

# Spectroscopic investigation of the interaction between rifabutin and bovine serum albumin

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## Abstract

The binding of rifabutin (RB) to bovine serum albumin (BSA) was investigated by fluorescence spectroscopy and circular dichroism (CD). RB effectively quenched the intrinsic fluorescence of BSA via a combination of static and dynamic quenching. The thermodynamic parameters,  $\Delta H^\circ$  and  $\Delta S^\circ$  were estimated to be  $-5.14 \text{ kJ mol}^{-1}$ ,  $+120.44 \text{ J mol}^{-1} \text{ K}^{-1}$  according to the van't Hoff equation. This indicates that hydrophobic interaction plays a major role in stabilizing the RB–BSA complex. The high order of magnitude of  $k_q$  ( $10^{15}$ ) for RB–BSA suggests that the process of energy transfer occurs through intermolecular interaction. Binding studies in the presence of fluorescence probe, 8-anilino-1-naphthalein-sulphonic acid (ANS), showed that RB competed with ANS for hydrophobic sites on the surface of BSA. The effect of metal ion on the binding constant of RB–BSA complex varied with metal ion.  $\text{Cu}^{2+}$  and  $\text{Ca}^{2+}$  increased the binding constant, whereas  $\text{Zn}^{2+}$  and  $\text{Mg}^{2+}$  decreased the binding efficacy of RB to BSA. Synchronous fluorescence spectra and CD data revealed that RB induced the conformational change of BSA.

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## 1. Introduction

Serum albumins are one of the most abundant proteins in blood plasma. Many drugs are transported in the blood upon binding to albumin. The binding ability of drug–albumin in blood stream may have a significant impact on distribution, free concentration, and metabolism of drug [1,2]. Thus, it is important and necessary to study the interaction of drug with serum albumins at molecular level [3–6].

Rifabutin (RB) (Scheme 1) is a potent semisynthetic spiro-piperidyl-rifamycin derivative. It possesses a broad spectrum of antibacterial activity and is particularly active against mycobacterium tuberculosis, including rifampicin-resistant strains, and atypical mycobacteria. The antimicrobial action of the RB results from the inhibition of bacterial DNA-dependent RNA polymerase. Prophylactic treatment with RB was shown to decrease the incidence of mycobacterium avium complex (MAC) by approximately 50% in patients infected with human immunodeficiency virus. RB exhibits lower toxicity and have a

longer half-life than rifampicin [7,8]. Previous studies suggested that protein binding of rifamycin antibacterials, e.g. rifampicin, rifabutin and rifapentine, may be a key parameter in their pharmacodynamics [9]. However, the binding mode and binding mechanism of RB with albumin are not clear so far. Thus, the interaction of RB with albumin needs to be investigated to provide binding parameters which are useful in studying the pharmacological response and design of dosage forms of RB.

Spectroscopic method has been widely applied in investigating drug binding with albumin under physiological conditions because of its accuracy, sensitivity, rapidity and convenience of usage [10–12]. It can reveal the accessibility of drugs to albumin's fluorophores, help understand the binding mechanisms of albumin–drug and provide information of the structural features that determine the therapeutic effectiveness of drug.

In this study, the interaction of RB with bovine serum albumin (BSA) was investigated via spectroscopic method. Fluorescence spectroscopy was employed to understand the quenching mechanism of RB–BSA binding as well as the impacts of common metal ions on RB–BSA interaction. Furthermore, binding of RB with BSA in the presence of fluorescence probe, 8-anilino-1-naphthalein-sulphonic acid (ANS), was conducted. Effects of RB on conformational changes of BSA were investigated by

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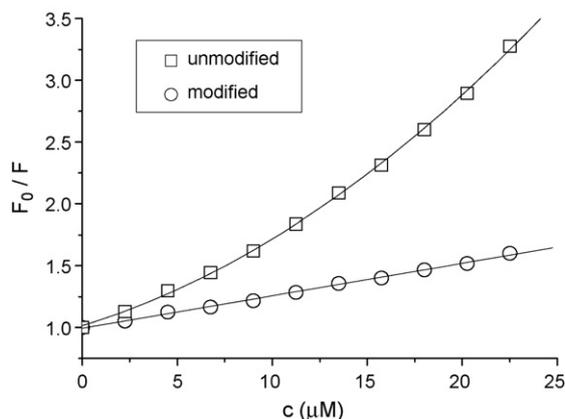


Fig. 2. Stern–Volmer and modified Stern–Volmer plots of RB interaction with BSA at 298 K;  $C_{\text{BSA}} = 10 \mu\text{M}$ ;  $\lambda_{\text{ex}} = 295 \text{ nm}$ .

