An analysis was carried out on the promoter region of the Drosophila DNA polymerase α 73-kDa subunit gene and the factor(s) activating the promoter. Transcription initiation sites were newly identified in the region downstream of the previously determined sites. Full promoter activity resided within the region from −285 to +129 base pairs with respect to the newly determined major site. Within this region, we found three sequences identical or similar to the DNA replication-related element (DRE), 5'-TATCGATA, which is known as a common promoter-activating element for the Drosophila DNA polymerase α 180-kDa subunit gene and the proliferating cell nuclear antigen gene. These sites were located at positions −77 to −70 (DREα-I), −44 to −37 (DREα-II), and +3 to +10 (DREα-III). Footprinting analysis using the recombinant DRE-binding factor (DREF) or Kc63 cell nuclear extract demonstrated that DREF can bind to all three DRE-related sites. Introduction of mutation in even one of the three DRE-related sequences caused extensive reductions of the promoter activity and also the DREF-binding activity of the promoter-containing fragment. The results indicate that the three DRE-binding sites cooperate to enhance promoter activity of the DNA polymerase α 73-kDa subunit gene.

Five distinct species of DNA polymerases (α, β, γ, δ, and ε) have been isolated from eukaryotes and characterized (1, 2). Of these, three are thought to be involved in chromosomal DNA replication including the DNA polymerase α-primase, which has been implicated in this process by many lines of evidence (1–5). The DNA polymerase α-primase consists of four subunits with molecular masses of 165–182, 68–86, 54–60, and 46–50 kDa (2). The largest polypeptide is known to be the DNA polymerase catalytic subunit (6), and the two smallest subunits are responsible for the primase activity (7). The function of the second largest subunit at 68–86 kDa is not clear yet. cDNA clones for the four subunits of the mouse DNA polymerase α-primase were isolated, and their expressions were examined in mouse cells during the cell cycle (8). When cells at the quiescent state are stimulated to proliferate, levels of mRNAs for all four subunits of the enzyme increase almost simultaneously prior to DNA synthesis (8), and therefore, transcription of these genes is likely regulated by a common mechanism.

In budding yeast, promoter regions of many DNA replication-related genes contain a common nucleotide sequence (5′-ACGCGT) named MCB (MluI cell cycle box) (9), and the specific transcription factor MBF (MCM-binding factor) is required for the transcription of these genes at the G1-S boundary (10, 11). In mammalian cells, the transcription factor E2F binds to the E2F-recognition site (5′-TTTCGCGC) and positively regulates transcription of a group of genes whose products are required for cell proliferation (12, 13) such as DNA polymerase α, thymidylate synthase, thymidine kinase, c-Myc, c-Myb, Cdc2, proliferating cell nuclear antigen (PCNA), and cyclin D and cyclin E (14–17). We have isolated Drosophila genes for DNA polymerase α 180-kDa subunit (18) and PCNA (19). Promoter regions of these genes contain a common 8-base pair (bp) palindromic sequence (5′-TATCGATA) named DNA replication-related element (DRE) (20). Three DREs are present in the DNA polymerase α 180-kDa subunit gene at nucleotide positions −217, −86, and −30 with respect to the transcription initiation site and one DRE in the PCNA gene at a position −100 (20). The requirement for DREs for the activities of promoters of these genes has been confirmed both in cultured cells (20) and in transgenic flies (21). Furthermore, we found a specific DRE-binding factor (DREF) consisting of an 80-kDa polypeptide homodimer (20). It is therefore of interest to determine whether the DRE/DREF transcriptional regulatory system functions in the transcription of genes for other DNA replication enzymes.

A cDNA and the genomic regions for the Drosophila DNA polymerase α 73-kDa subunit have been cloned, and their nucleotide sequences have been determined (22). This sequence apparently contains one DRE sequence and close to that two additional DRE-related sequences. However, all of these are located around the first ATG codon in the transcribed region. In the work presented here, we have carried out a more detailed analysis of the transcription initiation sites in the 73-kDa subunit gene and have determined new sites downstream of those previously identified. The DRE-related sequences are located at −76, −44, and −30 with respect to the most prominent new transcription initiation site. We have therefore examined the role of the DRE-related sequences in the promoter activity. The obtained results suggest that these sites cooperate to activate the promoter of the DNA polymerase α 73-kDa subunit gene.

