Compilation of sequence-specific DNA-binding proteins implicated in transcriptional control in fungi

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Received August 1, 1993; Revised and Accepted September 7, 1993

INTRODUCTION

In recent years it has become abundantly clear that transcriptional regulation involves sequence-specific DNA-binding proteins and a large number of such proteins have been identified in various organisms. Some of these proteins control only one specific gene while others are multifunctional and regulate many diverse cellular phenomena. Additionally, some protein factors interact in a combinatorial fashion in order to control/modulate gene expression. Many of these regulatory proteins appear to be evolutionarily conserved and show sequence homology as well as functional homology between diverse groups of organisms. Hence, the recent compilation of vertebrate-encoded transcription factors by Faisst and Meyer (1) is timely and valuable. Because numerous fungal DNA-binding proteins for which there are no vertebrate homologs have also been characterized, we felt that a compilation of fungal transcription factors will be helpful and will enhance our ability to rapidly identify putative regulatory DNA elements in the upstream regulatory sequences. In this compilation we have concentrated only on those fungal protein factors which have been implicated in regulating transcription by directly binding to specific upstream DNA elements. Factors that affect transcription by interacting with other proteins (instead of directly binding to DNA elements) have not been included. Similarly, DNA-binding proteins such as replication factors, single strand DNA-binding proteins, Z-DNA binding proteins, centromere/telomere binding proteins, chromatin binding proteins and the proteins involved in recombination, repair, transcript elongation and termination are not a part of this compilation. However, some multifunctional transcription factors included in this compilation are involved in some of these other activities.

As in Faisst and Meyer's compilation (1), the transcription factors in the following table are listed in alphabetical order. Synonyms are given in parentheses, and whenever possible the consensus binding sites, protein features, name of the fungus, target genes and references are given in the respective columns. In the remarks column we have mentioned some pertinent information including cellular phenomena affected by the listed factor. Although we have cited numerous relevant reports we refer the readers to the references cited in those original reports.

In some cases discrepancies exist in the literature. DNA-binding sequences reported in one publication were found to be different from those reported in another relevant publication. Whenever possible we have listed both sequences, however, it is possible that we have missed some discrepancies and/or elements. The information presented here may be restricted in some cases and we urge the readers to refer to the original reports cited in the

table. It is important to note that in many cases the *in vivo* roles of these factors are not clear and in some cases even the evidence suggesting the involvement of these factors in transcription is limited.

Although the genes for many fungal mating type factors have been cloned and sequenced, and analysis of the conceptual polypeptides shows that many of these factors contain homeodomains, suggesting that these factors might be involved in transcriptional regulation, their roles in transcriptional regulation have not been clearly demonstrated. Hence, these factors have been omitted from this compilation.

ACKNOWLEDGEMENTS

This work was supported by the NIH grant 1R15GM47556-01. We thank Dr G.A.Marzluf at Ohio State University (Columbus, OH) for helpful hints and suggestions.

REFERENCES

1. Faisst, S. and Meyer, S. (1992) Nucl. Acids Res. 20, 3–26.
2. Tymon, M., Kües, U., Richardson, W. V. J. and Casselton, L. A. (1992) EMBO J. 11, 1805–1813.
3. Kovari, L. Z. and Cooper, T. G. (1991). J. Bacteriol. 173, 6332–6338.
4. Rhode, P. R., Elsasser, S. and Campbell, J.L. (1992) Mol. Cell. Biol. 12, 1064–1077.
5. Trawick, J. D., Kraut, N., Simon, F. R. and Poyton, R. O. (1992) Mol. Cell. Biol. 12, 2302–2314.
6. Gonçalves, P. M., Maurer, K., Mager, W. H. and Planta, R. J. (1992) Nucl. Acids Res. 9, 2211–2215.
7. Luche, R. M., Sumrada, R. and Cooper, T. G. (1990). Mol. Cell. Biol. 10, 3884–3895.
8. Buchman, A. R., Kimmerly, W. J., Rine, J. and Kornberg, R. D. (1988) Mol. Cell. Biol. 8, 210–225.
9. Evans, C. F., Engelke, D. R. and Thiele, D. J. (1990) Mol. Cell. Biol. 10, 426–429.
10. Fürst, P. and Hamer, D. (1989) Proc. Natl. Acad. Sci. USA 86, 5267–5271.
11. Gralla, E. B., Thiele, D. J., Silar, P. and Valentine, J. S. (1991) Proc. Natl. Acad. Sci. USA 88, 8558–8562.
12. Casas-Finet, J. R., Hu, S., Hamer, D. and Karpel, R. L. (1992) Biochemistry 31, 6617–6626.
13. Dameron, C. T., Winge, D. R., George, G. N., Sansone, M., Hu, S. and Hamer, D. (1991) Proc. Natl. Acad. Sci. USA 88, 6127–6131.
14. Buchman, C., Skroch, P., Welch, J., Fogel, S. and Karin, M. (1989) Mol. Cell. Biol. 9, 4091–4095.
15. Vincent, A. C. and Struhl, K. (1992) Mol. Cell. Biol. 12, 5394–5405.
16. Thukral, S. K., Eisen, A. and Young, E. T. (1991) Mol. Cell. Biol. 11, 1566–1577.

