CHAPTER 5

EFFECT OF SODIUM DODECYL BENZENE
SULPHONATE ON FLOW PROPERTIES OF
SOLUBLE OVALBUMIN

INTRODUCTION

Viscosity is of great significance in the macromolecular chemistry amongst various transport properties like sedimentation, diffusion, viscosity etc. used for studying rheological nature of colloids. Two main reasons behind are :

(i) The property being measured is not only one of the most important measures of gross conformation but it reflects particle volume.

(ii) The measurement of viscosity of polymers in solution requires relatively simple instrumentation.

Interaction of proteins with surfactants is a great importance in the fields of industrial (cosmetics, paints, foods), biological and pharmaceutical sciences (1). Owing to the existence of nonpolar and ionic amino acids side chains in protein molecules, the formation of these complexe is driven by electrostatic interaction between the charged head groups of the surfactants and the oppositely charged units of the proteins, as well as by hydrophobic interaction between the alkyl chains and different parts of the proteins(2, 3).

The application of surfactants in the field of biochemistry has given importance to studies the nature of the interaction between protein and surface active agents in biological phenomena such as biological membrane (3) and protein solubilization. It has also suggested the surfactant-protein systems can be used as a model of biological membrane (4-7). This implies the interactions between surfactants and proteins are complex processes, involving different types of
intermolecular forces. Therefore, the ionic head groups of surfactants may bind to oppositely charged groups on the protein surface by electrostatic forces, whereas non-polar tail groups of surfactants may bind to non-polar sites on the protein surface through hydrophobic forces (8).

It is known in general that anionic surfactant interact strongly with proteins and form protein-surfactant complexes, which would induced the unfolding of proteins (9). The sensitivity of viscosity to molecular structure makes it useful for monitoring processes that result in overall protein conformation (10, 11). Similar interaction has been observed between coagulant protein and the anionic surfactant sodium bis (2-ethyl-1-hexyl) sulfosuccinate (AOT) when monitored by surface tension probe (12).

The interaction of SDS with Casein (13), transfusion gelatin (14) and ovalbumin (15) has been investigated with the help of viscometric method. Arora et al. have reported the interaction between triethanolamine lauryl sulphate (TEALS) and gelatin by viscometric method (16). The interaction between TEALS-bovine serum albumin and ovalbumin has been examined viscometrically (17).

The intrinsic viscosity values have been used to explain the changes produced due to unfolding of protein molecule in the presence of surfactant. Bovine serum albumin was found to be more reactive than ovalbumin. Singh et al. (18) have studied the interaction between anionic surfactants (SDS and CPB) and gliadin (a fraction of wheat protein) and the effect of pH and temperature on viscosity behaviours were also studied. Some other workers have also studied the interaction between surfactant and proteins (19-28). In order to extend knowledge of rheological phenomena, viscometric studies on soluble ovalbumin in presence of anionic surfactant, sodium dodecyl benzene sulphonate (SDBS) are made in this chapter. The average molecular weight and
the temperature co-efficient of interaction has been critically discussed at pH 7.50.

**EXPERIMENTAL**

**Reagents** : The soluble ovalbumin was prepared from ovalbumin (Sigma product) by the method of Smith and Back (as described in Chapter 1) and its concentration determined by drying a known aliquot in an air oven 105°C-110°C. Sodium dodecyl benzene sulphonate (SDBS) were purchased from Sigma Chemical Company. It was purified from acetone and its purity was checked by the method of Gold Smith (29). Its stock solutions was prepared in double distilled water. A solution of sodium acetate and acetic acid (BDH) used for making buffer of pH 5.80 and 1.0 M KCl (BDH) solution was used for maintaining the ionic strength at 0.15.

**pH-measurements** : These measurements were carried out as described in Chapter 2.

**Viscosity measurements** : Ostwald viscometer of relatively long capillary having flow time for water 65 second was used for viscosity measurement at temperature of 35°C at all pH’s and at 25°C, 30°C, 35°C and 40°C, at pH 7.50 in a water bath. Kinetic energy correction was found to be negligible. Viscometer stand was arranged in a manner that it was always situated in the same position in the bath. Protein and SDBS stock solutions were centrifuged at 16,000 rpm for 60 minutes to remove particulate matter. The densities of solvent and solutions were determined with the help of pyknometer. The viscosity values were calculated by the following relation.

\[
\eta_{\text{rel}} = \frac{\eta}{\eta_0} = \frac{t_d}{t_0s_0}
\]

\(\eta_{\text{rel}}\) is relative viscosity, \(t\) and \(d\) are the flow time and density of the solution, where as \(t_0\) and \(d_0\) are time and density for the solvent (water).

