Anti-mutagenic Activity of DNA Damage-binding Proteins Mediated by Direct Inhibition of Translesion Replication*

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DNA lesions that block replication can be bypassed in Escherichia coli by a special DNA synthesis process termed translesion replication. This process is mutagenic due to the miscoding nature of the DNA lesions. We report that the repair enzyme formamido-pyrimidine DNA glycosylase and the general DNA damage recognition protein UvrA each inhibit specifically translesion replication through an abasic site analog by purified DNA polymerases I and II, and DNA polymerase III (a subunit) from E. coli. In vivo experiments suggest that a similar inhibitory mechanism prevents at least 70% of the mutations caused by ultraviolet light DNA lesions in E. coli. These results suggest that DNA damage-binding proteins regulate mutagenesis by a novel mechanism that involves direct inhibition of translesion replication. This mechanism provides anti-mutagenic defense against DNA lesions that have escaped DNA repair.

Mutations caused by DNA-damaging agents play a key role in cancer via activation of oncogenes and inactivation of tumor suppressor genes (1). DNA repair is the major defense mechanism of cells against DNA damage and its deleterious effects. The major repair strategy in both prokaryotes and eukaryotes is excision repair. It involves excision of the damaged region from DNA, followed by re-synthesis using the complementary undamaged strand as a template (2). Two excision repair mechanisms are known for DNA damage: nucleotide excision repair (NER),1 which operates on a wide variety of DNA lesions (3),1 and base excision repair (BER),1 which operates on a wide variety of DNA lesions (3), and base excision repair (BER) which is more limited in its range of substrate specificity (4). The key step in these mechanisms is the recognition of DNA damage. In the bacterium Escherichia coli, the protein UvrA is responsible for the recognition of a broad range of DNA lesions that are repaired by NER, whereas in BER a series of DNA glycosylases with a much narrower range of specificity recognize and excise damaged or foreign bases from DNA (2). A DNA lesion that has escaped repair can cause a discontinuity in DNA in the form of a ssDNA region carrying the lesion. This occurs when the replication fork is blocked at the lesion (5, 6), or occasionally because of complications in nucleotide excision repair (7). This gap/lesion structure poses a problem for excision repair; an attempt to eliminate the lesion will cause a double-strand break, which is highly lethal, but on the other hand, the gap must be filled in for DNA replication to be completed and cell division to occur.

Two tolerance mechanisms that operate in E. coli are responsible for filling in the gap/lesion structures (2). A recombination repair mechanism patches the gap via recombination using homologous sequences from the sister chromatid. This process does not remove the damaged base, but it enables an error-free bypass, resulting in the restoration of genome continuity. An alternative bypass mechanism, which is regulated by the SOS stress response, involves filling in of the gap by DNA synthesis. This translesion replication reaction is potentially mutagenic because of the miscoding properties of most DNA lesions (6, 8). The process was termed SOS mutagenesis, or error-prone repair, because the gap is repaired (though the damaged nucleotide remains) with the concomitant formation of mutations. It is responsible for mutations caused by a large spectrum of DNA lesions, including UV lesions, bulky carcinogen adducts, and abasic sites, which share the property of being blocks to DNA replication (2).

Biological regulation is often achieved by a combination of both positive and negative affectors; however, so far little is known on negative affectors that act directly on error-prone repair (9, 10). In this study, we examined the possibility that proteins that bind lesions on ssDNA act as inhibitors of mutagenesis by directly inhibiting translesion replication.

EXPERIMENTAL PROCEDURES

Materials—UvrA and RecA were purified as described (11–13). DNA polymerase I (6000 units/mg) was obtained from Boehringer Mannheim. DNA polymerase II, purified according to Ref. 14, was a gift from M. Goodman (University of Southern California, Los Angeles, CA), and DNA polymerase III (a subunit), purified as described (15), was a gift from M. O'Donnell (Rockefeller University, New York, NY). Fpg was a gift from J. Laval (Institut Gustave Roussy, Villejuif, France).

