were excised, then isolated using the QIAquick gel extraction kit (Qiagen). Both strands of the purified DNAs were sequenced with the use of the Taq DyeDeoxy Terminator Cycle sequencing kit (Perkin-Elmer/Applied Biosystems) and a total of 51 WN-specific primers spaced about 400 bases apart on the genome (primer sequences are available upon request). Cycle sequencing was performed by combining ~400 ng of gel-purified DNA (0.2 pmol) with 30 pmol of WN-specific primer and following the manufacturer's protocol.

2. C. M. Rice *et al.*, *Science* **229**, 726 (1985).
3. M. K. Gentry, E. A. Henchal, J. M. McCown, W. E. Brandt, J. M. Dalrymple, *Am. J. Trop. Med. Hyg.* **31**, 548 (1982).
4. E. A. Henchal, J. M. McCown, D. S. Burke, M. C. Seguin, W. E. Brandt, *Am. J. Trop. Med. Hyg.* **34**, 162 (1985).
5. J. T. Roehrig *et al.*, *Am. J. Trop. Med. Hyg.* **42**, 394 (1990).
6. E. A. Gould, A. Buckley, S. Higgs, S. Gaidamovich, *Arch. Virol.* (suppl. 1) (1990), p. 137.
7. R. A. Hall, G. W. Burgess, B. H. Kay, P. Clancy, *Immunol. Cell Biol.* **69**, 47 (1991).
8. S. C. Adams *et al.*, *Virology* **206**, 49 (1995).
9. J. T. Roehrig, J. H. Mathews, D. W. Trent, *Virology* **128**, 118 (1983).
10. R. A. Hawkes, J. T. Roehrig, A. R. Hunt, G. A. Moore, *J. Gen. Virol.* **69**, 1105 (1988).
11. C. H. Calisher *et al.*, *J. Gen. Virol.* **70**, 37 (1989).
12. H. M. Savage *et al.*, *Am. J. Trop. Med. Hyg.*, in press.
13. F.-X. Berthet *et al.*, *J. Gen. Virol.* **78**, 2293 (1997).
14. S. Kumar, K. Tamura, M. Nei, *MEGA: Molecular Evolutionary Genetics Analysis*, version 1 (Pennsylvania State University, University Park, PA, 1993).
15. D. L. Swofford, *PAUP*: Phylogenetic Analysis Using Parsimony (*And Other Methods)*, version b4 (Sinauer Associates, Sunderland, MA, 1998).
16. G. J. Olsen, H. Matsuda, R. Agstrom, R. Overbeek, *Comput. Appl. Biosci.* **10**, 41 (1994).
17. J. Felsenstein, *J. Mol. Evol.* **17**, 368 (1981).
18. R. S. Lanciotti and M. B. Crabtree, data not shown.
19. T. Briese, X.-Y. Jia, C. Huang, L. J. Grady, W. I. Lipkin, *Lancet* **354**, 1261 (1999).
20. T. H. Work, H. S. Hurlbut, R. M. Taylor, *Am. J. Trop. Med. Hyg.* **4**, 872 (1955).
21. T. F. Tsai, F. Popovici, C. Cernescu, G. L. Campbell, N. I. Nedelcu, *Lancet* **352**, 767 (1998).
22. A. Rzhetsky and M. Nei, *Mol. Biol. Evol.* **9**, 945 (1992).
23. ———, *Mol. Biol. Evol.* **10**, 1073 (1993).
24. We thank K. Tsuchiya, A. Kerst, B. Holloway, K. Gottfried, M. Godsey, N. Panella, B. R. Miller, A. H. Hunt, R. S. Nasci, B. J. Biggerstaff, and C. J. Mitchell (CDC) for technical assistance and valuable scientific discussions; S. Murri and M.-T. Drouet (Institut Pasteur), G. Gustafson, J. Pedersen, D. Petersen, K. Moser, and D. Johnson (NVSL), K. Hynes and R. Diana (New York State Department of Environmental Conservation), L. Sileo and K. Converse (National Wildlife Center), A. Ngbokoli and R. Manduca (Wildlife Conservation Society), and D. J. White (New York State Department of Health) for technical assistance; E. Gould (Institute of Virology and Environmental Microbiology, Natural Environment Research Council, UK) for providing WN-specific mAb H5.46; M. Layton, A. Fine, J. Miller, D. Nash, A. Ramon, and I. Poshni (New York City Department of Health) for providing human specimens for testing; K. Reibner (New York City Office of the Chief Medical Examiner) for performing the autopsies; and R. Deavours and A. Mather (CDC) for secretarial and editorial assistance.