**EXPERIMENTAL PROCEDURES**

Cell Culture—Kc63 cells derived from Drosophila melanogaster embryos were grown at 25 °C in M36F medium (23) supplemented with

---

1. The abbreviations used are: PCNA, proliferating cell nuclear antigen; DRE, Drosophila DNA replication-related element; DREF, DRE binding factor; CAT, chloramphenicol acetyltransferase; PCR, polymerase chain reaction; bp, base pair(s); GST, glutathione S-transferase; PIPES, 1,4-piperazinediethanesulfonic acid.
Plasmid Constructions—All nucleotide positions of the 73-kDa subunit gene in the following paper were expressed with respect to one of the major transcription initiation sites, which were determined in the present study. Plasmid A contains all of the transcribed region and at least 5 kilobases of the upstream region of the Drosophila DNA polymerase α 73-kDa subunit gene (22). Plasmid B contains about 1.2 kilobases of the upstream region from the position +7 of the 73-kDa subunit gene in the vector pBluescript (22). The plasmid pDhp70-L contains firefly luciferase DNA combined with the Drosophila hsp70 gene promoter was used for cotransfection with CAT plasmids as an internal control (21).

To construct the plasmid that contained the upstream region from the position −302 to the position +129 of the 73-kDa subunit gene, PCR was performed using plasmid A DNA as a template and a combination of primers B-1 and B-2. The PCR product was blunt-ended using T4 DNA ligase and then self-ligated using T4 DNA ligase. By this treatment, two base pairs, GC, were inserted at the center of the DRE sequence. To construct the plasmids that contained mutations in the DRE-related sequences (DRE-I, II, and both), the plasmid containing the mutation(s) in site I, site II, or both were digested with ClaI and then blunt-ended using T4 DNA ligase, followed by self-ligation using T4 DNA ligase.

Plasmid Constructions—All nucleotide positions of the 73-kDa subunit gene in the following paper were expressed with respect to one of the major transcription initiation sites, which were determined in the present study. Plasmid A contains all of the transcribed region and at least 5 kilobases of the upstream region of the Drosophila DNA polymerase α 73-kDa subunit gene (22). Plasmid B contains about 1.2 kilobases of the upstream region from the position +7 of the 73-kDa subunit gene in the vector pBluescript (22). The plasmid pDhp70-L contains firefly luciferase DNA combined with the Drosophila hsp70 gene promoter was used for cotransfection with CAT plasmids as an internal control (21).

To construct the plasmid that contained the upstream region from the position −302 to the position +129 of the 73-kDa subunit gene, PCR was performed using plasmid A DNA as a template and a combination of primers B-1 and B-2. The PCR product was blunt-ended using T4 DNA ligase, digested with XhoI, and then used to replace the region containing the mutated DRE-related sequence. These products were digested with BamHI and XhoI and then used to replace the region carrying the wild type sequence between BamHI and XhoI sites of p-302DpOLA73CAT to create the plasmids p-302DpOLA73CATmutI and p-302DpOLA73CATmutII.

To construct the plasmid p-302DpOLA73CATmutIII containing a mutation in the DRE sequence (DRE-I, II), p-302DpOLA73CAT was digested at the center of the DRE sequence with ClaI and then blunt-ended using T4 DNA ligase, digested with XhoI, and then used to replace the region containing the mutated DRE-related sequence. These products were digested with BamHI and XhoI and then used to replace the region carrying the wild type sequence between BamHI and XhoI sites of p-302DpOLA73CAT to create the plasmids p-302DpOLA73CATmutI and p-302DpOLA73CATmutII.
sonicated calf thymus DNA (average size, 0.2 kilobase) on ice for 5 min. When necessary, unlabeled DNA fragments were added as competitors at this step. Then, the E. coli lysate containing GST-DREF(16–608) fusion protein or Kc cell nuclear extract was added, and a reaction mixture was incubated for 15 min on ice. DNA-protein complexes were electrophoretically resolved on a 4% polyacrylamide gel in 50 mM Tris borate, pH 8.3, 1 mM EDTA containing 2.5% glycerol at 25 °C. The gel was dried and autoradiographed.

