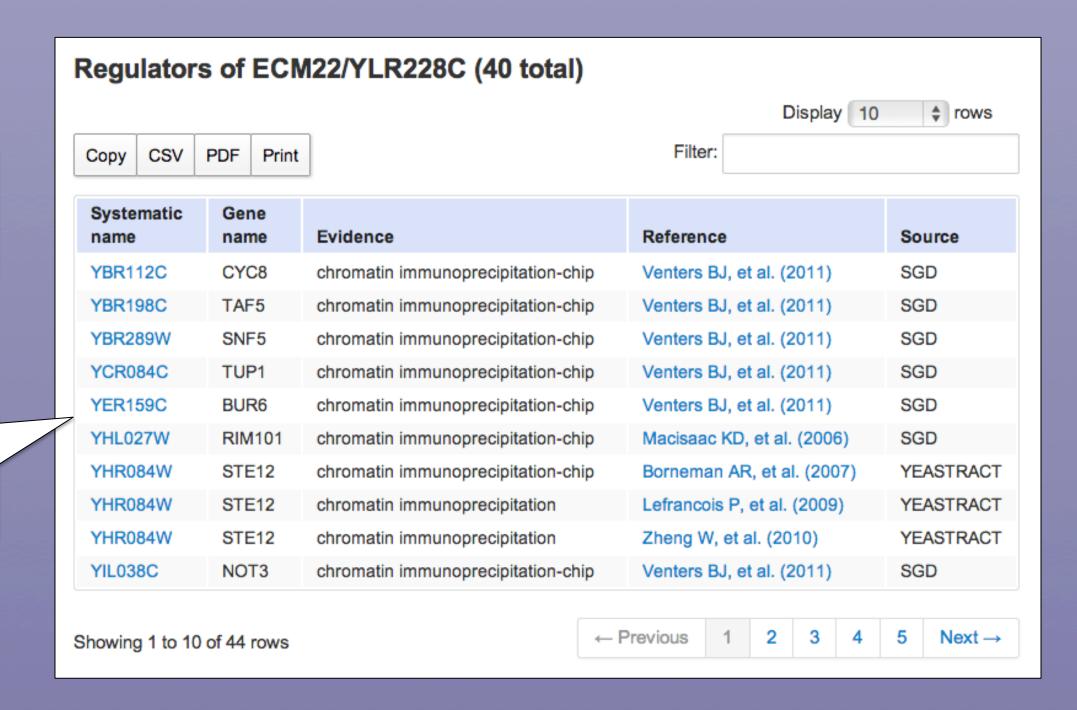- HTP data curated by SGD

**Shared GO Processes Among Ecm2p Regulatory Targets (9 total)**

| 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 |

Showing 1 to 10 of 13 rows

GO Process enrichment of TF targets

Regulators whose target is this TF

**Regulators of ECM22/YLR228C (40 total)**

| 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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