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THE KINETICS FOR EXCHANGE OF THE IMINO PROTONS OF THE d(C-G-C-G-A-A-T-T-C-G-C-G) DOUBLE HELIX IN COMPLEXES WITH THE ANTIBIOTICS NETROPSIN AND/OR ACTINOMYCIN

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August 1982

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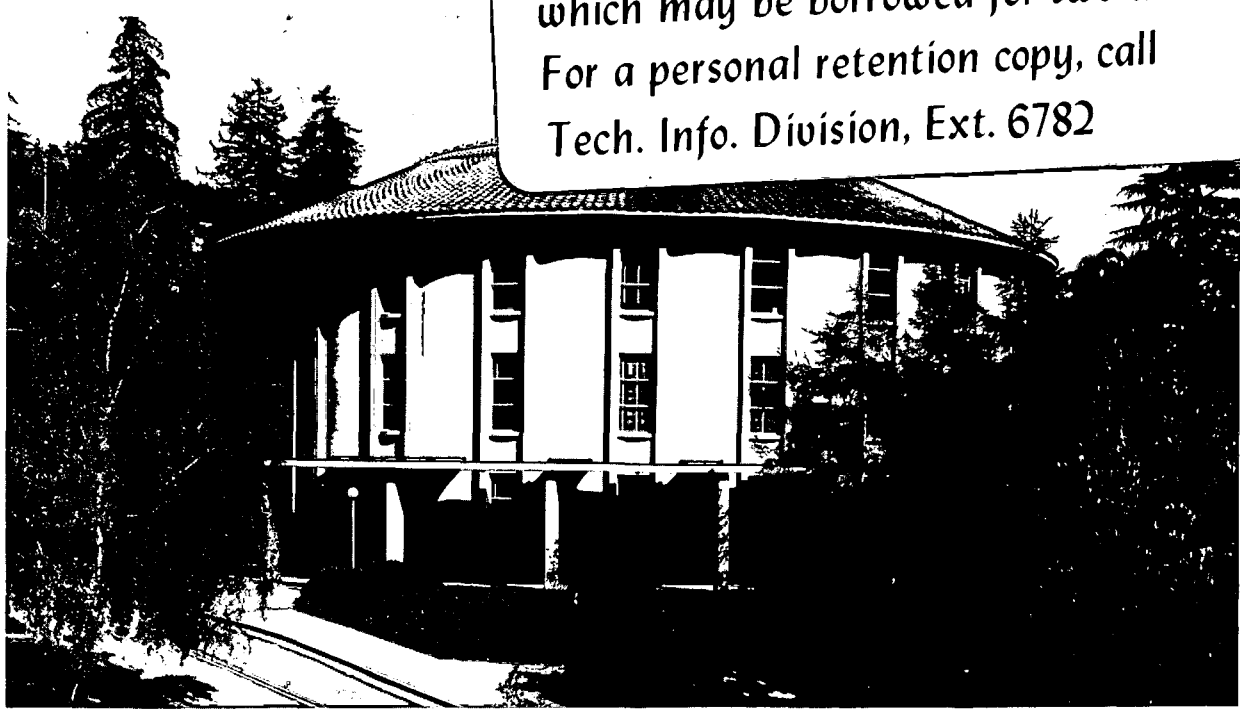

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# The Kinetics for Exchange of the Imino Protons of the d(C-G-C-G-A-A-T-T-C-G-C-G) Double Helix in Complexes with the Antibiotics Netropsin and/or Actinomycin†

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List of Abbreviations:

NMR, nuclear magnetic resonance

EDTA, ethylenediamine tetra acetic acid

ABSTRACT

The lifetimes for exchange of the imino protons in the dodecanucleotide d(C-G-C-G-A-A-T-T-C-G-C-G) upon binding of netropsin and/or actinomycin have been measured by proton nuclear magnetic resonance experiments. At high temperature these lifetimes were found to measure the lifetimes for opening of the base pairs in the double helix. Comparison of the opening rates in the dodecamer with those in the complex with netropsin (which binds at the -A-A-T-T-sequence) shows that there is not only a large kinetic stabilization of the A•T base pairs at the binding site, but also a significant stabilization of the G•C base pairs adjacent to the netropsin binding site. For the complex with actinomycin, which intercalates at the G-C sites in the double strand, the lifetimes of the base pairs at the binding site increase upon binding of actinomycin, but the A•T base pairs in the central core are slightly kinetically destabilized by the actinomycin binding. The activation energies for exchange of the imino protons were also measured in the complexes and indicate that the mechanism for exchange of the imino protons is individual base-pair-opening, where one base pair opens independently of the others. The effects of drug binding on the dynamics of individual base pairs in a double-stranded helix are discussed.

Nuclear magnetic resonance (NMR) experiments have been used to probe the conformation of drug-oligonucleotide complexes in the past mainly by observation of the chemical shift changes of the drug and/or nucleotide upon complex formation (Krugh & Nuss, 1979; Patel, 1979; Patel, 1980). The kinetic behavior of drug-nucleic acid interactions has been studied on oligonucleotides, or polynucleotides by temperature-jump experiments (Bresloff & Crothers, 1975; Davanloo & Crothers, 1976) and hydrogen-deuterium exchange method (Priesler et al., 1981). In this work we present results on the kinetics of opening of individual base pairs in drug-oligonucleotide complexes as studied by proton NMR.

Actinomycin D is an antibiotic drug which has been shown to intercalate in double-stranded DNA specifically at G(3'-5')C sites (Meienhofer & Atherton, 1977; Sobell, 1973; Krugh et al., 1977). Netropsin is a peptide antibiotic which binds in the minor groove of DNA duplexes specifically at A•T rich regions (Zimmer, 1975; Wartell et al., 1974). The structure of the dodecanucleotide d(C-G-C-G-A-A-T-T-C-G-C-G), referred to as the 12-mer, has been solved by X-ray crystallographic techniques (Wing et al., 1980; Drew & Dickerson, 1981). The conformation of this molecule in solution has been studied by NMR experiments (Patel et al., 1982). The conformation of the 12-mer in complexes with netropsin and actinomycin bound separately, and simultaneously, has recently been studied by observation of the $^{1}H$ and $^{31}P$ NMR chemical shifts in these complexes (Patel et al., 1981).

