
energy of DNA binding to change the helical twist, resulting in an overwinding of the DNA. Changes in helical twist may destabilize histone-DNA ${ }^{23}$ as well as histone-histone interactions ${ }^{24}$, so the ability of the SWI/SNF complex to modulate both DNA structure and topology may be important in SWI/SNF-dependent disruption of nucleosome structure.

[^0]FIG. 4 SWI/SNF introduces positive supercoils into relaxed plasmid DNA in the presence of bacterial topoisomerase I. a, SWI/SNF induces supercoiling. Closed relaxed plasmid DNA (lane 2) was incubated with the SWI/ SNF complex and bacterial topoisomerase I (topo I; 3 units). Molar ratios of SWI/SNF to plasmid are indicated above each set of lanes. A ratio of 20:1 corresponds to 3 nM SWI/SNF. Addition of ATP to a subset of the reactions is indicated. Arrows to the right denote topology standards, lane 1 contains linear plasmid (form III), lane 3 contains supercoiled plasmid (form I) and some nicked circles (comigrate with form II, closed relaxed DNA). The bracket to the right denotes SWI/SNF-induced topoisomers. $b$, SWI/SNF introduces positive supercoils. Plasmid DNA was supercoiled with SWI/SNF ( 3 nM ) and bacterial topo I as in a. DNA was purified (lane 6) and retreated with either bacterial topo I (3 units; lane 7), calf thymus topo I ( 3 units; lane 8 ), or calf thymus topo II (7 units; lane 9). Lanes 1-4 show control reactions in which negatively supercoiled plasmid DNA (lane 1) was incubated with each topoisomerase under conditions identical to those for lanes 7-9. Lane 5 shows the starting relaxed substrate DNA. Reactions that contained calf thymus topo II contained 1 mM ATP.
METHODS. Supercoiling reactions $(20 \mu)$ contained $1 \times$ supercoiling buffer ( 20 mM HEPES, $\mathrm{pH} 7.5,7 \mathrm{mM} \mathrm{MgCl} 2,15 \mathrm{mM} \mathrm{KCl}, 0.5 \mathrm{mM}$ DTT, $50 \mu \mathrm{~g} \mathrm{per}$ ml BSA), $50 \mathrm{ng} \mathrm{pJH} 28, \mathrm{SWI} / \mathrm{SNF}$, and topoisomerases where indicated. Reactions were incubated for 45 min at $30^{\circ} \mathrm{C}$, stopped with $80 \mu \mathrm{l} 1 \%$ SDS, 10 mM EDTA, $100 \mu \mathrm{gml}{ }^{-1}$ proteinase $\mathrm{K}, 50 \mu \mathrm{gml}^{-1}$ tRNA, and incubated for 30 min at $37^{\circ} \mathrm{C}$. Samples were extracted with phenol/chloroform, ethanol-precipitated, and electrophoresed on $0.8 \%$ agarose gels without ethidium bromide and then Southern-blotted. DNA was purified and electrophoresed in the presence of chloroquine as described ${ }^{27}$. Blots were probed with pJH 28 labelled with [ $\alpha{ }^{-32}$ P]dCTP by random priming. Plasmid pJH28 contains SUC2 sequences from $-1,100$ to +14 in plasmid pRS316.

## ERRATA

## Crystal structure of a G-protein $\boldsymbol{\beta} \gamma$ dimer at 2.1 A resolution

John Sondek, Andrew Bohm, David G. Lambright, Heidi E. Hamm \& Paul B. Sigler

Nature 379, 369-374 (1996)
In this title, a typographical error caused the substitution of a subscripted 'A' for a hyphen in 'G-protein'. The correct title is given here.

# Bifurcations of the Atlantic thermohaline circulation in response to changes in the hydrological cycle 

## Stefan Rahmstorf

Nature 378, 145-149 (1995)
The shaded areas A and B of Fig. $1 a$ of this Article were lost during printing. The correct figure is shown here.



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