(132)
**Procedure**: Different amounts of soluble ovalbumin (0.2 to 0.6%) were mixed with different amounts of sodium dodecyl benzene sulphonate (0.5 to 2.0%). These sets were arranged at pH values 1.99, 3.95, 5.50, 7.50 and 10.50 using buffers keeping total volume 15.0 ml. The viscosity of these mixtures were determined at 35°C. At pH 7.50 all these sets were arranged at 25°C, 30°C, 35°C and 40°C, respectively. Viscosity measurement data are shown graphically and results are recorded in Tables 1 to 3.

**Viscosity Relation**: Following relation applies for dilute suspensions of solid particles.

\[
\eta_{sp} = \frac{\eta - \eta_0}{\eta_0} = \eta_{rel-1} = V\phi \quad............ \quad (i)
\]

where \(\eta_{sp}\) is specific viscosity, \(\eta\) is the viscosity of suspension, \(\eta_0\) is the viscosity of pure solvent, \(V\) is the Simha shape factor, and \(\phi\) the volume fraction of the particles in the suspension. At higher concentrations the solute-solute interaction is considered and a quadratic term is to be added.

\[
\eta_{sp} = V\phi + K\phi^2 \quad............ \quad (ii)
\]

The value \(\phi\) in eqn. (ii) can be expressed in terms of the product \(VC\) where \(V\) is specific solute volume and \(C\) is the concentration in g/cm³

\[
\eta_{sp} = \gamma V C + K V^2 C^2 \quad............ \quad (iii)
\]

Dividing by \(C\) gives

\[
\eta_{sp} = \gamma V + K V^2 C \quad............ \quad (iv)
\]

The limiting value of \(\eta_{sp/c}\) limit \(C \rightarrow 0\) is called intrinsic viscosity or the intrinsic viscosity number \([\eta]\). It is measure of effective hydrodynamic volume per gram of macromolecule. Equation (iv) now assumes the following form

\[
\eta_{sp/c} = [\eta] + K [\eta]^2 C \quad............ \quad (v)
\]

(133)
where \( K \) is huggin’s constant. For random coils, following important relation of flory and fox (30) applies:

\[
[\eta] = \phi (\gamma)^{3/2} \quad \text{.......... (vi)}
\]

where \( \phi' \) is flory-fox constant and it changes with polymer molecular weight (\( M \)) and the solvent. Accordingly in a \( \phi \) solvent we have

\[
[\eta] = \frac{\phi'_0 (\gamma)^{3/2}}{M} \quad \text{.......... (vii)}
\]

Various theoretical values have been obtained for \( \phi'_0 \) but it has been established empirically that the most appropriate one is \( 2.5 \times 10^{23} \) (CGS Units). From equation (vi), the semi empirical relation

\[
[\eta] = K'M^a \quad \text{.......... (viii)}
\]

can be derived. The constant \( K' \) and ‘a’ are characteristics of the solute solvent pair at particular temperature. For random coils the value of ‘a’ is ordinarily between 0.5 and 1.0. For \( \phi \), solvent equation (viii) takes the form

\[
[\eta]_0 = K'M^a \quad \text{.......... (ix)}
\]

Reynolds and Tanford (31) have shown that the intrinsic viscosity for protein - sodium dodecyl benzene sulphonate complex obeys the following relation:

\[
\log [\eta]_0 = \log K' + 1.2 \log M \quad \text{(x)}
\]

Molecular weight can also be determined by the following relation (32):

\[
[\eta] = 8.69 \times 10^{-5} \text{Mn}^{-0.70} \quad \text{(in Benzene)}
\]

\[
[\eta] = 8.69 \times 10^{-5} \text{Mn}^{-1.00} \quad \text{(in Water)}
\]

The value of ‘a’ is 1 for best solvent and \( M \) is the average molecular weight. The quantity \([\eta]\) is also used in determining the hydrodynamic radius (Re) according the following relation:

\[
\text{Re} = \left[ \frac{3M}{10\pi n[\eta]} \right]^{1/3}
\]

Where \( M \) is molecular weight, \( N \) is Avagadro’s number. It also
used in determining end to end root mean square distance

\[(r^2)^{1/2} = \left[ \frac{M[n]}{\phi} \right]^{1/2} \]

where \(\phi\) is a shape factor and is independent of solvent. The quantity [n] gives valuable information about the shape and dimensions of macromolecule and their complexes in solution.