In this work we probe the dynamics of the 12-mer-antibiotic complexes by studying the kinetics of exchange of the imino protons of the double strand in the complexes. The theory for interpretation of the exchange behavior of imino protons measured by NMR has been discussed by Johnston and Redfield (1981) and Pardi and Tinoco (1982). We have recently studied the kinetics for

exchange of the imino protons in the 12-mer and two related double helices, one with a G•T base pair and one with an extra adenine base (Pardi et al., 1982). The NMR of these three helices and also the NMR of the 12-mer-antibiotic complexes, including preliminary reports of some of the kinetic experiments performed here, have recently been reviewed (Patel, Pardi, & Itakura, 1982). The kinetics for exchange in the free 12-mer are compared here with the 12-mer-antibiotic complexes to study the effect of drug binding on the dynamics of base-pair-opening. The studies confirm results obtained from chemical shifts indicating perturbations at the binding sites and give additional information on changes in the dynamics of base pairs adjacent to the binding site. Comparing the lifetimes of exchange in the 12-mer and 12-mer-antibiotic complexes gives a more quantitative measure of the location and extent of perturbations induced by drug binding. The activation energies for exchange of the imino protons in the 12-mer-antibiotic complexes were determined and compared with those found in the 12-mer. The mechanism for exchange of the imino protons in the 12-mer-drug complexes is discussed.

## MATERIALS AND METHODS

The 12-mer was synthesized by a modified triester method followed by deprotection and purification (Patel et al., 1982). The actinomycin and netropsin were obtained from Merck and Famitalia (Milan, Italy), respectively. The NMR samples contained 12.5 mg/ml of d(C-G-C-G-A-A-T-T-C-G-C-G). Samples were made up in 0.2 ml of buffer containing 0.1 M phosphate and 2.5 mM EDTA with chemical shifts referenced to the internal standard 3-(trimethylsilyl)-1-propanesulfonate (DSS). Samples containing antibiotics had 2 equivalents of actinomycin or 1 equivalent of netropsin or both. The NMR experiments were performed on the HXS-360 MHz instrument at the Stanford Magnetic Resonance Laboratory. Temperature was controlled to ±1°C and was calibrated

by placing a thermocouple in an NMR tube (containing only $D_2O$) while it was in the probe. Data were collected on a Nicolet 1180 computer with 8K data points and a sweep width of ±5000 Hz. The large water signal was attenuated by the Redfield 214 pulse (Redfield et al., 1975) and the use of a tunable notch filter (Marshall et al., 1979). Saturation recovery experiments were performed as previously described (Pardi & Tinoco, 1982). Inversion recovery experiments were performed using methods similar to the long pulse inversion recovery technique described by Early et al. (1980). Lifetimes of the saturation recovery experiments were analyzed as previously described (Pardi & Tinoco, 1982) and the inversion recovery analysis was done using a 3 parameter nonlinear least squares fit to the inversion recovery function. Errors in the lifetimes are not more than ±20%. No significant differences were found in the lifetimes measured by the two techniques. Typically 10-15 different delay times were taken with 200-250 scans for each point.

RESULTS

Figure 1 shows the 360 MHz spectra of the low field resonances of the 12-mer, the 12-mer-actinomycin complex, the 12-mer-netropsin complex and the 12-mer-netropsin-actinomycin complex. The assignment of the imino protons in these complexes has been previously discussed (Patel et al., 1981; Patel, Pardi, & Itakura, 1982). In this paper we will be discussing only imino protons from base pairs 3-6 as the protons from base pairs 1 and 2 exchange too rapidly to allow sufficient data to be obtained in the presence or absence of bound antibiotics. The chemical shifts <u>versus</u> temperature for the imino protons in G•C base pairs in all the complexes is shown in Figure 2.

For the 12-mer-actinomycin complex the resonances for the A•T base pairs 5 and 6 overlap at all temperatures, except 15°C where two peaks are observed which have equal lifetimes for exchange. The temperature dependence of the

lifetimes for the imino protons in the 12-mer-actinomycin complex are given for base pairs 3-6 from 15-60°C in Table I. Arrhenius plots for the imino protons in this complex are given in Figure 3. The activation energies for exchange of imino protons 5 and 6 are given in Table IV and are calculated to be 17 kcal/mol.

The lifetimes of the imino protons in the 12-mer-netropsin complex from 15-80°C are in given in Table II. Arrhenius plots for these protons are given in Figure 4. The activation energies determined from these plots are given in Table IV and range from 12-18 kcal/mol.

For the 12-mer-netropsin-actinomycin complex the lifetimes of the imino protons from 20-80°C are given in Table III. Arrhenius plots for the imino protons in base pairs 4-6 are given in Figure 5; the corresponding activation energies for exchange of imino protons are given in Table IV and range from 17-18 kcal/mol.

DISCUSSION

We will use the chemical shifts of the imino protons of the 12-mer upon complex formation with actinomycin and/or netropsin to obtain information on the extent of binding of these drugs to the 12-mer duplex. The temperature dependence of the chemical shifts of the G·C imino protons in the 12-mer alone and the 12-mer in a complex with actinomycin are shown in Figures 2a and 2b, respectively. As seen in Figure 2b the imino protons on base pairs 2 and 3 shift upfield by at least 0.4 ppm upon complex formation with 2 actinomycins per 12-mer. If the free 12-mer and the 12-mer in the complex were in fast exchange on the NMR time scale, then we would expect to observe a weight average chemical shift for the imino protons. Because of the large shift upon binding we conclude that if the free and bound 12-mer are in fast exchange, then, even at high temperature (60°C), the concentration of the free 12-mer is

very small. If there is slow exchange on the NMR time scale between free and bound 12-mer, then one would observe two separate peaks for the imino protons in these two states. We see no such behavior in the 12-mer-actinomycin complex and can thus still conclude that the concentration of free 12-mer must be small (<10%). Intermediate exchange is ruled out by the absence of broadening of the resonances except at the highest temperature where the imino protons do broaden due to chemical exchange of the imino protons with water, as will be discussed later. Thus for the 12-mer-actinomycin complex we observe that over the whole temperature range used in this study the concentration of free 12-mer is small (<10%) and that the 12-mer is essentially totally bound in the complex at all temperatures.

For the netropsin complex one A•T imino proton resonance shifts downfield at least 0.5 ppm from its position in the free 12-mer at all temperatures observed (see Figure 2 in Patel et al., 1981). We can again use this large difference in chemical shifts upon complex formation to conclude that the concentration of free 12-mer is very small.. A similar conclusion is reached for the 12-mer-netropsin-actinomycin complex as revealed by the chemical shift changes of the G•C imino protons in Figure 2 and the A•T imino proton in Figure 2 of Patel et al. (1981). Thus in all the 12-mer-drug complexes studied here the concentration of the free 12-mer is less than 10% of the total and therefore the observed NMR parameters arise essentially from the 12-mer in the complex.

