Identification of Functional Domains in the RAD51L2 (RAD51C) Protein and Its Requirement for Gene Conversion*

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The RAD51 protein plays a key part in the process of homologous recombination through its catalysis of homologous DNA pairing and strand exchange. Additionally, five novel mammalian RAD51-like proteins have been identified in mammalian cells, but their roles in homologous recombination are much less well established. These RAD51-like proteins form two different complexes, but only the RAD51L2 (RAD51C) protein is a part of both complexes. By using site-directed mutagenesis of RAD51L2, we show that non-conservative mutation of the putative ATP-binding domain severely reduces its function, whereas a conservative mutation shows partial loss of function. We find that the protein is localized to the nucleus by tagging RAD51L2 with the green fluorescent protein and provisionally identify a C-terminal domain that acts as a nuclear localization signal. Further, a RAD51L2-deficient cell line was found to have significantly reduced homology-directed repair of a DNA double-strand break by gene conversion. This recombination defect could be partially restored by ectopic expression of the human RAD51L2 protein. Therefore, we have identified protein domains that are important for the correct functioning of RAD51L2 and have shown that there is a specific requirement for RAD51L2 in gene conversion in mammalian cells.

Homologous recombination (HR)† is an essential process in mammalian cells for the reassortment of genetic material and for the repair of DNA damage. RAD51 is the key eukaryotic protein for HR, mediating homologous pairing of DNA sequences and strand exchange (1). Five novel RAD51-like proteins have recently been identified in mammalian cells; these proteins have limited homology to RAD51, and their functions are relatively unknown (2, 3). The RAD51-like protein RAD51L2 (RAD51C) was first identified from data base searches through partial homology to RAD51 and other members of this protein family (4). Recently, we (5) and others (6) have described DNA damage-sensitive cell lines that specifically lack RAD51L2 activity. It was shown that the RAD51L2 gene function was not redundant to other RAD51-like genes or RAD51 itself, because only RAD51L2 was able to restore DNA damage resistance to these cell lines. It was further suggested that RAD51L2 has a role in RAD51-dependent HR because RAD51L2-deficient cells show a reduction in sister-chromatid exchange and a decrease in damage-dependent RAD51 focus formation (5, 6). However, a direct role in homologous recombination processes has not been shown.

Human RAD51L2 shares only 27% sequence identity with the human RAD51 protein, with the most well conserved residues being those with homology to the nucleotide-binding or “Walker motif” (2). The Walker motif (7) consists of two separate sequences, A and B, which come together to form a nucleotide binding site. These residues are highly conserved in the RAD51 family and in its prokaryotic counterpart RecA. The Walker A motif, also known as the phosphate-binding loop (P-loop), is defined by the consensus sequence GXXXXGKT/S, where X is any amino acid. In RecA, non-conservative mutation of any of the four residues that identify the P-loop results in a non-functional protein but restricted mutation at other positions is tolerated (8, 9). A well characterized mutation in this motif is the conservative lysine to arginine (K72R) substitution: this mutant protein is able to bind but not hydrolyze ATP and can promote limited strand exchange in vitro (10). However, this mutant has been shown to lack RecA activity in vitro (9). Data obtained from the RecA crystal structure suggests that Lys-72 interacts directly with the β- and γ-phosphates of the bound ATP molecule (11). Mutagenesis has also been used to investigate the function of the A motif in the yeast Saccharomyces cerevisiae Rad51p. Rad51p with a lysine to arginine (K191A) mutation in this motif is unable to complement the DNA-damage sensitivity and recombination defects of a RAD51-null strain (12). Similarly, a K133A mutation in the Walker A motif of human RAD51 did not rescue the RAD51L2-deficient lethal phenotype of chick cells, whereas a K133R mutation gave a partially defective phenotype (13).

However, the presence of homology to the Walker motifs does not seem to be as functionally relevant in some of the RAD51-like proteins. In S. cerevisiae, mutation of the P-loop lysine results in increased γ-ray sensitivity and defective sporulation for Rad55p but not for Rad57p (14). In addition, P-loop mutations (K54R, K54A, and ΔG53/ΔK54) in the RAD51-like human protein XRCC2 have little effect on its function (15).