Fluorescence intensity data was then analyzed according to Stern–Volmer quenching equation [13]:

$$\frac{F_0}{F} = 1 + K_{\text{sv}}[Q] \quad (1)$$

where  $F_0$  and  $F$  are the steady state fluorescence intensities of BSA at 343 nm before and after the addition of quencher (RB).  $K_{\text{sv}}$  and  $[Q]$  are the Stern–Volmer dynamic quenching constant and the concentration of quencher RB, respectively.

Stern–Volmer plot of BSA with RB at 298 K is shown in Fig. 2. The plot shows a positive deviation (concave towards the y axis), suggesting the presence of a combination of static and dynamic quenching by the same fluorophore. According to Eftink and Ghiron [14,15], the upward curvature in the Stern–Volmer plot indicates that both tryptophan residues of BSA are exposed to the quencher. Accordingly, a modified Stern–Volmer equation that describes quenching data for both dynamic and as static quenching was applied [14]:

$$\frac{F_0}{F} = 1 + K_{\text{sv}}[Q] \exp(V[Q]) \quad (2)$$

where  $V$  is the static quenching constant and the value of  $V$  can be obtained from Eq. (2) by plotting  $F_0/F \exp(V[Q]) - 1$  versus  $[Q]$  for varying  $V$  until a linear plot is acquired. The  $K_{\text{sv}}$  can be then obtained from slope of  $F_0/F \exp(V[Q]) - 1$  versus  $[Q]$  plot. Values of  $V$  and  $K_{\text{sv}}$  at three different temperatures (298, 304 and 310 K) are consequently presented in Table 1.

Table 1  
Static and collisional quenching constants for RB–BSA system at different temperatures

$T$ (K)	$V$ ( $\times 10^6 \text{ M}^{-1}$ )	$K_{\text{sv}}$ ( $\times 10^6 \text{ M}^{-1}$ )	$R^2$
298	3.18	2.63	0.9979
304	2.95	1.95	0.9938
310	1.99	1.83	0.9973

$C_{\text{BSA}} = 10 \mu\text{M}$ ,  $\lambda_{\text{ex}} = 295 \text{ nm}$ .

As for a bimolecular quenching process, Eq. (3) is employed for the evaluation of the quenching rate constant  $k_q$ :

$$k_q = \frac{K_{\text{sv}}}{\tau_0} \quad (3)$$

where  $\tau_0$  is the average lifetime of biomolecules in the absence of quencher and the typical value of  $\tau_0$  for tryptophan fluorescence in BSA is  $10^{-9} \text{ s}$  [11]. The  $k_q$  value was thus calculated to be of the order of  $10^{15} \text{ M}^{-1} \text{ s}^{-1}$ . The  $k_q$  depends on the probability of a collision between fluorophore and quencher and it is a measurement of exposure of tryptophan residues to drugs. This probability depends on their rate of diffusion ( $D$ ), their size and concentration as shown in the following equation:

$$k_q = 4\pi a D N a \times 10^{-3} \quad (4)$$

where  $D$  is the sum of diffusion coefficients of quencher and fluorophore,  $a$  the sum of molecular radii and  $Na$  is the Avogadro's number. Upper limit of  $k_q$  expected as a diffusion-controlled bimolecular process is  $10^{10} \text{ M}^{-1} \text{ s}^{-1}$  [16]. High magnitude of  $k_q$  observed here ( $10^{15} \text{ M}^{-1} \text{ s}^{-1}$ ) can only occur by the process of energy transfer, indicating that the quenching of BSA fluorescence by RB is through intermolecular interaction forces [9].