## Spin-Lattice Relaxation versus Chemical Exchange

In previous studies on the 12-mer we found that at high temperature, chemical exchange with water was the dominant relaxation mechanism for the imino protons in the duplex (Pardi et al., 1982). The spin-lattice relaxation, $T_1$, is dominant in the 12-mer only at temperatures lower than

30°C. Similar results are observed in the 12-mer-antibiotic complexes studied here. For the 12-mer-netropsin complex the observed lifetimes increase sharply with decreasing temperature from 80°C down to around 45°C where they level off (see Table II). This is more clearly seen in the Arrhenius plots in Figure 4. We will concentrate on the high temperature range where exchange is the dominant relaxation mechanism and so will use temperatures from 45-80°C for analysis of exchange in the 12-mer-netropsin complex. Table I and Figure 3 show that similar behavior is observed for the less stable 12-mer-actinomycin complex and we will use temperatures from 35-60°C for analysis of chemical exchange lifetimes of the imino protons. The behavior of the observed lifetimes in the 12-mer-netropsin-actinomycin complex, as seen in Table III and Figure 5, indicates that chemical exchange is the dominant relaxation pathway for the imino protons from 55-80°C.

Exchange Lifetimes in the 12-mer Antibiotic Complexes

We have recently shown that the imino protons of base pairs 3-6 in the 12-mer duplex were in the open-limited region (Pardi et al., 1982), which means that every time the base pair opens the imino protons exchange with water. The longer lifetimes for the 12-mer-antibiotic complexes compared to those found in the free 12-mer indicates that exchange of the imino protons in these complexes will also be in the open-limited region. Thus the lifetimes for exchange studied here will measure the kinetics of base-pair-opening in these complexes.

Patel et al. (1981) have shown that two actinomycins bind per duplex in the 12-mer-actinomycin complex. Table I gives the lifetimes for exchange of the imino protons in this complex; they can be compared with the lifetimes for the free 12-mer (Pardi et al., 1982). The lifetimes for the overlapping A•T base pairs 5 and 6 are 30 msec in the complex at 55°C; this is shorter than

the 35 msec and 55 msec found for A•T base pairs 5 and 6 in the free 12-mer. The lifetime for G•C base pair 4 is essentially unchanged by actinomycin binding; at 55°C it is 75 msec in the complex and 80 msec in the free 12-mer. However, the lifetime of G•C base pair 3 is strongly increased; at 55°C it is 85 msec in the complex, but only 35 msec in the free 12-mer. Thus, binding actinomycin between G•C base pairs 2 and 3 decreases the rate of opening of G•C base pair 3 by over a factor of two. It leaves G•C base pair 4 unchanged, and it slightly increases the rate of opening of A•T base pairs 5 and 6. Actinomycin kinetically stabilizes G•C base pair 3 at the binding site; it has little effect on base pair 4, but it destabilizes the two A•T base pairs 5 and 6. The effect of binding actinomycin at each G(3'-5')C site is propagated into the helix, perhaps inducing some conformational changes in the A•T base pairs.

Netropsin is known to bind with a specificity for A•T regions in the minor groove of DNA duplexes (Zimmer, 1975; Wartell et al., 1974). It has been shown that in the complex only one netropsin is bound per 12-mer duplex (Patel et al., 1981). Netropsin, which lacks a center of symmetry, removes the 2-fold symmetry of the 12-mer as revealed by up to a 0.02 ppm chemical shift difference for base pairs 3-6 on different ends of the helix (Patel et al., 1981). However, no measurable difference in the exchange lifetimes for individual base pairs on different ends of the 12-mer helix in the netropsin complex was observed.

The lifetimes for the 12-mer netropsin complex are given in Table II. First consider the A•T base pairs; the netropsin increases the lifetime for exchange of base pair 5 by over a factor of five from 35 msec in the free 12-mer to 190 msec in the 12-mer-netropsin complex at 55°C. Base pair 6 is kinetically stabilized by a factor of three at 55°C: the lifetimes for

exchange of the free 12-mer is 55 msec while that of the 12-mer-netropsin complex is 165 msec. Thus base pair 5 has the largest change in kinetics of the A•T base pairs upon netropsin binding. Base pair 5 has also been found to have a very large downfield shift of the imino proton resonance upon netropsin binding (Patel et al., 1981). What is the effect on base pairs adjacent to the binding site? The lifetime for exchange of G•C base pair 3 in the free 12-mer at 55°C is 35 msec; comparing this with a lifetime of 50 msec in the 12-mer-netropsin complex shows an increase of about 50% upon drug binding. However, the lifetime for exchange of G•C base pair 4 is increased by almost a factor of three upon netropsin binding: from 80 msec for the free 12-mer to 225 msec in the 12-mer-netropsin complex. Thus we see that binding of netropsin at the central core of the 12-mer duplex affects the dynamics of the G•C base pairs which are distant from the binding site. The binding of netropsin is known to span 2-4 base pairs, therefore its binding presumably includes all four A•T base pairs. It is interesting to note that upon complex formation the relative increase in the lifetime for opening of the G•C base pair at position 4 is as large as that found at the netropsin binding site at A•T base pair 6. This result could be due to netropsin directly interacting with the G•C 4 site or could be an effect propagated down the helix from netropsin binding at the A•T sites.

The 12-mer has been shown to form a complex having two actinomycins and one netropsin simultaneously bound at adjacent G•C and A•T blocks (Patel et al., 1981). The lifetime in the 12-mer-netropsin-actinomycin complex at 55°C for G•C base pair 4 is 130 msec compared to 80 msec in the free 12-mer; for A•T base pair 5 the lifetime is 130 msec in the complex compared to 35 msec in the free 12-mer, and A•T base pair 6 has a lifetime of 135 msec in the complex and 55 msec in the free 12-mer. Thus we observe that the lifetimes for ex-

change of all the imino protons have increased in the complex relative to the free 12-mer.

In comparing the lifetimes of the 12-mer-actinomycin complex with those in the 12-mer-netropsin-actinomycin complex we see that the complex with both drugs bound has lifetimes for all the imino protons which are significantly larger than the corresponding lifetimes when only actinomycin is bound in the complex (130 msec, 130 msec, 135 msec compared to 75 msec, 30 msec, 30 msec; Tables I and III). Thus netropsin kinetically stabilizes base pairs 4-6 of the double helix when it binds to the 12-mer-actinomycin complex. Just the opposite is true for the 12-mer-netropsin complex; the lifetimes of the imino protons on base pairs 4-6 are greater in the 12-mer-netropsin complex than in the 12-mer-netropsin-actinomycin complex (225 msec, 190 msec, 165 msec compared to 130 msec, 130 msec, 135 msec; Tables II and III). Thus the actinomycin kinetically destabilizes these base pairs in the double helix when it binds to the 12-mer-netropsin complex. Notice that the increase or decrease in the lifetimes of the 12-mer-netropsin-actinomycin complex compared to the 12-mer with only actinomycin or netropsin bound extends beyond the binding site of the second antibiotic.