Searches for other potential functional motifs in the RAD51L2 protein yield few clues. Given its anticipated role in DNA-damage metabolism, RAD51L2 might be expected to be localized to the nucleus, and to carry a nuclear localization signal (NLS) sequence, but this has not been identified. The NLS usually consists of one or two short sequences of positively charged lysines and arginines, which are bound by a family of importins or transportins for active transport into the nucleus through the nuclear pores (16).

We used site-directed mutagenesis and deletion analysis to...
look at the importance of putative functional domains in the RAD51L2 protein by testing for the ability of the mutant protein to restore DNA damage resistance to a RAD51L2-deficient hamster cell line (irs3). In addition we have for the first time made direct measurements of HR efficiency in the irs3 cell line and compared it with its wild-type parent line.

EXPERIMENTAL PROCEDURES

Mammalian Cell and Bacterial Culture Methods—Wild-type V79 and RAD51L2-deficient irs3 cells (5, 17) were grown as monolayers at 37 °C in minimal essential medium (Invitrogen) supplemented with 10% fetal calf serum and antibiotics. To assay the sensitivity of individual clones to the DNA cross-linking agent mitomycin C (MMC), cells were respread into 24-well plates containing graded concentrations of MMC (0–100 nM), and survival was assessed visually as described previously (5). To quantitate MMC resistance, three independent repeat experiments were made with cells from pooled clones (five to six per experiment). To quantitate MMC resistance, three independent repeat experiments were made with cells from pooled clones (five to six per experiment) to assay the sensitivity of individual clones to MMC (0–100 nM), and survival was assessed visually as described previously (5).

Functional Domains in RAD51L2

Expression of RAD51L2-GFP Protein in irs3 Cells—RAD51L2 cDNA was cloned into pEGFP-N1 vector (Clontech) to create an in-frame fusion of the EGFP gene to the 3′ end of RAD51L2 and checked by sequencing. After transfection of RAD51L2-GFP into irs3 cells, G418-resistant clones were tested for MMC resistance using 24-well plates (as above) to demonstrate RAD51L2 function. Cells were grown on glass coverslips, and the fusion protein was visualized at 488 nm using a Bio-Rad MRC600 laser scanning confocal microscope.

Homologous Recombination Repair Assay—The recombinase reporter p59xDR-GFP6, carrying two mutant GFP genes positioned at either side of the pgk-puro selection cassette (19), was kindly provided by Dr. Maria Jasin (Memorial Sloan-Kettering Cancer Center, New York). V79 and irs3 cells were stably transfected with XhoI-linearized reporter DNA, and clones were isolated in 5 μg/ml puromycin. Subsequent clones were transiently transfected by electroporation (conditions as above) with 50 μg of pcBAse (1.5-kb expression vector) or transiently cotransfected with 50 μg of pcBAsec and 20 μg of RAD51L2 expression vector. Transfected cells were put into non-selective medium for 45 h, after which they were harvested and washed twice in phosphate-buffered saline. Flow cytometry analysis was carried out on 2 × 105 cells, and data were recorded on a green (FL1) versus red (FL3) fluorescence plot. Southern blotting was used to determine copy number and integrity of the DR-GFP construct in stably transfected clones. Two different digestion and probing strategies were used: (i) digestion with HindIII and probing with a GFP gene fragment to assess reporter copy number; and (ii) digestion with XcmI and probing with pgk-puro to assess linkage of the two mutant GFP genes. The HindIII digest yields one detectable fragment of known size (806 bp) that corresponds to one GFP gene (gGFP) and a second fragment of variable size that corresponds to ScGFP. Because this HindIII fragment size will vary with different copies of the reporter, it reveals copy number.

Sequence Analysis—Nuclear localization signals were searched for with PredictNLS and PSORT. Homologues of RAD51L2 were found by searching current EST and protein databases using BLAST (20) and manipulated for alignment by using programs within the GCG suite (Genetics Computer Group, Madison, WI).