17. Thukral, S. K., Morrison, M. L. and Young, E. T. (1992) *Mol. Cell. Biol.* 12, 2784–2792.
18. Thukral, S. K., Tavianini, M. A., Blumberg, H. and Young, E. T. (1989) *Mol. Cell. Biol.* 9, 2360–2369.
19. Blumberg, H., Eisen, A., Sledziewski, A., Bader, D. and Young, E. T. (1987) *Nature* 328, 443–445.
20. Taylor, W. E. and Young, E. T. (1990) *Proc. Natl. Acad. Sci. USA* 87, 4098–4102.
21. Kulmburg, P., Sequeval, D., Lenouvel, F., Mathieu, M. and Felenbok, B. (1992) *Mol. Cell. Biol.* 12, 1932–1939.
22. Kulmburg, P., Judewicz, N., Mathieu, M., Lenouvel, F., Sequeval, D. and Felenbok, B. (1992) *J. Biol. Chem.* 267, 21146–21153.
23. van Heeswijk, R. and Hynes, M. J. (1991) *Nucl. Acids Res.* 19, 2655–2660.
24. Littlejohn, T. G. and Hynes, M. J. (1991) *Mol. Gen. Genet.* 235, 81–88.
25. Andrianopoulos, A. and Hynes, M. J. (1988) *Mol. Cell. Biol.* 8, 3532–3541.
26. Davis, M. A. and Hynes, M. J. (1989) *Trends in Genetics* 5, 11–19.
27. Wang, W. X., Hynes, M. J. and Davis, M. A. (1992) *Gene* 122, 147–154.
28. Zhou, P., Szczypka, M. S., Sosinowski, T. and Thiele, D. J. (1992) *Mol. Cell. Biol.* 12, 3766–3775.
29. Nagata, O., Takashima, T., Tanaka, M., Tsukagoshi, N. (1993) *Mol. Gen. Genet.* 237, 251–260.
30. Harshman, K. D., Moye-Rowley, W. S. and Parker, C. S. (1988) *Cell* 53, 321–330.
31. Schnell, N., Krems, B. and Entian, K.-D. (1992) *Curr. Genet.* 21, 269–273.
32. Kudla, B., Caddick, M. X., Longdon, T., Martinez-Rossi, N. M., Bennet, C. F., Sibley, S., Davies, R. W. and Arst, H. N. Jr. (1990) *EMBO J.* 9, 1355–1364.
33. de Rijcke, M. D., Seneca, S., Punyammalee, B., Glansdorff, N. and Crabeel, M. (1992) *Mol. Cell. Biol.* 12, 68–81.
34. Dubois, E., Bercy, J. and Messenguy, F. (1987) *Mol. Gen. Genet.* 207, 142–148.
35. Dubois, E., Bercy, J., Descampes, F. and Messenguy, F. (1987) *Gene* 55, 265–275.
36. Dubois, E. and Messenguy, F. (1991) *Mol. Cell. Biol.* 11, 2162–2168.
37. Qiu, H. F., Dubois, E. and Messenguy, F. (1991) *Mol. Cell. Biol.* 11, 2169–2179.
38. Messenguy, F., and Dubois, E. (1993) *Mol. Cell. Biol.* 13, 2586–2592.
39. Messenguy, F., Dubois, E. and Boonchird, C. (1991) *Mol. Cell. Biol.* 11, 2852–2863.
40. Lin, Y.-S. and Green, M. R. (1989) *Proc. Natl. Acad. Sci. USA* 86, 109–113.
41. Jones, R. H., and Jones, N. C. (1989) *Proc. Natl. Acad. Sci. USA* 86, 2176–2180.
42. Schulz, B., Banuett, F., Dahl, M., Schlesinger, R., Schäfer, W., Martin, T., Herskowitz, I. and Kahmann, R. (1990) *Cell* 60, 295–306.
43. Daignan-Fornier, B. and Fink, G. R. (1992) *Proc. Natl. Acad. Sci. USA* 89, 6746–6750.
44. Tice-Baldwin, K., Fink, G. R. and Arndt, K. T. (1989) *Science* 246, 931–935.
45. Bürglin, T. R. (1988) *Cell* 53, 339–340.
46. Sengstag, C. and Hinnen, A. (1987) *Nucl. Acids Res.* 15, 233–246.
47. Chang, Y. C. and Timberlake, W. E. (1993) *Genetics* 133, 29–38.
48. Adams, T. H., Deising, H. and Timberlake, W. E. (1990) *Mol. Cell. Biol.* 10, 1815–1821.
49. Ebbola, D. J., Paluh, J. L., Plamann, M., Sachs, M. S. and Yanofsky, C. (1991) *Mol. Cell. Biol.* 11, 928–934.
50. Paluh, J. L., Orbach, M. J., Legerton, T. L. and Yanofsky, C. (1988) *Proc. Natl. Acad. Sci. USA* 85, 3728–3732.
51. Paluh, J. L. and Yanofsky, C. (1991) *Mol. Cell. Biol.* 11, 935–944.
52. Bram, R. J. and Kornberg, R. D. (1987) *Mol. Cell. Biol.* 7, 403–409.
53. Cai, M. and Davis, R. W. (1990) *Cell* 61, 437–446.
54. Cai, M. and Davis, R. W. (1989) *Mol. Cell. Biol.* 9, 2544–2550.
55. Baker, R. E. and Mason, D. C. (1990) *Mol. Cell. Biol.* 10, 2458–2467.
56. Mellor, J., Rathjen, J., Jiang, W. and Dowell, S. J. (1990) *Nucl. Acids Res.* 19, 2961–2969.
57. Dowzer, C. E. A. and Kelly, J. M. (1991) *Mol. Cell. Biol.* 11, 5701–5709.
58. Kulmburg, P., Mathieu, M., Dowzer, C., Kelly, J. and Felenbok, B. (1993) *Mol. Microbiol.* 7, 847–857.
59. Fu, Y.-H., Paietta, J. V., Mannix, D. G. and Marzluf, G. A. (1989) *Mol. Cell. Biol.* 9, 1120–1127.
60. Fu, Y.-H. and Marzluf, G. A. (1990) *J. Biol. Chem.* 265, 11942–11947.
61. Kanaan, M. N. and Marzluf, G. A. (1991) *Mol. Cell. Biol.* 11, 4356–4362.
62. Paietta, J. V. (1992) *Mol. Cell. Biol.* 12, 1568–1577.
63. Paietta, J. V., Akins, R. A., Lambowitz, A. M. and Marzluf, G. A. (1987) *Mol. Cell. Biol.* 7, 2506–2511.
64. Coornaert, D., Vissers, S. and Andre, B. (1991) *Gene* 97, 163–171.
65. Coornaert, D., Vissers, S., Andre, B. and Grenson, M. (1992) *Curr. Genet.* 21, 301–307.
66. Andre, B., Hein, C., Grenson, M. and Jauniaux, J.-C. (1993) *Mol. Gen. Genet.* 237, 17–25.
67. Andre, B. (1990) *Mol. Gen. Genet.* 220, 269–276.
68. Cunningham, T. S. and Cooper, T. G. (1991) *Mol. Cell. Biol.* 11, 6205–6215.
69. Olive, M. G., Daugherty, J. R. and Cooper, T. G. (1991) *J. Bacteriol.* 173, 255–261.
70. Mai, B. and Lipp, B. (1993) *FEBS Letters* 321, 153–158.
71. Gardner, K. H., Pan, T., Narula, S., Rivera, E. and Coleman, J. E. (1991) *Biochemistry* 30, 11292–11302.
72. Johnston, M. (1987) *Microbiol. Rev.* 51, 458–476.
73. Pan, T. and Coleman, J. E. (1990) *Biochemistry* 29, 3023–3029.
74. Donald, R. G. K., Schindler, U., Batschauer, A. and Cashmore, A. R. (1990) *EMBO J.* 9, 1727–1735.
75. Mösch, H.-U., Scheier, B., Lahti, R., Mäntsälä, P. and Braus, G. H. (1991) *J. Biol. Chem.* 266, 20453–20456.
76. Arndt, K. and Fink, G. R. (1986) *Proc. Natl. Acad. Sci. USA* 83, 8516–8520.
77. Türkler, S. and Farabaugh, P. J. (1993) *Mol. Cell. Biol.* 13, 2091–2103.
78. Suckow, M., von Wilcken-Bergmann, B. and Müller-Hill, B. (1993) *EMBO J.* 12, 1193–1200.
79. Baker, H. V. (1991) *Proc. Natl. Acad. Sci. USA* 88, 9443–9447.
80. Uemura, H. and Jigami, Y. (1992) *Mol. Cell. Biol.* 12, 3834–3842.
81. Uemura, H. and Jigami, Y. (1992) *J. Bacteriol.* 174, 5506–5532.
82. Willett, C. E., Gelfman, C. M. and Holland, M. J. (1993) *Mol. Cell. Biol.* 13, 2623–2633.
83. Huie, M. A., Scott, E. W., Drazinic, C. M., Lopez, M. C., Hornstra, I. K., Yang, T. P. and Baker, H. V. (1992) *Mol. Cell. Biol.* 12, 2690–2700.
84. Dorsman, J. C., van Heeswijk, W. C. and Grivell, L. A. (1990) *Nucl. Acids Res.* 18, 2769–2776.
85. Minehart, P. L. and Magasanic, B. (1991) *Mol. Cell. Biol.* 11, 6216–6228.
86. Miller, S. M. and Magasanic, B. (1991) *Mol. Cell. Biol.* 11, 6229–6247.
87. Daugherty, J. R., Rai, R., El Berry, H. M. and Copper, T. G. (1993) *J. Bacteriol.* 175, 64–73.
88. Pfeifer, K., Arcangioli, B. and Guarente, L. (1987) *Cell* 49, 9–18.
89. Pfeifer, K., Kim, K.-S., Kogan, S. and Guarente, L. (1989) *Cell* 56, 291–301.
90. Pfeifer, K., Prezant, T. and Guarente, L. (1987) *Cell* 49, 19–27.
91. Zhang, L., Bermingham-McDonogh, O., Turcotte, B. and Guarente, L. (1993) *Proc. Natl. Acad. Sci. USA* 90, 2851–2855.
92. Forsburg, S. L. and Guarente, L. (1989) *Genes Dev.* 3, 1166–1178.
93. Olesen, J. T., Hahn, S. and Guarente, L. (1987) *Cell* 5, 953–961.
94. Olesen, J. T., Fikes, J. D. and Guarente, L. (1991) *Mol. Cell. Biol.* 11, 611–619.
95. Zhu, G., Muller, E. G. D., Amacher, S. L., Northrop, J. L. and Davis, T. N. (1993) *Mol. Cell. Biol.* 13, 1779–1787.
96. Silar, P., Butler, G. and Thiele, D. (1991) *Mol. Cell. Biol.* 11, 1232–1238.
97. Sorger, P. K. and Nelson, H. C. M. (1989) *Cell* 59, 807–813.
98. Sorger, P. K. and Pelham, H. R. B. (1987) *EMBO J.* 6, 3035–3041.
99. Peteranderl, R. and Nelson, H. C. M. (1992) *Biochemistry* 31, 12272–12276.
100. Yang, W., Gahl, W. and Hamer, D. (1991) *Mol. Cell. Biol.* 11, 3676–3681.
101. Wiederrecht, G., Shuey, D. J., Kibbe, W. A. and Parker, C. S. (1987) *Cell* 48, 507–515.
102. Witte, M. M. and Dickson, R. C. and Coleman, J. E. (1990) *Mol. Cell. Biol.* 10, 5128–5137.
103. Pan, T., Halvorsen, Y.-D., Dickson, R. C. and Coleman, J. E. (1990) *J. Biol. Chem.* 265, 21427–21429.
104. Salmeron, J. M. and Johnston, S. A. (1986) *Nucl. Acids Res.* 14, 7767–7781.
105. Wray, C. V., Witte, M. M., Dickson, R. C. and Riley, M. I. (1987) *Mol. Cell. Biol.* 7, 1111–1121.
106. Zhou, K. and Kohlhaw, G. B. (1990) *J. Biol. Chem.* 265, 17409–17412.
107. Martinez-Arias, A., Yost, H. J. and Casadaban, M. J. (1984) *Nature* 307, 740–742.
108. Sze, J.-Y., Wontner, M., Jaehning, J. A. and Kohlhaw, G. B. (1992) *Science* 258, 1143–1144.
109. Sze, J.-Y. and Kohlhaw, G. B. (1993) *J. Biol. Chem.* 268, 2505–2512.
110. Kim, J. and Michels, C. A. (1988) *Curr. Genet.* 14, 319–323.