Table III shows that the lifetimes of base pairs 4-6 are approximately the same at a given temperature in the 12-mer-netropsin-actinomycin complex. This result could be explained by a cooperative mechanism where all the imino protons exchange together. As will be discussed in the following section, the activation energies for exchange of the imino protons rule out a cooperative mechanism for exchange. Base pairs 4-6 in the 12-mer-netropsin-actinomycin complex thus exchange independently of one another, but have similar rates for exchange.

Activation Energies for the 12-mer-Antibiotic Complexes

Activation energies for the imino protons in the 12-mer were previously measured and it was shown that exchange takes place by an individual base-pair-opening mechanism (Pardi et al., 1982). The activation energies for the imino protons on base pairs 3-6 for the 12-mer-netropsin complex range from 12-18 kcal/mol (Table IV), and are similar to those found in the 12-mer under similar conditions. The activation energies for the A•T base pairs remained essentially the same; a 2-3 kcal/mol decrease from the free 12-mer was observed. The low values for activation energies indicate that an individual base-pair-opening mechanism is the dominant exchange process in this complex (Pardi et al., 1982).

The activation energies for base pairs 5 and 6 for the 12-mer-actinomycin complex are given in Table IV. Activation energies for G•C base pairs 3 and 4 were not calculated as it is difficult to determine from the data where chemical exchange becomes dominant. An Arrhenius plot of the data is shown in figure 3a. The activation energies for base pairs 4-6 for the 12-mer-netropsin-actinomycin complexes are given in Table IV. The activation energies for both of these complexes are again similar to those found in the free 12-mer and indicate that exchange in both complexes takes place by an individual base-pair-opening mechanism. Thus a process involving a cooperative exchange of several base pairs does not seem to be an important mechanism in the kinetics for exchange of the imino protons for any of the 12-mer-antibiotic complexes studied here.

The high temperature points used to determine the activation energies will have some contribution due to magnetic spin-lattice relaxation. Any contribution from $T_1$ would result in a lifetime for chemical exchange which is greater than the observed lifetime. It is difficult to determine the effect

of $T_1$ accurately because the low-temperature data, where $T_1$ is dominant, are limited to temperatures above 0°C. However, we estimate that $T_1$ will increase both the lifetimes for chemical exchange and the activation energies by at most 50%. This does not change our qualitative conclusions that exchange takes place by an individual base-pair-opening mechanism, that actinomycin kinetically stabilizes base pairs at the binding site with little effect elsewhere and that netropsin kinetically stabilizes base pairs at the binding site and affects base pairs adjacent to the binding site.

## SUMMARY AND CONCLUSIONS

The lifetimes for exchange of the imino protons have been investigated in complexes of a dodecanucleotide double strand with the antibiotics netropsin and/or actinomycin. These lifetimes of base-pairing protons in the double strand upon drug binding give information on the changes in the kinetic stability of base pairs at the binding site and at different distances from the binding site. The lifetimes were measured by saturation recovery experiments or inversion recovery experiments and were shown to correspond at high temperatures to lifetimes of chemical exchange of the protons. Comparison with previous work on the 12-mer shows that the exchange of each imino proton is a measure of the rate of opening of each base pair in the complex. That is, every time the base pair is broken, the imino proton exchanges with water.

Actinomycin intercalates at the G(3'-5')C site between base pair 2 and 3 in the 12-mer (Patel et al., 1981). G•C base pair 3 at the binding site was significantly stabilized by actinomycin binding, but the lifetime of G•C base pair 4 was unaffected. The binding kinetically destabilized the A•T base pairs at the central core of the 12-mer slightly. However, in the 12-mer-netropsin complex the lifetimes of all the base pairs increase upon drug

binding. The netropsin is known to bind in the minor groove at A•T rich sites in DNA and binds in the central A•T core of the 12-mer. There is a large increase in the lifetime for exchange of G•C base pair 4 next to the A•T netropsin binding site, indicating that the netropsin may interact with this G•C residue, or at least induces a perturbation in the helix which stabilizes this base pair. Comparing the lifetimes of the imino protons in the complex when both drugs are bound with those when only one drug is bound, one sees that the binding of netropsin stabilizes the A•T base pairs as well as G•C base pair 4 relative to the 12-mer-actinomycin complex, whereas the binding of actinomycin to a 12-mer-netropsin complex destabilizes all of these base pairs. It is clear that the effects of binding of a drug at a specific site in the helix can be propagated along the double strand and alter the dynamics for opening of base pairs beyond the nearest-neighboring residues.

The activation energies for exchange of the imino protons in the 12-mer complexes were studied by measuring the temperature dependence of the exchange rates. The activation energies are not dramatically different from those found in the free 12-mer, with values ranging from 12-18 kcal/mol. These relatively small values for exchange of imino protons in the three 12-mer-antibiotic complexes studied here show that exchange takes place by an individual base-pair-opening mechanism. The activation energies change only slightly with and without bound drugs, indicating that the open states may have quite similar structure.

Studies on the kinetics of binding of the antibiotics netropsin and/or actinomycin to the 12-mer would be extremely useful in probing the dynamics of these complexes in solution. Correlations between base-pair-opening and drug-dissociation in the complexes could then be studied to try to understand the general dynamics of drug-nucleic acid interactions.