RESULTS

RAD51L2 Translation Initiation Site—The functional activity of wild-type and mutated RAD51L2 protein was studied by transfection of human RAD51L2 cDNA into hamster cells (either the RAD51L2-deficient irs3 mutant or its wild-type V79 parent line). This procedure allowed the presence and expression of the transfected cDNA to be distinguished from any endogenous (hamster) RAD51L2 cDNA copies present. We have shown previously that the human cDNA substantially complements the RAD51L2 defect in irs3 (5) and found subsequently that the hamster RAD51L2 cDNA is no better at functional complementation than the human cDNA (data not shown). The human cDNA has been reported to have two potential start codons, 27 base pairs apart, neither of which is in an ideal sequence context compared with the Kozak consensus (21). The identification of both mouse (22) and hamster (5) RAD51L2 cDNAs showed that the first potential start codon is not conserved in these rodent species. We cloned the full-length human cDNA (including both potential start sites) or a cDNA of the protein. The products were cloned into the multiple cloning site of the pEGFP-N1 vector (Clontech) to create an in-frame fusion of the EGFP gene to the 3′ end of RAD51L2 and checked by sequencing. After transfection of RAD51L2-GFP into irs3 cells, G418-resistant clones were tested for MMC resistance using 24-well plates (as above) to demonstrate RAD51L2 function. Cells were grown on glass coverslips, and the fusion protein was visualized at 488 nm using a Bio-Rad MRC600 laser scanning confocal microscope.
truncated at the 5’ end to delete the first ATG (Fig. 1) into a vector with an internal ribosome entry site (pIRESneo2) to optimize selection of clones expressing RAD51L2 along with the selectable neo gene. These constructs were separately transfected into the irs3 cell line; after selection for the linked marker gene, clones were checked for the presence of the human RAD51L2 sequence in genomic DNA and for gene expression by RT-PCR. Very few clones (15%) transfected with the full-length cDNA had successfully integrated and expressed RAD51L2. Conversely, irs3 transfected with the 5’-truncated cDNA showed larger numbers (60%) of clones with successful RAD51L2 integration and expression. Clones with either the full-length or the 5’-truncated construct in genomic DNA were able to complement the MMC sensitivity to a very similar level (data not shown). We interpret these data to indicate that the second ATG of the human gene is capable of yielding a functional product in hamster cells, and therefore we used constructs including only this site in all subsequent experiments (Fig. 1).

Walker A Motif Is Important for RAD51L2 Function—The invariant lysine residue in the RAD51L2 Walker A motif was altered by site-directed mutagenesis to give either a non-conservative K131A mutation or a conservative K131R mutation (Fig. 1). Clones of irs3 cells transfected with the RAD51L2 K131A or K131R constructs were selected and checked for the presence of the mutant gene in genomic DNA and for gene expression by RT-PCR (data not shown). Growth tests of six individual clones expressing the RAD51L2 K131A construct in different MMC concentrations showed that each had no better ability to grow than untransfected irs3 cells. Full survival curves on pooled clones confirmed this finding (Fig. 2A). However, 5/5 clones expressing the RAD51L2 K131R construct were able to grow at higher MMC levels than irs3 in growth tests. Full survival curves of pooled clones carrying RAD51L2 K131R showed a level of MMC resistance between that of untransfected irs3 cells and cells transfected with wild-type RAD51L2 cDNA (Fig. 2A). These data strongly support the importance of the Lys-131 residue and, by inference, the Walker A motif in the function of the RAD51L2 protein.

Localization of the RAD51L2 Protein and Effect of Loss of the C Terminus—RAD51L2 cDNA was fused with EGFP and the construct was transfected into irs3 cells. The proportion of selected clones expressing RAD51L2 was lower than for the experiments reported above, because the EGFP vector does not carry an internal ribosome entry site. However, those clones expressing the RAD51L2-EGFP fusion gene were as resistant to MMC as clones expressing wild-type RAD51L2 cDNA, indicating that the EGFP tag did not affect function (data not shown). Assessment of the localization of the fluorescent fusion protein by confocal microscopy showed it to be predominantly nuclear, apart from the nucleoli, although some cytoplasmic
speckles were also visible (Fig. 3A). Clones transfected with the EGFP vector alone showed fluorescence throughout the cell (data not shown). Although search programs for an NLS motif in RAD51L2 did not identify any sequence at high probability, there is a short sequence of hydrophilic residues common to known NLS motifs (-RKRSR-) at the C terminus of the human protein (Fig. 1, amino acids 366–370, in bold). Compared with surrounding residues, we found that this sequence is highly conserved in RAD51L2 proteins from different mammals, and the conservation of the arginine and lysine residues extends to the predicted proteins of other newly identified RAD51L2 genes in lower vertebrates (Fig. 3C). To test the importance of this C-terminal region, a second EGFP fusion construct was generated with an 11 amino acid C-terminal deletion including the putative NLS (Fig. 1, amino acids 366–376). Several clones were selected after transfection of this construct, and those expressing the 3’ truncated RAD51L2 cDNA were tested for MMC resistance. Tests on individual clones showed that they had substantially reduced MMC resistance compared with wild-type RAD51L2 cDNA (data not shown), and full survival curves on pooled clones confirmed and quantified this result (Fig. 2B). Importantly, confocal imaging of the clones showed EGFP fluorescence distributed throughout the cell rather than localized to the nucleus (Fig. 3B).