The 40-nucleotide-long templates AB1 (5′-GCT GTA CAA CGT CGT GAC TGG GAA AAC CTT GCC GTT ACC C-3′) and AB2 (5′-GGGA AAA CCC TGG CGT TAC CCF ACT TAA TCG TCT TGC AGC A-3′), each containing a site-specific abasic site analog (marked F), were synthesized and purified as described (16) and were gifts from M. Takeshita (State University of New York, Stony Brook, NY). Similar oligonucleotides with no damage were synthesized by the Synthesis Unit of The Weizmann Institute of Science.

The substrates were prepared each by annealing the complementary 9P-end-labeled 17-mer primer to the 40-nucleotide-long synthetic DNA template as described (17). Essentially, all template molecules contain the abasic site analog (>99.98%), as deduced from the complete arrest of DNA synthesis at the lesion when bypass was assayed with pol I in the presence of 0.1 mM KCl (<0.02% bypass, representing the limit of detection; Ref. 18).

Translesion Replication—The assay was performed essentially as described (17, 18). The in vitro replication reaction mixture (25 or 50 μl) contained 20 mM Tris-HCl, pH 7.5, 8 μg/ml bovine serum albumin, 5 mM dithiothreitol, 0.1 mM EDTA, 4% glycerol, 10 mM MgCl₂, 1 mM ATP and

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1 The abbreviations used are: NER, nucleotide excision repair; BER, base excision repair; ssDNA, single-stranded DNA; MMS, methylmethanesulfonate.
0.5 mM dNTPs. In addition the mixtures contained 70 nM pol I and 70 nM template AB1, 24 nM pol II and 36 nM template AB2, or 150 nM pol III (α subunit) and 85 nM template AB1. The time course of bypass was performed in the absence or the presence of 0.8 μM Fpg or 0.2 μM UvrA. These concentrations are comparable with the estimated intracellular concentrations of UvrA (0.3 μM; Ref. 19) and Fpg (0.15–0.30 μM; Ref. 20), which are minimal estimated concentrations that might be further increased by compartmentalization. Reactions were carried out at 30 °C for the indicated time periods, after which they were treated with proteinase K and fractionated by electrophoresis on 20% polyacrylamide gels containing 8 M urea. End-labeled oligonucleotides were used as size standards. Samples were run at 1500–1600 V for 3–4 h, after which they were visualized and quantified using a Fuji BAS 1000 phosphorimager.

**Strain Construction**—The *E. coli* mutants used were derived from AB1157 argE3 his4 leuB6 proA2 thr1 ara14 galK2 lacY1 mtl1 xyl5 thi1 tpx3 rpmL3 supE44 by P1 transduction as described (21). WBY130 was prepared by moving the ΔuvrA ΔuvrB mutation from strain M1H1 (obtained from P. van de Putte, Leiden University, Leiden, The Netherlands) to AB1157. WBY131 is AB1157 but also uvrC279::Thr10 (transduced from strain N3124 obtained from R. G. Lloyd, University of Nottingham, Nottingham, England). Strains WBY136 and WBY137 are Δphr::kan derivatives of strains WBY130 and WBY131, respectively. The mutation was moved from strain UNC523 (obtained from A. San- car, University of North Carolina, Chapel Hill, NC).

