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RESEARCH ARTICLE

Dissociation Kinetics of the Streptavidin–Biotin Interaction Measured Using Direct Electrospray Ionization Mass Spectrometry Analysis

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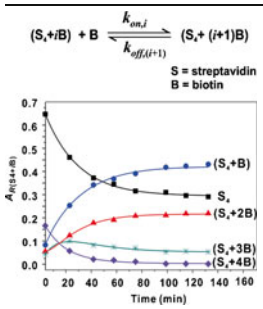

Abstract. Dissociation rate constants (k_{off}) for the model high affinity interaction between biotin (B) and the homotetramer of natural core streptavidin (S_4) were measured at pH 7 and temperatures ranging from 15 to 45 °C using electrospray ionization mass spectrometry (ESI-MS). Two different approaches to data analysis were employed, one based on the initial rate of dissociation of the (S_4 + 4B) complex, the other involving nonlinear fitting of the time-dependent relative abundances of the (S_4 + iB) species. The two methods were found to yield k_{off} values that are in good agreement, within a factor of two. The Arrhenius parameters for the dissociation of the biotin–streptavidin interaction in solution were established from the k_{off} values determined by ESI-MS and compared with values measured using a radiolabeled biotin assay. Importantly, the dissociation activation energies determined by ESI-MS agree, within 1 kcal mol^{-1}, with the reported value. In addition to providing a quantitative measure of k_{off}, the results of the ESI-MS measurements revealed that the apparent cooperative distribution of (S_4 + iB) species observed at short reaction times is of kinetic origin and that sequential binding of B to S_4 occurs in a noncooperative fashion with the four ligand binding sites being kinetically and thermodynamically equivalent and independent.

Key words: Electrospray ionization mass spectrometry, Rate constants, Protein–ligand complexes

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Introduction

Noncovalent interactions between proteins and between proteins with other biopolymers, small molecules, or metal ions are critical to most cellular processes. The abundances of protein complexes and their lifetimes reflect the rates of the corresponding association and dissociation reactions. Quantification of the kinetic parameters—the association and dissociation rate constants (k_{on} and k_{off}, respectively)—under specific solution conditions (e.g., pH, temperature, ionic strength) is important in understanding the structure and function of protein complexes and is relevant to drug design [1–3]. There exist a number of established experimental techniques for measuring the rates of biochemical reactions, including association and dissociation reactions. These include surface plasmon resonance [4, 5], spectroscopic methods (e.g., atomic force spectroscopy, circular dichroism, or fluorescence-based approaches) [6–10], kinetic capillary electrophoresis [11, 12], radiolabeling combined with filtration/dialysis [13, 14] and NMR [15]. Many of these techniques require the labeling of one of the binding partners, their attachment to a surface or some other manipulation of the system, which can complicate the interpretation of the kinetic data and, in some instances, influence the rates of the reactions being investigated [16].

Electrospray ionization mass spectrometry (ESI-MS) has emerged as an important addition to the arsenal of techniques available for measuring the kinetics of chemical and biochemical reactions [17–28]. The ESI-MS approach is attractive as there is no requirement for labeling or immobilization since the identity of reactants and products and, possibly intermediates, can usually be established directly from the measured mass-to-charge ratios (m/z) [18, 29]. Moreover, ESI-MS analysis allows for multiple reactions to be monitored simultaneously, a feature not associated with most kinetic assays. The determination of reaction rates by ESI-MS analysis normally follows one of two general strategies: on-line (real-time) monitoring of the reaction mixture, and off-line analysis, usually following a quench step that stops the reaction. The advantage of the on-line approach is that it allows, in principle, for direct analysis of

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the time-dependent distribution of reactants, intermediates, and products. The minimum acquisition time for an ESI mass spectrum, which is typically in the s to min range (although it varies between instruments and the nature of the sample being analyzed), places restrictions on the speed of reactions that can be reliably analyzed using the on-line approach. For this reason, real-time ESI-MS kinetic measurements are most commonly applied to relatively slow reactions, with time-scales>min. However, there are examples where ESI-MS has been successfully applied to relatively fast reactions, in the ms to s range [17, 18, 20, 22, 24, 25]. The measurement of fast kinetics typically requires the use of rapid mixing systems, such as a continuous-flow [17, 18, 20, 22], rapid quenched-flow apparatus [24], or stopped-flow [25, 26]. The off-line approach is generally easier to implement and affords greater flexibility in terms of the experimental conditions under which the reactions are carried out. For example, this approach is suitable for the analysis of enzyme kinetics under solution conditions that are not amenable to direct ESI-MS analysis, such as high concentrations of salts or non-volatile buffers (e.g., PBS, citrate, HEPES, or TRIS) that are commonly used to stabilize proteins and ensure relevance to physiological conditions. Following the quench step, the solvent composition can be altered in order to facilitate detection of reactants or products by ESI-MS. However, a limitation of the off-line approach is that information on the distribution of species present under the reaction conditions of interest may be lost.