### 3.2. Analysis of binding equilibria

Fluorescence intensity data can also be used to obtain the binding constant ( $K_a$ ) and the number of binding sites ( $n$ ). Equilibrium between free and bound molecules is given by Eq. (5) providing that small molecules bind independently to a set of equivalent sites on a macromolecule [16,17]:

$$\log \frac{(F_0 - F)}{F} = \log K_a + n \log [Q] \quad (5)$$

where  $K_a$  is the binding constant or the apparent association constant for drug–protein interaction, and  $n$  is the number of binding sites. Values of  $K_a$  and  $n$  can thereby be determined from the intercept and slope by plotting  $\log(F_0 - F)/F$  versus  $\log[Q]$ . As can be seen in Table 2, the value of  $K_a$  as obtained is of the order of  $10^5$ , which indicates that there is a strong interaction between RB and BSA. Value of  $n$  is approximately equal to 1, indicating that there is one class of binding site for RB towards BSA.

Table 2  
Apparent binding constants  $K_a$  and binding sites  $n$  of the interaction of RB with BSA at different temperatures

$T$ (K)	$K_a$ ( $\times 10^5 \text{ M}^{-1}$ )	$n$	$R^2$
298	10.8	1.23	0.9961
304	5.43	1.19	0.9929
310	3.14	1.17	0.9973

$C_{\text{BSA}} = 10 \mu\text{M}$ ,  $\lambda_{\text{ex}} = 295 \text{ nm}$ .

### 3.3. Interacting forces between BSA and RB

Thermodynamic parameters relying on temperatures were analyzed to characterize the acting forces between drug and BSA. Basically, four types of interactions play vital roles in protein–drug binding, that is, hydrogen bonds, van der Waals forces, electrostatic forces, and hydrophobic interactions. Thermodynamic parameters, free energy changes ( $\Delta G^\circ$ ) enthalpy changes ( $\Delta H^\circ$ ) and entropy changes ( $\Delta S^\circ$ ) of interactions are essential to interpret the binding mode. For the purpose of clarifying interaction of RB with BSA, the temperature dependence of binding constant was resulted from binding studies carried out at three different temperatures: 298, 304 and 310 K. When enthalpy change ( $\Delta H^\circ$ ) does not vary significantly in the temperature range studied, both enthalpy change ( $\Delta H^\circ$ ) and entropy change ( $\Delta S^\circ$ ) can be determined from van't Hoff equation:

$$\ln K = -\frac{\Delta H^\circ}{RT} + \frac{\Delta S^\circ}{R} \quad (6)$$

In Eq. (6),  $K$  corresponds to the binding constant at specific temperature and  $R$  is the gas constant.  $\Delta H^\circ$  and  $\Delta S^\circ$  can be calculated from slopes and ordinates of the van't Hoff relationship.  $\Delta G^\circ$  was consequently obtained according to the following equation:

$$\Delta G^\circ = \Delta H^\circ - T\Delta S^\circ \quad (7)$$

Values of  $\Delta G^\circ$ ,  $\Delta H^\circ$ , and  $\Delta S^\circ$  are summarized and listed in Table 3.

As can be seen in Table 3, the negative values of  $\Delta G^\circ$  and  $\Delta H^\circ$  along with the positive values of  $\Delta S^\circ$  are obtained for the RB–BSA interaction. Negative values of  $\Delta G^\circ$  reveal that the binding process is spontaneous. Positive values of  $\Delta S^\circ$  are evidence of hydrophobic interactions [18]. Moreover, a positive value of  $\Delta S^\circ$  along with a negative  $\Delta H^\circ$  value is characteristic of electrostatic interactions in aqueous solution. Thus, it is more likely that hydrophobic and electrostatic interactions are involved in binding process. Nevertheless, it is less possible that RB interacting with albumin through electrostatic interactions under our experimental conditions. Consequently, hydrophobic interaction plays a major role in the binding of RB with albumin.