DNA Transfection and CAT Assay—Kc cells (2 × 10^6/dish) were grown in 60-mm plastic dishes for 24 h and cotransfected with 10 μg of the reporter plasmid DNA and 50 ng of pDHsp70-L DNA by a calcium phosphate coprecipitation method as described (27). Cells were harvested 48 h after DNA transfection. Cell extracts for determination of CAT activities were prepared as described (28). Radioactivities of spots corresponding to acetylated [14C]chloramphenicol were quantified with the imaging analyzer BAS2000 (Fuji Film). The luciferase assay was carried out by means of a PicoGene assay kit (Toyo Inc.) as described previously (29). All assays were performed within the range of linear relation of the activities to incubation time and protein amounts.

CAT activities were normalized to luciferase activities.

DNase I Footprinting Analysis—DNase I footprinting analysis was performed essentially as described (20). The DNA fragment obtained from digestion of pDPOLA73BLU with BamHI and XhoI was labeled at 5'-end of the upper or lower strand (1 ng, 1 × 10⁶ cpm) and added to 30 μl of a reaction mixture containing 25 mM Hepes, pH 6.7, 40 mM KCl, 5 mM MgCl₂, 0.1 mM EDTA, 1 μg of sonicated calf thymus DNA, 1 μg of poly(dI-dC). E. coli lysate containing GST-DREF(16–242) or Kc cell nuclear extract were added last, and the binding reaction was performed for 15 min on ice. DNase I (2 μl, 100 units/μl) that was freshly diluted in 10 mM Hepes, pH 7.6, 5 mM CaCl₂, 10 mM MgCl₂, and 100 μg/ml bovine serum albumin was added to each reaction. After 1 min of digestion at 25 °C, reactions were terminated by adding 100 μl of a solution containing 40 mM EDTA, 0.4% SDS, 0.3 mM NaCl, 40 μg/ml E. coli RNA, and 100 μg/ml proteinase K. The samples were incubated for 30 min at 45 °C and then extracted with phenol-chloroform. The reaction products were precipitated with ethanol and then loaded on a 6% polyacrylamide/8 M urea sequencing gel in parallel with products of Maxam-Gilbert sequencing reactions using the same DNAs as probes for sequencing controls. After electrophoresis, gels were dried and autoradiographed.

RESULTS

Determination of Transcription Initiation Sites of the DNA Polymerase α 73-kDa Subunit Gene—DNA and the gene for the Drosophila DNA polymerase α 73-kDa subunit gene—cDNA and the gene for the Drosophila DNA polymerase α 73-kDa subunit were isolated, and their nucleotide sequences were determined (22). We found a sequence identical to DRE (5′-TATCGATA) and two sequences similar to DRE around the previously identified ATG translation initiation codon (ATG1 in Fig. 1). These locations are several hundred base pairs downstream from the previously determined multiple transcription initiation sites (22). Because these three sites were found to be bound by DREF as described below, we named these sites as DREα-1, DREα-11, and DREα-111. In our previous studies on the genes for DNA polymerase α 180-kDa subunit and PCNA, DREs are localized...
Thus, the polypeptide coded by the new sequence is 44 amino
acid shorter than that coded by the previously determined sequence. Homology searches indicate that amino acid sequence of the N-terminal end of the newly suggested sequence corresponds to that of the mammalian 73-kDa subunit sequence, and therefore, the previously determined coding frame has an extra sequence of 44 amino acid residues that is absent in the mammalian homolog.