UV Light and Methylmethanesulfonate (MMS) Mutagenesis—The His reversion assay was performed essentially as described (10). Derivatives of *E. coli* AB1157 cells were UV-irradiated at 254 nm with the indicated doses using a germicidal lamp, after which they were plated on M9 minimal plates supplemented with 100 μg/ml each of Pro, Arg, Thr, Leu, Ile, and Val, and a limited amount of 2 mg/liter His. His on M9 minimal plates supplemented with 100 mg/liter each of Pro, Arg, Ile, and Val, and 1.2% agar was raised to 100 mg/liter, and that of Arg was lowered to 3 mg/liter. UV light-induced reversion of Arg auxotrophy was conducted according to the same procedure except that the concentration of His in the plates was raised to 100 mg/ml, and that of Arg was lowered to 3 mg/liter. MMS-induced His reversions were assayed as follows; cells were grown to OD<sub>600</sub> 0.5, after which they were washed, resuspended in 10 mM Tris-HCl, pH 7.5, 0.15 M NaCl, and incubated for 30 min at 37 °C with 0.5–2.0 μg/ml MMS. His<sup>−</sup> mutants were assayed as described above for UV mutagenesis.

**RESULTS**

Formamido-pyrimidine DNA Glycosylase Inhibits Translesion DNA Synthesis through an Abasic Site Analog—Abasic sites are a classical example of miscoding and replication-blocking DNA lesions, which cause mutations via the SOS response (22). Although polymerization frequently terminates at DNA lesions, which cause mutations via the SOS response (22). Although polymerization frequently terminates at DNA lesions, which cause mutations via the SOS response (22). Although polymerization frequently terminates at DNA lesions, which cause mutations via the SOS response (22). Although polymerization frequently terminates at DNA lesions, which cause mutations via the SOS response (22).

To examine the effects of Fpg on bypass synthesis by each of the three known DNA polymerases of *E. coli*. We have shown previously that when the appropriate reaction conditions are used, each of the DNA polymerases can bypass the abasic site analog, unassisted by other proteins, at frequencies higher than reported previously (17). We used DNA polymerase I, DNA polymerase II, and the α subunit of DNA polymerase III (pol IIIα). In this bypass assay system, pol III core showed little bypass, and thus its α subunit, which contains the polymerase active site, was used instead (17). As can be seen in Fig. 1, each of the DNA polymerases was capable of replicating through the abasic site analog, albeit at different rates. Addition of Fpg caused an inhibition of translesion replication by each of the DNA polymerases of up to 10–20-fold (Fig. 1, B and C). This was evident from the decreased amount of bypass products, and from the accumulation of termination products at the lesion (Fig. 1B).

The UvrA Damage Recognition Protein Inhibits Bypass Synthesis—To examine whether other DNA damage-binding proteins inhibit translesion synthesis, we analyzed the effect of the UvrA protein on bypass of the abasic site analog. UvrA is the general DNA damage recognition protein of *E. coli* (2). It recognizes a large spectrum of DNA lesions (19), including abasic sites (30). When purified UvrA protein was added to the bypass reaction, it caused a strong 10–20-fold inhibition of bypass synthesis by DNA polymerase I or by pol IIIα, and it completely inhibited (900-fold) translesion synthesis by pol II (Fig. 2; Table I). The termination of DNA synthesis in these experiments and in the experiments with Fpg was not caused by cleavage of the template by Fpg or by UvrA at the abasic site analog, because the abasic site analog is insensitive to the enzyme (29) and UvrA has no nuclease activity (2). This was confirmed by repeating the bypass reactions in the presence of Fpg or UvrA with a DNA substrate in which the 5′-end of the template strand was radiolabeled (data not shown). Thus, DNA damage-binding proteins of both the NER and BER pathways of repair strongly inhibit translesion replication.

The Inhibition of Bypass Synthesis by UvrA and Fpg Is Specific—The dependence of the inhibitory effect on the presence of the lesion in DNA was addressed by repeating the inhibition experiments with a control template with no damage, and the results are shown in Table I. DNA synthesis on the undamaged DNA by each of the three DNA polymerases was not affected by Fpg, compared with the 10–20-fold inhibition on the damaged template. Thus, inhibition of bypass by Fpg was DNA damage-specific. The UvrA protein caused an inhibition of DNA synthesis on the undamaged template; however, its extent depended on the polymerase. DNA synthesis by pol II was inhibited only 2.7-fold, much weaker than the 900-fold inhibition of bypass synthesis. For pol I and pol IIIα, inhibition by UvrA of DNA synthesis on the damaged template was 2–3-fold stronger than on the undamaged template (Table I).