111. Miller, A. M., MacKay, V. L. and Nasmyth, K. A. (1985) *Nature* 314, 598–603.
112. Covitz, P. A., Herskowitz, I. and Mitchell, A. P. (1991) *Genes Dev.* 5, 1982–1989.
113. Goutte, C. and Johnson, A. D. (1988) *Cell* 55, 875–882.
114. Ammerer, G. (1990) *Genes Dev.* 4, 299–312.
115. Glass, N. L., Grotelueschen, J. and Metznerberg, R. L. (1990) *Proc. Natl. Acad. Sci. USA* 87, 4912–4916.
116. Jarvis, E. E., Hagen, D. C. and Sprague, G. F. (1988) *Mol. Cell. Biol.* 8, 309–320.
117. Johnson, A. D. and Herskowitz, I. (1985) *Cell* 42, 237–247.
118. Wolberger, C., Vershon, A. K., Liu, B., Johnson, A. D. and Pabo, C. O. (1991) *Cell* 67, 517–528.
119. Vershon, A. K. and Johnson, A. D. (1993) *Cell* 72, 105–112.
120. Keleher, C. A., Goutte, C. and Johnson, A. D. (1988) *Cell* 53, 927–936.
121. Herschenbach, B. M. and Johnson, A. D. (1993) *Mol. Cell. Biol.* 13, 4029–4038.
122. Kelly, M., Burke, J., Smith, M., Klar, A. and Beach, D. (1988) *EMBO J.* 7, 1537–1547.
123. Dirick, L., Moll, T., Auer, H. and Nasmyth, K. (1992) *Nature* 357, 508–512.
124. Sidorova, L. and Breeden, L. (1993) *Mol. Cell. Biol.* 13, 1069–1077.
125. Breeden, L. and Nasmyth, K. (1987) *Cell* 48, 389–397.
126. Lowndes, N. F., McInerney, C. J., Johnson, A. L., Fantes, P. A. and Johnston, L. H. (1992) *Nature* 355, 449–452.
127. Lowndes, N. F., Johnson, A. L., Breeden, L. and Johnston, L. H. (1992) *Nature* 357, 505–506.
128. Lowndes, N. F., Johnson, A. L. and Johnston, L. H. (1991) *Nature* 350, 247–249.
129. Wynne, J. and Treisman, R. (1992) *Nucl. Acids Res.* 20, 3297–3303.
130. Passmore, S. and Tye, B.-K. (1989) *Genes Dev.* 3, 921–935.
131. Elble, R., Tye, B.-K. (1991) *Proc. Natl. Acad. Sci. USA* 88, 10966–10970.
132. Christ, C. and Tye, B.-K. (1991) *Genes Dev.* 5, 751–763.
133. Errede, B. (1993) *Mol. Cell. Biol.* 13, 57–62.
134. Thomas, D., Jacquemin, I., Surdin-Kerjan, Y. (1992) *Mol. Cell. Biol.* 12, 1719–1727.
135. Nehlin, J. O. and Ronne, H. (1990) *EMBO J.* 9, 2891–2898.
136. Nehlin, J. O., Carlberg, M. and Ronne, H. (1991) *EMBO J.* 10, 3373–3377.
137. Hohman, S., Huse, K., Valentin, E., Mbonyi, K., Thevelein, J. M. and Zimmermann, F. K. (1992) *J. Bacteriol.* 174, 4183–4188.
138. Jang, S. H. and Jaehning, J. A. (1991) *J. Biol. Chem.* 266, 22671–22677.
139. Riemen, G. and Michaelis, G. (1993) *Mol. Gen. Genet.* 237, 49–57.
140. Lisowski, T. (1990) *Mol. Gen. Genet.* 220, 186–190.
141. Ticho, B. S. and Getz, G. S. (1988) *J. Biol. Chem.* 263, 10096–10103.
142. Burger, G., Strauss, J., Scazzocchio, C. and Lang, B. F. (1991) *Mol. Cell. Biol.* 11, 5746–5755.
143. Yuan, G. F., Fu, Y.-H. and Marzluf, G. A. (1991) *Mol. Cell. Biol.* 11, 5735–5744.
144. Fu, Y.-H. and Marzluf, G. A. (1990) *Proc. Natl. Acad. Sci. USA* 87, 5331–5335.
145. Fu, Y.-H. and Marzluf, G. A. (1990) *Mol. Cell. Biol.* 10, 1056–1065.
146. Fu, Y.-H. and Marzluf, G. A. (1987) *Mol. Cell. Biol.* 7, 1691–1696.
147. Dickman, M. B. and Leslie, J. F. (1992) *Mol. Gen. Genet.* 235, 458–462.
148. Kang, S. and Metznerberg, R. L. (1990) *Mol. Cell. Biol.* 10, 5839–5848.
149. Bartuv, J., Valansi, C. and Shalit, C. (1993) *Biochem. Biophys. Res. Commun.* 191, 750–758.
150. Toda, T., Shimanuki, M., Saka, Y., Yamano, H., Adachi, Y., Shirakawa, M., Kyogoku, Y. and Yanagida, M. (1992) *Mol. Cell. Biol.* 12, 5474–5484.
151. Toda, T., Shimanuki, M. and Yanagida, M. (1991) *Genes Dev.* 5, 60–73.
152. Jones, R. H., Moreno, S., Nurse, P. and Jones, N. C. (1988) *Cell* 53, 659–667.
153. Meyers, S., Schauf, W., Balzi, E., Wagner, M., Goffeau, A. and Golin, J. (1992) *Curr. Genet.* 21, 431–436.
154. Balzi, E., Chen, W., Ulaszewski, S., Capiaux, E. and Goffeau, A. (1987) *J. Biol. Chem.* 262, 16871–16879.
155. Ruden, D. M. (1990) *Mol. Cell. Biol.* 10, 1432–1438.
156. Fisher, F., Jayaraman, P.-S. and Goding, C. R. (1991) *Oncogene* 6, 1099–1104.
157. Sophianopoulou, V., Suarez, T., Dhalluin, G. and Scazzocchio, C. (1993) *Mol. Gen. Genet.* 236, 209–213.
158. Kammerer, B., Guyonvarch, A. and Hubert, J. I. (1984) *J. Mol. Biol.* 180, 239–250.
159. Roy, A., Exinger, F. and Losson, R. (1990) *Mol. Cell. Biol.* 10, 5257–5270.
160. Sebastian, J. and Sancar, G. B. (1991) *Proc. Natl. Acad. Sci. USA* 88, 11251–11255.
161. Siddiqui, A. H. and Brandiss, M. C. (1989) *Mol. Cell. Biol.* 9, 4706–4712.
162. Siddiqui, A. H. and Brandiss, M. C. (1988) *Mol. Cell. Biol.* 8, 4634–4641.
163. Marczak, J. E. and Brandiss, M. C. (1991) *Mol. Cell. Biol.* 11, 2609–2619.
164. Asch, D. K., Orejas, M., Geever, R. F. and Case, M. E. (1991) *Mol. Gen. Genet.* 230, 337–344.
165. Baum, J. A., Geever, R. F. and Giles, N. H. (1987) *Mol. Cell. Biol.* 7, 1256–1266.
166. Geever, R. F., Huiet, L., Baum, J. A., Tyler, B. M., Patel, V. B., Rutledge, B. J., Case, M. E. and Giles, N. H. (1989) *J. Mol. Biol.* 207, 15–34.
167. Tyler, B. M., Geever, R. F., Case, M. E. and Giles, N. H. (1984) *Cell* 36, 493–502.
168. Henry, Y. A., Chambers, A., Tsang, J. S. H., Kingsman, A. J. and Kingsman, S. M. (1990) *Nucl. Acids Res.* 18, 2617–2624.
169. Hardy, C. F. J., Balderes, D. and Shore, D. (1992) *Mol. Cell. Biol.* 12, 1209–1217.
170. Hardy, C. F. J., Sussel, L. and Shore, D. (1992) *Genes Dev.* 6, 801–814.
171. Kyron, G., Boakye, K. A. and Lustig, A. J. (1992) *Mol. Cell. Biol.* 12, 5159–5173.
172. Shore, D. and Nasmyth, K. (1987) *Cell* 51, 721–732.
173. Chambers, A., Tsang, J. S. H., Stanway, C., Kingsman, A. J. and Kingsman, S. M. (1989) *Mol. Cell. Biol.* 9, 5516–5524.
174. McNeil, J. B., Dykshorn, P., Huy, J. N. and Small, S. (1990) *Curr. Genet.* 18, 405–412.
175. Buchman, A. R., Lue, N. F. and Kornberg, R. D. (1988) *Mol. Cell. Biol.* 8, 5086–5099.
176. Devlin, C., Tice-Baldwin, K., Shore, D. and Arndt, K. T. (1990) *Mol. Cell. Biol.* 11, 3642–3651.
177. Scott, E. W. and Baker, H. V. (1993) *Mol. Cell. Biol.* 13, 543–550.
178. Trueblood, C. E. and Poyton, R. O. (1988) 120, 671–680.
179. Morrow, B. E., Ju, Q. and Warner, J. R. (1990) *J. Biol. Chem.* 265, 20778–20783.
180. Ju, Q., Morrow, B. E. and Warner, J. R. (1990) *Mol. Cell. Biol.* 10, 5226–5234.
181. Wang, H., Nicholson, P. R. and Stillman, D. J. (1990) *Mol. Cell. Biol.* 10, 1743–1753.
182. Estruh, F. (1991) *Nucl. Acids Res.* 19, 4873–4877.
183. Covitz, P. A., Herskowitz, I. and Mitchell, A. P. (1991) *Genes Dev.* 5, 1982–1989.
184. Lowry, C. V., Cerdan, M. E. and Zitomer, R. S. (1990) *Mol. Cell. Biol.* 10, 5921–5926.
185. Keng, T. (1992) *Mol. Cell. Biol.* 12, 2616–2623.
186. Zitomer, R. S. and Lowry, C. V. (1992) *Microbiol. Rev.* 56, 1–11.
187. Fujita, A., Kikuchi, Y., Kuhara, S., Misumi, Y., Matsumoto, S. and Kobayashi, H. (1989) *gene* 85, 321–328.
188. Blumberg, H. and Silver, P. (1991) *Gene* 107, 101–110.
189. Nehlin, J. O., Carlberg, M. and Ronne, H. (1992) *Nucl. Acids Res.* 20, 5271–5278.
190. Okazaki, N., Okazaki, K., Tanaka, K. and Okayama, H. (1991) *Nucl. Acids Res.* 19, 7043–7047.
191. Sugimoto, A., Yuichi, I., Maeda, T., Watanabe, Y. and Yamamoto, M. (1991) *Genes Dev.* 5, 1990–1999.
192. Errede, B. and Ammerer, G. (1989) *Genes Dev.* 3, 1349–1361.
193. Dolan, J. W., Kirkman, C. and Fields, S. (1989) *Proc. Natl. Acad. Sci. USA* 86, 5703–5707.
194. Kirkman-Correa, C., Stroke, I. L. and Fields, S. (1993) *Mol. Cell. Biol.* 13, 3765–3772.
195. Yuan, Y. O. and Fields, S. (1991) *Mol. Cell. Biol.* 11, 5910–5918.
196. Nasmyth, K., Adolf, G., Lydall, D. and Seddon, A. (1990) *Cell* 62, 631–647.
197. Nagai, K., Nakaseko, Y., Nasmyth, K. and Rhodes, D. (1988) *Nature* 332, 284–286.
198. Stillman, D. J., Bankier, A. T., Seddon, A., Groenhout, E. G. and Nasmyth, K. A. (1988) *EMBO J.* 7, 485–494.
199. Hahn, S., Buratowski, S., Sharp, P. A. and Guarente, L. (1989) *EMBO J.* 8, 3379–3382.
200. Feaver, W. J., Gileadi, O. and Kornberg, R. D. (1991) *J. Biol. Chem.* 266, 19000–19005.
201. Cavallini, B., Faus, I., Matthes, H., Chipoulet, J. M., Winsor, B., Egly, J. M. and Chambon, P. (1989) *Proc. Natl. Acad. Sci. USA* 86, 9803–9807.