25 October 1999; accepted 18 November 1999

Binding of Transcription Termination Protein Nun to Nascent RNA and Template DNA

Randolph S. Watnick* and Max E. Gottesman†

The amino-terminal arginine-rich motif of coliphage HK022 Nun binds phage λ nascent transcript, whereas the carboxyl-terminal domain interacts with RNA polymerase (RNAP) and blocks transcription elongation. RNA binding is inhibited by zinc (Zn^{2+}) and stimulated by *Escherichia coli* NusA. To study these interactions, the Nun carboxyl terminus was extended by a cysteine residue conjugated to a photochemical cross-linker. The carboxyl terminus contacted NusA and made Zn^{2+}-dependent intramolecular contacts. When Nun was added to a paused transcription elongation complex, it cross-linked to the DNA template. Nun may arrest transcription by anchoring RNAP to DNA.

Transcription termination in bacteria may occur when elongating RNAP encounters a template sequence characterized by a region of dyad symmetry followed by a stretch of poly(dT). Alternatively, termination may require a factor that is not a component of the elongation complex, such as the *E. coli* Rho protein (*1*). Factor-dependent termination is generally not highly template- or site-specific. The Nun protein of phage HK022, in contrast, blocks transcription elongation uniquely on phage λ templates (*2*). Nun binds to boxB RNA (BOXB) of the nascent transcript of the λ pL and pR operons, blocks translocation of RNAP in vitro (*3*), and terminates transcription in vivo (*4*). Nun is a 109–amino acid protein that carries the arginine-rich motif (ARM) RNA binding motif found in several RNA binding proteins (Fig. 1A). The ARM motif is located in the Nun NH_2-terminus. The COOH-terminus of Nun inhibits RNA binding, particularly in the presence of Zn^{2+} (*5*). The *E. coli* transcription factor NusA binds the COOH-terminus of Nun and stimulates RNA binding (*5*). Deletion of the COOH-terminus eliminates the association between Nun and RNAP in solution and prevents transcription arrest or termination (*5*).

Within the COOH-terminal region, a tryptophan residue at position 108 is also necessary for termination and arrest, as determined by λ plaque-forming assays (*6*) (Fig. 1B). Mutant Nun protein Trp^{108}→Ala (W108A) promotes template switching, the movement of RNAP from the end of one template to a second without release of nascent transcript (*7*, *8*). We postulated that Trp^{108} intercalates into DNA template and brakes RNAP translocation. This model is supported by the finding that wild-type (WT) Nun cannot arrest transcription on single-stranded template (*8*).

Here we describe photochemical cross-linking and directed DNA cleavage assays that identify contacts made by the Nun COOH-terminus. Nun, which lacks cysteine residues, was modified by the addition of cysteine to the COOH-terminus, by polymerase chain reaction (PCR)–directed mutagenesis (Fig. 1A). This modified Nun protein, Nun Cys^{110}, was active in terminating transcription in a λ *pL-nutL-lacZ* fusion assay in which the pL promoter of λ was fused upstream of the gene for β-galactosidase. Tester strains carrying either WT or mutant Nun formed white (Lac^-) colonies on MacConkey-Lactose indicator plates, indicating that Nun was terminating transcription and preventing expression of β-galactosidase (*9*).