ESI-MS has been used to study the reaction rates for a variety of non-covalent protein interactions, including protein-protein [19, 20, 30], protein–small molecule [31] and protein–metal ion complexes [32], as well as for other biological complexes, such as DNA duplexes [33, 34]. However, to the best of our knowledge, absolute values of k_{on} and k_{off} for protein–ligand interactions measured using this approach have not been previously reported. Here, we describe the application ESI-MS for quantifying k_{off} for the high affinity interaction between biotin (B) and a truncated form (containing residues 13–139) of wild-type (WT) streptavidin. Streptavidin is a homotetrameric protein complex (S_4) that is isolated from *Streptomyces avidinii* [35]. Each streptavidin subunit is organized into an eight-stranded β-barrel, with a binding site for B at one end [36]. The streptavidin–biotin interaction is one of the most stable in nature and the exceptionally high affinity (K_a of ~2.5 × $10^{13}M^{-1}$ at pH 7.4 and 25 °C) arises from an unusually small dissociation rate constant (5.4 × $10^{-6}s^{-1}$ at pH 7.4 and 25 °C) [13]. The origin of the slow dissociation kinetics has been the focus of many experimental and theoretical studies [13, 14, 37–40]. For example, the temperature dependence of k_{off} for the interaction between B and WT streptavidin has been compared with values measured for a variety of single site mutants in an effort to elucidate the influence of the specific amino acid side chains on the kinetic barrier to dissociation [13, 14, 41]. These data were measured using a radiolabeled B assay, whereby the release of bound B from (S_4 + 4B) complex was monitored in the presence of an excess of unlabeled B. In the present study, values of k_{off} for the sequential loss of B from the (S_4 + 4B) complex, at pH 7 and temperatures ranging from 15 to 45 °C, were measured using ESI-MS. Two different approaches were used to analyze the ESI-MS data, one based on the initial rate of change in the relative abundance of the (S_4 + 4B) species, the other based on nonlinear fitting of the time-dependent relative abundances of all free and B-bound S_4 species. The Arrhenius parameters determined from the k_{off} values measured by ESI-MS were compared with the values obtained using the radiolabeled B assay [14]. In addition to providing a quantitative measure of the dissociation rate constants, the direct ESI-MS measurements provide a definitive answer to the question of whether the sequential binding of B to S_4 occurs in a cooperative or noncooperative fashion.

Experimental

Streptavidin and Biotin

The plasmid for natural core streptavidin (containing residues 13–139 of WT streptavidin, MW 13 271 Da) was a gift from Professor P. Stayton (University of Washington). Streptavidin was expressed in *E. coli* and purified using procedures described elsewhere [42]. Solutions of purified S_4 were exchanged directly into 100 mM aqueous ammonium acetate buffer using an Amicon microconcentrator with a MW cut-off of 10 kDa and lyophilized. Stock solutions of S_4 (100 μM) were prepared by dissolving a known amount of lyophilized streptavidin into 100 mM ammonium acetate and stored at –20 °C until needed. Biotin (B, MW 244.3 Da) was purchased from Sigma-Aldrich Canada (Oakville, Canada). The stock solution of B (800 μM) was prepared by dissolving B in Milli-Q water. All stock solutions were stored at –20 °C until needed.

Mass Spectrometry

All measurements were performed using an Apex Qe 9.4 T Fourier-transform ion cyclotron resonance (FTICR) mass spectrometer (Bruker, Billerica, MA, USA). Nanoflow ESI (nanoESI) was performed using borosilicate tubes (1.0 mm o.d., 0.68 mm i.d.), pulled to ~5 μm o.d. at one end using a P-97 micropipette puller (Sutter Instruments, Novato, CA, USA). The electric field required to spray the solution in positive ion mode was established by applying a voltage of 1.0–1.3 kV to a platinum wire inserted inside the glass tip. The solution flow rate was typically ~20 $nL\,min^{-1}$. Details of the instrumental and experimental conditions typically used for quantifying protein–ligand interactions can be found elsewhere [43].