To examine whether any protein that binds ssDNA inhibits bypass synthesis, we assayed the effect on translesion synthesis of RecA, a protein that binds ssDNA regardless of the presence of DNA damage (31). We found that RecA inhibited bypass synthesis by pol I and pol IIIα by 10% and 21%, respectively, and it stimulated bypass by pol II by 23%. Thus, RecA...
had only a marginal effect on bypass synthesis. This small effect was not due to lack of DNA binding, since under our conditions RecA caused a large retardation in the mobility of the template when assayed by the gel mobility shift assay (data not shown). Thus, not every ssDNA-binding protein inhibits translesion synthesis.

**The UvrA Protein and DNA Photolyase Inhibit UV Mutagenesis in Vivo in the Absence of DNA Repair**—The in vitro studies presented above raise the possibility that DNA damage-binding proteins have an anti-mutagenic activity separate from the one which is associated with the removal of DNA damage. If true in *vivo*, one would predict that SOS mutagenesis will be higher in a strain that lacks DNA damage-binding proteins when compared with a strain that contains these proteins. The examination of such a prediction should be made under conditions in which the repair capacity of the two strains is the same, and the only difference is the presence or absence of DNA damage-binding proteins. The mutagen that we examined was UV light. It was chosen because it provided a convenient experimental system (see below) in which the concept could be examined on DNA lesions other than abasic sites. UV light produces primarily cyclobutyl dimers and 6–4 pyrimidine–pyrimidone adducts (2). These lesions are chemically very different from abasic sites, and they are repaired by different error-free repair mechanisms. However, they give rise to mutations by the same SOS mutagenesis pathway, and thus they are functional homologues, as far as induced mutagenesis is concerned (6, 22, 32). In particular, the 6–4 photoadducts share with abasic sites the properties of being both blocking and miscoding (33). The cyclobutyl photodimers are blocking, but only weakly miscoding (34, 35).

Both types of UV lesions are repaired by the UvrABC NER
system, although the 6–4 adducts are repaired faster. The cyclobutyl dimers are also repaired by DNA photolyase, using light as a cofactor (2). By using a uvrC mutant (NER not operative) and working under yellow light (DNA photolyase not active), one creates a situation in which cyclobutyl dimers and 6–4 adducts are not repaired. Under these conditions, the repair capacity of the uvrC strain is the same as a uvrA phr double mutant, except that in the uvrC strain both UvrA and DNA photolyase are still present and bind UV lesions (photolyase also binds cyclobutyl dimers in the dark; Ref. 36).

The prediction was that if UvrA and photolyase inhibit translesion replication in vivo, UV mutagenesis would be higher in the uvrA phr double mutant as compared with the uvrC mutant (Table II).

We compared UV mutagenesis and survival of an isogenic series of single uvrA and uvrC mutants, and the uvrA phr and uvrC phr double mutants. We used low UV doses, under which cell survival was high (70–90%), conditions that are physiologically relevant. As can be seen in Fig. 3A, the frequency of UV light-induced His$^-$ → His$^+$ reversions was 3.3-fold higher in
the uvrA phr strain, as compared with the uvrC strain. UV survival was identical, indicating that the repair capabilities of these strains were the same, as expected. Mutants carrying the uvrA or uvrC phr mutations exhibited intermediate mutagenicity. We also examined the same mutants in the Arg reversions, UV-induced Arg $^{+} \rightarrow$ Arg$^{-}$ reversions were higher in the uvrA phr strain, as compared with the uvrC strain, although the effect was slightly lower (2.5-fold). These results indicate that, when present, UvrA and DNA photolyase eliminate as much as 70% of the UV-induced His$^{+}$ mutations by a mechanism that does not involve DNA damage removal.