We used the modified protein to conjugate a photoreactive cross-linker, ^{125}I-*N*-[(2-pyridyldithio) ethyl]-4-azidosalicylamide (AET), to the added cysteine residue via a disulfide bond (*10*). By using this cross-linker, radiolabeled ^{125}I can be transferred to the target of the cross-link by treatment with dithiothreitol (DTT). The labeled ^{125}I-AET-Nun conjugate was irradiated with ultraviolet (UV) light in the presence or absence of Zn^{2+} and NusA (*11*). Zn^{2+} promoted formation of intramolecular Nun cross-links (Fig. 2). Thus, the ^{125}I-labeled Nun protein migrated with the same mobility on an SDS–polyacrylamide gel before and after DTT treatment. NusA and ^{125}I-AET-Nun formed an ^{125}I-labeled complex after UV irradiation. The ^{125}I-label was transferred to NusA after DTT treatment (Fig. 2).

This intramolecular cross-linking supports the model that the Nun COOH-terminus inhibits RNA binding in the presence of Zn^{2+} by occluding the NH_2-terminal RNA binding

Department of Biochemistry and Molecular Biophysics and Institute of Cancer Research, Columbia University, New York, NY 10032, USA.

*Present address: Whitehead Institute, 9 Cambridge Center, Cambridge, MA 02142, USA.
†To whom correspondence should be addressed. E-mail: gottesma@cuccfa.ccc.columbia.edu

domain (*5*). We have not yet, however, defined the point of contact made by the COOH-terminus.

We next used ^{125}I-AET-Nun to locate the COOH-terminus in an arrested transcription complex. To determine whether the COOH-terminus contacts the DNA template, we paused RNAP at the +15 site on a ^{32}P-labeled pL template by incubation with ATP, GTP, and CTP but withholding UTP (*4*). The paused complexes were exposed to ^{125}I-AET-Nun, irradiated, and analyzed by denaturing polyacrylamide gel electrophoresis (PAGE) (*11*). Before DTT treatment, an ^{125}I-labeled band migrated at a slower rate than template DNA (Fig. 3A, lane 2). After treatment with DTT this band migrated at the same position as template DNA (Fig. 3A, lane 3). ^{125}I-AET-Nun did not cross-link DNA in the absence of RNAP (Fig. 3, lane 4). Thus, the Nun COOH-terminus cross-links with DNA in a transcription elongation complex (TEC). Two termination-defective Nun mutants, H98A and W108A, failed to cross-link template (Fig. 3A, lanes 5 and 6), although, unlike the 13–amino acid COOH-terminal truncation mutant T-Nun, they bound RNAP in solution (Fig. 3B) (*12*).

Nun H98A may not be situated in the elongation complex in proximity to template DNA. Nun W108A lacks the tryptophan residue that may intercalate into double-stranded template DNA (Fig. 1A) (*8*). This indicates that the interaction with template DNA is an

Fig. 1. (**A**) Sequence of Nun110C. The residues in bold represent the ARM region that binds to λ BOXB; the residues in italics represent the region of the protein that interacts with *E. coli* RNAP and NusA, and with λ *nutL* and *nutR*. (**B**). Efficiency of λ plating on *E. coli* N99 carrying plasmids with WT Nun, NunW108A, NunW108L, NunW108Y, and the parent vector (pET23d) alone. Abbreviations for the amino acid residues are as follows: A, Ala; C, Cys; D, Asp; E, Glu; F, Phe; G, Gly; H, His; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.

A

VKKTI YVNPD SGQNR KVSDR GLTS**R**$_{25}$

DRRRI ARWEK RIAYA LKNSV TPGFN$_{50}$

AIDDG PEYKI NEDPM DKVDK ALATP$_{75}$

FPRDV EKIED EKYED VM*HRV* *VNHAH*$_{100}$

QRNPN KKWSC$_{110}$

B

Host	λ Plating Efficiency
N99	1
N99 + WT-Nun	<1x10^6
N99 + W108ANun	1
N99 + W108LNun	1
N99 + W108YNun	<1x10^6