Kinetic Measurements

For the kinetic measurements, the reaction mixtures were prepared by mixing aliquots of the stock solutions to achieve the desired concentrations of S_4 (10 μM), B (10–26 μM) and ammonium acetate (5 mM). The reaction

mixtures were kept at constant temperature (15–45 °C) using a water bath (Colora, Germany). Aliquots of the reaction mixtures were removed at specific reaction times (t) and analyzed by ESI-MS. Three ESI mass spectra were measured for each aliquot. An acquisition time of approximately 1 min was used for each mass spectrum.

Data Analysis

Assuming that the four ligand binding sites of S_4 are kinetically equivalent and independent, vide infra, the apparent rate constants for ligand association and dissociation reactions ($k_{on,i}$ and $k_{off,(i+1)}$, respectively) for each (S_4 + iB) species Equation (1) are related to the intrinsic (microscopic) rate constants (k_{on} and k_{off}) through statistical factors, which reflect the number of free and occupied binding sites, Equations (2a) and (2b):

$$(S_4 + iB) + B \underset{k_{off,(i+1)}}{\overset{k_{on,i}}{\rightleftarrows}} (S_4 + (i+1)B) \tag{1}$$

$$k_{on,i} = (4 - i)k_{on} \tag{2a}$$

$$k_{off,(i+1)} = (i+1)k_{off} \tag{2b}$$

It follows that the rate of change of the concentration of each (S_4 + iB) species can be described by Equations (3a)–(3e):

$$\frac{d([S_4])}{dt} = -4k_{on}[B][S_4] + k_{off}[S_4 + B] \tag{3a}$$

$$\frac{d([S_4+B])}{dt} = -\left(3k_{on}[B] + k_{off}\right)[S_4 + B] + 4k_{on}[B][S_4] + 2k_{off}[S_4 + 2B] \tag{3b}$$

$$\frac{d([S_4 + 2B])}{dt} = -\left(2k_{on}[B] + 2k_{off}\right)[S_4 + 2B] + 3k_{on}[B][S_4 + B] + 3k_{off}[S_4 + 3B] \tag{3c}$$

$$\frac{d([S_4 + 3B])}{dt} = -\left(k_{on}[B] + 3k_{off}\right)[S_4 + 3B] + 2k_{on}[B][S_4 + 2B] + 4k_{off}[S_4 + 4B] \tag{3d}$$

$$\frac{d([S_4 + 4B])}{dt} = -4k_{off}[S_4 + 4B] + k_{on}[B][S_4 + 3B] \tag{3e}$$

where $[S_4 + iB]$ is the concentration of the (S_4 + iB) species and [B] is the concentration of free B.

Because the rate of association of B to S_4 is very high, [B] will be extremely small when substoichiometric amounts of ligand are used (which is the case in the present study). Consequently, it is reasonable to assume that [B] exists at a steady-state over the course of the entire reaction. Therefore, the ik_{on}[B] terms can be approximated as ik_1, where k_1 is a pseudo first-order rate constant. Equations (3a)–(3e) can then be rewritten in terms of the normalized abundances $\left(A_{R(S_4 + iB)}\right)$ of the (S_4 + iB) species, Equations (4a)–(4e):

$$\frac{dA_{R\,S_4}}{dt} = -4k_1 A_{R\,S_4} + k_{off} A_{R(S_4 + B)} \tag{4a}$$

$$\frac{dA_{R(S_4 + B)}}{dt} = -\left(3k_1 + k_{off}\right)A_{R(S_4 + B)} + 4k_1 A_{RS_4} + 2k_{off} A_{R(S_4 + 2B)} \tag{4b}$$

$$\frac{dA_{R(S_4 + 2B)}}{dt} = -\left(2k_1 + 2k_{off}\right)A_{R(S_4 + 2B)} + 3k_1 A_{R(S_4 + B)} + 3k_{off} A_{R(S_4 + 3B)} \tag{4c}$$

$$\frac{dA_{R(S_4 + 3B)}}{dt} = -\left(k_1 + 3k_{off}\right)A_{R(S_4 + 3B)} + 2k_1 A_{R(S_4 + 2B)} + 4k_{off} A_{R(S_4 + 4B)} \tag{4d}$$

$$\frac{dA_{R(S_4 + 4B)}}{dt} = -4k_{off} A_{R(S_4 + 4B)} + k_1 A_{R(S_4 + 3B)} \tag{4e}$$