We searched this by a primer extension experiment using the new primer (Primer 2 shown in Fig. 1), and several new transcription initiation sites of the 73-kDa subunit gene were identified in addition to those previously determined using Primer 1 (22) (Fig. 1 and 2). The most prominent of the newly determined transcription initiation sites was now defined as the nucleotide position +1 and was mapped 3 bp downstream of the first ATG codon as suggested previously (22) (Fig. 1). Both previously and newly identified sites seem to be frequently used in early embryos. The signal of newly identified site was especially prominent with RNA extracted from Kc cells (Fig. 2), and those corresponding to previously determined ones were rather weak. A TFIID target sequence, 5’-TTATTG (30), was found 12 bp upstream of the major site of the new transcription initiation sites but not around the previously determined sites.

In the region downstream of the newly determined transcription initiation site, the ATG codon (ATG2 in Fig. 1) was found in the position of +130, and its location is 132 bp downstream from the previously determined first ATG (ATG1 in Fig. 1). Thus, the polypeptide coded by the new sequence is 44 amino acids shorter than that coded by the previously determined sequence. Homology searches indicate that amino acid sequence of the N-terminal end of the newly suggested sequence corresponds to that of the mammalian 73-kDa subunit sequence, and therefore, the previously determined coding frame has an extra sequence of 44 amino acid residues that is absent in the mammalian homolog.

Determination of the Promoter Region of the DNA Polymerase α 73-kDa Subunit Gene—The fragment spanning positions about −1200 to +129, which contains both previously and newly determined transcription initiation sites, was placed adjacent upstream of the CAT gene (pDPOLA73CAT). Deletions were made unidirectionally from its 5’-end, and then the plasmids carrying various deletions were transfected into Drosophila Kc cells. A deletion from position −1200 to position −508 did not show any significant change in CAT expression (data not shown). Further deletions to position −285 also did not affect CAT activity significantly (Fig. 3). About 60% reduction of CAT expression was observed with a deletion from −285 to −266. Because this region contains a sequence similar to the E2F-binding site, 5’-TTTCCGG, the transcription factor E2F might play a role for activation of the promoter of this gene as reported with the PCNA gene (31). Further deletions resulted in progressive reduction of the CAT expression level. Therefore,
the region containing DRE and DRE-related sequences are required for high promoter activity.

A deletion construct from the 3'-end was also made. The plasmid carrying the region from −302 to +129 showed high CAT expression. However, the plasmid carrying the region from −302 to +12 showed no detectable level of CAT expression, although it contained the DRE, the DRE-related sequences, and the major transcription initiation site (Fig. 3). These results indicate that the region from +12 to +129 contains an element(s) essential for the promoter activity. Taken together, it is concluded that the promoter region of the DNA polymerase α 73-kDa subunit gene is localized between positions −285 and +129.

Determination of the DREF-binding Sites in the DNA Polymerase α 73-kDa Subunit Gene—To examine whether DRE and its related sequences can be recognized by DREF, the DRE-binding factor identified previously (20), we carried out a gel mobility shift assay using the GST-DREF (16–242) fusion protein (26) and Kc cell nuclear extract, in which four DNA fragments from various regions of the gene (Fig. 1) were used as probes. The shifted band was observed with the 430-bp fragment C but not with fragments A, B, and D (Fig. 4A). The shifted band was competed by adding an excess amount of the probe. Similar complexes were observed with the fragment C and the Kc cell nuclear extract (Fig. 4C). Furthermore, the addition of the anti-DREF monoclonal antibody (monoclonal antibody 4) (26) to the binding reaction resulted in super-shift of the DNA-protein complex (Fig. 4D, lanes d–f). These results indicate that DREF can specifically bind to the fragment C-containing DRE and its related sequences of the DNA polymerase α 73-kDa subunit gene.

DNase I footprinting analysis was performed to determine the exact DREF-binding site(s) in the DNA fragment C. The 5' end of either the upper or lower strand of the fragment spanning from position −302 to +129 was 32P-labeled and was used for the analysis. As shown in Fig. 5A, GST-DREF (16–242) fusion protein protected three regions of the upper strand corresponding to positions from −78 to −62 (α-I), from −55 to −34 (α-II), and from −4 to +18 (α-III). Similar regions were protected when the lower strand was used as a probe (Fig. 5B). When the Kc cell nuclear extract was added in the reaction (Fig. 5C), three regions of about 22 bp corresponding to positions from −78 to −62, from −55 to −34, and from −4 to +18 were also protected. The region α-III contains the DRE sequence, whereas the regions α-I and α-II contain the DRE-related sequences that matches 5 bp out of the 8-bp DRE sequence.

