Links:

*Escherichia coli*
http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=genomeprj&cmd=Retrieve&dopt=Overview&list_uids=12319

TRCF
http://ca.expasy.org/uniprot/P30958

UvrA
http://ca.expasy.org/uniprot/P0A698

Thermotoga maritima
http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=genomeprj&cmd=Retrieve&dopt=Overview&list_uids=111

NusG
http://ca.expasy.org/uniprot/P0AFG0

BACTERIAL TRANSCRIPTION

# Smooth coupling

Alexandra Deaconescu and colleagues have solved the X-ray crystal structure of *Escherichia coli* transcription–repair coupling factor (TRCF) to 3.2 Å resolution, and the structure is described in a recent issue of *Cell*.

Transcription-coupled DNA repair is triggered when an elongating RNA polymerase (RNAP) stalls at a lesion in the DNA template. In bacteria, this process requires a single polypeptide, the TRCF, which is a double-stranded DNA (dsDNA) translocase with ATPase activity. TRCF has two distinct functions. First, the stalled RNAP is recognized and removed, which requires dissociation of the highly stable ternary elongation complex (TEC) and transcript termination, and second, DNA repair is stimulated by recruiting UvrA, a component of the nucleotide-excision-repair machinery.

So, has the structure provided any insight into the functions of TRCF? For TRCF to successfully carry out its two distinct functions, it is predicted that large conformational changes are required, and this prediction is supported by the structure. First, TRCF comprises a series of structured domains connected by flexible linker regions. Second, comparing the TRCF structure with the structure of the *Thermotoga maritima* RecG–ADP complex (RecG is also a dsDNA translocase) revealed several conformational changes in the translocation module, including in the relay helix that connects the RNAP-interacting domain with the translocation module and in the key TRG motif, which is essential for TRCF-mediated release of RNAP. The authors suggest

that bending of the relay helix and opening of the TRG motif could be crucial conformational changes for the function of TRCF.

In previous experimental work, a model for transcription-coupled repair was proposed in which TRCF translocates on the dsDNA and contacts the β-subunit of RNAP upstream of the area of transcription and effectively pushes the RNAP forward, causing the transcription bubble to collapse if a lesion is present, and so allowing DNA-repair proteins to access the lesion. One of the most important interactions for TRCF is therefore the interaction with RNAP, and the structure supports the proposed model as well as providing some new data, including a role for domain D4, which has structural similarity to the antiterminator NusG. In addition, the authors were able to construct a detailed model of the TRCF–TEC interaction, perhaps the most interesting aspect of which is a secondary interaction between a TRCF domain and the RNAP β-flap which covers the RNA exit channel.

As transcription-coupled repair is one of only three mechanisms of transcription termination in bacteria, researchers working on TRCF are keen to discover the mechanistic details of the reactions involved, and the TRCF structure is another stepping stone on the way.

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**ORIGINAL RESEARCH PAPER** Deaconescu, A. *et al.* Structural basis for bacterial transcription-coupled DNA repair. *Cell* **124**, 507–520 (2006)