202. Horikoshi, M., Yamamoto, T., Ohkuma, Y., Weil, P. A. and Roeder, R. G. (1990) *Cell* 61, 1171–1178.
203. Horikoshi, M., Wang, K., Fujii, H., Cromlish, J. A., Weil, P. A. and Roeder, R. G. (1989) *Nature* 341, 299–302.
204. Fikes, J. D., Becker, D. M., Winston, F. and Guarente, L. (1990) *Nature* 346, 291–293.
205. Goyer, C., Lee, H. S., Malo, D. and Sonenberg, N. (1992) *DNA Cell Biol.* 11, 579–585.
206. Struhl, K. (1987) *Cell* 49, 295–297.
207. Kuddus, R. and Schmidt, M. C. (1993) *Nucl. Acids Res.* 21, 1789–1796.
208. Zewel, L. and Reinberg, D. (1993) *Progress in Nucleic Acid Research and Molecular Biology* 44, 67–105.
209. Woychik, N. A. and Young, R. A. (1992) *Proc. Natl. Acad. Sci. USA* 89, 3999–4003.
210. Wang, C. K. and Weil, P. A. (1989) *J. Biol. Chem.* 264, 1092–1097.
211. Archambault, J., Milne, C. A. and Schappert, K. T., Baum, B., Friesen, J. D. and Segall, J. (1992) *J. Biol. Chem.* 267, 3282–3288.
212. Challice, J. M. and Segall, J. (1989) *J. Biol. Chem.* 264, 20060–20067.
213. Hanas, J. S., Gaskins, C. J., Smith, J. F. and Ogilvie, M. K. (1992) *Progress in Nucleic Acid Research and Molecular Biology* 43, 205–239.
214. Kassavetis, G. A., Braun, B. R., Nguyen, L. M. and Geiduschek, E. P. (1990) *Cell* 60, 235–245.
215. Kassavetis, G. A., Riggs, D. L., Negri, R., Nguyen, L. H. and Geiduschek, E. P. (1989) *Mol. Cell. Biol.* 9, 2551–2566.
216. Kassavetis, G. A., Bartholomew, B., Blanco, J. A., Johnson, T. E. and Geiduschek, E. P. (1991) *Proc. Natl. Acad. Sci. USA* 88, 7308–7312.
217. Klekamp, M. S. and Weil, P. A. (1986) *J. Biol. Chem.* 261, 2819–2827.
218. Bartholomew, B., Kassavetis, G. A. and Geiduschek, E. P. (1991) *Mol. Cell. Biol.* 11, 5181–5189.
219. Gabrielsen, O. S. and Sentenac, A. (1991) *Trends Biochem. Sci.* 16, 412–416.
220. Bartholomew, B., Kassavetis, G. A., Braun, B. R. and Geiduschek, E. P. (1990) *EMBO J.* 9, 2197–2205.
221. Swanson, R. N., Conesa, C., Lefebvre, O., Carles, C., Ruet, A., Quemeneur, E., Gagnon, J. and Sentenac, A. (1991). *Proc. Natl. Acad. Sci. USA* 88, 4887–4891.
222. Evans, C. F. and Engelke, D. R. (1991) *Biochem. Biophys. Res. Commun.* 176, 826–832.
223. Lefebvre, O., Carles, C., Conesa, C., Swanson, R. N., Bouet, F., Riva, M. and Sentenac, A. (1992) *Proc. Natl. Acad. Sci. USA* 89, 10512–10516.
224. Parsons, M. C. and Weil, P. A. (1990) *J. Biol. Chem.* 265, 5095–5103.
225. Kobayashi, N. and McEntee, K. (1993) *Mol. Cell. Biol.* 13, 248–256.
226. Suarez, T., Oestreicher, N., Peñalva, M. A. and Scazzocchio, C. (1991) *Mol. Gen. Genet.* 230, 369–375.
227. Campbell, W. H. and Kinghorn, J. R. (1990) *Trends Biochem. Sci.* 15, 315–319.
228. Kulkens, T., Riggs, D. L., Heck, J. D., Planta, R. J. and Nomura, M. (1991) *Nucl. Acids Res.* 19, 5363–5370.
229. Mei, B., Budde, A. D. and Leong, S. A. (1993) *Proc. Natl. Acad. Sci. USA* 90, 903–907.
230. Luche, R. M., Smart, W. C. and Cooper, T. G. (1992) *Proc. Natl. Acad. Sci. USA* 89, 7412–7416.
231. Park, H.-D., Luche, R. M. and Cooper, T. G. (1992) *Nucl. Acids Res.* 20, 1909–1915.