### 3.4. Binding studies in the presence of ANS

It is known that ANS quenches the intrinsic fluorescence of BSA through hydrophobic and electrostatic interactions, and on the other hand, the fluorescence of ANS itself increases due to transfer of ANS from an aqueous to non-polar environment as a

Table 3  
Apparent binding constants  $K_a$  and thermodynamic parameters of RB–BSA interaction

$T$ (K)	$K_a$ ( $\times 10^5 \text{ M}^{-1}$ )	$\Delta G^\circ$ (kJ mol $^{-1}$ )	$\Delta H^\circ$ (kJ mol $^{-1}$ )	$\Delta S^\circ$ (J mol $^{-1}$ K $^{-1}$ )
298	10.8	−35.90	−5.14	120.44
304	5.43	−36.62		
310	3.14	−37.34		

result of hydrophobic interactions with BSA [19,20]. Therefore, ANS can be used as a fluorescence probe to understand the interaction of RB with BSA.

Fluorescence spectra of BSA upon addition of ANS/RB were first recorded upon excitation at wavelength of 295 nm. Fraction of bound ( $\theta$ ) was then determined according to equation as follows [21]:

$$\theta = \frac{F_0 - F}{F_0} \quad (8)$$

The value of  $\theta$  for ANS bound to BSA was calculated to be 82%. While for RB bound to BSA, the value of  $\theta$  was around 53% under the same conditions. This indicated that the interaction of ANS with BSA was stronger than that of RB with BSA.

Additionally, ANS–BSA interaction upon sequentially addition of RB was studied by recording fluorescence spectra of ANS in range of 390–550 nm upon excitation at 370 nm. It was observed that fluorescence intensity of ANS exhibited a slight decrease upon addition of RB. This is similar to the effect of rifampicin on the BSA–ANS interaction [9]. Thus RB, like rifampicin, may compete with ANS for binding to hydrophobic sites on the albumin surface.

### 3.5. Energy transfer between rifabutin and BSA

Föster's theory of non-radiative energy transfer was used as determining the distances between the BSA residue and RB bound to BSA. According to the Föster's theory, the energy transfer effect is not only related to the distance between the donor (tryptophan residue) and acceptor (RB), but also influenced by the critical energy transfer distance  $R_0$ , that is:

$$E = 1 - \frac{F}{F_0} = \frac{R_0^6}{R_0^6 + r^6} \quad (9)$$

where  $r$  is the distance between the acceptor and the donor, and  $R_0$  is the critical energy transfer distance, at which 50% of the excitation energy is transferred to the acceptor is defined by the following equation:

$$R_0^6 = 8.8 \times 10^{-25} k^2 N^{-4} \Phi J \quad (10)$$

In Eq. (10),  $k^2$  is the orientation factor related to the geometry of the donor–acceptor of dipole,  $N$  the refractive index of medium, and  $\Phi$  is the fluorescence quantum yield of the donor. Spectra overlap integral  $J$  between the donor emission spectrum and the acceptor absorbance spectrum is then calculated by the equation:

$$J = \frac{\sum F(\lambda)\varepsilon(\lambda)\lambda^4\Delta\lambda}{\sum \varepsilon F(\lambda)\Delta\lambda} \quad (11)$$

where  $F(\lambda)$  is the fluorescence intensity of fluorescence donor at wavelength of and  $\varepsilon(\lambda)$  is molar absorbance coefficient of the acceptor when wavelength is  $\lambda$ . Under experimental conditions, it had been noted that  $k^2 = 2/3$ ,  $N = 1.336$  and  $\Phi = 0.15$  for BSA [22].

The spectral overlap of UV absorption spectrum of RB and fluorescence emission spectrum of BSA is illustrated in

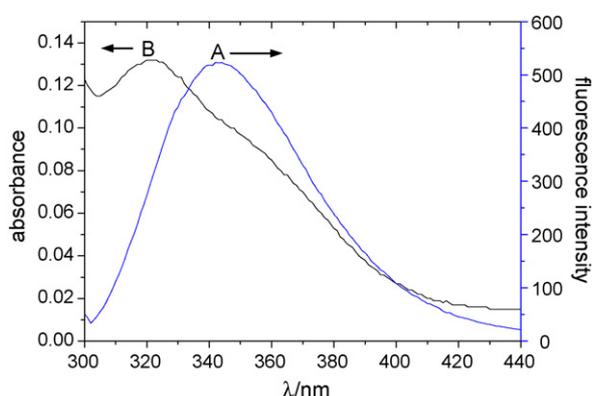


Fig. 3. Spectral overlap between (A) BSA fluorescence spectrum and (B) RB absorbance spectrum.  $C_{\text{BSA}} = 10 \mu\text{M}$ ,  $C_{\text{RB}} = 10 \mu\text{M}$ .