**RAD51L2-deficient Cells Have a Reduced Frequency of Homologous Recombination**—To measure HR, the irs3 cell line and its wild-type counterpart (V79 line) were transfected with a recombination reporter substrate consisting of tandem defective genes encoding the GFP (19). One of the GFP genes is inactivated by the incorporation of an I-SceI endonuclease site, allowing a double-strand break (DSB) to be generated within the gene, whereas the other is truncated at both ends. Recombination by gene conversion can generate an intact GFP gene, the expression of which can be detected by flow cytometry (23).

![Copy number and recombination frequency (GFP fluorescence) data following integration of recombination reporter constructs into wild-type (V79) and RAD51L2-deficient (irs3) cells.](image)

A. Southern analysis of copy number of introduced recombination reporter construct in several clones, after DNA digestion with HindIII and probing with a GFP gene fragment. M, markers (PerkinElmer Life Sciences, 1-kb ladder); c, recombinant reporter p59xDR-GFP. B, representative GFP-fluorescence FACS data from a clone of RAD51L2-deficient cells (irs3–5) and wild-type cells (V79). Left to right: data shown are from cells not transfected with I-SceI (No DNA), transfected with I-SceI (I-SceI), or transfected with both I-SceI and the human RAD51L2 gene (I-SceI + RAD51L2). Cells falling above the diagonal line in each display represent GFP-positive recombinants (23).
TABLE I
Frequency of recombination (GFP-positive cells) in wild-type and RAD51L2-deficient irs3 cells, as well as in cells transected with wild-type RAD51L2 cDNA

| Clone     | Copy number | GFP-positive cells/SE | Mean GFP-positive cells | (I-Sce1 + L2)/S.E. | (I-Sce1)/S.E. |
|-----------|-------------|-----------------------|-------------------------|-------------------|---------------|
| irs3–5    | 2           | 0.29 ± 0.05           | 3.3                     |                   |               |
| irs3–17   | 2           | 0.13 ± 0.06           | 1.8                     |                   |               |
| irs3–24   | 1           | 0.26 ± 0.02           | 2.2                     |                   |               |
| V79–7     | 1           | 2.76 ± 0.25           | 1.1                     |                   |               |
| V79–10    | 2           | 1.00 ± 0.29           | 1.72 ± 0.29             | 0.93              |               |
| V79–15    | 1           | 1.41 ± 0.33           | 0.93                    |                   |               |

a Number of integrated copies of recombination substrate, determined by Southern analysis (see Fig. 4A; clone irs3–17 had one copy of smaller-than-expected size, so it may have only one functional copy).

b Averaged from 2–3 experiments per clone.

c Relative increase in recombination frequency following transfection of RAD51L2 cDNA.

Ten clones of each cell line carrying the recombination reporter substrate were analyzed for GFP fluorescence after transfection of a plasmid expressing the I-SceI endonuclease (pCBASce) to show that they retained at least one intact copy of the substrate. Clones with the potential for GFP expression were then assessed for copy number and linkage of the two GFP genes in the substrate using two different digestion/probing strategies on Southern blots (see “Experimental Procedures”; Fig. 4A and data not shown). In this way, three clones from each cell line carrying a single copy or two copies of the substrate were identified and used in recombination frequency measurements (Fig. 4B).

Although there was some clone-to-clone variation, all irs3-derived clones showed a significantly lower percentage of GFP-positive cells than the V79-derived clones (Table I). Thus, irs3 cells showed on average an ~7-fold decrease in the ability to repair an induced DSB by HR. To test directly whether the recombination deficiency in irs3 was caused by the lack of RAD51L2 protein, human RAD51L2 cDNA was co-transfected with pCBASce plasmid into both irs3-derived and V79-derived cells. Consistent with partial complementation shown in other tests (5), the expression of RAD51L2 gave a 2- to 3-fold increase in the frequency of GFP-positive cells in the irs3-derived clones, compared with I-SceI expression alone, whereas no increase was seen in the V79-derived clones (Table I and Fig. 4B).