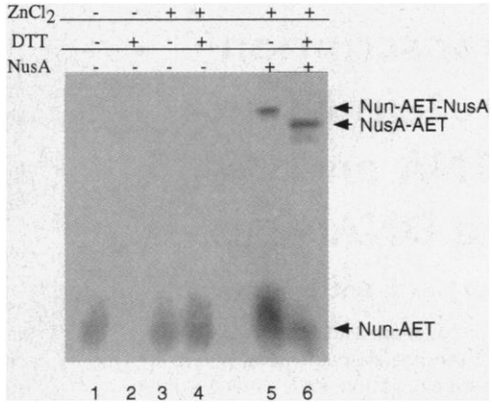

Fig. 2. Nun110C was conjugated to ^{125}I-AET and incubated without (lanes 1 and 2) or with (lanes 3 and 4) $ZnCl_2$ (100 μM) and irradiated with UV light to induce cross-linking. The reactions were then divided in half, and one sample was treated with DTT (lanes 2 and 4). DTT reduces the disulfide linkage between Nun and AET and transfers the ^{125}I label of the cross-linker to its target. In the unreduced sample, ^{125}I-AET-Nun and its cross-linked target remain cross-linked. The reduced and unreduced samples were then subjected to gel electrophoresis on a 15% SDS-polyacrylamide gel. ^{125}I-AET-Nun was also incubated with NusA in the presence of $ZnCl_2$ (100 μM) and irradiated with UV light to induce cross-linking. The cross-linking reaction was then treated as described above, comparing the unreduced (lane 5) and reduced (lane 6) samples on the same gel.

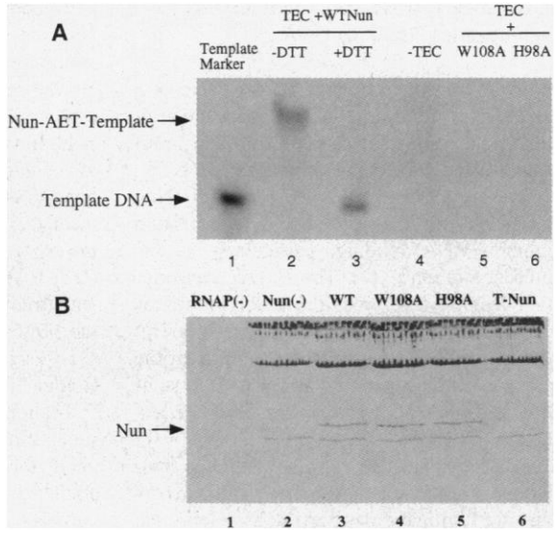

Fig. 3. (**A**) ^{125}I-AET-Nun was incubated with TEC that had been paused at the +15 site on the DNA template (*4*). The reaction was then UV-irradiated and transcription halted by the addition of EDTA. After purification of template (*4*), the reaction was divided into two samples. The unreduced sample (lane 2), in which Nun is cross-linked to the DNA, and the reduced sample (lane 3), in which the disulfide bond has been cleaved and the ^{125}I label transferred to the DNA, were subjected to electrophoresis on a urea–polyacrylamide gel. The ^{32}P-labeled template was run as a marker (lane 1). A control reaction, in which ^{125}I-AET-Nun was incubated with template DNA in the absence of RNAP and rNTPs, was subjected to electrophoresis in lane 4. Lanes 5 and 6 show the lack of cross-linking with the mutant Nun proteins W108A and H98A, respectively. (**B**) SDS-PAGE analysis of excluded fractions from a Sepharose G100 chromatography column of WT (lane 3) and the Nun mutants W108A and H98A in the presence of RNAP (lanes 4 and 5). In the absence of RNAP, W108A is retained (lane 1), as are H98A and WT Nun (*5*, *17*). Both mutant proteins are excluded from the column only in the presence of RNAP, indicating an interaction between these proteins and RNAP in solution, unlike T-Nun (lane 6).