Our model predicts that the anti-mutagenic effect of a particular DNA damage-binding protein will be directed only against the DNA lesions to which it binds. Thus, no anti-mutagenic effect of UvrA and DNA photolyase is predicted, for example, for alkylation damage in DNA. This prediction was examined by assaying MMS mutagenesis in the various mutants. Like UV mutagenesis, MMS mutagenesis is SOS-dependent. However, in contrast to UV light DNA damage, the alkylation DNA damage caused by MMS is repaired primarily by demethylation and by BER (2). Thus, it was expected that MMS mutagenesis would be the same in the uvr and phr mutants. As can be seen in Fig. 3C, there were no differences in MMS mutagenesis among the four strains, as expected, suggesting that the effect is specific for the appropriate combination of DNA damage-binding proteins and the DNA lesions to which they bind.

The most likely explanation for the lower UV mutagenesis in the uvrC mutant as compared with the uvrA phr mutant is binding of UvrA and DNA photolyase to UV lesions present on ssDNA regions, and physical obstruction of the bypass attempt by the polymerase, similar to our in vitro results with the abasic site analog. The magnitude of the inhibition of translesion DNA synthesis by DNA-binding proteins in vivo may be larger than the 3.3-fold effect observed in our UV mutagenesis experiments, because there may be other proteins that bind pre-mutagenic UV lesions in addition to UvrA and DNA photolyase.

### Table II

Phenotypes of E. coli strains that were constructed in order to examine the effect of DNA damage-binding proteins on UV mutagenesis

| Phenotype                                      | Genotype        | uvrA phr | uvrC |
|-----------------------------------------------|-----------------|----------|------|
| Relevant proteins present                     | None            | UvrA, photolyase |
| Repair by NER and PR                          | No              | No       | Yes  |
| Binding to UV dimers and 6–4 adducts          | No              | Yes      |      |
| UV mutagenesis (predicted)                    | + + +           | -        |      |

**DISCUSSION**

This study addressed the possibility that DNA damage-binding proteins can intervene directly in the mutagenic bypass reaction and inhibit it, thus providing extra anti-mutagenic protection to the cell. Our results with the in vitro model system showed that the Fpg and UvrA repair proteins specifically inhibited in vitro translesion replication through an abasic site analog by purified DNA polymerases. These effects can be explained by the binding of the DNA damage-binding proteins to the damaged site in DNA, forming a physical obstacle to polymerization by the DNA polymerases. As the polymerase encounters the lesion, it pauses and readily dissociates from DNA (25, 37, 38). The presence of a DNA damage-binding protein may facilitate dissociation and/or inhibit rebinding of the polymerase to the primer-lesion site, leading to an inhibition of bypass synthesis. Such a mechanism could be common to many types of DNA lesions and the proteins that specifically bind them. In particular, replication of strongly blocking lesions is expected to be prone to this type of inhibition, because the DNA polymerases have difficulty in replicating them in the first place, strongly favoring dissociation over bypass (6).

UV lesions and abasic sites give rise to mutations by a similar translesion replication mechanism (6, 8, 22). Our findings that, in the absence of DNA repair, UV mutagenesis was higher in a strain lacking UvrA and DNA photolyase and that Fpg and UvrA inhibit bypass synthesis in vitro can be explained by the same basic molecular mechanism. According to this mechanism, a DNA lesion that has escaped repair and is located in a ssDNA region is recognized by both specific and general DNA damage-binding proteins. These proteins are unable to eliminate the lesion by excision repair, because that would cause a lethal double strand break. Instead, the binding of these proteins to the lesion inhibits bypass synthesis, and thus causes a reduction in mutagenesis.
DNA Damage-binding Proteins Inhibit Translesion Replication

Consistent with our suggestion is the observation that overproduction of DNA photolyase reduced in vivo UV mutagenesis (39). A related observation was the report that mutations due to a site-specific O6-butylguanine in phage dx174 increased 8-fold in a uvrA mutant. However, the interpretation of this experiment is complicated by the fact that a missense uvrA mutant, rather than a deletion mutant, was used, and because repair mechanisms responsible for removal of alkylated damage were not neutralized in the cell (40).