DISCUSSION

RAD51L2 is thought to play an important role in the repair of damage in genomic DNA by homologous recombination. Consistent with this role, the RAD51L2-EGFP fusion protein localizes to the nucleus, probably utilizing a C-terminal nuclear localization signal. At present, our experiments have refined the region for nuclear localization to the final 11 amino acids, and more precise site-directed mutagenesis would be required to show that the RKRSR motif is directly involved. However, it should be noted that the remaining residues at the C terminus are not completely conserved (Fig. 3C), suggesting that they do not necessarily have an essential function, and that the sequence (R/K/K/BRCA2-RAD51/L1-RAD51/L2/L3-IRS, when compared with other recombination-deficient cell lines, could relate to the nature of the mutation in the respective genes or to differing roles of the recombination proteins involved. Recombination in BRCA2 mutant cells is reduced by 6- to >100-fold, depending on the nature of the mutation (19).

It is important to note that the reporter construct used in our analysis measured repair of a DSB by providing a homologous template from which genetic information could be copied. This RAD51L2-dependent process has been shown to involve mostly non-reciprocal events, termed gene conversion (33). Recently another measure of recombination, gene targeting frequency, was used to suggest that a RAD51L2-deficient chick lymphoblastoid cell line had a reduced level of HR at two loci (by 6-fold and 13-fold, respectively) (34). However, it was not possible to demonstrate that this targeting defect was directly related to the RAD51L2 gene, because the defect could not be complemented by cDNA transfection (although other chick cell responses could be complemented in this way). Gene targeting may be achieved by mechanisms other than gene conversion, perhaps including non-homologous events (35, 36). In our experiments, the human RAD51L2 gene was able to substantially complement the recombination deficiency of the irs3 line, similar to other responses we have shown here (Fig. 2A) and in previous work (5). Therefore, we have demonstrated a specific effect of RAD51L2 on homologous recombination efficiency for the first time.
As noted above, RAD51L2 has a unique role among the human RAD51-like proteins in forming part of both the heterodimeric (L2:X3) and heterotetrameric (L1:L2:L3:X2) complexes. The roles identified for RAD51L2 in this study, its requirement for the ATP-binding domain, for nuclear localization, and for gene conversion, give a sound basis for further functional analysis of this protein. Although the biochemical steps of RAD51-dependent HR are known in outline, especially from studies with yeast (36), the importance of the RAD51-like proteins in the different HR stages is still the subject of intense research efforts. There is evidence for their involvement in early HR stages by helping RAD51 polymerize onto DNA, in helping to displace single-stranded DNA binding protein (31, 37), as well as in the strand invasion step (38, 39). However, some recent data point to a potential role of these proteins in later stages of HR (5, 29, 40, 41). The challenge now is to integrate these various data into a coherent picture of the functioning of RAD51L2 and its partners in HR and related processes.

