

The basis for much of our understanding of transcriptional regulation has been learned from the budding yeast *Saccharomyces cerevisiae*. Studies with yeast have also provided powerful insights into the diversity of protein complexes and the cellular pathways in which they are involved. We will present an update on new developments at the *Saccharomyces* Genome Database (SGD; <http://www.yeastgenome.org/>), the premier community resource for budding yeast. We have expanded the scope of SGD to include high quality manually curated information regarding transcriptional regulation and protein complexes. These new categories are provided in meaningful ways allowing data mining and discovery by integrating these data into this encyclopedic online resource. In addition to introducing our presentation of these newly curated data we will highlight other new developments, such as methods to display the depth of sequence variation within the many available genomes of *S. cerevisiae*. We already provide access to many of the strain genomes, in addition to the reference genome sequence of strain S288C. We will annotate and provide comparative analyses of these additional genomes, correlating sequence changes with variations in cellular phenotypes and protein function. SGD maintains these different datatypes, and distributes them to the scientific community via the web and file transfer. These expanded outreach efforts are part of our continuing mission to educate students, enable bench researchers and facilitate scientific discovery. This work is supported by a grant from the NHGRI (U41 HG001315).

### Transcriptional Regulation

SWI4/YER111C

Transcriptional Regulation

Summary

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SWI4/YER111C

Regulation

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#### Regulation Summary

SWI4 encodes a transcription factor of the Ig-fold superfamily, which contacts DNA using a series of flexible loops. As part of the SBF complex (Swi4p/Swi6p cell-cycle box (SCB) binding factor), Swi4p binds and activates G1/S genes with SCB-containing promoters, including G1 cyclins (CLN1, CLN2, PCL1, PCL2) and the HO endonuclease. Swi4p recognizes sequences of the form 5'-ACGCGAAA-3'. Swi4p binding DNA requires association with Swi6p, and is restricted to late M and G1, when Swi6p is located in the nucleus. Free Swi4p is subject to intramolecular interactions that physically prevent DNA binding. Association with Swi6p induces conformational changes in Swi4p which alleviate this inhibition, allowing Swi4p to bind DNA. Swi4 transcription is activated in late M/early G1 phase by an early cell cycle box (ECB), and the SWI4 promoter also contains binding sites for the SBF and MBF (Mbp1p/Swi6p cell-cycle box (MCB) binding factor) complexes, which confer late G1-specific transcription. This promoter structure ensures that Swi4p activity persists throughout G1, enabling sufficient quantities of its targets to be expressed to promote the transition to S phase.

Tennen RI, et al. (2013) Cell-cycle and DNA damage regulation of the DNA mismatch repair protein Msh2 occurs at the transcriptional and post-transcriptional level. DNA Repair (Amst) 12(2):97-109 PMID:23261051  
SGD Paper PubMed Full-Text PMC

Breeden LL (2003) Periodic transcription: a cycle within a cycle. Curr Biol 13(1):R31-8 PMID:12526763  
SGD Paper PubMed Full-Text

Baetz K and Andrews B (1999) Regulation of cell cycle transcription factor Swi4 through auto-inhibition of DNA binding. Mol Cell Biol 19(10):6729-41 PMID:10406812  
SGD Paper PubMed PMC

Siegmund RF and Nasmyth KA (1996) The Saccharomyces cerevisiae Start-specific transcription factor Swi4 interacts through the ankyrin repeats with the mitotic Clb2/Cdc28 kinase and through its conserved carboxy terminus with Swi6. Mol Cell Biol 16(6):2847-55 PMID:8649372  
SGD Paper PubMed PMC

Transcriptional Targets and Regulators for SWI4

Targets

Regulators

185

7

0

50

100

150

200

Genes

Domains and Classification

13

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Search:

Protein Coordinates	Accession ID	Description	Source
1-1093	MA0401.1	Class: Ig-fold, Family: Rel	JASPAR
3-681	SSF48403	Ankyrin repeat	SUPERFAMILY
34-159	SSF54616	DNA-binding domain of MluI-box binding protein MBP1	SUPERFAMILY
37-171	G3DSA:3.10.260.10	Transcription regulator HTH, APSEs-type binding domain	
57-122	PF04383	KIUA-N	
478-680	G3DSA:1.25.40.20	Ankyrin repeat-containing domain	
520-549	SM00248	ankyrin repeats	
521-550	PF00023	Ank	
641-670	SM00248	ankyrin repeats	
642-672	PF00023	Ank	
814-835	coll	coiled-coil	
891-912	coll	coiled-coil	
935-956	coll	coiled-coil	

