

## Rapid Isolation and Identification of Bacteriophage T4-Encoded Modifications of *Escherichia coli* RNA Polymerase: A Generic Method to Study Bacteriophage/Host Interactions

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Bacteriophages are bacterial viruses that infect bacterial cells, and they have developed ingenious mechanisms to modify the bacterial RNA polymerase. Using a rapid, specific, single-step affinity isolation procedure to purify *Escherichia coli* RNA polymerase from bacteriophage T4-infected cells, we have identified bacteriophage T4-dependent modifications of the host RNA polymerase. We suggest that this methodology is broadly applicable for the identification of bacteriophage-dependent alterations of the host synthesis machinery.

**Keywords:** *Escherichia coli* • bacteriophage • RNA polymerase • bacteriophage infection • affinity isolation • MALDI MS

### Introduction

In the bacterium *Escherichia coli* (*Ec*), transcription is dependent upon a single ~400 kDa multisubunit RNA polymerase (RNAP) that can exist in two forms: the catalytic core enzyme ( $\alpha_2\beta\beta'\omega$ ) and the promoter-specific holoenzyme ( $\alpha_2\beta\beta'\omega\sigma$ ). Transcription can be divided into three distinct stages: initiation, elongation, and termination. Regulation of RNAP can occur at each stage of transcription by protein, RNA, and small molecule *trans*-acting factors that associate with the enzyme to modulate its activity.

Bacteriophages (phages) are bacterial viruses dependent upon a host organism to propagate; therefore, phages are endowed with mechanisms that subvert the host's cellular processes to serve the needs of the virus. Consequently, bacteriophages offer an exciting and tractable system by which to study developmental processes. Recently, a resurgence in the use of bacteriophages for the treatment or prophylaxis of bacterial infectious diseases—bacteriophage therapy—has increased the demands for understanding bacteriophage/host interactions.<sup>1</sup> In particular, identification of phage proteins that bind to and inhibit essential host enzymes should allow the identification of novel drug targets. Therefore, it is highly

desirable to have efficient methods for the identification of phage-encoded proteins that associate with host proteins.

Many phages encode proteins that directly bind to and regulate the activity of the bacterial host RNAP, and some phages encode enzymes that covalently modify the host transcriptional apparatus. These phage-induced modifications ensure coordinated temporal transcription of the phage genome and inhibition of host transcription.<sup>2</sup>

Bacteriophage T4 (T4) does not encode its own RNAP and relies on *Ec* RNAP for expression of its genes. To appropriate the host RNAP, T4 employs several redundant mechanisms that target *Ec* RNAP to the T4 genome<sup>2</sup> and promote the transcription of T4 DNA. One such mechanism involves the T4-encoded Alc protein that functions to increase the pool of host RNAP available for transcribing T4 DNA by selectively terminating RNAP transcription on *Ec* DNA without affecting transcription of T4 DNA.<sup>3–5</sup>

In this paper, we present a method for the rapid isolation of RNAP from phage-infected *Ec* cells, followed by matrix-assisted laser desorption ionization mass spectrometric (MALDI MS) analysis of proteins co-isolating with RNAP. This method allowed unequivocal identification of most of the known T4-encoded proteins that bind directly to host RNAP and identification of Alc whose binding to RNAP had not previously been reported, and also identified covalent modifications of the host RNAP by T4-encoded enzymes. This general procedure should be broadly applicable for the identification of phage-encoded proteins that interact with components of the host macromo-

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lecular synthesis machinery and should become increasingly important in characterizing the many bacteriophage/host systems.

## Experimental Section

**Ec Strains and Growth Conditions.** A strain of *Ec* MG1655 encoding two Fc-binding repeats of the Protein A (2PrA) affinity tag<sup>6</sup> appended to the 3' end of the *rpoC* gene (which encodes the RNAP  $\beta'$  subunit) was constructed as previously described.<sup>7</sup> Both the MG1655 *Ec* wild-type and MG1655 *Ec rpoC::2PrA* strains exhibited almost identical growth curves in Luria–Bertani broth (LB; data not shown) and doubling times (*Ec* wild-type,  $25.3 \pm 1.6$  min; *Ec rpoC::2PrA*,  $28.5 \pm 2.1$  min).