Fig. 5. Mapping of DREF-binding sites by DNase I footprinting analysis. DNase I footprinting analysis was performed as described under "Experimental Procedures." The 32P-labeled upper (A and C) or lower (B) strand of BamHI-XhoI fragment of the 73-kDa subunit gene was incubated with GST-DREF or GST (A and B) or with Kc cell nuclear extract (C) and then digested with DNase I. The three regions protected from DNase I digestion are indicated by brackets with α, α-I, and α-III. T and T+G sequencing reactions were put in the first two lanes.

Fig. 6. Roles of DRE-related sequences for promoter activity of the DNA polymerase α 73-kDa subunit gene. A, schematic features of reporter CAT plasmids are illustrated. DRE-related sequences are indicated by open circles. Bases identical to DRE consensus sequences are indicated by dots above the sequences. The mutated bases are indicated by underlined italic letters. B, these reporter CAT plasmids (10 μg each) carrying various mutations were transfected into Kc cells, and the CAT activities were determined. The CAT activities are expressed as percentages of the p-302DPOLA73CAT value.
almost at the center of each protected region. The results indicate that DREF can bind to the DRE-related sequences as well as the DRE sequence.

Effects of Mutations in DRE and Its Related Sequences on Promoter Activity of the DNA Polymerase α 73-kDa Subunit Gene—To examine roles of DREF-binding sequences for promoter activity of the 73-kDa subunit gene, we constructed CAT expression plasmids having mutations in the DRE and its related sequences (Fig. 6A), and CAT transient expression assays in Kc cells were performed.

Mutation of either of three DREF-binding sequences resulted in extensive reduction (75-95%) of the CAT expression (Fig. 6B). Mutations in any two DRE-related sequences completely abolished the CAT expression. The results indicate that all of the three DREF-binding sequences are required for the high promoter activity.

The above evidence suggests that the three sites cooperate to enhance the promoter activity. To gain further insight into the molecular mechanism, we examined the effects of the mutations on the DREF binding to the DNA fragments by a gel mobility shift assay. When GST-DREF fusion protein was incubated with the 32P-labeled BamHI-HindIII fragments (fragment C) without competitor fragments, the shifted bands were detected (Fig. 7A, lane c). When a fragment containing intact DRE and DRE-related sequences was added to the reaction as a competitor, the shifted band was decreased extensively (Fig. 7A, lane d). In contrast, when any of mutant fragments with mut I, mut II, or mut III was added to the reactions, shifted bands were decreased to only a limited extent. (Fig. 7A, lanes h–k, l–o, and p–s, and quantified results in Fig. 7B). Therefore, the presence of all three DREF-binding sequences in intact forms is required for formation of the strong DNA-protein complex, and an extensive decrease of the promoter activity by mutation in any of three DREF-binding sequences might be due to loss of affinity of DREF to the three DRE sequences. Thus, three DREF-binding sequences appear to cooperate to conduct high promoter activity.

DISCUSSION

In the present study, we have mapped new transcription initiation sites for the Drosophila DNA polymerase α 73-kDa subunit gene, which are downstream of those previously reported. The sites in both upstream and downstream regions seem to be utilized in Drosophila early embryos, whereas the newly mapped sites are prominent in the cultured Kc cells. The newly mapped major transcription initiation site was located 3 bp downstream of the first ATG codon that was previously predicted as a translation initiation site (22). These results suggest that the second ATG codon located at 132 bp downstream of the first ATG codon functions as a translation initiation site in the mRNA, which is synthesized from the newly mapped transcription initiation sites. Thus, the previously predicted open reading frame contains 44 additional amino acid residues to the N terminus of the polypeptide started from the second ATG. Comparison of amino acid sequences of these predicted amino acid sequences with that of the mammalian 73-kDa subunit (8) revealed that the N-terminal of mammalian homolog corresponds to that predicted by the second ATG. However, this does not rule out the possibility that Drosophila embryos also contain a 73-kDa subunit with the extra N-terminal sequence. Biological significance of the possible heterogeneity of the DNA polymerase α 73-kDa subunit remains to be clarified.