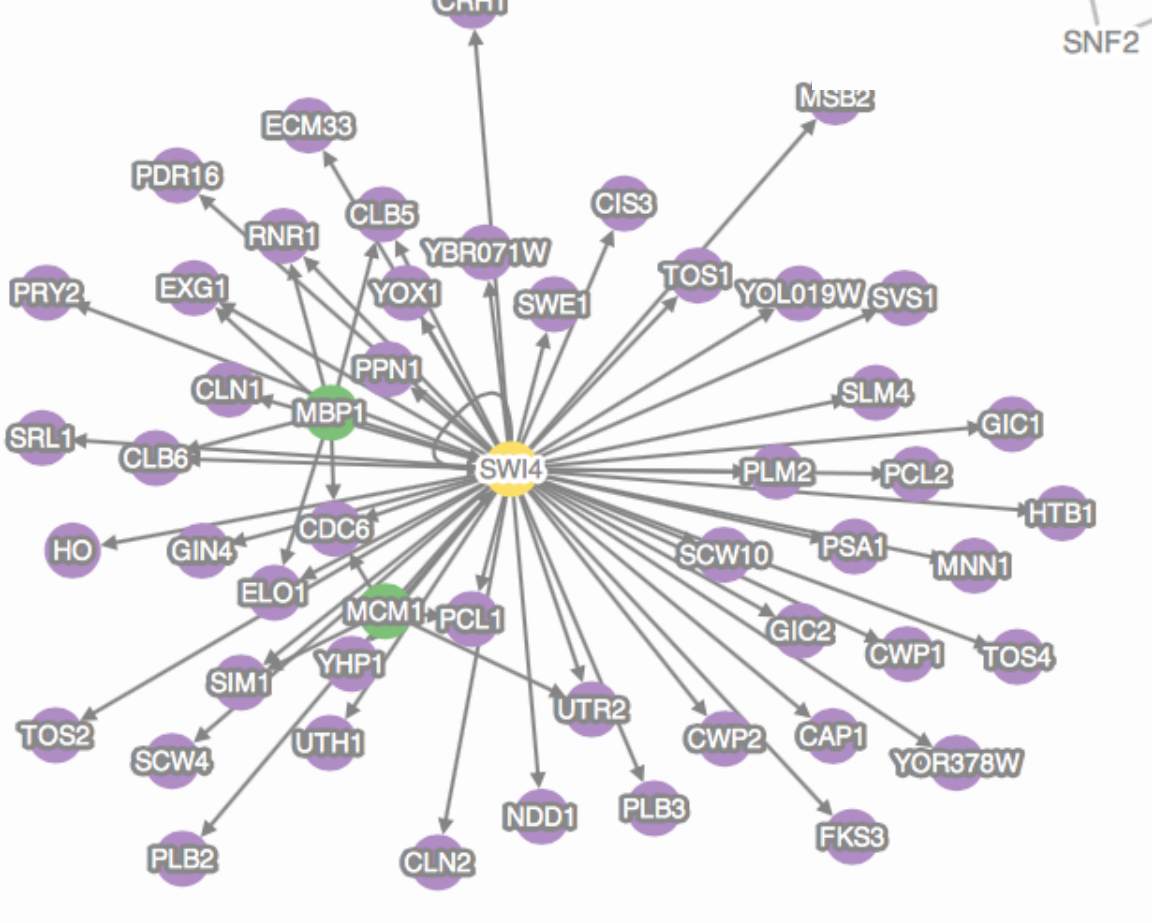
Showing 1 to 13 of 13 entries

DNA Binding Site Motifs

Click on a motif to view YeTFaSCO record.



Network Visualization



### Protein Complexes

Complex: SBF transcription complex

Summary

Associated Gene Ontology Term: SBF transcription complex

Cellular Localization: nucleus

Definition: A protein complex that binds to the Swi4/6 cell cycle box (SCB) promoter element, consensus sequence CRCGAAA, and activates transcription during the G1/S transition of the cell cycle. In Saccharomyces, the complex contains a heterodimer of the DNA binding protein Swi6p and the activator Swi4p, and is associated with additional proteins known as Whi5p and Msa1p.

Genes

4

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Analyze

Gene Name

Description

STB1

Protein with role in regulation of MBF-specific transcription at Start; phosphorylated by Cln-Cdc28p kinases in vitro; unphosphorylated form binds Swi6p, which is required for Stb1p function; expression is cell-cycle regulated; STB1 has a paralog, YOL131W, that arose from the whole genome duplication

SWI4

DNA binding component of the SBF complex (Swi4p-Swi6p); a transcriptional activator that in concert with MBF (Mbp1-Swi6p) regulates late G1-specific transcription of targets including cyclins and genes required for DNA synthesis and repair; Sid2p-independent regulator of cold growth; acetylation at two sites, K1016 and K1066, regulates interaction with Swi6p

SWI6

Transcription cofactor; forms complexes with Swi4p and Mbp1p to regulate transcription at the G1/S transition; involved in meiotic gene expression; also binds Stb1p to regulate transcription at START; cell wall stress induces phosphorylation by Mpk1p, which regulates Swi6p localization; required for the unfolded protein response, independently of its known transcriptional coactivators

WHI5

Repressor of G1 transcription; binds to SCB binding factor (SBF) at SCB target promoters in early G1; phosphorylation of Whi5p by the CDK, Cln3p/Cdc28p relieves repression and promoter binding by Whi5; periodically expressed in G1; WHI5 has a paralog, SRL3, that arose from the whole genome duplication

Showing 1 to 4 of 4 entries

Shared GO Processes

15 entries for 4 genes

Download

10

records per page

Search:

GO Term	Number of genes	P-Value
regulation of transcription involved in G1/S transition of mitotic cell cycle	4	1.35e-08
G1/S transition of mitotic cell cycle	4	2.84e-07
cell cycle phase transition	4	1.16e-06
mitotic cell cycle phase transition	4	1.16e-06
positive regulation of transcription involved in G1/S transition of mitotic cell cycle	2	0.00019
mitotic cell cycle	4	0.00019
regulation of transcription from RNA polymerase II promoter	4	0.00019

Shift your reference!