All *Ec* strains were grown in LB at 37 °C with shaking. To prepare T4-infected biomass, wild-type *Ec* and *Ec rpoC::2PrA* strains (4 L of each) at an  $A_{600\text{ nm}}$  of 0.5–0.6 were infected with T4 (*alt*-) at a multiplicity of infection of 10. Infection was halted 15 min postinfection by rapidly cooling the samples in icy water baths. Cells were harvested by centrifugation, washed once with ice-cold 10% (v/v) glycerol, and frozen as pellets in liquid nitrogen. Cells were cryogenically disrupted with a Retsch MM301 mixer mill (Retsch) that was maintained at liquid nitrogen temperature and stored at  $-80$  °C.<sup>8</sup>

**Affinity Isolation and Mass Spectrometric Identification of Protein Complexes.** Cryogenically lysed cells (1 g) were suspended in 5 mL of extraction buffer (20 mM Hepes (pH 7.4); 2 mM MgCl<sub>2</sub>; 150 mM NaCl) supplemented with one protease inhibitor cocktail tablet (Roche Diagnostics). Suspended lysate was treated with 0.002% (w/v) DNase I (Sigma-Aldrich) with agitation. The soluble fraction was isolated by centrifugation at 27,200 g for 10 min, and the supernatant was decanted and subjected to another 10 min centrifugation step. The supernatant was incubated with 25 mg of Dynabeads (Invitrogen) cross-linked to rabbit IgG (MP Biomedicals) with gentle agitation for 10 min. For  $\beta'$ -2PrA, and other affinity tagged proteins, rapid affinity isolations are optimal (data not shown<sup>9</sup>). Dynabeads were collected with a magnet and washed with wash buffer (20 mM Hepes (pH 7.4); 150 mM NaCl). The  $\beta'$ -2PrA-tagged protein and copurifying proteins were eluted from the IgG Dynabeads with 0.5 M NH<sub>4</sub>OH and 0.5 mM EDTA. The eluted proteins were frozen in liquid nitrogen and evaporated to dryness in a SpeedVac (Thermo Savant). Dried protein samples were dissolved in SDS-PAGE loading buffer and heated at 95 °C. Samples were resolved by SDS-PAGE with 4–12% (w/v) Bis-Tris polyacrylamide gels (Invitrogen), and bands due to proteins were visualized by Coomassie blue staining. The entire gel lane was sliced into 1 mm slices, and the proteins in each gel slice were destained with a mixture of 50% (v/v) acetonitrile and 50 mM ammonium bicarbonate. After destaining, the proteins were reduced with 10 mM TCEP-HCl (Pierce) for 30 min and then alkylated with 50 mM iodoacetamide (Sigma-Aldrich) for 1 h. Finally, proteins in each gel slice were digested with Trypsin (Roche Diagnostics) at 37 °C for 4 h. The resulting peptides were extracted on reverse phase resin (Poros 20 R2, PerSeptive Biosystems), eluted with 50% (v/v) methanol, 20% (v/v) acetonitrile, and 0.1% (v/v) trifluoroacetic acid, and subjected to MALDI MS analysis. Proteins were identified by MALDI-QqTOF single-stage MS and MALDI-ion-trap MS<sup>2</sup> as previously described.<sup>10,11</sup> Single-stage and multistage mass spectrometric data were used for protein identification with the programs ProFound<sup>12</sup> and Sonar MS/MS,<sup>13</sup> respectively.

**Cloning and Overexpression of Alc.** Due to the toxicity of T4 Alc to *Ec* cells, a T7 RNAP-directed Alc overexpression

plasmid was constructed in several steps. First, using purified T4 genomic DNA as a template, the DNA encoding Alc was amplified by the polymerase chain reaction (PCR). The resultant PCR product was blunt-end cloned into pT7Blue (Novagen) in an antisense orientation relative to the T7 RNAP  $\phi$ 10 and *Ec* RNAP *lacUV5* promoters to reduce basal expression of Alc, creating pT7-alcrev. Second, pT7-alcrev was cleaved with *Afl*III, treated with Klenow DNA polymerase to generate blunt ends, and digested with *Bam*HI to obtain a fragment encoding Alc and the  $\phi$ 10 and *lacUV5* promoters. The resultant fragment was cloned into pET28a (Novagen) cleaved with *Hind*III, treated with Klenow to generate blunt ends, and then cleaved with *Bam*HI to create pET28-alc(T7-*lacUV5*). Finally, a DNA fragment encoding only the *lacUV5* promoter was generated by digesting pUC19 with *Afl*III, followed by incubation with Klenow to generate blunt ends, and then cleaved with *Hind*III. The resultant *lacUV5* fragment was cloned between the *Not*I site, also treated with Klenow, and the *Hind*III site of pET28-alc(T7-*lacUV5*), thus creating pET28-alc(*lacUV5*). Thus, Alc overexpression is under the control of the plasmid-encoded T7 RNAP  $\phi$ 10 promoter, while the *Ec* RNAP *lacUV5* promoter drives transcription antisense to Alc reducing Alc toxicity.