Table.

Protein factor	Recognition Site ^b	Protein features ^c	Organism(s)	Target gene(s) ^d	References	Remarks ^f
A42		unusual homeodomain, POU related	<i>Coprinus cinereus</i>		2	Transcriptional activator, <i>A</i> mating type factor, regulates formation of clamp cells.
ABF1 (May be the same as GF1, TAF, TyBF, BAP1, BAF1, OBF1, SUF and SBF-B).	RTCRY N ₃ ACG, TATCATTTNNACGA	atypical zinc finger domain in N-terminal region	<i>Saccharomyces cerevisiae</i> , <i>Kluyveromyces fragilis</i>	<i>CAR1</i> , <i>COX6</i> , <i>ARS</i> elements, silencer elements in mating type loci HMR and HML, ribosomal/mitochondrial proteins and glycolytic enzymes.	3, 4, 5, 6, 7, 8	Involved in replication, transcriptional activation and repression. Multifunctional DNA binding protein. Related to RAP1.
ACE1 (CUP2)	UAS _c TC(T) ₄₋₆ GCTG	monomer, polynuclear Cu(I)-cysteine thiolate cluster	<i>S. cerevisiae</i>	<i>CUP1</i> , <i>SOD1</i>	9, 10, 11, 12, 13, 14	Transcriptional activator. Binds to UAS _c of metallothionein gene at multiple sites in a Cu and Ag inducible manner.
ACR1	ATGACGTCAT	bZIP homodimer	<i>S. cerevisiae</i>	<i>HIS3</i>	15	Similar to mammalian cAMP-responsive transcriptional regulators CREB and CREM, less similar to yeast GCN4 and YAP1. Repressor.
ADR1	TCTCAACTTATAA-GTTGGAGA (UAS1)	two zinc fingers, binds as a dimer	<i>S. cerevisiae</i>	<i>ADH2</i>	16, 17, 18, 19, 20	Activation of glucose repressible <i>ADH2</i> gene.
ALCR	CCGCA (half site)	binuclear zinc binding domain, contains 6 cysteines. (C6 class)	<i>Aspergillus nidulans</i>	<i>alcR</i> , <i>alcA</i> , <i>aldA</i>	21, 22	Activator in ethanol utilization pathway, three binding sites; two direct repeats and one inverted repeat of the half site.
amdR	TCGGCGAAGCCAGC-CAATCA (CCAAT-box is underlined)	six zinc fingers	<i>A. nidulans</i> , <i>Aspergillus oryzae</i>	<i>amdS</i> , <i>gatA</i> , <i>lamA</i> , <i>lamB</i>	23, 24, 25, 26, 27	Induces transcription of genes involved in lactam and acetamidase catabolism by omega-amino acids.
AMT1	WTWHNGCTGW	monomer, metal binding domain.	<i>Candida glabrata</i>	<i>MT-I</i> , <i>MT-II_a</i> , <i>SOD1</i>	11, 28	Similar to ACE1. Activates metallothioneins in response to Cu or Ag. Multiple ATM binding sites are found in both the <i>MT-I</i> , <i>MT-II_a</i> promoters.
AnCF	CCAAT		<i>A. nidulans</i>	<i>amdS</i>	23	Binds to CCAAT-box adjacent to or in regions overlapping that of amdR.
AnCP1	CCAAT		<i>A. nidulans</i>		29	Binds to the same site as AnCP2. Present in glucose grown cells.
AnCP2	CCAAT		<i>A. nidulans</i>		29	See AnCP1.