As described below, under the solution conditions used in the present study, there is a significant difference in the ligand association and dissociation rates immediately upon mixing S_4 and B [9, 13, 14]. Because of this and the fact that the initial concentration of B is less than the total concentration of binding sites, mixing S_4 with B initially produces a non-equilibrium distribution of (S_4 + iB), one that favors the S_4 and (S_4 + 4B) species. As the reaction proceeds, the relative abundance of (S_4 + 4B) will decrease and system will eventually achieve an equilibrium distribution of (S_4 + iB) species. Because $A_{R(S_4 + 3B)}$ is initially relatively small, the rate of change of $A_{R(S_4 + 4B)}$, described by Equation (4e), can be approximated by Equation (5):

$$\frac{dA_{R(S_4 + 4B)}}{dt} \approx -4k_{off} A_{R(S_4 + 4B)} \tag{5}$$

and k_{off} can be evaluated from a linear least squares fit of the plot of the natural logarithm of $A_{R(S_4 + 4B)}$ versus t, Equation (6):

$$\ln A_{R(S_4 + 4B)} = -4k_{off} \times t + b \quad (6)$$

where b is a constant that is equal to $\ln A_{R(S_4 + 4B)}$ at $t = 0$. In this case, $t = 0$ corresponds to the earliest reaction time for which ESI mass spectra were acquired. It should be noted that the magnitude of b depends on the initial concentrations of S_4 and B.

An alternative approach to determining k_{off} involves applying nonlinear regression analysis to the time-dependence of $A_{R(S_4 + iB)}$ for each (S_4 + iB) species. This approach is more general than the initial rate method described above since there are no simplifying assumptions needed and k_1, in addition to k_{off}, can be determined. Moreover, this approach is not limited to data measured early in the reaction. In fact, inclusion of data measured at longer times, where the system is approaching equilibrium, enhances the reliability of the fitting procedure. Expressions for the time-dependent $A_{R(S_4 + iB)}$ for each (S_4 + iB) species are obtained by solving Equations (4a)–(4e) (as a system) using Maple 14 (Maplesoft, Waterloo, Canada). The experimental $A_{R(S_4 + iB)}$ values at $t = 0$ (the earliest time point measured) served as a boundary conditions. Shown in Supplementary Data is a set of solutions (functions) corresponding to experimental data acquired at 44.8 °C. Origin (OriginLab, Northampton, MA, USA) was used to fit the functions (with k_{off} and k_1 as adjustable parameters) to the experimental breakdown curves ($A_{R(S_4 + iB)}$ values plotted versus t). At each temperature, k_{off} and k_1 values were calculated for each (S_4 + iB) species; the reported k_{off} and k_1 values in Table 1 correspond to the average of these values.

The temperature dependence of the measured k_{off} values was analyzed according to the Arrhenius equation, Equation (7):

$$\ln(k_{off}) = -\frac{E_a}{RT} + \ln(A) \quad (7)$$

The activation energy (E_a) and pre-exponential factor (A) were calculated from the slope and intercept, respectively, of a linear least-squares fit of the plot of ln(k_{off}) versus 1/T.