**RESULTS AND DISCUSSION**

1. **Effect of pH on specific viscosity of soluble ovalbumin**: The changes in the specific viscosity of different protein concentration against pH are shown in Figure 1. There is minima in each curve at pH 5.50 and maxima on either side of this pH. The minima at pH 5.50 indicates isoelectric point in the buffered medium. Malik and Ashraf using unbuffered solutions had reported the minima at pH 5.00 (14). The higher pH of minima in this case could be due to the influenc of cation binding from the buffer components similar shift of minima was observed by us in binding of surfactant cations with protein (33). The minima in specific viscosity at isoelectric point may be due to contracted state of molecules cause by attractive forces between balanced positive and negative charges on the protein (zwitter ion) on either side of isoelectric point, specific viscosity increased due to increase in hydrodynamic volume. In this region the molecules have net charge and repulsive forces between them brings about the extension of the molecule. Near more lower or higher pH, the repulsive forces shall be again reduced due to increase in the free ions in mixture with the result that hydrodynamic volume and viscosity decreases.

2. **pH effect on specific viscosity of sodium dodecyl benzene sulphonate (SDBS) and soluble ovalbumin**: Specific viscosity variation against pH becomes anomalous in presence of
increasing amount of SDBS as shown in Figure 2 to 5. Figure 2 represents change on viscosity of 0.002 to 0.006 g/ml of protein in presence of 0.5% of SDBS. The interesting feature of SDBS addition is the minima shift to pH 4.0 in place of 5.60 and becomes maxima while viscosity at pH 1.99 also assumes the same pattern as viscosity at pH 5.50. The displacement of isoelectric point towards lower pH could be due to the reaction of surfactant anions with cationic groups on protein. A result of interaction, the total positive charge on protein decreases. The maxima on either side of new isoelectric point shows similar characteristics as it was without addition of surfactant. In presence of 1.0% of SDBS, the minima starts abolishing with rising protein concentration (Figure 3). At 1.5% and 2.0% SDBS the minima completely abolishes (Figures 4 and 5) with 2.0% SDBS a sharp break is observed pH 7.50 beyond which the specific viscosity continuously increases. This indicates that the pattern of binding is identical between pH 4.00 to 7.50 and somewhat different above this pH.

3. **Effect of varying sodium dodecyl benzene sulphonate concentration at constant soluble ovalbumin concentrations:**

Change in specific viscosity obtained upon addition of SDBS within certain ranges of SDBS concentrations is shown in Figure 6. At 3.95 pH, the initial decrease of viscosity at 0.5% SDBS is due to the tightening of protein molecule owing to interaction with surfactant anions which caused a marked decrease in viscosity. This concentration is shown as threshold concentration (9). In presence of large amount of SDBS the viscosity again increases. This rise in viscosity is due to formation of a second absorption layer by van der Waals attractive forces between carbon chains (34) of already bound and oncoming SDBS molecules and the mixture exhibits nearly Newtonian viscosity.
Table 1: **Intrinsic viscosity (η) and hydrodynamic radius (Re) of soluble ovalbumin at different pH at 35°C.**

<table>
<thead>
<tr>
<th>SDBS in %</th>
<th>pH 1.99</th>
<th>pH 3.95</th>
<th>pH 5.50</th>
<th>pH 10.50</th>
</tr>
</thead>
<tbody>
<tr>
<td>[η]</td>
<td>Re</td>
<td>[η]</td>
<td>Re</td>
<td>[η]</td>
</tr>
<tr>
<td>0.00</td>
<td>4.90</td>
<td>42.50</td>
<td>8.50</td>
<td>47.9</td>
</tr>
<tr>
<td>0.50</td>
<td>8.90</td>
<td>45.50</td>
<td>8.80</td>
<td>39.0</td>
</tr>
<tr>
<td>1.00</td>
<td>11.85</td>
<td>50.60</td>
<td>9.50</td>
<td>48.7</td>
</tr>
<tr>
<td>1.50</td>
<td>-</td>
<td>-</td>
<td>10.50</td>
<td>49.2</td>
</tr>
<tr>
<td>2.00</td>
<td>-</td>
<td>-</td>
<td>12.10</td>
<td>51.70</td>
</tr>
</tbody>
</table>