AnNP1	CTCTACGCATCGGA-CGCACCAT		<i>A. nidulans</i>		29	Binds just upstream of CCAAT-box. This factor and AnCP1/AnCP2 binding appears to be mutually exclusive.
yAP1 (PAR1, SNQ3, PDR4)	STGACTMA (ARE)	bZIP protein	<i>S. cerevisiae</i>	glutathione, oxygen detoxification enzymes	30, 31	Homolog of mammalian AP1. Involved in regulation of oxidative stress response/oxygen detoxification. May also be involved in heavy metal metabolism.
AREA		putative zinc finger	<i>A. nidulans</i>	genes involved in nitrogen catabolism, <i>amdS</i>	32	Transcriptional activator, involved in mediating nitrogen metabolite repression.
ARGRI (ARG80)	CCTCTAAAGG	DNA-binding domain similar to MCM1	<i>S. cerevisiae</i>	Arginine metabolism genes	33, 34, 35	Repressor of arginine biosynthesis and induction of arginine catabolism. May work in cooperation with ARGRII and ARGRIII.
ARGRII(ARG81)	AAGTACAGTTAAT-AACGR (AB1) (33)	zinc finger motif, RNase-like sequence and activation domain with two acidic regions	<i>S. cerevisiae</i>	<i>ARG3, ARG5,6, CAR1, CAR2</i>	33, 35, 36, 37, 38, 39	In presence of arginine ARGRI, ARGRII and ARGRIII are required to repress anabolic and induce catabolic genes. Interaction with MCM1 plays a role in regulation.
yATF	GTGACGTMR (40) KWCGTCA (41)		<i>S. cerevisiae, Schizosaccharomyces pombe</i>		40, 41	Homolog to mammalian ATF. Implicated in expression of cellular cAMP inducible genes.
<i>b</i> alleles		motif related to homeodomain in constant region	<i>Ustilago maydis</i>		42	Twenty five alleles at <i>b</i> locus, combination of any two forms a multimeric protein which governs the switch from the yeastlike, non-pathogenic form to the filamentous, pathogenic form.
BAF1	see ABF1, and GFI					
BAP1	see ABF1					
BAS1	TGACTC	DNA binding region similar to Myb proteins of higher organisms	<i>S. cerevisiae</i>	<i>ADE2, ADE5,7, HIS4</i>	43, 44	Regulates histidine pathway genes required for basal and induced transcription.
BAS2 (PHO2)	GGTAAATTAGTT-AATTAATTG	contains a region similar to a homeobox	<i>S. cerevisiae</i>	<i>HIS4, PHO5, ADE2</i>	43, 44, 45, 46	Appears to regulate the same target genes as <i>BAS1</i> .
BRL A	MRAGGGR	two zinc fingers	<i>A. nidulans</i>	<i>rod A</i>	47, 48	Transcriptional activator. Involved in conidiophore development.
yBTF1	see TFIID					
BUF	see URS1 factor					
CPC1	TGACTCA	bZIP protein, dimer	<i>Neurospora crassa</i>	<i>ARG2, ARG12, TRP-3</i>	49, 50, 51	Global transcriptional activator. Functionally homologous to GCN4 of <i>S. cerevisiae</i> . Bind to the same DNA sequence.
CP1 (CPF1, CBP1, CF1) (centromere binding protein)	RTCACRTG (CDE1 site)	contains 20% acidic residues (glutamate/aspartate), helix-loop-helix protein	<i>S. cerevisiae</i>	<i>MET25, GAL2, GAL4, TRP1</i> . For other putative target genes see (52).	52, 53, 54, 55, 56	Recognition sequence same as USF of HeLa cells. Binding site occurs in numerous non-centromeric genes. CBP1 might be a derivative of CP1.
CREA	SYGGGG	two zinc finger domains	<i>A. nidulans</i>	<i>alcR, alcA</i> and other genes repressed by carbon catabolites.	57, 58	Related to yeast MIG1 and mammalian Egr1 and Egr2, and Wilms' tumor proteins. Involved in carbon catabolite repression.
CUP2	see ACE1					
CYS-3	TTCGCT, GAGAA & one or more CAT or CAAT	bZip protein.	<i>N. crassa</i>	Sulfur-catabolism related enzymes.	59, 60, 61, 62, 63	Transcriptional activator of structural genes involved in sulfur uptake and assimilation. Shows homology to yeast GCN4, <i>Neurospora</i> CPC1, and the mammalian Fos, Jun, and C/EBP proteins.
DAL80 (UGA43)	GATAA	GAL4-type zinc finger, putative leucine zipper	<i>S. cerevisiae</i>	<i>DAL5, DAL7, DAL4, DURP, DUR1,2, UGA4</i>	64, 65, 66, 67, 68	Repression of GABA catabolism.
DAL81 (UGA35, DURL)	GATAA	zinc finger	<i>S. cerevisiae</i>	<i>UGA1, UGA2, UGA4, DURP, DUR1,2, CAR2, DAL4, DAL7</i>	64, 66	Transcriptional activator of genes involved in catabolism of GABA, urea, arginine, and allantoin for use as N source.

Table. (continued)

DAL82 (DURM)			<i>S. cerevisiae</i>	<i>DUR1,2</i>	69	Induction of allantoin system gene transcription.
DSC1	see MBF					
yE2F	GGCGGGAAA, GCGCGAAA	12kDa	<i>S. cerevisiae</i>	for a list of potential target gene see (70)	70	Homologous to human E2F. Smallest known yeast DNA binding protein. Exists as homodimer or single protein.
GAL4	CGGASGACWCA GSAGGC (UASG)	binuclear zinc binding domain with 6 cysteine residues, dimer	<i>S. cerevisiae</i>	galactose metabolizing enzymes	71, 72, 73	Transcriptional activation in response to galactose. Repressed by GAL80 in absence of galactose.
yGBF	MCACGTGGCA (G box)		<i>S. cerevisiae</i>	putative target genes listed in (74)	74	Homologous to plant G-box Binding Protein (GBP).
GCN4	RRTGACTCA	bZIP protein	<i>S. cerevisiae</i>	Binds to GCRC (GCN4 responsive element) in <i>ADE4</i> and other genes involved in protein and purine biosynthesis	75, 76, 77, 78	General transcriptional activator of precursors of protein synthesis in response to amino acid starvation and of purine biosynthesis. Homologous to Jun. Binds to same sequence as AP1. Implicated in activating transcription from Ty2 retroposon of <i>S. cerevisiae</i> .
GCR1	CTTCC (789), CATTG (82,82)	94kDa	<i>S. cerevisiae</i>	<i>ENO1, ENO2, TDHE, ADH1, TPI</i>	79, 80, 81, 82, 82	Appears to be a coactivator that binds to UAS in concert with RAP1. Regulates genes of glycolytic enzymes. Forms a complex with GCR2. Existence of GCR3 has been reported, which might interact with other proteins or bind DNA by itself.
GFI (SUF, TAF, ABF1, SBF-B, BAF1)	RTCRYYYNNACG	atypical zinc finger domain in N-terminal region	<i>S. cerevisiae, K. lactis</i>	For a list of potential target genes see (84)	84	Multifunctional transcriptional activator. More abundant in <i>S. cerevisiae</i> than in <i>K. lactis</i> . Implicated in controlling genes involved in mitochondrial function, cell growth, transcription and translation.
GFI (maybe identical to CP1/CBP1)	RTCACRTG		<i>S. cerevisiae, K. lactis</i>	CDEI element of yeast centromeres, genes involved in mitochondrial functioning, also <i>GAL2, TRP1</i> and <i>MET25</i>	55, 84	Abundant transcriptional activator in both <i>S. cerevisiae</i> and <i>K. lactis</i> . May be involved in a variety of cellular processes. Related to RAP1.
GLN3	GATAA	one putative zinc finger domain	<i>S. cerevisiae</i>	<i>GLN1, GDH2, DAL5, DAL7</i> also see (87)	85, 86, 87	Homologous to NIT2 of <i>N. crassa</i> , AREA of <i>A. nidulans</i> , and the erythroid specific transcription factor GATA1. Transcriptional activator of genes involved in allantoin and glutamate metabolism. Related to DAL 80 and DAL81.
GRF1 (RAP1/ TUF)	RMACCCANNCAYY		<i>S. cerevisiae</i>	silent mating type loci <i>HML E</i> and <i>HMR E, MATα</i> genes	8	General regulatory factor that binds to diverse genetic elements and appears to activate transcription.
GRF2	see REB1					
GRM	see MCM1					
HAP1	CCCTCGCTATTAT CGCTATTAGC (CYC7) TGGCCGGGGTTT ACGGACGATGA (CYC1)	binuclear zinc binding domain with 6 cysteine residues	<i>S. cerevisiae</i>	<i>CYC1, CYC7</i>	88, 89, 90, 91	Binds to region B of UAS of <i>CYC1</i> and <i>CYC7</i> , activates transcription in a heme-dependent manner. Region B also binds RC2.
HAP2/3/4 complex	CCAAT	heterotrimeric complex of HAP2, HAP3, and HAP4	<i>S. cerevisiae, Sch. pombe</i>	<i>CYC1</i> , and other genes involved in mitochondrial transport	92, 93, 94	Transcriptional activator. Complex conserved throughout evolution; a homolog has been identified in <i>Sch. pombe</i> .
HCM1		N-terminal end similar to fork head proteins	<i>S. cerevisiae</i>	<i>cmd1-1</i>	95	Protein shows 50% homology to fork head family of transcription factors. Functions as a dosage-dependent suppressor of a temperature-sensitive calmodulin mutant.