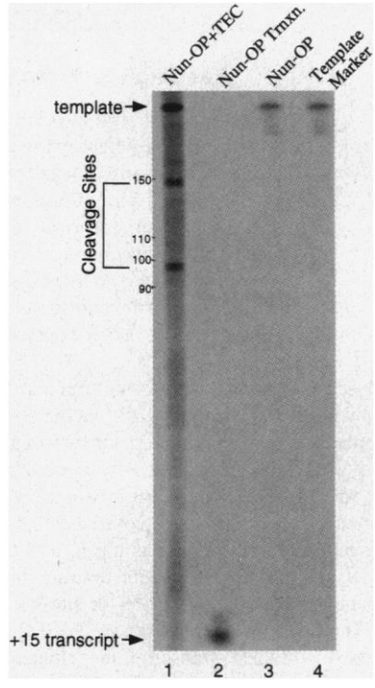

Fig. 4. DNA scission pattern of the +15 TEC treated with IOP-Nun. Lane 1, scission products of ^{32}P-labeled template after cleavage by Nun-OP (*5*). Lane 2, transcription (denoted as Trnxn.) products after treatment of the +15 TEC with Nun-OP. In a control reaction, Nun-OP was incubated with ^{32}P-labeled template in the absence of RNAP and rNTPs, and cleavage was induced (lane 3). Lane 4 is ^{32}P-labeled template run as a marker for uncleaved template. Numbers on the left denote where products of the size (in nucleotides) ran on a sequencing ladder (not shown).

integral step in the termination mechanism.

To confirm the cross-linking result and to define the location of the Nun-template interaction, *N*-(1,10-phenanthrolin-5-yl) iodacetamide (IOP) was conjugated to Nun C110, creating Nun-OP (*13*). Coordination of Cu^{2+} and treatment with 3-mercaptoproprionic acid and H_2O_2 converts IOP to a chemical nuclease that will cleave template DNA upon contact (*14*, *15*).

To perform the cleavage reaction, a TEC was paused at +15 on a 250–base pair (bp) λ DNA template that was ^{32}P-labeled at both 5′ ends in the same manner described above. Although the template alone was resistant to cleavage by Nun-OP, TEC treated with Nun-OP yielded two major cleavage products of about 100 and 150 bp (Fig. 4, compare lanes 1 and 3). The recovery of two bands of equivalent intensity from the reaction, with a combined size of template, indicates that Nun-OP cleaved both template strands with equal efficiency. This implies that the Nun COOH-terminus contacts double-stranded DNA. The major site of DNA cleavage correlated well with the location of RNAP on the template, as determined by a transcription arrest assay with Nun-OP (Fig. 4, lane 2) (*12*) (note that transcription initiates 77 bp from the template end). The sizes of the major cleavage products are consistent with a contact between the Nun COOH-terminus and template about 8 bp promoter-distal to the active center of RNAP and to the RNA:DNA hybrid. Assuming that the paused TEC did not undergo upstream translocation, Nun contacted double-stranded template in the DNA binding site of RNAP (*8*). This observation supports our findings that Nun requires double-stranded template for transcription arrest in vitro (*9*). The contact between Nun and template may involve the intercalation of W108 into double-stranded DNA. As shown, W108 can be substituted with tyrosine, another planar aromatic amino acid, but not with leucine or alanine (Fig. 1B). It has been postulated that movement of nascent RNA and template DNA through a "double-sliding clamp" in the β′ subunit of RNAP is coupled (*16*). As a result of this coupling, the disruption of either motion would compromise the processivity of RNAP.

Like polymerase, Nun binds by different domains to both RNA and DNA. Although not proven, Nun probably contacts both transcript and template simultaneously. Nun is the first auxiliary transcription factor with such properties to be described.