Table 2: **Intrinsic viscosity (η) and other parameters at pH 7.50 and different temperatures**

<table>
<thead>
<tr>
<th>SDBS in %</th>
<th>Temp. 25°C</th>
<th>Temp. 30°C</th>
<th>Temp. 35°C</th>
<th>Temp. 40°C</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.00</td>
<td>8.40</td>
<td>400</td>
<td>6.60</td>
<td>475</td>
</tr>
<tr>
<td>0.50</td>
<td>10.50</td>
<td>722</td>
<td>8.60</td>
<td>480</td>
</tr>
<tr>
<td>1.00</td>
<td>13.20</td>
<td>740</td>
<td>12.40</td>
<td>525</td>
</tr>
<tr>
<td>1.50</td>
<td>16.50</td>
<td>865</td>
<td>14.50</td>
<td>540</td>
</tr>
<tr>
<td>2.00</td>
<td>19.00</td>
<td>1180</td>
<td>17.50</td>
<td>570</td>
</tr>
</tbody>
</table>

Table 3: **Energy of activation x 10⁷ of soluble ovalbumin in absence and presence of SDBS at pH 7.50 using Huggins constant K’.**

<table>
<thead>
<tr>
<th>SDBS in %</th>
<th>Protein (g/ml) 0.002</th>
<th>Protein (g/ml) 0.003</th>
<th>Protein (g/ml) 0.004</th>
<th>Protein (g/ml) 0.005</th>
<th>Protein (g/ml) 0.006</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.00</td>
<td>2.22</td>
<td>2.28</td>
<td>2.50</td>
<td>2.50</td>
<td>2.50</td>
</tr>
<tr>
<td>0.50</td>
<td>2.70</td>
<td>2.98</td>
<td>3.10</td>
<td>3.15</td>
<td>3.35</td>
</tr>
<tr>
<td>1.00</td>
<td>2.12</td>
<td>3.04</td>
<td>3.15</td>
<td>3.25</td>
<td>3.40</td>
</tr>
<tr>
<td>1.50</td>
<td>2.75</td>
<td>3.12</td>
<td>3.25</td>
<td>3.30</td>
<td>3.50</td>
</tr>
<tr>
<td>2.00</td>
<td>3.70</td>
<td>3.50</td>
<td>3.65</td>
<td>3.87</td>
<td>4.25</td>
</tr>
</tbody>
</table>

(137)
The phenomenon may be considered as, the more or less expended protein molecule at the acidic side of isoelectric point may be changed into folded, hydrophobic state by the continuous combination of SDBS and consequently the viscosity decreases. On adding excess of SDBS, viscosity increases and the solutions behave similar to the solution at isoelectric point without addition of surfactant.

At pH 5.50 the specific viscosity first increased linearly and then becomes nearly constant with rising SDBS concentration (Figure 7). The surfactant-protein ratio depends upon the mixing behaviour with increasing protein concentration, the protein to surfactant ratios were found to be 1:2.0, 1:1.5, 1:10 and 1:0.5, respectively. This stoichiometry shows that surfactant binding decreased as the protein concentration increased. This could be attributed to swelling and then extensive hydration of protein molecule in a dilute solution. Ray et al. (35) observed that 1% bovine serum albumin solution bound less SDBS and dodecanol than 0.1% protein solution. Several hypothesis have been offered to explain the effect of protein concentration (35, 36). The most satisfactory explanation appears to be that the kinetics of equilibrium may be slower in case of concentrated protein solutions. However, no such experiment were performed in the present investigations. At pH 7.50 the viscosity increases linearly without attaining any limiting value (Figure 8) whereas at pH 10.50, viscosity was not affected by 0.5% SDBS. It increases instantaneously with rising SDBS concentrations (Figure 9). The nature of viscosity curves indicate unfolding of protein molecule.