### Sequences & Strains

Reference Strain: S288C

Location - S288C

Chromosome III: 293835 - 294321

View in: GBrowse | ORF Map

5'

YCR095W-A

HMR

YCRWdelta13

3'

OCA4

ARS317

HMR2

ARS318

GIT1

289000

290000

291000

292000

293000

294000

295000

296000

297000

298000

299000

Subfeatures - S288C

5 entries

CDS

Intron

CDS

Intron

CDS

1

50

100

150

200

250

300

350

400

450

Feature Type

Relative Coordinates

Coordinates

Coord. Version

Seq. Version

CDS

1-105

293835-293939

2011-02-03

1997-01-28

intron

106-159

293940-293993

2011-02-03

1997-01-28

CDS

160-405

293994-294239

2011-02-03

1997-01-28

intron

406-457

294240-294291

2011-02-03

1997-01-28

CDS

458-487

294292-294321

2011-02-03

1997-01-28

Download (txt)

Sequence - S288C

Genomic DNA

CDS

Intron

1

ATGGATGATA

TTTGTAGTAT

GGCGAAAAC

ATAAACAGAA

CTCTGTTTAA

CATTCTAGGT

61

ACTGAGATTG

ATGAATACAA

TCTCAATACT

ATAATCTTT

ATAATGTATG

TTTTCATTTC

121

AAGGATAGCC

TTTGAATCAA

TTTACTAACA

ATACTTCAGT

TTATATGGA

AAGTAATTG

181

ACTAAAGTAG

AGCAACATAC

ATTACACAAA

ATATTTCTTA

ACAATAGOTT

AGAAATATAC

241

CACCACTTAA

AAAAAGAGAA

GAGCCCAAG

GGAATATCAT

CAATATCACC

CAAAGCAGCG

301

GCATTTTATG

AACAGGTTTT

TAGAAGAAG

CAAGCCTTA

ATTCCAAGGA

AAAGAGAGAA

361

GTTCGAAGA

AATGTGGCAT

TACTCCACTT

CAAGTAAGAG

TTTGGGTATG

TAAATGAGA

421

ATCAACTCTA

AAATATACCT

ATACTAACA

TTTGTAGTTC

ATAAATAAAC

GTATGAGATC

481

TAAATAAA

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Alternative Reference Strains

Strain

W303

- lab strain constructed by Rodney Rothstein

Location - W303

W303\_contig00042: 92958 - 93444

5'

YCR095W-A

ARS317

H...

AR...

YCR097W-A

YCRWdelta13

3'

OCA4

HMR2

YCRdelta14

GIT1

88000

89000

90000

91000

92000

93000

94000

95000

96000

97000

98000

Sequence - W303

Genomic DNA

CDS

Intron

1

ATGGATGATA

TTTGTAGTAT

GGCGAAAAC

ATAAACAGAA

CTCTGTTTAA

CATTCTAGGT

61

ACTGAGATTG

ATGAATACAA

TCTCAATACT

ATAATCTTT

ATAATGTATG

TTTTCATTTC

121

AAGGATAGCC

TTTGAATCAA

TTTACTAACA

ATACTTCAGT

TTATATGGA

AAGTAATTG

181

ACTAAAGTAG

AGCAACATAC

ATTACACAAA

ATATTTCTTA

ACAATAGOTT

AGAAATATAC

241

CACCACTTAA

AAAAAGAGAA

GAGCCCAAG

GGAATATCAT

CAATATCACC

CAAAGCAGCG

301

GCATTTTATG

AACAGGTTTT

TAGAAGAAG

CAAGCCTTA

ATTCCAAGGA

AAAGAGAGAA

361

GTTCGAAGA

AATGTGGCAT

TACTCCACTT

CAAGTAAGAG

TTTGGGTATG

TAAATGAGA

421

ATCAACTCTA

AAATATACCT

ATACTAACA

TTTGTAGTTC

ATAAATAAAC

GTATGAGATC

481

TAAATAAA

Download (txt)

Other Strains

Strains Available for Download

AWRI1631

- Haploid derivative of South African commercial wine strain N96

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Resources

GBrowse | Gene/Sequence Resources | ORF Map


S288C only


ATCC/WashU Clones | BLASTN | BLASTP | Design Primers | Restriction Fragment Map | Restriction Fragment Sizes | Six-Frame Translation


S288C vs. other species


BLASTN vs. fungi | BLASTP at NCBI | BLASTP vs. fungi | Fungal Alignment | Synteny Viewer

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