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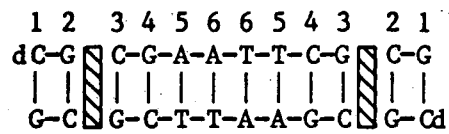
TABLE I. Lifetimes (msec) of Imino Protons in 12-mer-Actinomycin Complex



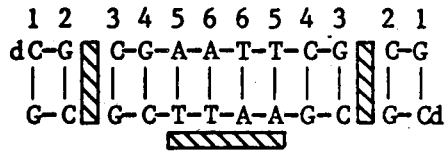

| Temperature (°C) | Proton | | | |
|---|---|---|---|---|
| | #3 | #4 | (#5 | #6) |
| 15 | | | (190 | 185) |
| 25 | | | 160 | |
| 30 | | | 185 | |
| 35 | | | 150 | |
| 40 | 170 | 135 | 100 | |
| 45 | 105 | 140 | 70 | |
| 50 | — | 135 | 50 | |
| 55 | 85 | 75 | 30 | |
| 60 | 70 | 40 | 17 | |

TABLE II. Lifetimes (msec) of Imino Protons in 12-mer-Netropsin Complex

```
 1 2 3 4 5 6 6 5 4 3 2 1
dC-G-C-G-A-A-T-T-C-G-C-G
 | | | | | | | | | | | |
 G-C-G-C-T-T-A-A-G-C-G-Cd
```

| Temperature (°C) | Proton #2 | #3 | #4 | #5 | #6 |
|---|---|---|---|---|---|
| 15 | | | | 320 | 325 |
| 20 | | | | 340 | 375 |
| 25 | | | | 305 | 370 |
| 30 | | | | 420 | 335 |
| 35 | 45 | 240 | 400 | 405 | 360 |
| 40 | | — | — | 415 | 310 |
| 45 | 13 | 95 | — | 515 | 290 |
| 50 | | | 315 | 280 | 230 |
| 55 | | 50 | 225 | 190 | 165 |
| 60 | | 35 | 210 | 235 | 130 |
| 65 | | 17 | 150 | 135 | 105 |
| 70 | | | 100 | 120 | 85 |
| 75 | | | 60 | 75 | 65 |
| 80 | | | 35 | 60 | 40 |

TABLE III. Lifetimes (msec) of Imino Protons in 12-mer-Netropsin-Actinomycin Complex




| Temperature (°C) | Proton #3 | #4 | #5 | #6 |
|---|---|---|---|---|
| 20 | | | | 160 |
| 25 | | | | 180 |
| 35 | | | | 180 |
| 45 | | 155 | 175 | 160 |
| 55 | | 130 | 130 | 135 |
| 60 | | 85 | 75 | 75 |
| 65 | 55 | 65 | 55 | 55 |
| 70 | | 35 | 50 | 45 |
| 75 | | 35 | 25 | 25 |
| 80 | 12 | 18 | 19 | 19 |

TABLE IV.

Activation Energies (kcal/mol) for Exchange of Imino Protons in 12-mer Antibiotic-Complexes

| Complex | Proton | | | |
|---|---|---|---|---|
| | #3 | #4 | #5 | #6 |
| 12-mer alone[a] (pH = 6) | | | 14 ± 2 | 15 ± 2 |
| 12-mer-actinomycin | | | 17 ± 3[b] | 17 ± 3[b] |
| 12-mer-netropsin | 18 ± 3 | 16 ± 2 | 12 ± 2 | 12 ± 2 |
| 12-mer-netropsin-actinomycin | — | 17 ± 3 | 18 ± 3 | 17 ± 3 |

[a]Data taken from
[b]Resonances from base pairs 5 and 6 overlap in this complex (see text).

FIGURE LEGENDS

Figure 1. The 360 MHz NMR spectra, low field region, of: (a) the 12-mer duplex, 20°C, pH = 6.8; (b) the complex with the 12-mer duplex and two equivalents of actinomycin, 15°C, pH = 7; (c) the complex with the 12-mer duplex and one equivalent of netropsin, 20°C, pH = 7; and (d) the complex with the 12-mer duplex with both two equivalents of actinomycin and one equivalent of netropsin, 20°C, pH = 7.

Figure 2. The temperature dependence of the G·C imino protons on base pairs 2, 3, and 4 in: (a) the 12-mer; (b) the 12-mer-actinomycin complex; (c) the 12-mer-netropsin complex; and (d) the 12-mer-netropsin-actinomycin complex.

Figure 3. Arrhenius plots for the observed lifetimes of the 12-mer-actinomycin complex for: (a) the G·C base pairs; and (b) the A·T base pairs. The activation energy was calculated for temperatures of 35°C and above.

Figure 4. Arrhenius plots for the observed lifetimes of the 12-mer-netropsin complex for: (a) the G·C base pairs; and (b) the A·T base pairs. The activation energy was calculated for temperatures of 45°C and above.

Figure 5. Arrhenius plots for the observed lifetimes of the 12-mer-netropsin-actinomycin complex for: (a) the G·C base pair; and (b) the A·T base pairs. The activation energy was calculated for temperatures of 55°C and above.

