

**Table 6.**

Factor name	Consensus
ABF1-A	[AG]TC[AG][CT]NNNNNACG
ABF1-B	TATCATTNNNACGA
ABF3	ACAAATGGTGTAAAAGAC
ADR1	GGAGAN(1,12)TCTCC
AFT1	[CT][AG]CACCC[AG]
ARGR1	CACCTCTA
ARR1	TTACTAA
BAS1/CAT8	TGACTC
BAS2/PHO2/GRF10	AAA[AT][GT]AGTTAATT[AG]A[AT]T
CAD1/YAP2	TTACTAA
CBF1-A	[AG]TCAC[AG]TG
CBF1-B	[AG]TCAC[AG]TGA
CBF1-C	AA[AT]T[AT]A[AG][AT]CAC[AG]TGATA[AT]A[AT][AT]T
CCBF	NN[CT]CACGAAAA
CIN5/YAP4	TTACTAA
DAL80/81/GLN3	GATAAGN(21)GATAAG
GAL4-A	CGGN(11)CCG
GAL4-B	CGGA[CG]GACAGTC[CG]TCCG
GCN4-A	ATGACTCAT
GCN4-B	[AG][AG]TGACTCA
GCN4-C	GACTCA
GCR1/2/3	C[AT]TCC[AT]
GFI	[AG]TC[AG][CT][CT][CT]NNNACG
GFII	[AG]TCAC[AG]TG
GRF1/RAP1	[AG][AC]ACCCANNCA[CT][CT]
GRF2/REB1-A	CCGGGTAA
GRF2/REB1-B	[CT]NN[CT][CT]ACCCG
GRF2/REB1-C	[CT]NN[CT][CT]ACCCT
GRF10/BAS2/PHO2	AAA[AT][GT]AGTTAATT[AG]A[AT]
GZF3	GATAAC
HAP1-A	CGGN(6)CGG
HAP1-B	CGGNNNTANCGG
HAP1-C	CGCNNNTANCGC
HAP1-D	TGGCCGGGGTTTACGGACGATGA
HAP1-E	GCTAATAGCGATAATAGCGAGGG
HAP2	TNATTGGT
HAP2/3/4	TN[AG]TTGGT
HO	TNNN[CT]GC{GA}N{CA}AN{TG}
HSF1-A	CNNGAANNTTCNNG
HSF1-B	GAAN(2,3)TTC
HSF1-C	TTCTAGAA
IME1	T[AG]G[CG]CG[GC]C[GT]A
INO2	CATGTGAAAT
LEU3	GCCGNNNNCGGC
LYS14	[AT][AT][AT]TCC[AG]N[CT]GGA[CT][CT][CT]
MATalpha1	TCAATGNCAG
MATalpha2-A	CATGTAANNNNNNNNNNNNNNNNTTACATG

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MATalpha2-B	GCTTCCCAATGTAAAAGTACATCATAG
MATalpha2-C	[CT]C[AG]TGTNN[AT]NANNTACATCA
MATalpha1-Q-BOX	TTGA[AT]GG
MBP1/MBF1	ACGCGTNA
MCM1/PRTF/GRM	CCTAATT[AG]GG
MET4	TGGCAAATG
MET31/32	AAACTGTGG
MIG1-A	GCGGGG
MIG1-B	[AT][AT][AT][AT][CG][CT]GGGG
MSN2/4	CCCCT
MTF1-A	TATAAT
MTF1-B	TATAAA
MTF1-C	ATATAAGTA
MTF2	TATAAGTA
OCR1-A	CAAGTGCCGTGCATAATGATGTGGGT
OCR1-B	TACGTCTTTGTCATTATATACCCAAAGG
OCR1-C	TCGTATTTAGTGATTATAATAC
PHO2/BAS2/GRF10	AAA[AT][GT]AGTTAATT[AG]A[AT]T
PHO4	CACGTG
PDR1	CCGCGG
PDR3	CCGCGG
PPR1	CGGN(2,1)CCG
PUT3	CGGN(10)CCG
RAP1-A	CAAAAACCCAT
RAP1-B	AAAAACCCA
RAP1-C	[AG][AC]ACCCANNCA[CT][CT]
REB1-A	CCGGGTAA
REB1-B	TTTTTACCCG
REB2	TCTATTATAATATACGATGA
RLM1	CTA[TA][TA][TA][TA]TAG
RME1	G[AT]ACCTCAA[AG]A
ROX1/REO1	[CT]NN[CT][CT]ACCCG
RPN4	GGTGGCAAAA
SBF-B	[AG]NN[CT]CACGAAAA
SKO1	[GT][GT]ACGTC[AT]
SMP1	ACTACTA[TA][TA][TA][TA]TAG
STE12-A	[AG]TGAAACA
STE12-B	TGAAACA
SWI4	CACGAAAA
TBF1	TTAGGG
TFIID-TBP-A	TATAA
TFIID-TBP-B	TATAAA
TFIID-TBP-C	TATATAAA
TFIID-TBP-D	TATTTAA
TFIIIA-A	GNGN(2)GNGGGNG
TFIIIA-B	GNGGGNGNG
TFIIIB	[CT]CACCA
TFIIIC-A-Box	AGTGGCANNAGT
TFIIIC-B-Box-A	GGTTCGANTCC
TFIIIC-B-Box-B	GGTTCAANTCC

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THI5-A	GAGATT
THI5-B	GAAAATG
TSF1	CCCCT
TUF1	ACACCCATACATTT
Ty2BF	GTCATCATAGA[CT]
UVind	ATGATT
yAP1	[CG]TGACT[AC]A
yATF-B	[GT][AT]CGTCA

binding site predictions from Jennifer 10/09/03

PIP2-OAF1	CGGN(3)TN[AG]N(8,12)CCG
ADR1	C[TC]CC[AG][ATG]N(4,36)[TAC][TC]GG[AG]G
HAP4-A	TN[AG]TTGGT
HAP4-B	TGATTGGT
YAP6	TTACTAA
CAT8	[CT]CGGA[CT][AG][AG]A[AT]GG
LYS14	[AT][AT][AT]TCC[AG]N[CT]GGA[AT][AT][AT]
MCM1	CCNNN[AT][AT][AG]GG

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