HSF (HSTF)	(NGAAN) _n (HSE)	binds as trimer, trimerization via a coiled coil α -helical motif	<i>S. cerevisiae</i>	Heat shock proteins, mutant form binds to CUP1	96, 97, 98, 99, 100, 101	Transcriptional activator, no homology to any known DNA-binding proteins. Substitution of one amino acid in HSF allows it to bind to <i>CUP1</i> and activate transcription of metallothioneins. The binding sequence, HSE (heat shock element), is highly conserved.
LAC9	UAS _G (see GAL4)	binuclear zinc binding domain with 6 cysteine residues	<i>K. lactis</i>	Galactose and lactose metabolizing enzyme	102, 103, 104, 105	Homologous to GAL4.
LEU3	GCCGGAACCGGC (UAS1)	binuclear zinc binding domain with 6 cysteine residues	<i>S. cerevisiae</i>	<i>LEU1</i> , <i>LEU2</i> , <i>LEU4</i> , <i>ILV2</i> , <i>ILV5</i> , <i>GDH1</i>	106, 107, 108, 109	Transcriptional regulator of branched amino acid biosynthesis. Activates/represses transcription depending on presence/absence of the metabolite α -IPM.
MAL63		zinc finger, binuclear zinc domain	<i>S. cerevisiae</i>	<i>MAL11</i> , <i>MAL 62</i> .	110	Transcriptional activator of maltose fermentation genes.
MATa1		homeodomain	<i>S. cerevisiae</i>	haploid specific and a-specific genes, <i>HO</i>	111	Represses transcription, homologous to $\alpha 2$ in homeodomain.
MATa1- $\alpha 2$	ATGT N ₇ TACATCA	helix-turn-helix	<i>S. cerevisiae</i>	<i>RME1</i>	111, 112, 113	Represses transcription of inhibitor of meiosis <i>RME1</i> in a/ α cells.
MAT $\alpha 1$ ($\alpha 1$)	TTGAWGG (Q box) (113), CTGTCATTGA (115)		<i>S. cerevisiae</i>	<i>STE3</i> , <i>MF$\alpha 1$</i> , <i>MF$\alpha 2$</i>	114, 115, 116	Inducer of α -specific genes, synergistic interaction with MCM1. Homologous to <i>mt A-1</i> of <i>N. crassa</i> and <i>mat M_c</i> of <i>Sch. pombe</i> .
MAT $\alpha 2$ ($\alpha 2$)	TGGACTAATTAG-GAAA (P box)	homeodomain, helix-turn-helix, dimer	<i>S. cerevisiae</i>	<i>STE2</i> , <i>STE6</i> , <i>MF$\alpha 1$</i> , <i>MF$\alpha 2$</i> , <i>BAR1</i>	114, 116, 117, 118, 119, 120, 121, 122	Represses transcription of a-specific mating type genes in α cells by binding to DNA and MCM1. A homeodomain extension is involved in binding to MCM1. Has been shown to repress transcription by RNA polymerase I and II, but not III. Homologous to <i>Pi</i> mating regulator of <i>Sch. pombe</i> .
MBF (DSC1)	ACGCGTNA (MCB)		<i>S. cerevisiae</i> , <i>Sch. pombe</i>	<i>TMP1</i> , <i>POL1</i> , <i>CDC21</i>	123, 124, 125, 126, 127, 128	Composed of SWI6 and a 120 kDa protein, involved in modulating cell cycle start-specific protein. Homologous to <i>Sch. pombe cdc10</i> .
MCM 1 (PRTF or GRM)	CCTAATTRGG (MCE/P box), see (128) for a list of potential target sequences.	DNA binding and acidic domain (MADS box motif)	<i>S. cerevisiae</i>	<i>a</i> and α mating type specific genes, <i>CAR1</i> , <i>CAR2</i> , <i>ARG5,6</i>	38, 114, 129, 130, 131, 132, 133	Homologous to vertebrate serum response factor (SRF). General regulator of mating. Co-activation of α specific genes when bound to $\alpha 2$ in α cells and <i>a</i> specific activation in <i>a</i> cells. Affects replication, minichromosome maintenance, arginine metabolism, and TY1 transcriptional activation.
MET4	TGGCAAATG	bZip	<i>S. cerevisiae</i>	<i>MET5</i>	134	Transcriptional activator of sulfur metabolism genes. CBP1 and MET4 both are required for activation. MET4 may directly or indirectly recognize the binding sequence.
MIG1	WWWSYGGGG (core underlined)	2 zinc fingers	<i>S. cerevisiae</i>	<i>GAL</i> genes, <i>SUC2</i>	135, 136, 137	Involved in glucose repression. Zinc fingers resemble mammalian Egr and Wilms tumor proteins.
MTF1	TATAAT, TATAAA, ATATAAGTA	43 kDa	<i>S. cerevisiae</i>	mitochondrial genes	138, 139	Transcriptional activator, mitochondrial RNA polymerase specificity factor, similar to TFIID and bacterial sigma factor.
MTF2	TATAAGTA	70kDa	<i>S. cerevisiae</i>	mitochondrial genes	140, 141	Confers selectivity for promoter.
NIRA		binuclear zinc finger	<i>A. nidulans</i>	<i>niaD</i> and <i>niiA</i>	142	Pathway specific regulator mediating nitrate induction.

Table. (continued)

NIT-4		binuclear-type zinc finger and a glutamine-rich domain	<i>N. crassa</i>	<i>nit-3</i> and <i>nit-6</i>	143	Pathway specific in the nitrogen circuit involved in nitrate induced expression, shows homology to NIRA of <i>A. nidulans</i> .
NIT-2	(TATCTA) _{2-n}	One zinc finger	<i>N. crassa</i>	<i>nit3</i> and many other nitrogen related enzymes	144, 145, 146, 147	Major regulatory gene. Positively controls nitrogen catabolic enzymes. Functionally homologous to <i>Aspergillus</i> AREA. Has been shown to complement <i>nnu</i> mutants of <i>Gibberella zeae</i> .
NUC-1		helix-loop-helix	<i>N. crassa</i>		148	Appears to function like PHO2 and PHO4 proteins in controlling phosphorus acquisition.
Yp20	WTTTATRTTTW (ARS)	20kDa	<i>S. cerevisiae</i>	TRP1,ARS elements	149	Similar, but not identical to ABFII. Heat stable. Novel ARS binding protein, abundant chromatin associated protein that may enhance replication by repressing transcription.
PAP1	TKAGTCA (AP1) TTACGTAA (PLD)	leucine zipper	<i>Sch. pombe</i>	p25	150, 151, 152	Transcriptional activator. Both AP1 and PLD sites are necessary for positive regulation of p25.
PAR1 PDR1	see yAP1	binuclear Zinc binding domain with 6 cysteine residues	<i>S. cerevisiae</i>	PDR5	153, 154	Transcriptional activator, controls expression of membrane proteins that export small molecules across the membrane. Involved in drug resistance.
PDR4 PGA4	see yAP1 UAS _G (see GAL4)		<i>Sch. pombe</i>		155	Transcriptional activator. Homologous to GAL4 of <i>S. cerevisiae</i> .
PHO4	CACGTG	helix-loop-helix	<i>S. cerevisiae</i>	PHO5	156	Positively regulates PHO5, similar to C-MYC
PRNA		binuclear zinc binding domain, GAL4-like zinc finger	<i>A. nidulans</i>	<i>prnB</i> , <i>prnC</i> , <i>prnD</i>	157	Transcriptional activator proline utilization genes mediated by proline.
PPR1		Binuclear zinc binding domain with 6 cysteine residues.	<i>S. cerevisiae</i>	URA3, URA1, URA4,	158, 159	Transcriptional activator of inducible enzymes of the pyrimidine biosynthetic pathway.
PRTF PRP	see MCM1 GTGAAAGTATGCTT- ACTTTGAC (URS1 _{PHR1})		<i>S. cerevisiae</i>	PHR1	160	Damage responsive protein. Increases transcription of DNA repair enzyme photolyase.
PUT3	TCGGGAAGCCAA CTCCGAAGC (PUT2) CCGGAAAGCCAT TGCCGAAAG (PUT1)	979 amino acids, 2 acidic domains	<i>S. cerevisiae</i>	PUT1, PUT2	161, 162, 163	Transcriptional activator, mediates induction of genes involved in the proline utilization pathway. Has homology to GAL4, LAC9, PPR1 and PDR1.
qa-1F	GGRTAARYRYTT TATCC	binuclear zinc binding domain with 6 cysteine residues	<i>N. crassa</i> and other <i>Neurospora</i> ssp.	qa cluster genes	164, 165, 166, 167	Transcriptional activator of qa structural genes, which allow for the utilization of quinic acid as carbon source.
RAP1 (GRF1, TUF, TBA, SBF-E)	RMACCCANNCAYY (same as GCN4) ACACCTGGACACC (176)	827 amino acids, unusually large DNA binding domain	<i>S. cerevisiae</i>	ADHI, HIS4, PYK, PGK, ENOI, ENOII, TP1 ribosomal proteins, regulatory subunit of PKA, MAT α locus, membrane ATPase, silencer element of HMR and HML, ARS elements,	168, 169, 170, 171, 172, 173, 174, 175, 176, 177	Transcriptional activator of glycolytic gene products. Transcriptional repressor at silent mating type loci HML and HMR. May work in combination with other factors such as SIR1-SIR4, ABF, GCR1 or GAL11. Involved in telomere and protein stability. Required for BAS1/BAS2 and GCN4 dependent transcription of HIS4 gene.
RC2	recognizes the same site as HAP1		<i>S. cerevisiae</i>	CYC1	88	Transcriptional regulator. Its binding to the target gene excludes the binding of HAP1.