4. **Intrinsic viscosity of soluble ovalbumin at different fixed amount of SDBS at different pH values**: At intrinsic viscosity $[\eta]$ of protein in presence of different fixed amounts of SDBS
were determined by plotting the reduced viscosity \( \eta_r / C \) against protein concentration (g/ml) and then extrapolating to zero protein concentration (Figure 10 -17). The Huggins constant \( K' \) (37) representing the ratio of the slope to the square of the intercept [\( \eta \)] and are given in Table 1 and 2 along with intrinsic viscosity values. The quantity [\( \eta \)] in each case was used for evaluating the hydrodynamic radius (Re) and end to end distance assuming the shape factor (\( \phi \)) equal to 2.6 x 10^21 and are compiled along with other parameters.

It is observed that the reduced viscosities and other related parameters increased as the amount of SDBS increased. The values were found to be greater in presence of surfactant at the isoelectric point showing higher degree of disorder at this pH as compared to other pH values. At isoelectric point (pH 5.50) the protein has negligible [\( \eta \)] i.e. 0.901 g/cm² which represent a highly tight conformation of the protein molecule. The intrinsic viscosity of protein decreases in presence of 0.5% SDBS at pH 3.95 and 5.50 which suggests the contraction of protein molecule owing to complexation and then increased regularly on adding further quantity of SDBS (Figure 18). At other pH value the intrinsic viscosity increased with increasing surfactant concentration (Figure 19). It indicates an expansion of protein coil in the cluster because of enhanced electrostatic repulsions (9, 38). The small [\( \eta \)] and low radius of gyration at isoelectric point is in favour of dehydration and a special configuration is being maintained because of hydrogen bonding between the several hydroxyl groups of hydroxyproline and hydroxylysine residues of protein.

5. **Temperature effect on binding parameters at pH 7.50**: The effect of temperature on [\( \eta \)] of protein has been determined at pH 7.50 (Figure 20). The intrinsic viscosity of protein in absence
and presence of SDBS decreases with rising temperature. The surfactant appears to open the helixes and the extent of opening is being facilitated due to breaking off inter-chain hydrogen bonding and other cohesive forces responsible for the stability of the protein structure. The increasing temperature forces the helixes to become more and more complicated, hence intrinsic viscosity and hydrodynamic radius decreases. The decrease in viscosity with rise in temperature indicates the helix coil transition as reported in the case of phosphoglucomutase (39) or could be due to increasing chain flexibility with increasing temperature(40). The pH and temperature dependence of the viscosity must be attributed to disorganization of the helical contents of the protein. Jirgensons(41) observed that the protein possesses high α-helical, contents became slightly disorganized after treatment with anionic surfactant while those devoid of helical contents get converted to partly α-helical conformation on treatment with anionic surfactant (SDBS).

From higher [η] values, it is probable to suppose that protein in presence of varying amounts of SDBS forms either highly asymmetric particles or highly solvated while reverse process occurred at higher temperatures which may be due to collapsing of higher association because of hydrophobic interactions. The hydrocarbon part of the SDBS may bound over the hydrocarbon part of protein molecule with rising temperature. The temperature coefficient of binding process was determined from plots of log [η] against temperature at pH 7.50. The slope of the straight line corresponds to the temperature coefficient. These are found to be 25.3 x 10^{-2}, 21.9 x 10^{-2}, 15.2 x 10^{-2}, 14.3 x 10^{-2} and 14.2 x 10^{-2} in presence of 0.00, 0.50, 1.00, 1.50 and 2.00% SDBS. These values show that the energy of the system decreases with rising concentration of surfactant i.e.
initially the unfolding is rapid and then become slower. This shows that SDBS-protein interaction is a two stage process, one involving ionic and the other hydrophobic and other types of bonding. The energy of activation of the system was calculated with the help of slope of curve which is plotted between log η vs 1/T (Figure 23). These values increase with increasing protein and SDBS concentration and becomes constant at higher concentration which supported the involvement of ionic and hydrophobic nature of SDBS-protein combination.