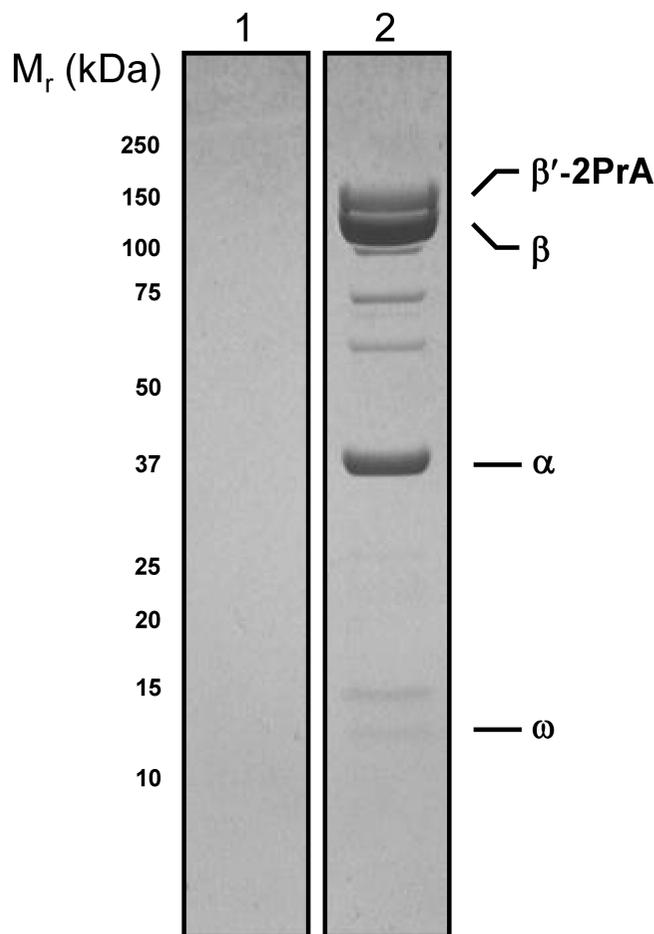
The expression plasmid pET28-alc(*lacUV5*) was transformed into *Ec* cells harboring the *paf rpoB* allele<sup>3</sup> (which partially nullifies the toxicity of Alc) and the  $\lambda$  (DE3) lysogen encoding T7 RNAP, and transformants were selected in the presence of 50  $\mu$ g/mL of kanamycin. Cultures were grown at 37 °C to an  $A_{600\text{ nm}} \sim 0.6$  and induced with 1 mM IPTG for 14 h at 37 °C. Cells containing overexpressed proteins were harvested by centrifugation and stored at  $-80$  °C.

**Protein Purification.** Recombinant Alc formed inclusion bodies and was solubilized by adding urea to a final concentration of 8 M. A polyhistidine tag (derived from the vector) was appended to the amino terminus of Alc, thus Alc was purified by HiTrap Ni<sup>2+</sup>-charged affinity chromatography (GE Healthcare) with 8 M urea present in all the column buffers. Purified (His)<sub>6</sub>-Alc was exchanged into renaturation buffer (40 mM Tris-HCl (pH 8.0), 0.1 M NaCl, 0.5 mM EDTA, 2 mM  $\beta$ -mercaptoethanol, 5% (v/v) glycerol) by dialysis and concentrated using centrifugal concentration units (Pall Life Sciences). Finally, the protein was exchanged into storage buffer (20 mM Tris-HCl (pH 8.0), 0.1 M NaCl, 1 mM EDTA, 0.5 mM DTT, 50% (v/v) glycerol) by dialysis and stored at  $-20$  °C.