The exact events that occur in a cell following UV irradiation are not fully understood. However, it is clear that ssDNA regions are formed due to the inhibition of DNA replication by blocking UV lesions that were not repaired (5, 6). These regions may serve as binding sites for DNA damage-binding proteins, thus suppressing the error-prone translesion replication. The final mutagenicity is the outcome of the activity of factors that facilitate UV mutagenesis, such as RecA, UmuD, and UmuC, and factors that inhibit the process, such as UvrA and DNA photolyase. How does the binding of UvrA and photolyase lead to an anti-mutagenic effect? One possibility is that this intermediate cannot be repaired and will lead to cell death. This would have predicted differences in UV survival of uvrA phr and uvrC mutants; however, such a difference was not observed. We favor the idea that, while inhibitory to the mutagenic translesion synthesis, the binding of DNA damage-binding proteins does not interfere with error-free recombinational repair. This enables continuation of chromosome replication and cell division, without creating a mutation.

In summary, our results suggest that the mutagenic effects caused by agents such as UV light, which produce replication blocks, are suppressed by DNA damage-binding proteins. This provides a second line of defense, which reduces the mutagenic effects of DNA lesions that have escaped DNA repair. It operates by the direct inhibition of translesion replication, mediated via binding of DNA damage-binding proteins to the pre-mutagenic ssDNA regions carrying the DNA lesions. This represents a new regulatory mechanism of induced mutagenesis, and a new anti-mutagenic function for DNA damage-binding proteins. At this point, we do not know whether a similar mechanism operates in eukaryotes. However, based on the great similarity in basic DNA repair mechanisms between E. coli and eukaryotes, direct inhibition of translesion DNA synthesis by DNA damage-binding proteins, such as the human XPA or the yeast Rad14 proteins, is likely to be involved in the regulation of induced mutagenesis in eukaryotes as well.