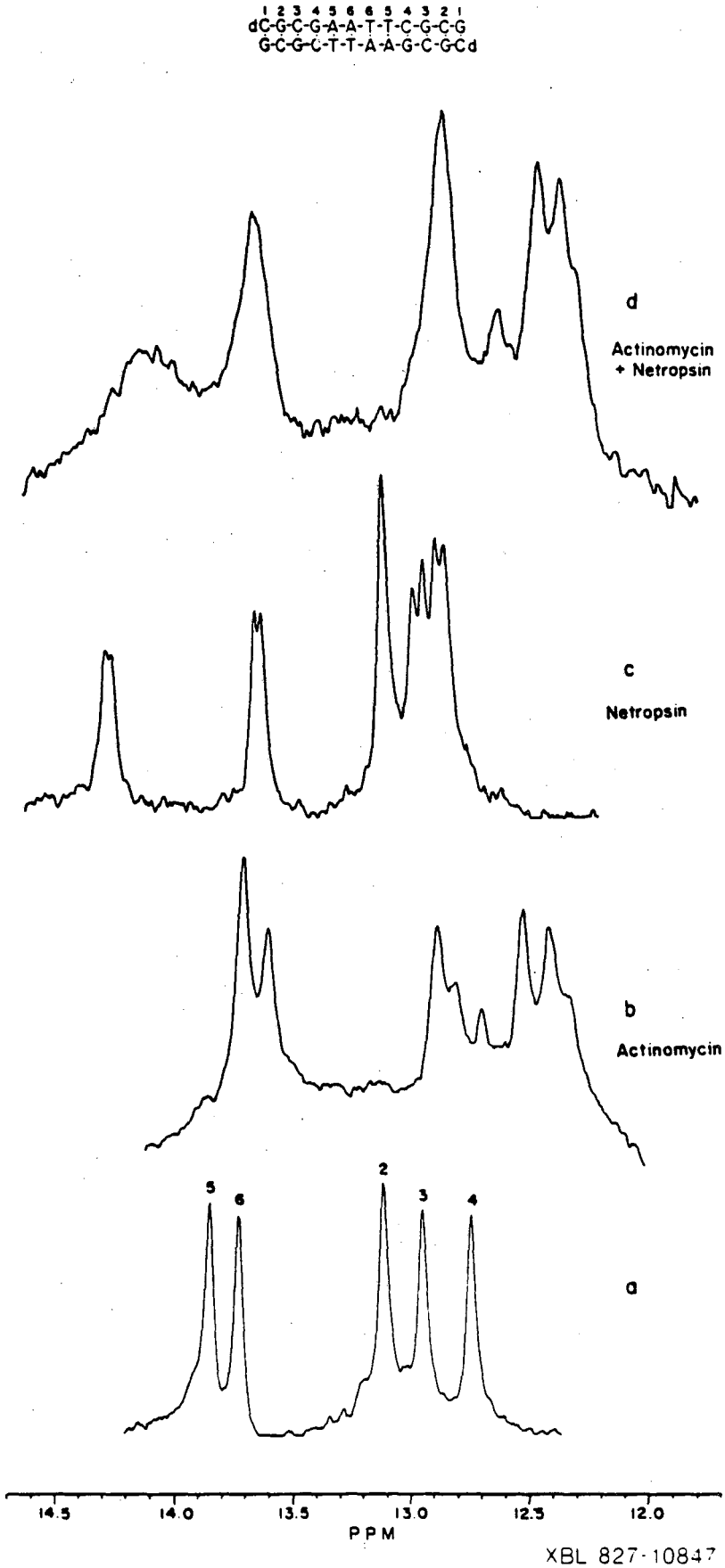

1 2 3 4 5 6 6 5 4 3 2 1
dC-G-C-G-A-A-T-T-C-G-C-G
G-C-G-C-T-T-A-A-G-C-G-Cd
d
Actinomycin
+ Netropsin
c
Netropsin
b
Actinomycin
5
6
2
3
4
a
14.5
14.0
13.5
13.0
12.5
12.0
PPM
XBL 827-10847

Fig. 1

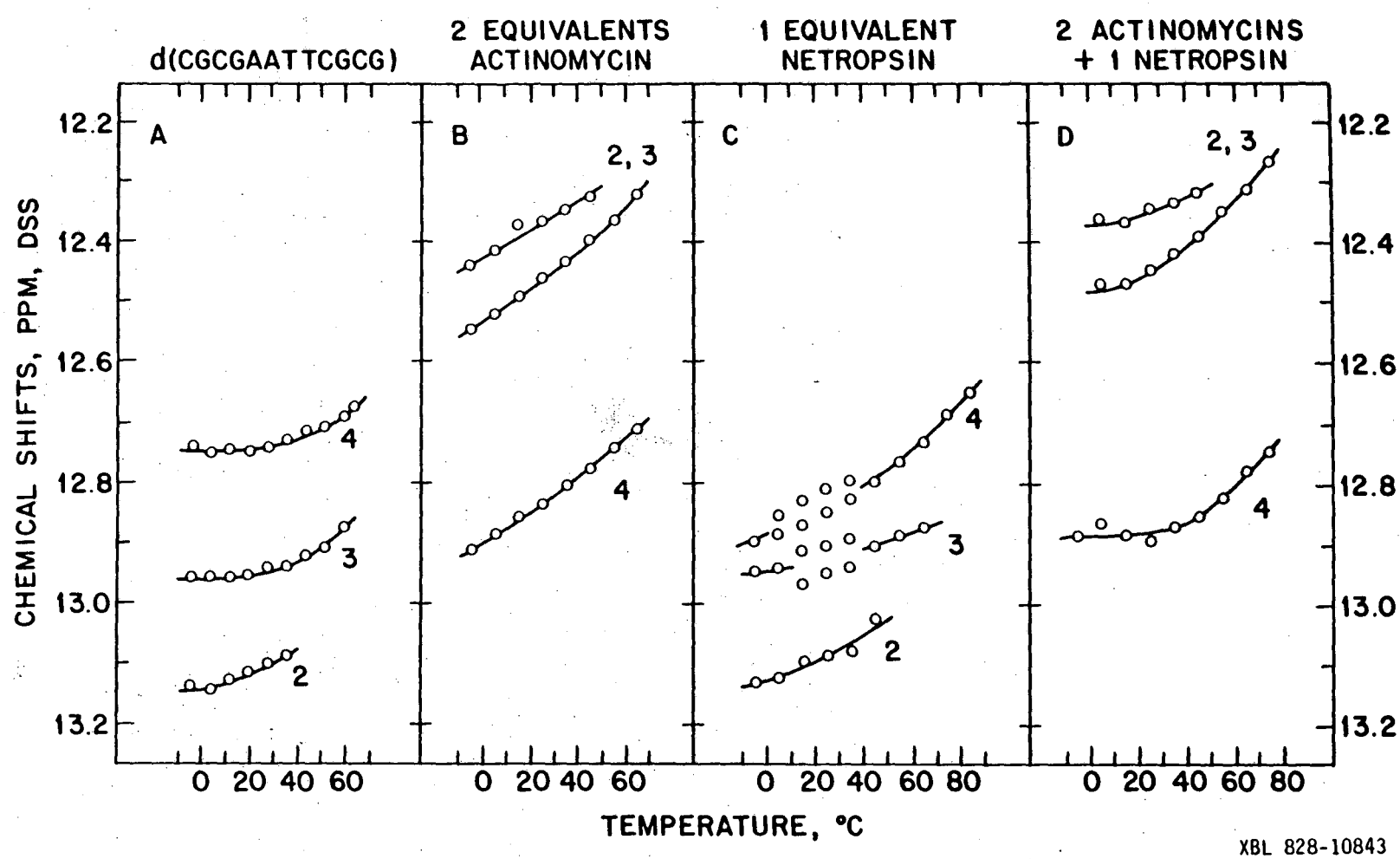

d(CGCGAATTCGCG)
2 EQUIVALENTS ACTINOMYCIN
1 EQUIVALENT NETROPSIN
2 ACTINOMYCINS + 1 NETROPSIN
A
B
C
D
2, 3
4
3
2
CHEMICAL SHIFTS, PPM, DSS
12.2
12.4
12.6
12.8
13.0
13.2
0 20 40 60
0 20 40 60 80
TEMPERATURE, °C
XBL 828-10843