Wild-type *Ec*  $\sigma^{70}$  was purified as previously described.<sup>14</sup> The *Ec* core enzyme and  $\sigma^{70}$ -associated holoenzyme were reconstituted in vitro<sup>14</sup> and fractionated by anion-exchange chromatography (Mono Q; GE Healthcare<sup>15</sup>). Fractions containing core and  $\sigma^{70}$ -associated enzymes were pooled separately and stored as described previously.<sup>15</sup>

**Analysis of Alc/RNAP Interactions.** Reactions (8  $\mu$ L) containing 0.75  $\mu$ g of Alc and either 0.125  $\mu$ g of core RNAP or 0.07  $\mu$ g of  $\sigma^{70}$ -associated holoenzyme in transcription buffer (30 mM Tris-HCl (pH 7.9), 40 mM KCl, 10 mM MgCl<sub>2</sub>, 1 mM  $\beta$ -mercaptoethanol) were incubated at room temperature for 10 min.

Samples (4  $\mu$ L of each reaction mixture) were resolved by nondenaturing PAGE on a 4–15% (w/v) gradient polyacrylamide gel, and the bands due to proteins were stained with Coomassie blue. To determine the composition of the bands due to proteins separated by gel electrophoresis under nondenaturing conditions, the bands were excised from the nondenaturing gel and equilibrated in SDS-PAGE loading buffer, and their composition was determined by electrophoresis on a 10% (w/v) SDS-PAGE denaturing gel.



**Figure 1.** affinity isolation of  $\beta'$ -2PrA and co-isolating proteins from T4-infected *Ec* cells. Complexes were isolated via a PrA tag under conditions that co-isolated interacting proteins. Proteins were resolved by denaturing SDS-PAGE, visualized by Coomassie blue staining, and analyzed by MALDI MS. Lanes are loaded as follows: lane 1, affinity isolated proteins from *Ec* wild-type cells infected with T4; lane 2, affinity isolated proteins from *Ec rpoC::2PrA* cells infected with T4. RNAP subunits in the 2PrA-tagged sample (lane 2) are labeled.

## Results and Discussion

**Noncovalent Modifications of *Ec* RNAP: Affinity Isolation and Mass Spectrometric Identification of T4-Encoded Proteins that Coisolate with *Ec* RNAP.** To identify T4-encoded *Ec* RNAP co-isolating proteins, we affinity isolated RNAP from T4-infected *Ec* cells (Figure 1, lane 2). Isolation was performed using the genomically 2PrA-tagged  $\beta'$  subunit of RNAP. The conditions of affinity isolation were sufficiently gentle and rapid to maintain interactions with other cellular macromolecules.<sup>8,9,16–19</sup> As a control, parallel isolation of proteins from T4-infected wild-type cells (untagged  $\beta'$ ) was performed. Little or no protein bands are present in the control, indicating that our conditions are stringent enough to prevent nonspecific association of most *Ec* and T4 proteins with the immunoaffinity matrix (Figure 1, lane 1). The material from the tagged strain contained major bands corresponding to the RNAP subunits (Figure 1, lane 2), indicating that the procedure allowed specific single-step purification of RNAP from whole-cell lysates.

Affinity isolated T4-encoded proteins were identified by mass spectrometry (Table 1). Traces of contaminating proteins that were present in the untagged control sample that nonspecifically