Results and Discussion

Shown in Figure 1a–c are representative ESI mass spectra acquired in positive ion mode for a solution (pH 7 and 22.1 °C) of S_4 (10 μM) and B (14 μM) and ammonium acetate (5 mM) immediately after mixing (i.e., reaction time ~0 min), and after 112 min and 1602 min (1.1 d). In each mass spectrum, signals corresponding to the protonated (S_4 + iB)$^{n+}$ ions with $0 \le i \le 4$, at n = 12 – 16, are evident. Initially, the S_4^{n+} and (S_4 + 4B)$^{n+}$ ions represent the dominant species present (Figure 1a). The observation of predominantly free and fully ligand-bound protein shortly after mixing B with S_4 is consistent with results of Sano and Cantor [44]. These authors used gel electrophoresis to analyze solutions of B and S_4, immediately after mixing, and observed only two major bands, which corresponded to S_4 and (S_4 + 4B) [44]. The authors interpreted these results as evidence of cooperative ligand binding [44]. However, the observation of abundant S_4 and (S_4 + 4B) in the ESI mass spectra does not necessarily imply cooperative binding of B to S_4. Instead, mixing of S_4 and B could lead initially to a non-equilibrium distribution of streptavidin-biotin species due to the fast association kinetics and extremely slow dissociation kinetics. The latter explanation finds support in the observation that the distribution of (S_4 + iB) species changes at longer reaction times. For example, after 112 min, abundant signal is observed for all five of the (S_4 + iB) species (i.e., with i from 0 to 4) although S_4 remains the dominant species detected (Figure 1b); after 1602 min, the (S_4 + B) species dominates (Figure 1c). At much longer times, a constant distribution of (S_4 + iB) species is observed, indicating that an equilibrium distribution of (S_4 + iB) species was reached. As an example, shown in Figure 1d is a representative ESI mass spectrum acquired after 13080 min (9 d). Notably, the measured distribution of (S_4 + iB) species agrees with the distribution expected in the case of four identical and independent ligand binding sites, each with a microscopic K_a of $2.5 \times 10^{13} M^{-1}$ (at pH 7.4 and 25 °C) (Figure 1e) [13]. These results establish, unambiguously, that B binding to S_4 is not a cooperative process, in agreement with the findings of Jones and Kurzban [45] and Fidelio and co-workers [46], and that the binding sites are thermodynamically equivalent and independent. It is also concluded that the apparent cooperative distributions of the (S_4+iB) species observed at short reaction times are, in fact, of kinetic and not thermodynamic origin.

Table 1. Microscopic Rate Constants (k_{off}) for the Dissociation of the Streptavidin-Biotin Interaction at pH 7 and Temperatures Ranging from 15 to 45 °C Measured Using Direct ESI-MS Analysis [a,b]

$[S_4]_o$ (μM)	$[B]_o$ (μM)	T (°C)	k_{off} (s^{-1})[a] Linear fitting	k_{off} (s^{-1}) [b] Nonlinear fitting	k_1 (s^{-1})[b] Nonlinear fitting
10	20	15.3	$(1.1\pm0.1)\times10^{-6}$	$(1.3\pm0.7)\times10^{-6}$	$(2.3\pm0.8)\times10^{-6}$
10	14	22.1	$(4.1\pm0.1)\times10^{-6}$	$(5.5\pm0.3)\times10^{-6}$	$(2.8\pm0.9)\times10^{-6}$
10	10	30.5	$(1.8\pm0.1)\times10^{-5}$	$(2.1\pm0.1)\times10^{-5}$	$(8.7\pm0.3)\times10^{-6}$
10	10	36.2	$(5.0\pm0.2)\times10^{-5}$	$(5.1\pm0.1)\times10^{-5}$	$(1.8\pm0.3)\times10^{-5}$
10	10	44.8	$(1.6\pm0.1)\times10^{-4}$	$(2.5\pm0.2)\times10^{-4}$	$(8.4\pm0.7)\times10^{-5}$

[a] k_{off} was obtained from the slope (k_{off}=1/4 slope) of a linear least squares fit of the plot of the natural logarithm of $A_{R(S_4+4B)}$ versus t. Reported errors correspond to one standard deviation.
[b] At each temperature, k_{off} and k_1 were obtained from nonlinear regression analysis of the time-dependent relative abundance of each of the (S_4+iB) species. The reported k_{off} and k_1 values correspond to the average of these values and errors are one standard deviation.