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REFERENCES

1. West, S. C. (2003) Nat. Rev. Mol. Cell Biol. 4, 435–445
2. Thacker, J. (1999) Trends Genet. 15, 166–168
3. Thompson, L. H., and Schild, D. (2001) Mutat. Res. 477, 131–153
4. Dosanjh, M. K., Collins, D. W., Fan, W., Lennon, G. G., Albala, J. S., Shen, Z., and Schild, D. (1998) Nucleic Acids Res. 26, 1179–1184
5. French, C. A., Masson, J. Y., Griffin, C. S., O’Regan, P., West, S. C., and Thacker, J. (2002) J. Biol. Chem. 277, 19322–19330
6. Godthelp, B. C., Wiegant, W. W., van Duijn-Goedhart, A., Scharer, O. D., van Buul, P. P., Kanaar, R., and Zdzienicka, M. Z. (2002) Nucleic Acids Res. 30, 2172–2182
7. Walker, J. E., Saraste, M., Runswick, M. J., and Gay, N. J. (1982) EMBO J. 1, 945–951
8. Logan, K. M., and Knight, K. L. (1993) J. Mol. Biol. 232, 1048–1059
9. Konsola, J. T., Logan, K. M., and Knight, K. L. (1994) J. Mol. Biol. 237, 20–34
10. Rehrauer, W., and Kowalczykowski, S. C. (1993) J. Biol. Chem. 268, 1292–1297
11. Story, R. M., and Steitz, T. A. (1992) Nature 355, 374–376
12. Shinohara, A., Ogawa, H., and Ogawa, T. (1992) Cell 69, 457–470
13. Morrison, C., Shinohara, A., Sonoda, E., Yamaguchi-Iwai, Y., Takata, M., Weichselbaum, R. R., and Takeda, S. (1999) Mol. Cell. Biol. 19, 6891–6897
14. Johnson, R. D., and Symington, L. S. (1995) Mol. Cell. Biol. 15, 4843–4850
15. O’Regan, P., Wilson, C., Townsend, S., and Thacker, J. (2001) J. Biol. Chem. 276, 22148–22153
16. Boopathi, T. (1994) J. Cell. Biochem. 55, 32–58
17. Jones, N. J., Cox, R., and Thacker, J. (1987) Mutat. Res. 183, 279–286
18. van den Hoff, M. J., Moorman, A. F., and Lamers, W. H. (1992) Nucleic Acids Res. 20, 2902
19. Moya, M. E., Pierie, A. J., and Jasin, M. (2001) Mol. Cell 7, 263–272
20. Autschel, S. F., Madden, T. L., Schaffer, A. A., Zhang, J., Zhang, Z., Miller, W., and Lipman, D. J. (1997) Nucleic Acids Res. 25, 3389–3402
21. Knazk, M. (1987) Nucleic Acids Res. 15, 8125–8148
22. Leasure, C. S., Chandler, J., Gilbert, D. J., Householder, D. B., Stephens, R., Copeland, N. G., Jenkins, N. A., and Sharan, S. K. (2001) Gene 271, 59–67
23. Pierie, A. J., Johnson, R. D., Thompson, L. H., and Jasin, M. (1999) Genes Dev. 13, 2633–2638
24. Coko, M., Nair, R., and Rost, B. (2000) EMBO Rep. 1, 411–415
25. Masson, J. Y., Tasouzas, M. C., Stasiak, A. Z., Stasiak, A., Shah, R., Meller, M. J., Benson, F. E., and West, S. C. (2001) Genes Dev. 15, 3296–3307
26. Wiese, C., Collins, D. W., Albala, J. S., Thompson, L. H., Kronenberg, A., and Schild, D. (2002) Nucleic Acids Res. 30, 1001–1008
27. Miller, K. A., Yoshikawa, D. M., McConnell, I. R., Clark, R., Schild, D., and Albala, J. S. (2002) J. Biol. Chem. 277, 8406–8411
28. Liu, N., Schild, D., Thelen, M. P., and Thompson, L. H. (2002) Nucleic Acids Res. 30, 1009–1015
29. Lio, Y. C., Mazin, A. V., Kowalczykowski, S. C., and Chen, D. J. (2003) J. Biol. Chem. 278, 2469–2478
30. Masson, J. Y., Stasiak, A. Z., Stasiak, A., Benson, F. E., and West, S. C. (2001) Proc. Natl. Acad. Sci. U. S. A. 98, 8440–8446
31. Sigurgardsson, S., Van Kemen, S., Bussen, W., Schild, D., Albala, J. S., and Sung, P. (2001) Genes Dev. 15, 3308–3318
32. Caldecott, K., and Jeggo, P. (1991) Mutat. Res. 255, 111–121
33. Johnson, R. D., and Jasin, M. (2000) EMBO J. 19, 3398–3407
34. Takata, M., Sasaki, M. S., Tachiiri, S., Fukushima, T., Sonoda, E., Schild, D., Thompson, L. H., and Takeda, S. (2001) Mol. Cell. Biol. 21, 2858–2866
35. Jasin, M. (1996) Trends Genet. 12, 224–228
36. Paques, F., and Haber, J. E. (1999) Microbiol. Mol. Biol. Rev. 63, 349–404
37. Sung, P. (1987) Genes Dev. 11, 1111–1121
38. Sugawara, N., Ivanov, E. L., Fishman-Lobell, J., Ray, B. L., Wu, X., and Haber, J. E. (1995) Nature 373, 84–86
39. Sugawara, N., Wang, X., and Haber, J. E. (2003) Mol. Cell 12, 209–219
40. Brenneman, M. A., Wagner, B. M., Miller, C. A., Allen, C., and Nickoloff, J. A. (2002) Mol. Cell 10, 387–395
41. Yokoyama, H., Kurumizaka, H., Iwaki, S., Yokoyama, S., and Shibata, T. (2003) J. Biol. Chem. 278, 2767–2772
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