**Table 1**

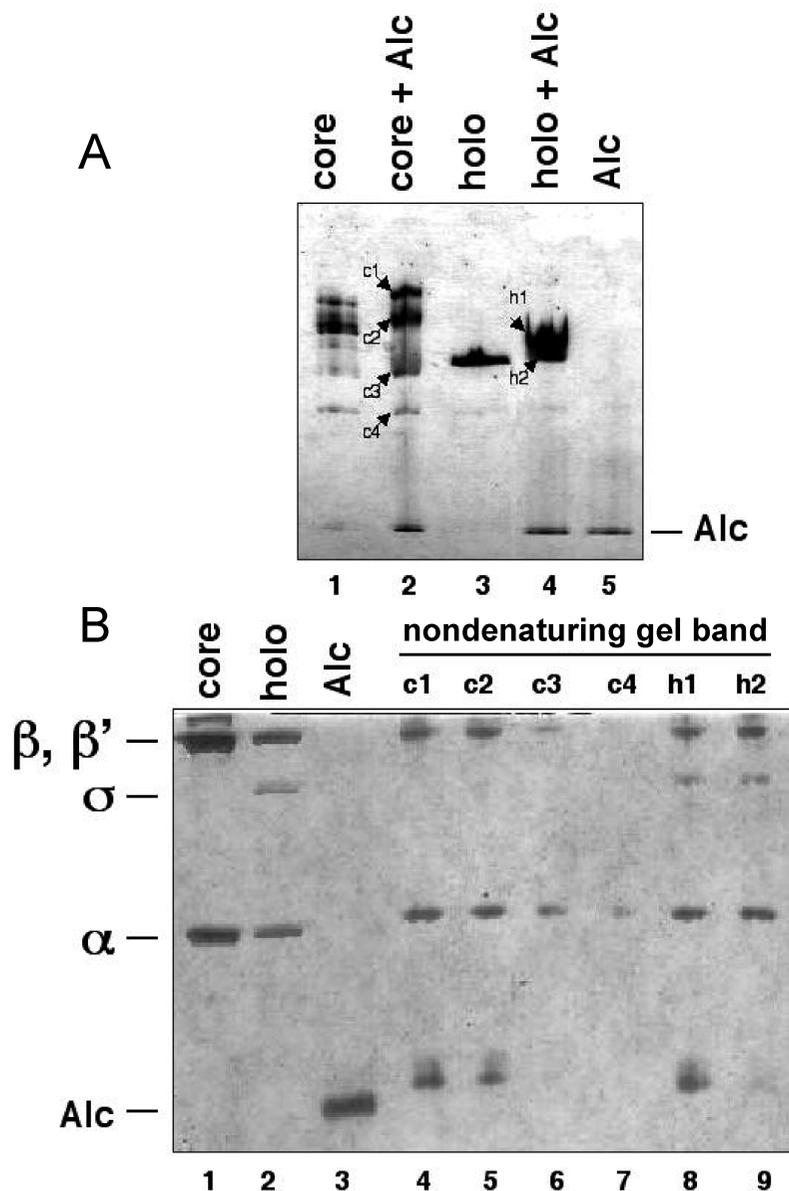
tagged protein	T4-encoded <i>Ec</i> RNAP-binding proteins	peptide coverage (%)	$M_r$ (kDa)	expectation value	
				profound	sonar
$\beta'$ -2PrA	MotA	58	23.6	$2.5 \times 10^{-4}$	$1.0 \times 10^{-11}$
	gp55	70	21.6	$6.2 \times 10^{-8}$	$5.0 \times 10^{-11}$
	Alc	57	19.2	$4.2 \times 10^{-4}$	$3.7 \times 10^{-12}$
	RpbA	81	14.8	$8.8 \times 10^{-8}$	$1.8 \times 10^{-5}$
	gp33	35	12.9	$2.5 \times 10^{-1}$	$6.2 \times 10^{-1}$
	AsiA	88	10.6	$2.6 \times 10^{-7}$	$2.0 \times 10^{-11}$

associated with the immunoaffinity matrix (Figure 1, lane 1) were computationally filtered out of the data set obtained from the tagged strain (Figure 1, lane 2). As is clearly seen in Figure 1, and as confirmed by MS analysis, all RNAP subunits were present in the sample affinity isolated from the tagged strain (Figure 1, lane 2) but were absent from the untagged control (Figure 1, lane 1).

Analysis of the affinity isolated material from the tagged strain (Figure 1, lane 2) revealed the presence of all T4-encoded proteins that are known to associate directly with RNAP: MotA, an activator of T4 middle promoters;<sup>20</sup> gp55, a T4-encoded  $\sigma$  factor that controls the expression of T4 late genes;<sup>21,22</sup> RpbA, a protein with unknown function; gp33, an activator of T4 late genes that coactivates T4 late genes with gp55;<sup>22</sup> and AsiA, a potent inhibitor of host-dependent transcription,<sup>23,24</sup> host RNAP appropriator, and coactivator of T4 middle genes.<sup>20</sup>

We also identified the T4-encoded transcription termination factor Alc. Alc increases the pool of host RNAP available for transcribing T4 DNA by selectively terminating RNAP transcription on *Ec* DNA without affecting transcription of T4 DNA.<sup>3–5</sup> On the basis of genetic studies, Alc is thought to bind directly to the  $\beta$  subunit dispensable region 1 ( $\beta$ DR1) of *Ec* RNAP, but no direct interaction between RNAP and Alc had been previously reported.<sup>3,4</sup> Since the affinity isolation experiment indicated an Alc/RNAP interaction, we tested this result using non-denaturing PAGE (Figure 2A). Under our conditions, purified core RNAP migrated as a diffuse set of bands (Figure 2A, lane 1); the  $\sigma^{70}$ -holoenzyme migrated as a single band (Figure 2A, lane 3); and purified Alc migrated with the dye front (Figure 2A, lane 5). From the gel, it is clear that the bands labeled c1 and c2 appear to have a slightly lower electrophoretic mobility than the corresponding bands from the RNAP core sample, suggesting an interaction between the core and Alc. With the mixture containing Alc and  $\sigma^{70}$ -holoenzyme (Figure 2A, lane 4), two poorly resolved bands are observed: one (labeled h2) has the same mobility as the  $\sigma^{70}$ -holoenzyme alone and the other (labeled h1) has a slightly decreased mobility compared to the  $\sigma^{70}$ -holoenzyme alone.