Fig. 2

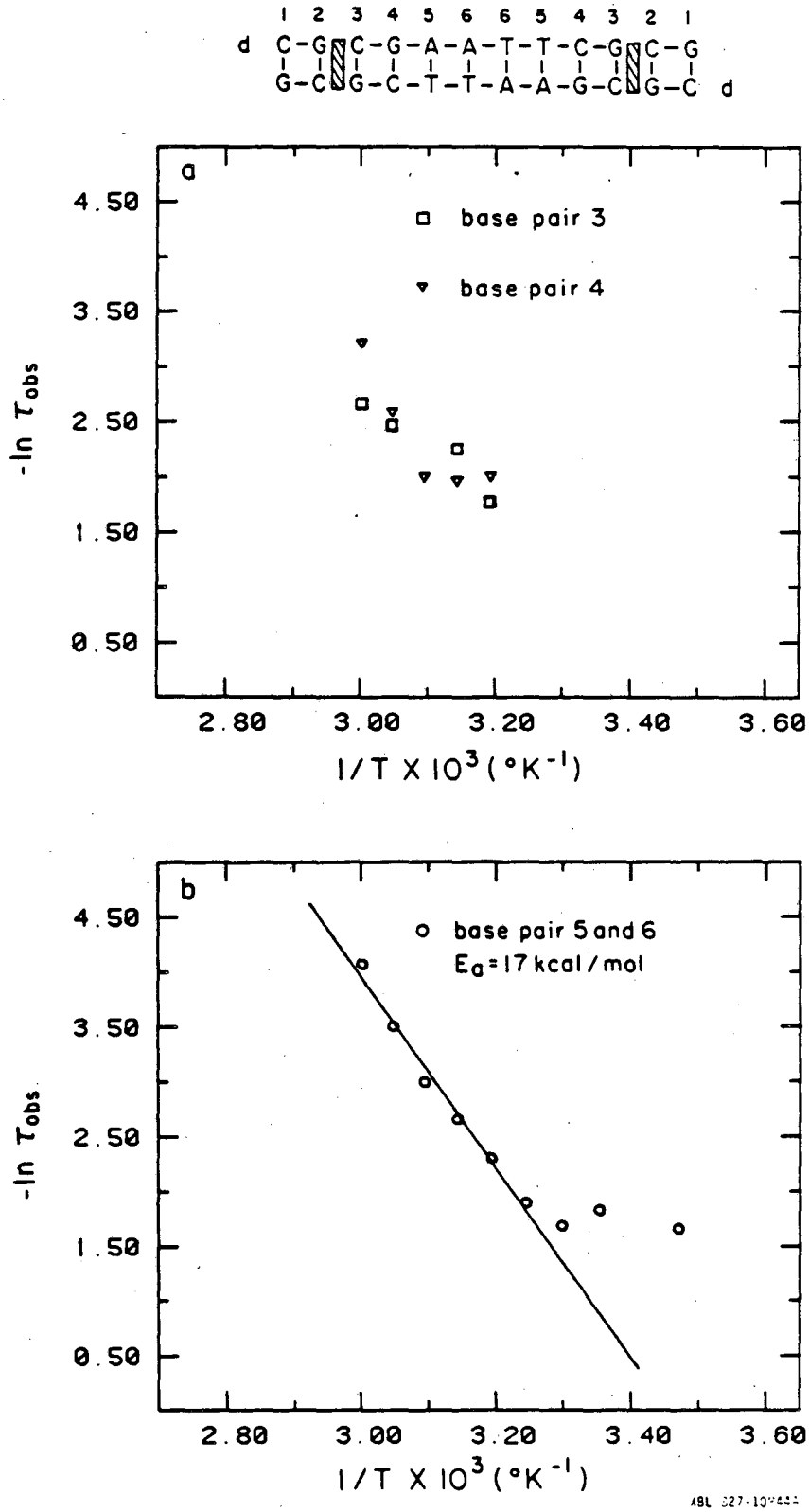

1 2 3 4 5 6 6 5 4 3 2 1
d C-G C-G-A-A-T-T-C-G C-G
G-C G-C-T-T-A-A-G-C G-C d
a
base pair 3
base pair 4
-ln τobs
4.50
3.50
2.50
1.50
0.50
2.80
3.00
3.20
3.40
3.60
1/T X 10³ (°K⁻¹)
b
base pair 5 and 6
Ea = 17 kcal/mol
-ln τobs
4.50
3.50
2.50
1.50
0.50
2.80
3.00
3.20
3.40
3.60
1/T X 10³ (°K⁻¹)