Previously, we reported that an 8-bp palindromic sequence of DRE and not neighboring sequences are responsible for activating promoters of the DNA polymerase α 180-kDa subunit and PCNA genes in both cultured cell and transgenic fly systems (20, 21). We also reported that the 2-base substitution within the 8-bp sequence of DRE abolished the binding to DREF (20). We found one DRE sequence and two DRE-related sequences in an adjacent region to the newly mapped transcription initiation sites. Although the nucleotide sequence of DRE
is identical to that reported previously, two DRE-related sequences match only 5 bp out of the 8-bp DRE sequence. However, gel shift analyses have shown that all these three sites are essential for formation of the DRE-protein complex. Furthermore, mutation in any one of these three DRE-binding sites resulted in extensive reduction of the promoter activity. Therefore, they probably cooperate to enhance the promoter activity.

Recently, a Drosophila homolog of the mammalian E2F1 was isolated (32–34), and E2F-binding sites were found in promoter regions of the DNA polymerase α 180-kDa subunit (32) and PCNA (31) genes. These sites appeared to function in both cultured Drosophila cells and living flies (31). A deletion of one of two E2F-recognition sequences in the DNA polymerase α 73-kDa subunit gene promoter remarkably reduced the promoter activity. Our observations therefore suggest that the 73-kDa subunit gene is also regulated by E2F like the 180-kDa subunit and PCNA genes, although further analysis is necessary to clarify this point. In addition, our results suggest that the region between positions +12 and +129 is also important for the promoter activity. However, the precise sequences responsible for the control have yet to be identified.

Organizations of transcriptional regulatory elements of Drosophila genes for the DNA polymerase α 73-kDa subunit, 180-kDa subunit, and PCNA are summarized in Fig. 8. DRE(s) and the E2F-binding sites are commonly observed among these genes. A similar organization of DRE and the E2F-binding site most likely represents a common regulatory mechanism for the expression of these three DNA replication-related genes.