The labeled bands were excised from the non-denaturing gel and their protein content established by denaturing SDS-PAGE (Figure 2B). It is apparent that the bands due to c1, c2, and h1 contained, in addition to the expected RNAP subunits, a band due to Alc (Figure 2B, lanes 4, 5, and 8, respectively), thus establishing that Alc binds both the core and  $\sigma^{70}$ -holoenzyme. The material in bands c3, c4, and h2 contained little or no Alc (Figure 2B, lanes 6, 7, and 9, respectively). The h2 band contained the free  $\sigma^{70}$ -holoenzyme; band c3 contained the RNAP assembly intermediate  $\alpha_2\beta$ ; and band c4 contained the free  $\alpha$  subunit. Thus, it appears that Alc fails to bind to  $\alpha_2\beta$  despite the fact that the genetically identified determinants for Alc binding are located in the  $\beta$  subunit.<sup>3</sup> This result suggests

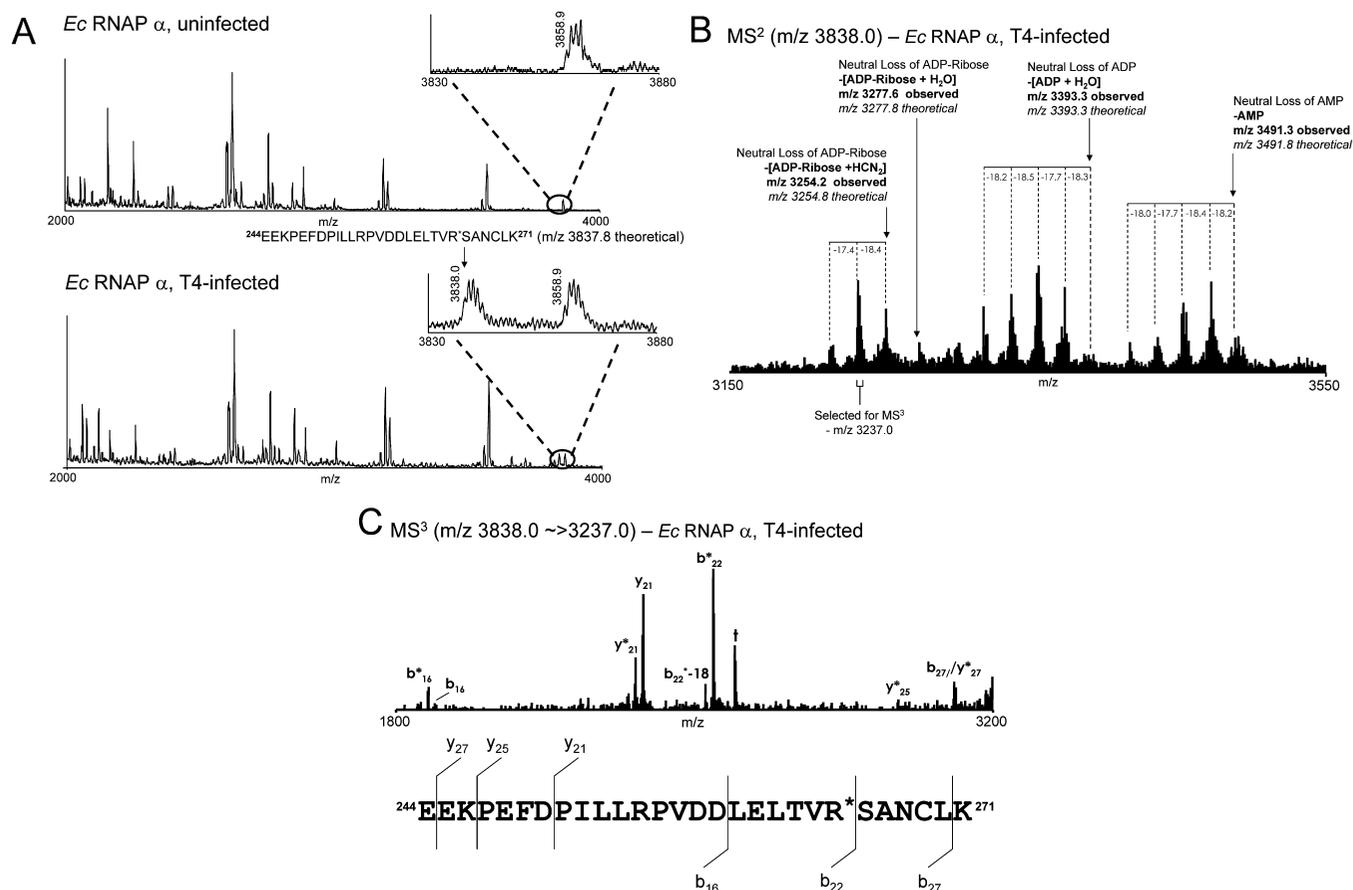


**Figure 2.** Nondenaturing PAGE and denaturing SDS-PAGE were used to probe the associations of Alc with the core enzyme and the  $\sigma^{70}$ -holoenzyme. (A) Different combinations of Alc, core, and  $\sigma^{70}$ -holoenzyme were incubated together and resolved under nondenaturing conditions. (B) Bands due to the proteins separated by nondenaturing PAGE, labeled in (A), were excised, and their composition was revealed by denaturing SDS-PAGE.

that Alc binding to RNAP may require determinants in both the  $\beta$  and  $\beta'$  subunits.

**Covalent Modifications of *Ec* RNAP: T4-Dependent ADP-Ribosylation of the *Ec* RNAP  $\alpha$  Subunit.** ADP-ribosyltransferases catalyze the transfer of the ADP-ribosyl moiety from substrate ADP-ribosyl-nicotinamide onto residues of a target protein.<sup>25</sup> T4 encodes two ADP-ribosyltransferases, Alt and ModA, that ADP-ribosylate Arg 265 of the RNAP  $\alpha$  subunit.