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REFERENCES

1. Vogelstein, B., and Kinzler, K. W. (1993) Trends Genet. 9, 138–141
2. Friedberg, E. C., Walker, G. C., and Siede, W. (1995) DNA Repair and Mutagenesis, ASM Press, Washington, D.C.
3. Sancar, A. (1994) Science 266, 1954–1956
4. Seeberg, R., Kiede, L., and Bjoras, M. (1995) Trends Biochem. Sci. 20, 391–397
5. Witkin, E. M. (1976) Bacteriol. Rev. 40, 869–897
6. Livneh, Z., Cohen-Fix, O., Skaliter, R., and Elizur, T. (1993) CRC Crit. Rev. Biochem. Mol. Biol. 28, 465–513
7. Tomer, G., Cohen-Fix, O., O'Donnell, M., Goodman, M., and Livneh, Z. (1996) Proc. Natl. Acad. Sci. U. S. A. 93, 1376–1380
8. Walker, G. C. (1995) Trends Biochem. Sci. 20, 416–420
9. Shawitt, O., and Livneh, Z. (1989) J. Bacteriol. 164, 11275–11281
10. Tadmor, Y., Ascarelli-Goell, R., Skaliter, R., and Livneh, Z. (1992) J. Bacteriol. 174, 2517–2524
11. Thomas, D. C., Levy, M., and Sancar, A. (1985) J. Biol. Chem. 260, 9875–9883
12. Yeung, A. T., Mates, W. B., Oh, E. Y., Yoakum, G. H., and Grossman, L. (1988) Nucleic Acids Res. 14, 8535–8556
13. Cox, M. M., McEntee, K., and Lehman, I. R. (1941) J. Biol. Chem. 256, 4676–4678
14. Cai, H., Yu, H., McEntee, K., Kunkel, T. A., and Goodman, M. F. (1995) J. Biol. Chem. 270, 15327–15335
15. Maki, H., and Kornberg, A. (1985) J. Biol. Chem. 260, 12987–12992
16. Takeshita, M., Chang, C., Johnson, F., Will, S., and Grollman, A. P. (1987) J. Biol. Chem. 262, 10171–10179
17. Paz-Elizur, T., Takeshita, M., Goodman, M. O'Donnell, M., and Livneh, Z. (1996) J. Biol. Chem. 271, 24662–24669
18. Paz-Elizur, T., Takeshita, M., and Livneh, Z. (1997) Biochemistry 36, 1766–1773
19. Van Houten, B. (1990) Microbiol. Rev. 54, 18–51
20. Boiteux, S. (1993) J. Photochem. Photobiol. B Biol. 19, 87–96
21. Miller, J. H. (1972) Experiments in Molecular Genetics, Cold Spring Harbor Laboratory Press, Cold Spring Harbor Laboratory, NY
22. Loeb, L. A., and Preston, B. D. (1986) Annu. Rev. Genet. 20, 201–230
23. Kunkel, T. A., Schaeper, R. M., and Loeb, L. A. (1983) Biochemistry 22, 2378–2384
24. Sagher, D., and Strauss, B. (1983) Biochemistry 22, 4518–4526
25. Hevroni, D., and Livneh, Z. (1988) Proc. Natl. Acad. Sci. U. S. A. 85, 5046–5050
26. Bonner, C. A., Randall, S. K., Rayssiguier, C., Radman, M., Eritiia, R., Kaplan, B. E., McEntee, K., and Goodman, M. F. (1988) J. Biol. Chem. 263, 18946–18952
27. O'Connor, T. R., and Laval, J. (1989) Proc. Natl. Acad. Sci. U. S. A. 86, 5222–5226
28. Tchou, J., Kasai, H., Shibutani, S., Chung, M. H., Laval, J., Grollman, A. P., and Nishimura, S. (1991) Proc. Natl. Acad. Sci. U. S. A. 88, 4690–4694
29. Castaigne, B., Boiteux, S., and Zelwer, U. (1992) Nucleic Acids Res. 20, 389–394
30. Snowden, A., Kow, Y. W., and Van Houten, B. (1990) Biochemistry 29, 7251–7259
31. Roca, A. I., and Cox, M. M. (1990) CRC Crit. Rev. Biochem. Mol. Biol. 25, 415–456
32. Sancar, G. B., Smith, F. W., Reid, R., Payne, G., Levy, M., and Sancar, A. (1987) J. Biol. Chem. 262, 478–485
33. Sancar, G. B., Smith, F. W., Reid, R., Payne, G., Levy, M., and Sancar, A. (1987) J. Biol. Chem. 262, 478–485
34. Horsfall, M. J., and Lawrence, C. W. (1994) J. Biol. Chem. 269, 2635–2639
35. Horsfall, M. J., Borden, A., and Lawrence, C. W. (1997) J. Biol. Chem. 272, 10518–10523
36. Sancar, G. B., Smith, F. W., Reid, R., Payne, G., Levy, M., and Sancar, A. (1987) J. Biol. Chem. 262, 478–485
37. Swarting, J., and Livneh, Z. (1987) J. Bacteriol. 169, 4518–4523
38. Swarting, J., and Livneh, Z. (1988) J. Bacteriol. 169, 4518–4523
39. Swarting, J., and Livneh, Z. (1988) J. Bacteriol. 169, 4518–4523
40. Chambers, R. B., Siedlewskaja-Goell, R., Hirani-Hoja, S., and Borowy-Borowsky, H. (1985) Proc. Natl. Acad. Sci. U. S. A. 82, 7173–7177