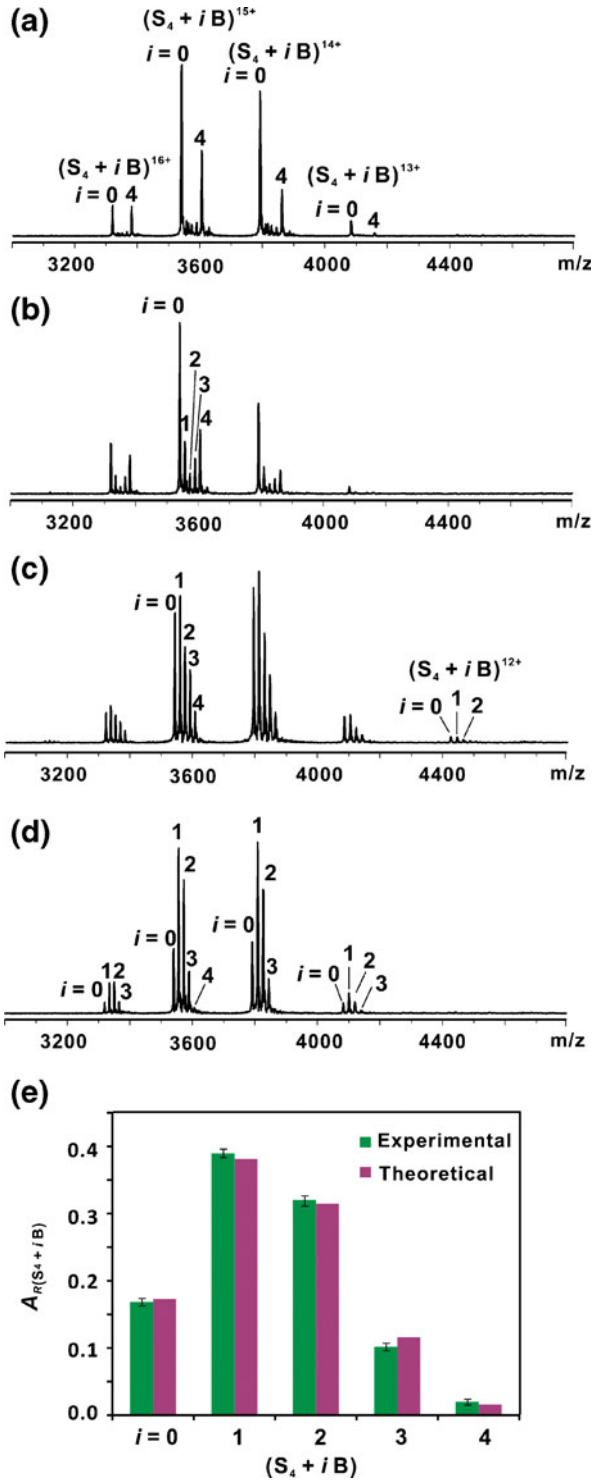

Figure 1. ESI mass spectra acquired for an aqueous ammonium acetate (5 mM) solution of S_4 (10 μM) and B (14 μM) at 22.1 °C and pH 7 and different reaction times (**a**) 0 s, (**b**) 112 min, (**c**) 1602 min (1.1 d), and (**d**) 13080 min (9 d). (**e**) Normalized distribution of (S_4 + i B) species, where i = 0 – 4, determined from the ESI mass spectrum shown in (**d**). The reported errors correspond to one standard deviation and were determined from three replicate measurements. Also shown is the calculated distribution for four equivalent ligand binding sites, each with a K_a of 2.5 × $10^{13}M^{-1}$

As noted in the Data Analysis section, two different approaches were used to quantify k_{off}. One approach is based on the initial rate of change of $A_{R(S_4 + iB)}$. Shown in Figure 2a are plots of the natural logarithm of $A_{R(S_4 + iB)}$ versus t, measured at the reaction temperatures indicated. Importantly, the plots exhibit excellent linearity. This result indicates that neglect of the ligand association reaction involving (S_4 + 3B) to $A_{R(S_4 + 4B)}$ in Equation (4e) is a reasonable assumption. The k_{off} values calculated at each reaction temperature are listed in Table 1. Notably, the value of 5.0 × $10^{-5}s^{-1}$ determined at 36.2 °C agrees very well with the reported value of 4.1 × $10^{-5}s^{-1}$, which was measured at 37 °C [14]. An alternative approach used to determine k_{off} involves