<sup>26–30</sup> Although ModA specifically modifies  $\alpha$ -Arg 265 of both  $\alpha$  subunits,<sup>30</sup> Alt modifies  $\alpha$ -Arg 265 on only one of the two  $\alpha$  subunits, multiple sites within *Ec* RNAP, and other host proteins.<sup>31–33</sup> The sites of Alt-dependent ADP-ribosylation within the  $\beta$ ,  $\beta'$ , and  $\sigma^{70}$  subunits remain to be elucidated. Residue  $\alpha$ -Arg 265 is involved in contacting both DNA and *trans*-acting factors,<sup>34–36</sup> thus ADP-ribosylation of this key residue alters  $\alpha$ /DNA and  $\alpha$ /protein interactions necessary for transcription activation.

To determine the facility of mass spectrometric analysis for elucidating posttranslational modifications of RNAP, we sought to identify the ModA-dependent ADP-ribosylation of the *Ec*  $\alpha$  subunit. To do this, tryptic peptides of the  $\alpha$  subunit affinity isolated from both uninfected and T4-infected *Ec* cells were prepared and analyzed by MALDI MS. Using a subtractive approach, the resulting mass spectra were scanned for peptides present in the T4-infected sample but absent from the uninfected sample. A peak due to a singly charged species at  $m/z$  3838.0 was observed in the T4-infected sample but not the uninfected sample (Figure 3A) and thus is likely due to T4-dependent modification of the  $\alpha$  subunit. The theoretical  $m/z$  for a singly protonated ADP-ribosylated tryptic peptide containing  $\alpha$  residues 244–271 is 3837.8. The match of both the theoretical and observed masses suggests that the species at  $m/z$  3838.0 is due to  $\alpha$  residues 244 to 271, encompassing an ADP-ribosyl group. This interpretation is further corroborated