REFERENCES

1. Linn, S. (1991) Cell 66, 185–187
2. Wang, T. S.-F. (1991) Annu. Rev. Biochem. 60, 513–552
3. Tsurimoto, T., Melendez, T., and Stillman, B. (1990) Nature 346, 534–539
4. Morrison, A., Araki, H., Clark, A. B., Hamatake, R. K., and Sugino, A. (1990) Cell 62, 1143–1151
5. Araki, H., Rapp, P. A., Johnson, A. L., Johnston, L. H., Morrison, A., and Sugino, A. (1992) EMBO J. 11, 733–740
6. Wong, S. W., Paborsky, L. R., Fisher, P. A., Wang, T. S.-F., and Korn, D. (1986) J. Biol. Chem. 261, 7958–7968
7. Bambara, R. A., and Jones, C. B. (1991) Biochem. Biophys. Acta 1088, 11–24
8. Miyazawa, H., Izumi, M., Tada, S., Takada, R., Masutani, M., Ui, M., and Hanaoka, F. (1993) J. Biol. Chem. 268, 8111–8122
9. Lowndes, N. F., Johnson, A. L., and Johnston, L. H. (1991) Nature 350, 270–275
10. Dirick, L., Moll, T., Auer, H., and Nasmyth, K. (1992) Nature 357, 508–513
11. Lowndes, N. F., Johnson, A. L., Breeden, L., and Johnston, L. H. (1992) Nature 357, 505–508
12. Slansky, J. E., Li, Y., Kadin, W. G., and Farhann, P. J. (1993) Mol. Cell. Biol. 13, 1610–1618
13. Li, R., Naeye, G. S., and Lee, A. S. (1993) Proc. Natl. Acad. Sci. U. S. A. 90, 3554–3558
14. Pearson, B. E., Nasheuer, H. P., and Wang, T. S.-F. (1991) Mol. Cell. Biol. 11, 2296–2302
15. Blake, M., and Azizkhan, J. C. (1989) Mol. Cell. Biol. 9, 4994–5002
16. Nevins, J. R. (1992) Science 258, 424–429
17. DeGregori, J., Kowalik, T., and Nevins, J. R. (1995) Mol. Cell. Biol. 15, 4215–4224
18. Hirose, F., Yamauchi, M., Nishida, Y., Masutani, M., Miyazawa, H., Hanaoka, F., and Matsukage, A. (1991) Nucleic Acids Res. 19, 4991–4998
19. Yamauchi, M., Nishida, Y., Moruchi, T., Hirose, F., Hui, C.-C., Suzuki, Y., and Matsukage, A. (1990) Mol. Cell. Biol. 10, 872–879
20. Hirose, F., Yamauchi, M., Hanada, H., Inomata, Y., and Matsukage, A. (1993) J. Biol. Chem. 268, 2092–2099
21. Yamauchi, M., Hayashi, Y., Nishimoto, Y., Hirose, F., and Matsukage, A. (1995) J. Biol. Chem. 270, 15808–15814
22. Cotterill, S., Lehman, T. R., and Mclachlan, P. (1992) Nucleic Acids Res. 20, 4325–4330
23. Cross, D. P., and Sang, J. H. (1978) J. Embryol. Exp. Morphol. 45, 161–172
24. Yamauchi, M., Hirose, F., Nishida, Y., and Matsukage, A. (1991) Mol. Cell. Biol. 11, 4909–4917
25. Cichon, P. J., and Sacchi, N. (1983) Anal. Biochem. 126, 156–159
26. Hirose, F., Yamauchi, M., Kuroda, K., Omori, A., Hachiya, T., Ikeda, M., Nishimoto, Y., and Matsukage, A. (1996) J. Biol. Chem. 271, 3930–3937
27. Di Noora, P., and Dawid, I. B. (1983) Proc. Natl. Acad. Sci. U. S. A. 80, 7095–7098
28. Yamauchi, M., Hayashi, Y., and Matsukage, A. (1988) Nucleic Acids Res. 16, 8773–8787
29. Echelarier, G., and Ohanesian, A. (1970) In Vitro 6, 162–172
30. Purnell, B. A., Emanuel, P. A., and Gilmour, D. S. (1994) Genes & Dev. 8, 830–842
31. Yamauchi, M., Hayashi, Y., and Matsukage, A. (1995) J. Biol. Chem. 270, 25159–25165
32. Ohtani, K., and Nevins, J. R. (1994) Mol. Cell. Biol. 14, 1603–1612
33. Dyrnlacht, B. D., Broek, A., Derbiski, M., Yenush, L., and Dyson, N. (1994) Proc. Natl. Acad. Sci. U. S. A. 91, 6359–6363
34. Hao, X. F., Alphey, L., Bandara, L. R., Lam, E. W.-F., Glover, D., and La Thangue, N. B. (1995) J. Cell Sci. 108, 2945–2954
35. Yamauchi, M., Hirose, F., and Matsukage, A. (1996) Genes to Cells, 1, 47–58

DRE in Regulation of DNA Polymerase α 73-kDa Subunit Gene 14547
DNA Replication-related Elements Cooperate to Enhance Promoter Activity of the
Drosophila DNA Polymerase α 73-kDa Subunit Gene
Yasuhiko Takahashi, Masamitsu Yamaguchi, Fumiko Hirose, Sue Cotterill, Jun Kobayashi,
Shigetoshi Miyajima and Akio Matsukage

J. Biol. Chem. 1996, 271:14541-14547.
doi: 10.1074/jbc.271.24.14541

Access the most updated version of this article at http://www.jbc.org/content/271/24/14541

Alerts:
• When this article is cited
• When a correction for this article is posted

Click here to choose from all of JBC's e-mail alerts

This article cites 35 references, 19 of which can be accessed free at http://www.jbc.org/content/271/24/14541.full.html#ref-list-1