Transcription factor binding sites used to build the PSSM

The following table gives the transcription factor binding sites (BS) used to build position-specific scoring matrices. Legend: * = direct experimental evidence. (a*) These genes have been discovered by deletion mapping (Rudolph & Hinnen, 1987); (b*) These BS have been characterized by deletion analysis and by protection from DNAse I digestion by Pho4p, etc. (Oshima et al., 1996); (c) These genes are regulated by the PHO system and possess one or more putative BS for Pho4p (Oshima et al., 1997). the co-regulation of these genes in the Pho4c mutant was also confirmed in microarray experiments of Ogawa et al. (2000).; (d*) These BS have been characterized by deletion analysis (Thomas et al., 1989; Thomas & Surdin-Kerjan, 1997); (e*) These BS have been characterized by mutation in the BS (O'Connell et al., 1995); (f) Northern experiments have shown that the expression of these genes do not occur in met4 mutant and that they possess one or more putative BS for Met4p (Thomas & Surdin-Kerjan, 1997); (g) Northern experiments have shown that these genes are less expressed in met28 mutant and that they possess one or more putative BS for Met4p (Thomas & Surdin-Kerjan, 1997); (h) These genes are structural genes involved in S metabolism and possess one or more putative BS to Met4p (Thomas & Surdin-Kerjan, 1997); (i*) This BS has been characterized by mobility shift assays and DNAse I protection experiment (Blaiseau et al., 1997; Thomas & Surdin-Kerjan, 1997); (j*) This BS has been characterized by mobility shift assays and by kinetics studies (Blaiseau & Thomas, 1998); (k*) This BS has been characterized by deletion analysis (Korch et al., 1991); (l) These structural genes are coregulated and involved in methionine biosynthesis (Blaiseau et al., 1997); (m) These structural genes have one or more putative BS for Met31p/Met32p and are involved in methionine biosynthesis (Korch et al., 1991).

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Pho4p binding gene	from	to	binding site (G/T)	ref.
PHO5	-260	-242	GCACTCACACGTGGGACTA (G)	(a,b,c)
PHO5	-368	-349	AATTAGCACGTTTTCGCATA (T)	(a,b,c)
PHO5	-202	-182	GAGATCGCACATGCCAAATTA (G)	(b,c)
PHO8	-540	-522	TCGGGCCACGTGCAGCGAT (G)	(b,c)
PHO8	-736	-718	ATATTAAGCGTGCGGGTAA (T)	(b,c)
PHO11	-290	-272	GCGTTCACACGTGGGTTTA (G)	(c)
PHO11	-423	-405	AAATTACCACGTTTTCGCA (T)	(c)
PHO81	-350	-332	TTATGGCACGTGCGAATAA (G)	(b,c)
PHO84	-421	-403	TTTCCAGCACGTGGGGCGG (G)	(b,c)
PHO84	-442	-425	TAGTTCCACGTGGACGTG (G)	(b,c)
PHO84	-884	-869	AGTGTCACGTGATAAA (G)	(b,c)
PHO84	-267	-250	TTAAAAACGTGCGTATTA (T)	(b,c)
PHO84	-592	-575	TTACGCACGTTGGTGCTG (T)	(b,c)
PHO86	-197	-179	GCGCCCGCACGTGCTCTTT (G)	(c)
PHO86	-503	-485	ACACACACACGTTAAGAGA (T)	(c)
PHO89	-330	-312	AATGCAGCACGTGGGAGAC (G)	(c)
PHO89	-470	-452	TCATCCCCACGTTGTGCCA (T)	(c)
SPL2	-368	-350	TTTTGCTCACGTGACCGAC (G)	(c)
SPL2	-154	-136	ATGTACGCACGTGGGCGAA (G)	(c)
SPL2	-97	-79	CTTTTCCCACGTGCTCCGC (G)	(c)
SPL2	-38	-20	CTGCAGCCACGTGCCTAGA (G)	(c)
Met4p-Met28p-Cbf1p binding gene	from	to	binding site	ref.
ECM17	-311	-293	ATTTCATCACGTGCGTATT	(f,h)
ECM17	-339	-321	TTTGTCCACGTGATATTTC	(f,h)
MET2	-360	-342	GTATTTTCACGTGATGCGC	(f,h)
MET2	-554	-536	TAATAATCACGTGATATTT	(f,h)
MET3	-367	-349	GAAAAGTCACGTGTAATTT	(f,g,h)
MET3	-384	-366	AAAAGGTCACGTGACCAGA	(f,g,h)
MET6	-540	-522	GCCACATCACGTGCACATT	(h)
MET6	-502	-484	AATATTTCACGTGACTTAC	(h)
MET10	-255	-237	CCACACCACGTGAGCTTAT	(f,g,h)
MET10	-237	-219	TAGAAGCACGTGACCACAA	(f,g,h)
MET14	-235	-217	CTAATTTCACGTGATCAAT	(f,g,h)
MET16	-185	-167	ATCATTTCACGTGGCTAGT	(e,h)
MET17	-306	-288	AAATGGCACGTGAAGCTGT	(d,h)
MET17	-332	-314	TTGAGGTCACATGATCGCA	(d,h)
SAM2	-329	-311	TCTACCCACGTGACTATAA	(h)
SAM2	-381	-363	TCTTCACATGTGATTCATC	(h)
Met31p/Met32p binding gene	from	to	binding site	ref.
MET1	-232	-212	CATAATAAACTGTGAACGGAC	(l)
MET14	-202	-182	CCTCAAAAAATGTGGCAATGG	(l)
MET14	-254	-233	GGAATAAAAGACCGTGCCACTA	(k)
MET14	-272	-251	TAGCTGCACGCTTTTCCAGGAA	(k)
MET14	-45	-24	CATCAAGAAAAGTTGGAATTAT	(k)
MET14	-21	-1	CTCCAAGCACACTGTACACCA	(k)
MET17	-227	-207	TCATGAAAACTGTGTAACATA	(i)
MET2	-313	-293	TGCAAAAAATTGTGGATGCAC	(l,m)
MET28	-159	-139	CTAACACCACAGTTTTGGGCG	(j)
MET3	-259	-239	ACAAAGCCACAGTTTTACAAC	(l,m)
MET30	-168	-148	GGGAAGCCACAGTTTGCGCGG	(l)
MET6	-313	-293	GTCGCAAAACTGTGGTAGTCA	(l)
MET8	-184	-164	GGAAAAAAAATGTGAAAATCG	(l,m)
MET8	-434	-414	TCTTGTCCGCAGTTTTATCTG	(l,m)
MUP3	-188	-168	CGGAAAAAACTGTGGCGTCGC	(l)
SAM1	-283	-263	ACAGGAAAACTGTGGTGGCGC	(l,m)
SAM2	-306	-286	GCTTGAAAACTGTGGCGTTTT	(m)
ZWF1	-173	-153	ATAAGCAAACTGTGGGTTCAT	(l)