**Figure 3.** Identification of T4-dependent ADP-ribosylation of RNAP  $\alpha$  subunit Arg 265. Bands due to the RNAP  $\alpha$  subunit isolated from uninfected and T4-infected cells were excised, digested with trypsin, and analyzed by MALDI MS. The resulting mass spectra were aligned and scanned for peptides present in the T4-infected sample, but absent from the uninfected sample. (A) Mass spectrum of tryptic peptides due to the RNAP  $\alpha$  subunit isolated from uninfected *Ec rpoC::2PrA* cells (top panel) and *Ec rpoC::2PrA* cells infected with T4 (bottom panel). The appearance of a peak at  $m/z$  3838.0, with a mass that corresponds to a singly protonated ADP-ribosylated peptide derived from  $\alpha$  residues 244–271 in the infected sample spectrum that is absent in the uninfected sample spectrum suggests that this peptide is ADP-ribosylated in vivo in a T4-dependent manner. (B) The mass spectrum of the MS<sup>2</sup> analysis of the species with  $m/z$  3838.0 described in (A) illustrates neutral loss of AMP, ADP, and ADP-ribose, together with various water/ammonia neutral losses. This fragmentation is consistent with the interpretation that the peptide ion at  $m/z$  3838.0 is indeed an ADP-ribosylated species. (C) MS<sup>3</sup> analysis of the ions in the MS<sup>2</sup> spectrum with  $m/z$  3237.0 (corresponding to the neutral loss of ADP-ribose + HCN<sub>2</sub> + water/ammonia) yielded backbone fragmentation providing partial sequence of the peptide. The fragmentation pattern is consistent with the interpretation that the original peptide ion at  $m/z$  3838.0 is indeed derived from  $\alpha$  residues 244–271. Observed are fragments corresponding to the preferential cleavage of the singly-protonated peptide ion carboxy-terminal to acidic residues and amino-terminal to Pro residues. Together, the MS, MS<sup>2</sup>, and MS<sup>3</sup> spectra in panels (A), (B), and (C) provide strong evidence that  $\alpha$  is ADP-ribosylated on Arg 265 within the tryptic peptide encoding residues 244–271.  $b^*$  indicates the loss of ammonia from a  $b$ -ion, and  $y^*$  indicates the loss of ammonia from a  $y$ -ion. ADP-ribosylated  $\alpha$ -Arg 265 is shown as  $R^*$ .

by the missed cleavage at  $\alpha$ -Arg 265, suggesting that ADP-ribosylation of this Arg residue may block tryptic cleavage.

Interrogation of this peptide ion using MALDI-ion-trap MS<sup>2</sup> mass spectrometry yielded a family of strong peaks corresponding to fragmentation of the ADP-ribosyl modification. Peaks consistent with the neutral losses of adenosine monophosphate, adenosine diphosphate, and ADP-ribose, combined with multiple water/ammonia losses were observed (Figure 3B). MS<sup>3</sup> of a peptide ion at  $m/z$  3237.0 (loss of ADP-ribose + water) yields a fragmentation pattern consistent with  $\alpha$  residues 244–271 (Figure 3C). The expected preferential fragmentations carboxy-terminal to acidic amino acid residues (Asp and Glu) and amino-terminal to Pro residues are observed.<sup>37</sup> Our data reveal that mass spectrometry can be used to probe for phage-dependent covalent modifications of host proteins and should allow the elucidation of those sites within *Ec* RNAP that are ADP-ribosylated by T4 Alt.

## Conclusion

We have affinity isolated *Ec* RNAP from T4-infected cells and analyzed the T4-encoded co-isolating proteins using MALDI MS. The T4 phage system has been studied extensively, and T4-encoded proteins that interact with and regulate the activity of host RNAP have been identified over the years by painstaking genetic and biochemical approaches. Our results show that optimized RNAP affinity isolations, coupled with mass spectrometric identification, allow rapid identification of many T4 proteins known to interact with *Ec* RNAP, as well as the novel identification of Alc as a binding partner, whose low affinity for RNAP prevented earlier identification. In addition, this method is also suitable for the identification of phage-dependent covalent modifications of the host transcription machinery, as demonstrated by our comprehensive mass spectrometric

analysis of an ADP-ribosylated peptide. The ADP-ribosylation of proteins is an important process in both prokaryotes and eukaryotes. Indeed, many bacterial exotoxins are ADP-ribosyltransferases<sup>38</sup> and function to manipulate and override host cellular processes. In eukaryotes, ADP-ribosylation is involved in regulating, among other things, the activity of histones and membrane traffic.<sup>39,40</sup> Elucidation of the MS<sup>2</sup> and MS<sup>3</sup> fragmentation characteristics of ADP-ribosylated peptides should facilitate the definition of control mechanisms and signaling pathways that are dependent upon ADP-ribosylation. Finally, we suggest that this methodology, coupled with phage genomic sequencing, will become an important tool for probing novel host/phage systems.

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