Table 4

Binding constants  $K_a$  of RB–BSA complex in the presence of various metal ions at 298 K

	$K_a (\times 10^5 \text{ M}^{-1})$	$R^2$
BSA–RB	10.8	0.9961
BSA–RB– $\text{Cu}^{2+}$	15.5	0.9916
BSA–RB– $\text{Zn}^{2+}$	8.12	0.9909
BSA–RB– $\text{Mg}^{2+}$	10.1	0.9952
BSA–RB– $\text{Ca}^{2+}$	15.3	0.9924

$C_{\text{BSA}} = 10 \mu\text{M}$ .

Fig. 3. It was then calculated that  $J = 1.29 \times 10^{-14} \text{ cm}^3 \text{ L mol}^{-1}$ ,  $R_0 = 2.63 \text{ nm}$ ,  $E = 0.422$ , and  $r = 2.77 \text{ nm}$ . As the distance of donor to acceptor for RB–BSA binding is in the 2–8 nm scale [23], the energy transfer from BSA to RB occurs with high probability.

### 3.6. Influences of common ions on binding constant

Metal ions, especially those of bivalent type, are vital to human body and playing an essentially structural role in many proteins based on coordinate bonds. The presence of metal ions in plasma may affect interaction of drugs with BSA.

Effects of common bivalent metal ions (e.g.  $\text{Cu}^{2+}$ ,  $\text{Zn}^{2+}$ ,  $\text{Mg}^{2+}$  and  $\text{Ca}^{2+}$ ) on binding constants of RB–BSA complex were investigated at 298 K. The values of binding constant  $K_a$  acquired in the present of metal ions are listed in Table 4.

It can be seen from Table 4 that the presence of  $\text{Cu}^{2+}$ ,  $\text{Ca}^{2+}$  ions increases the binding constant of RB–BSA complex, whereas, the binding constant between RB and BSA decreases to various degrees in the presence of  $\text{Zn}^{2+}$  and  $\text{Mg}^{2+}$ . The higher binding constant possibly results from the formation of metal ion–RB complexes via metal ion bridge [24]. This may prolong storage period of RB in blood plasma and enhance its maximum effects. On the contrary, the decrease in binding constant may due to the formation of metal ion–BSA complexes. The formation of metal ion–albumin complexes is likely to affect conformation of protein, which may influence RB binding kinetics and even inhibit RB–BSA binding.

### 3.7. Conformational investigations

Influences of RB on the conformational changes of BSA were assessed by synchronous fluorescence and CD. Synchronous fluorescence measurements provide information about the molecular microenvironment in the vicinity of the fluorophore functional groups. Synchronous fluorescence spectra were obtained by simultaneously scanning excitation and emission monochromators. As  $\Delta\lambda$  between excitation wavelength and mission wavelength is 15 nm, synchronous fluorescence offers characteristics of tyrosine residues, while when  $\Delta\lambda$  is 60 nm, it provides the characteristic information of tryptophan residues. Synchronous fluorescence spectra of BSA upon addition of RB gained at  $\Delta\lambda = 15$  and 60 nm are shown in Fig. 4.

As shown in Fig. 4, fluorescence intensity of both tryptophan and tyrosine decreases and a notable red shift at maximum emission upon addition of RB is observed, which indicates that the conformation of protein is changed. It is likely due to that the hydrophobic amino acid structure surrounding tryptophan and tyrosine residues in BSA tends to collapse slightly and thus tryptophan and tyrosine residues are exposed more to the aqueous phase.