REO1			<i>S. cerevisiae</i>	<i>COX5b, ANB1</i>	178	Aerobic repression of target genes.
REB1 (GRF2, RBP1)	CCGGGTAA	125 kDa	<i>S. cerevisiae</i>	<i>SIN3, SW15, CDC9, TOP1</i> and other UAS _G containing genes	179, 180, 181	Represses transcription by RNA polymerase II, also binds to rDNA.
RGM1		proline-rich zinc finger	<i>S. cerevisiae</i>		182	Zinc finger similar to and functionally homologous to mammalian Egr. Reduces cell growth when overexpressed.
RME1		At least 2 putative zinc finger domains	<i>S. cerevisiae</i>	<i>IME1</i>	183	Inhibits meiosis in α and α cells. Its expression is repressed by $\alpha 1$ - $\alpha 2$ in α/α cells, which can enter meiosis.
ROX1	YYYATTGTTCTC and TCGTTCGTTGCCT		<i>S. cerevisiae</i>	<i>CYC7, ANB1, HEM13, COX5b, ERG11, OLE1,</i>	184, 185, 186	Negative regulator of transcription, expression is transcriptionally activated by heme and partially dependent on HAP1.
SBF	CACGAAAA (SCB, cell cycle box)		<i>S. cerevisiae</i>	<i>CLN1, CLN2, CLN3, HCS26, CTS1, HO</i>	123, 124, 125	Composed of SWI4 and SWI6. Involved in cell cycle dependent transcriptional activation of HO endonuclease necessary for mating-type switching.
SBF-B	See ABF1 and GFI					
SFL1		767 amino acids, many 'PEST' sequences	<i>S. cerevisiae</i>		187	Homology to conserved regions of <i>c-myc</i> and the DNA binding domain of HSTF, involved in asexual cell aggregation.
SFP1		2 zinc finger domains	<i>S. cerevisiae</i>		188	Zinc finger domains are separated by 40 amino acids. Involved in cell growth and division.
STE4	TTCTTTGTTA CTAATATTCTAT	leucine zipper	<i>Sch. pombe</i>	genes involved in mating/meiosis	79, 190	Leucine zipper homologous to <i>jun</i> family. Essential for mating and meiosis, induces by nitrogen starvation. Transcription of STE4 is mediated by STE11.
STE11	TTCTTTGTTY	HMG-box protein	<i>Sch. pombe</i>	<i>matP, matM, mei2, STE4</i>	190, 191	Transcriptional activator of genes required for sexual development.
STE12	TGAAACA (PRE)	low level homology to homeodomain	<i>S. cerevisiae</i>	<i>STE2, TY1</i>	192, 193, 194, 195	Transcriptional activator. Binds to pheromone response element and interacts with MCM1. Conceptual protein, bears no homology to any known DNA-binding protein.
SUF	see ABF1 and GFI					
SWI4 (CCBF)	see SBF					
SWI5	ACATCAATTTAAAA-AAAAAACCGCAT GCTATAATGCT (URS1),	three zinc fingers	<i>S. cerevisiae</i>	<i>HO</i>	196, 197, 198	Mother-cell-specific transcriptional activator of <i>HO</i> endonuclease. First two zinc fingers are similar to TFIIIA of <i>Xenopus laevis</i> .
SWI6	see SBF and MBF					
TAF	see ABF1 and GFI					
TEC1		TEA domain	<i>S. cerevisiae</i>		45	
TFIID (yBTF1)	TATA element (TATAAA)	monomer, central cluster of basic residues	<i>S. cerevisiae</i> <i>Sch. pombe</i>	genes transcribed by RNA polymerase II	199, 200, 201, 202, 203, 204, 205, 206, 207, 208	Activates transcription by RNA polymerase II. TBP is a subunit of TFIID. Has been shown to be required for transcription by all 3 polymerases. Its binding follows the assembly of other transcription factors (TFIIA, B, C, E, % to enable start of transcription. Proposed to be a homolog of the bacterial sigma factor.
TFIIIA (PZF1)	GN10 GN2 GNGGGNG (208) N ₃ GNGGGNGN ₂ GN (209) TGTAAGTGGGTGACC (ICR, box C, 211)	nine zinc fingers	<i>S. cerevisiae</i>	5S rRNA genes	209, 210, 211, 212, 213	Assembly factor involved in RNA polymerase III mediated transcription.

Table. (continued)

TFIIIB	TAATGCAAGGATGA- CGATATCGATCATG- ATTTTC, for other potential target sequences see (214)	multisubunit protein containing at least 2 polypeptides	<i>S. cerevisiae</i>	5S rRNA and tRNA genes	214, 215, 216, 217, 218, 219	Central transcription factor responsible for specific recognition by RNA polymerase III. Requires prior binding of TFIIIA and TFIIIC to target genes.
TFIIIC (τ factor)	ATCGGTTCAAC (box A) GCAAGCTGAGG (box B), (220)	multisubunit protein containing at least four polypeptides. T_{95} subunit with helix-turn-helix and acidic domain.	<i>S. cerevisiae</i>	tRNA and 5S rRNA genes	220, 221, 222, 223, 224	Assembly factor for transcriptional initiation. Associates with TFIIIA and TFIIIB.
TSF	CCCCCT (TRS)	140 kDa polypeptide	<i>S. cerevisiae</i>	<i>DDR2</i>	225	Novel protein that binds to a site different from those of the known heat shock proteins. Transcriptional activator in response to thermal stress.
TUF	see GRF1 and RAP1					
TyBF	see ABF1 and GFI					
UAY		GAL4-like zinc finger (CYS_6/Zn_2)	<i>A. nidulans</i>	structural genes involved in purine transport and degradation	226, 227	Transcriptional activator. Mediates induction by uric acid of purine utilization pathway.
UBF	core domain and UCE (upstream control element)		<i>S. cerevisiae</i>	rRNA genes	228	Transcriptional activator of rRNA genes mediated by Polymerase I.
UBF1	see ABF1 and GFI					
UGA3		binuclear zinc binding domain with 6 cysteine residues	<i>S. cerevisiae</i>	<i>UGA1</i> , <i>UGA2</i> , <i>UGA4</i>	64, 67	Transcriptional activator. Involved in GABA catabolism.
UGA35	see DURL					
UGA43	see DAL80				64, 65, 66	
URBS1	GATA	two putative zinc fingers	<i>U. maydis</i>	<i>sid1</i>	229	Transcriptional regulator of siderophore biosynthesis.
URS1 factor (BUF)	AGCCGCCGA (URS1 site)	heterodimer (37.5 and 73.5 kDa)	<i>S. cerevisiae</i>	<i>CARI</i> , and many other genes containing the URS1 sequence.	3, 7, 230, 231	Generalized transcription factor, represses genes involved in nitrogen, carbon, and inositol metabolism, as well as those involved in electron transport, heat shock response, meiosis and sporulation.

^aSynonyms are listed in parenthesis^bWhenever possible consensus sequences are shown. Core sequences have been underlined. Abbreviations for the bases are: B=C/G/T, D=A/G/T, H=A/C/T, K=G/T, M=A/C, N=A/T/G/C, R=A/G, S=C/G, V=A/C/G, W=A/T, Y=C/T.^cThe molecular weights of the transcription factors were only included when no other information concerning features was available.^dIn some cases the transcriptional regulatory action of DNA-binding proteins have been demonstrated but their natural targets are not known. No target genes were listed in such cases.^eReferences listed here do not represent complete/exhaustive listing.^fOnly selected information is included.