References and Notes

1. E. Nudler, *J. Mol. Biol.* **288**, 1 (1999).
2. J. Robert *et al.*, *Cell* **51**, 483 (1987).
3. S. C. Hung and M. E. Gottesman, *J. Mol. Biol.* **247**, 428 (1995).
4. ———, *Genes Dev* **11**, 2670 (1997).
5. R. Watnick and M. E. Gottesman, *Proc. Natl. Acad. Sci. U.S.A.* **95**, 1546 (1998).
6. *Escherichia coli* N99 was grown to confluence on TB plates alongside strains carrying plasmids containing WT Nun, NunW108A, NunW108Y, and parent vector pET23d (Novagen) alone at 37°C. At this time, 1 × 10^2, 1 × 10^4, and 1 × 10^6 plaque-forming units of λ phage were spotted on the plates in a volume of 10 μl. The plates were incubated at 37°C overnight and plaques were counted.
7. E. Nudler *et al.*, *Cell* **89**, 33 (1997).
8. R. Watnick and M. Gottesman, in preparation.
9. E. Burova *et al.*, *Mol. Microbiol.* **31**, 1783 (1999).
10. Y. Chen, Y. Ebright, R. Ebright, *Science* **265**, 90 (1994).
11. Nun was purified as described (*5*). The purified protein was then dialyzed against 0.1 M sodium borate (pH 8.4) and treated with 50 mM DTT at 37°C for 30 min to reduce C110. The reduced protein was then passed through a G25 desalting column to remove the DTT. All of the following procedures were performed in the dark under red light illumination. Intramolecular cross-linking was performed by incubating 200 pmol of ^{125}I-AET-Nun at 4°C for 30 min in the presence or absence of 100 μM $ZnCl_2$. After incubation, the reaction mixtures were irradiated with a hand-held UV lamp for 1 min at the short-wavelength setting. Where indicated, cross-linked ^{125}I-AET-Nun protein was reduced by treatment with 50 mM DTT at room temperature for 10 min followed by removal of DTT by centrifugation through a G25 desalting column. Nun-NusA cross-linking was performed by incubating 300 pmol of NusA with 200 pmol of ^{125}I-AET-Nun in the presence of 100 μM $ZnCl_2$. Irradiation was performed as described above. Cross-linking reactions in the context of the transcription reaction were performed as follows: Transcription was allowed to proceed to the +15 position of the λ pL template by incubating RNAP at 32°C with a mixture of ribonucleoside triphosphates (rNTPs) lacking UTP for 15 min (*3*, *4*, *8*); ^{125}I-AET-Nun (200 pmol) was added to the paused elongation complex. After a 30-min incubation, the reaction mixture was irradiated as described above and stopped with 5 mM EDTA. The DNA was purified with the Qiaquick PCR purification kit (Qiagen) and divided into two samples, one of which was treated with 50 mM DTT to reduce the disulfide bond and cleave the cross-linker from Nun. As a control, ^{125}I-AET-Nun was incubated with template DNA in the absence of RNAP and rNTPs and irradiated with UV light in the same manner described above. The two samples were then heated to 95°C for 5 min to melt template DNA, and resolved on a 12% polyacrylamide–8 M urea denaturing gel after addition of one volume of 2× formamide loading buffer. As the marker, ^{32}P-labeled template, also melted at 95°C, was subjected to electrophoresis alongside the two samples.
12. Sepharose G100 exclusion chromatography was performed as described (*5*) with respect to protein concentrations, incubation times, and centrifugation conditions.
13. Purified, reduced Nun protein was conjugated to IOP by incubation at room temperature in 50 mM sodium phosphate (pH 7.0) for 1 hour in the dark. 3-Mercaptoproprionic acid (3 mM) was then added to inactivate any unreacted IOP. The reaction mixture was then passed through a G25 desalting column. Template DNA was treated with alkaline phosphatase and labeled with ^{32}P at both 5′ ends with T4 polynucleotide kinase. The transcription complex was allowed to proceed to the +15 site on the template in the same manner described above. Nun-OP was then added to the reaction along with 40 μM $CuSO_4$ and incubated at 32°C for 30 min (*11*). To induce scission, 3-mercapto-proprionic acid and H_2O_2 were then added to the reaction at a final concentration of 3 mM. The reaction was allowed to proceed for 45 min at 32°C. EDTA was then added to 5 mM to stop the transcription reaction, and the DNA was purified by ethanol precipitation. As a control, 3-mercapto-proprionic acid and H_2O_2 were withheld, and 150 μM ATP, UTP, GTP, and CTP were added to the reaction to determine whether Nun-OP was still termination competent. The purified DNA and RNA from the transcription reaction were then analyzed in the same manner as the cross-linked complexes. The size markers were determined on the basis of a combination of DNA markers of known length and the products of a Cycle Sequencing Reaction (Perkin-Elmer) of the pL template.
14. C. Chen, M. Gorin, D. Sigman, *Proc. Natl. Acad. Sci. U.S.A.* **90**, 4206 (1993).
15. J. Bullard, M. van Waes, D. Bucklin, W. Hill, *J. Mol. Biol.* **252**, 572 (1995).
16. E. Nudler *et al.*, *Science* **281**, 424 (1998).
17. R. S. Watnick and M. E. Gottesman, data not shown.