6. **pH effect on intrinsic viscosity**: The effect of pH on [η] of protein and its surfactant complexes is shown in Figure 21. The curve resembles to the well known specific viscosity vs pH curve (Figure 22). In presence of 0.5% SDBS minima is abolished and up to pH 4.6 the [η] of SDBS-protein complex is low while it is higher above this pH. In presence of 1.0 to 2.0% SDBS a maxima at the initial iso electric point develops while on either side the viscosities are lower. The occurrence of maxima at IEP in presence of SDBS may be explained by the fact that the additional surfactant caused unfolding rapidly due to cooperatively of linking. Most probably surfactant break the salt bridges between anionic and cationic groups and becomes attached there (42). The progressively rising values with increasing SDBS may be due to solubilization and unfolding. This behaviour depends upon chain length, nature of distribution of polar groups, flexibility of chains, tightness of packing and the number of cross-links. The increase in viscosity is due to the corresponding elongation of the molecule and a consequent increase in the dissymmetry of the macromolecular units.

7. **Molecular weight of soluble ovalbumin-SDBS complex at 30°C**: The quantity [η] has been used for determining the molecular weight by the following relation (32):

\[(141)\]
\[ \eta = 8.69 \times 10^{-3} \text{ M}^{-1} \]

where M is the average molecular weight and ‘a’ for water has been taken equal to one. The values of molecular weight are found to be 65598, 103835, 126255, 150575 and 174895 corresponding to intrinsic viscosities 5.7, 9.10, 11.0, 13.1 and 15.20, respectively at pH 7.50 at 30°C. The slope of log [\eta] vs log molecular weight is found to be 0.93 (Figure 24), which is characteristic for polymer with random coils. This indicates that protein and SDBS complexes are randomly coiled. Further this represents that SDBS causes unfolding of protein and consequently binds to polypeptide chains.

**PROPOSED MECHANISM OF PROTEIN-SURFACANT INTERACTION:**

From the nature of viscosity changes in protein and protein-surfactant mixtures tentative mechanism for the surfactant binding and consequent unfolding can be suggested.

The interactions of SDBS with protein probably involves two possible modes of linkage

a) Electrostatic, involving salt linkages of the protein.

b) Non-electrostatic involving forces which normally bind surfactant ions into micelle.

In initial stage when smaller quantity of surfactant are added, type ‘a’ interaction dominates while in presence of large amounts of SDBS, type ‘b’ is more probable. This is also evident from the values of interaction index [Huggin Constant (K)], hydrodynamic radius (Re) and average molecular weight which go on increasing continuously showing large amount of electrostatic interaction when concentration of surfactant are low. The phenomenon of unfolding seems to be more towards completion with increasing SDBS concentration. A sudden change in intrinsic viscosity and other parameters would suggest that
viscosity behaviour of protein in presence of SDBS is cooperative and the changes are certainly due to change in asymmetry of the molecule. The view of Lundgren (36) that the secondary association of anionic surfactant is in the form of loose combination due to a polar attraction with one which is already electrostatically bound gives support to the present experimental data. At higher surfactant concentration if interaction was due to apolar attraction, there should be less particle-particle interaction and the increase in the values of binding parameters should not be as much as observed in the initial stages of surfactant addition. The large number of aliphatic hydroxyl groups from the hydroxy proline and lysine residues of protein may also be involved in surfactant binding through hydrogen bonding resulting increase in viscosities, Huggin constant, hydrodynamic radius (Re) and average molecular weight. It may, therefore, be concluded that surfactant-protein interaction involves ionic, hydrophobic and hydrogen bonding in forming the complex depending upon pH, concentration of protein and that of surfactant. The temperature coefficient of interaction also supported two stages of binding i.e. ionic and hydrophobic causing extensive unfolding of protein. Since SDBS concentration used are well above CMC and charges perfectly neutralized hence the expansion caused as a result of unfolding may be co-related to hydrophobic bond formation between alkyl part of micelles and hydrophobic groups of protein. Side by side the negatively charged oxygen atoms of the ionic micelle head may be treated as forming hydrogen bonds with hydrogen of the aliphatic hydroxyl groups.

Oakes (43) has found that both surfactant head groups and alkyl side chains are associated with bovine serum albumin (BSA) at the initial binding sites. A higher binding all surfactant molecules have an alpha-methylene chemical shift equal to an alkyl chain and head group mobility similar to those in simple surfactant micelle. It appears that in present situation the clusters of SDBS molecules are also
formed on with the protein. In present investigation the high molecular weights of SDBS-protein complexes are in favour of clustering SDBS micelles on the protein.

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REFERENCES


34. H.P. Lundgren, Advances in Protein Chemistry, 5, 319 (1949).