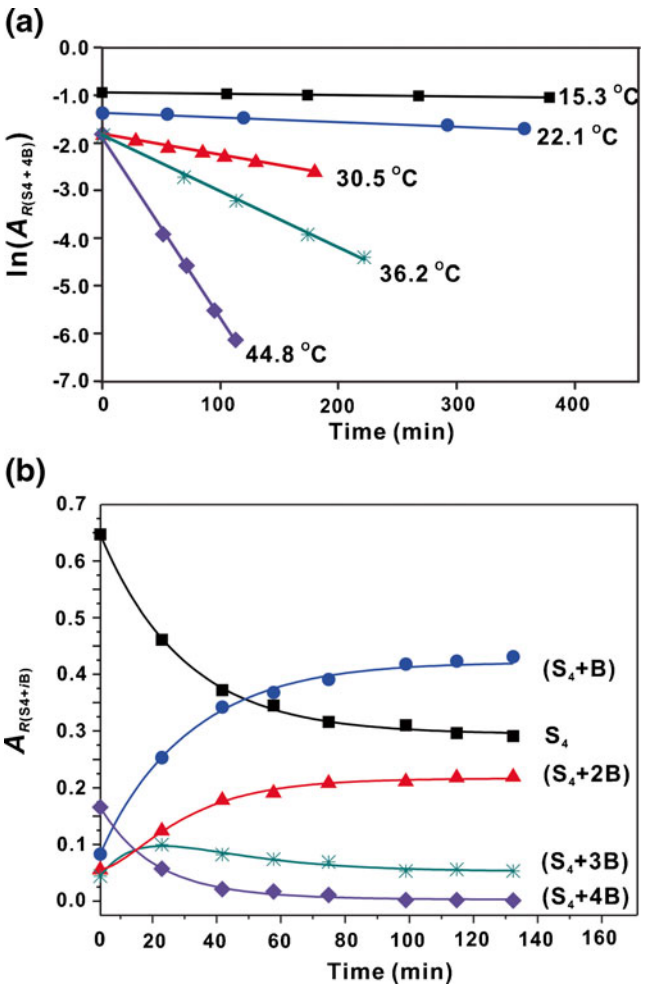

Figure 2. (**a**) Plots of the natural logarithm of $A_{R(S_4 + iB)}$ versus reaction time measured by ESI-MS for neutral aqueous ammonium acetate (5 mM) solutions of S_4 (10 μM) and B (10–20 μM) at 15.3 °C, 22.1 °C, 30.5 °C, 36.2 °C, and 44.8 °C. The solid curves represent linear least squares fits of the experimental data. (**b**) Plots of $A_{R(S_4 + iB)}$ versus reaction time measured by ESI-MS neutral aqueous ammonium acetate (5 mM) solution of S_4 (10 μM), B (10 μM) at 44.8 °C. The solid curves were determined from nonlinear regression analysis to the time-dependent $A_{R(S_4 + iB)}$ values

nonlinear fitting of the solutions of Equations (4a)–(4e) to the time-dependent $A_{R(S_4 + iB)}$ values. Plotted in Figure 2b are the $A_{R(S_4 + iB)}$ values measured at 44.8 °C and the curves obtained from the nonlinear fitting procedure. It can be seen that the calculated curves describe the experimental data very well. The average kinetic parameters, determined at each temperature investigated, are summarized in Table 1. Notably, the k_{off} values determined by the two different methods agree very well, within a factor of 2, at all of the temperatures investigated. For example, a k_{off} value of $5.0 \times 10^{-5} s^{-1}$ was determined at 36.2 °C with the nonlinear fitting method, which is indistinguishable from the value of $5.1 \times 10^{-5} s^{-1}$ determined from the initial rates approach. With the nonlinear fitting method, the k_1 ($=k_{on}[B]$) terms were also established at each temperature investigated (Table 1). Although [B] is not accurately known (and, in fact, varies over the course of the reaction), it is nevertheless possible to estimate k_{on} by assuming that [B] (at all reaction times) is similar in magnitude to the $[B]_{eq}$, the concentration of free B at equilibrium. Following this approach, k_{on} was estimated to be $1.3 \times 10^8 M^{-1} s^{-1}$ at 22.1 °C using a $[B]_{eq}$ of $2.2 \times 10^{-14} M$, which was calculated for a solution of S_4 (10 μM) and B (14 μM) and a microscopic K_a of $2.5 \times 10^{13} M^{-1}$ [13]. This value of k_{on} agrees reasonably well with a value of $4.5 \times 10^7 M^{-1} s^{-1}$, which was determined from measurements carried out at ambient temperature (not specified) using droplet microfluidics integrated with a confocal fluorescence detection system [9].

Shown in Figure 3 are the Arrhenius plots constructed from the k_{off} values determined from the ESI-MS data using the two different data analysis approaches. The corresponding Arrhenius parameters (E_a, A) are listed in Table 2. Also shown in Figure 3 is the calculated curve based on the reported activation enthalpy and entropy, for the loss of B from the (S_4 + 4B) complex in aqueous solution at pH 7.4 [14]. Inspection of Figure 3 (and Table 2) reveals that the Arrhenius plots for the loss of B from the (S_4 + 4B) complex from linear and nonlinear fitting are similar, with E_a values of 30.4 ± 0.7 and 31.7 ± 0.8 kcal mol^{-1}, respectively. Moreover, the E_a values agree with the reported value of 31.0 ± 0.2 kcal mol^{-1} [14]. These findings indicate that both approaches to the analysis of the time-resolved ESI-MS data can provide a reliable determination of the temperature-dependence of k_{off}. However, the nonlinear fitting approach is more general and, in principle, can be applied in cases where sequential ligand binding exhibits cooperativity or where multiple, nonequivalent binding sites are present.