18. We thank E. Nudler for his helpful comments and suggestions.

30 April 1999; accepted 11 November 1999

Requirement of Yeast *SGS1* and *SRS2* Genes for Replication and Transcription

Sung-Keun Lee, Robert E. Johnson, Sung-Lim Yu, Louise Prakash, Satya Prakash*

The *SGS1* gene of the yeast *Saccharomyces cerevisiae* encodes a DNA helicase with homology to the human Bloom's syndrome gene *BLM* and the Werner's syndrome gene *WRN*. The *SRS2* gene of yeast also encodes a DNA helicase. Simultaneous deletion of *SGS1* and *SRS2* is lethal in yeast. Here, using a conditional mutation of *SGS1*, it is shown that DNA replication and RNA polymerase I transcription are drastically inhibited in the *srs2*Δ *sgs1-ts* strain at the restrictive temperature. Thus, *SGS1* and *SRS2* function in DNA replication and RNA polymerase I transcription. These functions may contribute to the various defects observed in Werner's and Bloom's syndromes.

Patients with Bloom's syndrome (BS) and Werner's syndrome (WS) suffer from growth retardation and a high incidence of cancers. In addition, individuals with WS age prematurely (*1*). Both syndromes display hyperrecombination and an increased incidence of karyotypic abnormalities (*1*). The *SGS1* gene of *Saccharomyces cerevisiae* is a member of the RecQ family of DNA helicases (*2*), and it shares extensive homology with the human Bloom's syndrome gene *BLM* and the Werner's syndrome gene *WRN* (*3*). The helicases

References and Notes

[5] **Escherichia coli NusA is Required for Efficient RNA Binding by Phage HK022 Nun Protein**
Randolph S. Watnick; Max E. Gottesman
Proceedings of the National Academy of Sciences of the United States of America, Vol. 95, No. 4. (Feb. 17, 1998), pp. 1546-1551.
Stable URL:
http://links.jstor.org/sici?sici=0027-8424%2819980217%2995%3A4%3C1546%3AECNIRF%3E2.0.CO%3B2-U

[10] **Identification of the Target of a Transcription Activator Protein by Protein-Protein Photocrosslinking**
Yan Chen; Yon W. Ebright; Richard H. Ebright
Science, New Series, Vol. 265, No. 5168. (Jul. 1, 1994), pp. 90-92.
Stable URL:
http://links.jstor.org/sici?sici=0036-8075%2819940701%293%3A265%3A5168%3C90%3AIOTTOA%3E2.0.CO%3B2-R

[14] **Sequence-Specific Scission of DNA by the Chemical Nuclease Activity of 1, 10-Phenanthroline-Copper (I) Targeted by RNA**
Chi-Hong B. Chen; Michael B. Gorin; David S. Sigman
Proceedings of the National Academy of Sciences of the United States of America, Vol. 90, No. 9. (May 1, 1993), pp. 4206-4210.
Stable URL:
http://links.jstor.org/sici?sici=0027-8424%2819930501%2990%3A9%3C4206%3ASSODBT%3E2.0.CO%3B2-A

LINKED CITATIONS

[16] **Spatial Organization of Transcription Elongation Complex in Escherichia coli**
Evgeny Nudler; Ivan Gusarov; Ekaterina Avetissova; Maxim Kozlov; Alex Goldfarb
Science, New Series, Vol. 281, No. 5375. (Jul. 17, 1998), pp. 424-428.
Stable URL:
http://links.jstor.org/sici?sici=0036-8075%2819980717%293%3A281%3A5375%3C424%3ASOOTEC%3E2.0.CO%3B2-Q