Further evidence of conformational changes of BSA upon addition of RB was provided by CD data. CD is a sensitive technique to monitor conformational changes in protein upon interaction with ligand. CD spectra of BSA with various concentrations of RB are shown in Fig. 5. It is apparently

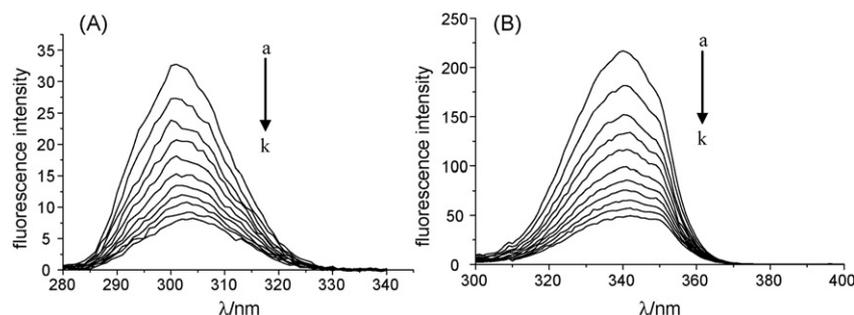


Fig. 4. Synchronous fluorescence spectra of BSA upon addition of RB at 298 K. (A)  $\Delta\lambda = 15 \text{ nm}$ , (B)  $\Delta\lambda = 60 \text{ nm}$ .  $C_{\text{BSA}} = 10 \mu\text{M}$ ;  $C_{\text{RB}}$  from (a) to (k): 0  $\mu\text{M}$  (a), 2.25  $\mu\text{M}$  (b), 4.5  $\mu\text{M}$  (c), 6.75  $\mu\text{M}$  (d), 9  $\mu\text{M}$  (e), 11.25  $\mu\text{M}$  (f), 13.5  $\mu\text{M}$  (g), 15.75  $\mu\text{M}$  (h), 18  $\mu\text{M}$  (i), 20.25  $\mu\text{M}$  (j) and 22.5  $\mu\text{M}$  (k).

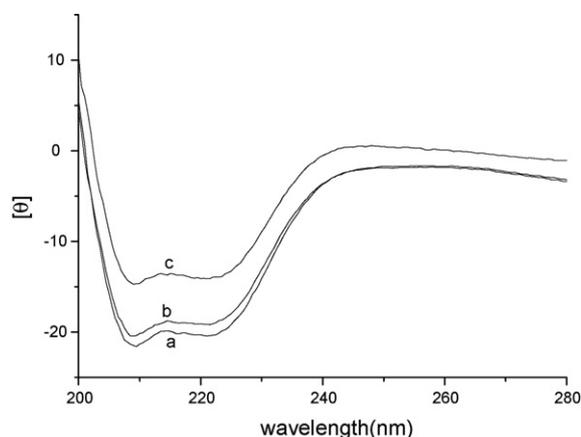


Fig. 5. CD spectra of BSA in the absence and presence of RB from 200 to 280 nm. (a)  $C_{\text{BSA}} = 1 \mu\text{M}$ , (b)  $C_{\text{BSA}} = 1 \mu\text{M}$ ,  $C_{\text{RB}} = 1 \mu\text{M}$ , and (c)  $C_{\text{BSA}} = 1 \mu\text{M}$ ,  $C_{\text{RB}} = 3 \mu\text{M}$ .

observed that CD spectral bands of BSA are at 208 and 222 nm, characteristic of a predominantly  $\alpha$ -helical structure of BSA [25]. The addition of RB, however, led to a decrease in band intensity along all wavelengths of CD spectra without any significant shift of the peaks, indicating that RB changes the secondary structure of BSA. Moreover, the decrease in negative ellipticity means that the peptide strand extended even more, while the hydrophobicity was decreased. This conclusion agrees with the synchronous fluorescence result.

#### 4. Conclusions

Interaction mechanism between RB and BSA was investigated by fluorescence spectroscopy and CD technique. The results show that RB is a strong quencher and interacts with BSA through a combination of dynamic and static quenching. The values of thermodynamic parameters  $\Delta H^\circ$ ,  $\Delta S^\circ$  and  $\Delta G^\circ$  at different temperatures demonstrate that the binding reaction is mainly entropy-driven and hydrophobic interactions play a major role in the reaction. Synchronous spectra and CD data reveal that RB could change the conformation of BSA. Moreover, the presence of  $\text{Cu}^{2+}$  and  $\text{Ca}^{2+}$  increases the binding constants of RB–BSA complex, this may prolong storage period of RB in blood plasma and enhance its maximum effects.

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