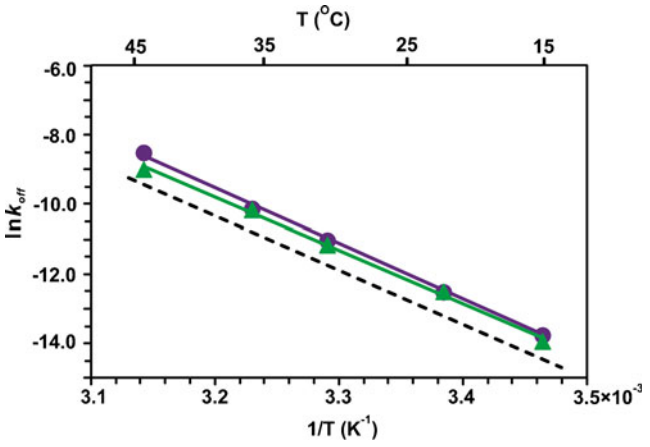

Figure 3. Arrhenius plots the loss of B from the (S_4 + 4B) complex at pH 7 constructed from k_{off} values measured by ESI-MS [linear fitting (▲), nonlinear fitting (●)] and corresponding plot (– – –) calculated from the activation enthalpy and entropy reported in [14]

Table 2. Arrhenius Activation Parameters (E_a, A) for the Loss of B from the (S_4 + 4B) Complex Determined from k_{off} Values Measured by ESI-MS (Using Linear and Nonlinear Data Analysis Methods) at pH 7, and Arrhenius Parameters Measured at pH 7.4 Using a Radiolabeled Biotin Assay

	E_a (kcal mol^{-1})	A (s^{-1})
ESI-MS (linear fitting)	30.4±0.7[a]	$10^{17.1 \pm 0.5}$ [a]
ESI-MS (nonlinear fitting)	31.7±0.8[a]	$10^{18.2 \pm 0.6}$ [a]
Radiolabeled biotin assay	31.0±0.2[b]	$10^{17.3 \pm 0.1}$ [b]

[a]Reported errors correspond to one standard deviation.
[b]Values calculated from the activation enthalpy and entropy reported in [14].

The streptavidin–biotin interaction is unusually kinetically stable and it takes several days to achieve an equilibrium distribution of (S_4 + iB) species at the temperatures investigated. However, it is important to note that this same experimental approach could be applied, in an on-line fashion, to determine k_{off} and, in principle, k_{on} for protein–ligand interactions that require less time to reach an equilibrium distribution. Given that ~1 min is typically required to acquire an ESI mass spectrum (with a high signal-to-noise ratio) for solutions of protein–ligand complexes [47], it should be possible to apply this approach to complexes that take >10 min (under the desired solution conditions) to reach equilibrium. Although this approach will not be suitable for all protein–ligand complexes (those that exhibit both fast association and dissociation kinetics), the kinetic parameters for many protein–ligand interactions are expected to be accessible with this technique [48, 49].

Conclusion

In summary, ESI-MS measurements have been used to quantify k_{off} for the sequential loss of B from the (S_4 + 4B) complex at pH 7 and temperatures ranging from 15 °C to 45 °C. Two different general strategies for data analysis were considered, one based on the initial rate of dissociation of the (S_4 + 4B) complex, and the other employing nonlinear fitting of the time-dependent $A_{R(S_4 + iB)}$ values of the (S_4 + iB) species. The two methods were found to yield k_{off} values that agree within a factor of two. Importantly, the dissociation E_a values measured by ESI-MS agree within 1 kcal mol^{-1} with the reported value, which was measured using a radiolabeled B assay. In addition to providing a quantitative measure of k_{off} at the temperatures investigated, the ESI-MS

measurements also revealed, unambiguously, that sequential B binding to S_4 occurs in a non-cooperative fashion and that the four ligand binding sites are kinetically and thermodynamically equivalent and independent.

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