Fig. 3

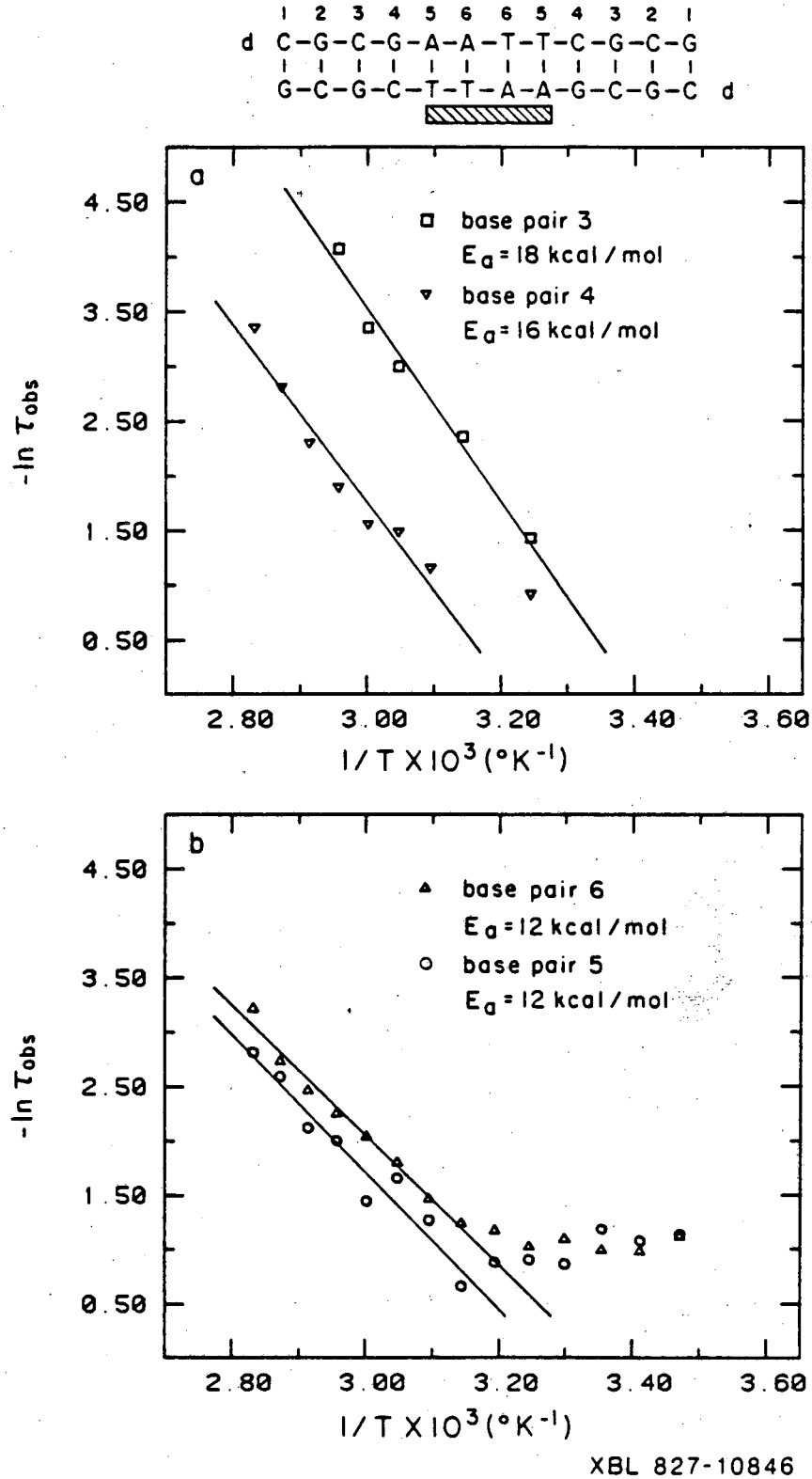

1 2 3 4 5 6 6 5 4 3 2 1
d C-G-C-G-A-A-T-T-C-G-C-G
G-C-G-C-T-T-A-A-G-C-G-C d
a
base pair 3
$E_a$ = 18 kcal / mol
base pair 4
$E_a$ = 16 kcal / mol
-ln $\tau_{obs}$
4.50
3.50
2.50
1.50
0.50
2.80
3.00
3.20
3.40
3.60
1/T X 10$^3$ (°K$^{-1}$)
b
base pair 6
$E_a$ = 12 kcal / mol
base pair 5
$E_a$ = 12 kcal / mol
-ln $\tau_{obs}$
4.50
3.50
2.50
1.50
0.50
2.80
3.00
3.20
3.40
3.60
1/T X 10$^3$ (°K$^{-1}$)
XBL 827-10846

Fig. 4

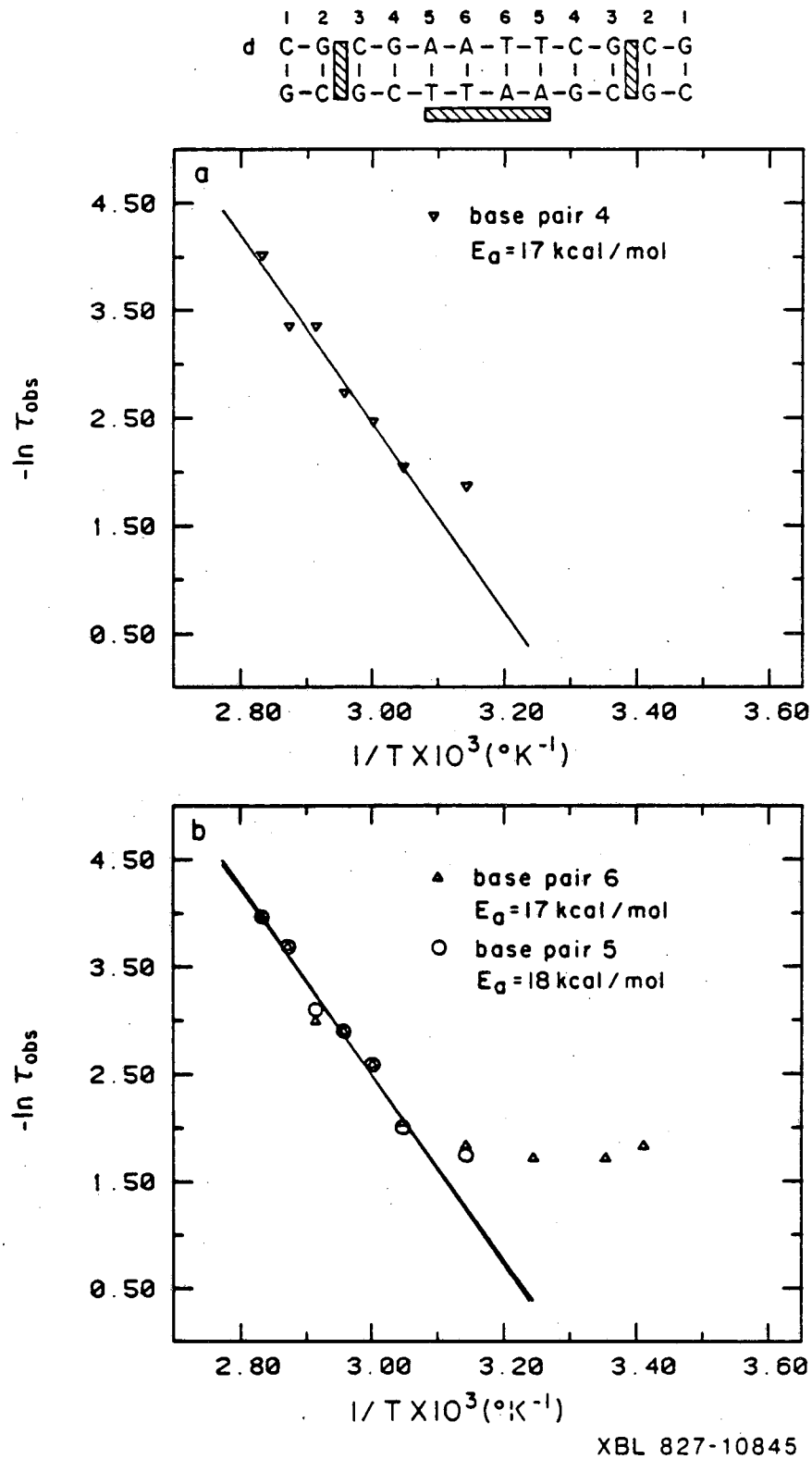

1 2 3 4 5 6 6 5 4 3 2 1
d C-G C-G-A-A-T-T-C-G C-G
G-C G-C-T-T-A-A-G-C G-C
a
base pair 4
Ea=17 kcal/mol
-ln τobs
4.50
3.50
2.50
1.50
0.50
2.80
3.00
3.20
3.40
3.60
1/T X10³(°K⁻¹)
b
base pair 6
Ea=17 kcal/mol
base pair 5
Ea=18 kcal/mol
-ln τobs
4.50
3.50
2.50
1.50
0.50
2.80
3.00
3.20
3.40
3.60
1/T X10³(°K⁻¹)
XBL 827-10845

Fig. 5

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