Phase separation in solutions of monoclonal antibodies and the effect of human serum albumin

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Detailed Terms

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Phase separation in solutions of monoclonal antibodies and the effect of human serum albumin

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We report the observation of liquid-liquid phase separation in a solution of human monoclonal antibody, IgG2, and the effects of human serum albumin, a major blood protein, on this phase separation. We find a significant reduction of phase separation temperature in the presence of albumin, and a preferential partitioning of the albumin into the antibody-rich phase. We provide a general thermodynamic analysis of the antibody-albumin mixture phase diagram and relate its features to the magnitude of the effective interprotein interactions. Our analysis suggests that additives (HSA in this report), which have moderate attraction with antibody molecules, may be used to forestall undesirable protein condensation in antibody solutions. Our findings are relevant to understanding the stability of pharmaceutical solutions of antibodies and the mechanisms of cryoglobulinemia.

Antibodies are widely used in research and biotechnology, as well as in medical and pharmaceutical applications. In some cases, concentrated solutions of specific antibodies are required. In particular, monoclonal antibodies (MAb) have become a major category of drugs in the treatment of a variety of diseases (1). In some drug delivery routes e.g., subcutaneous administration, formulations with concentrated antibody solutions are required to achieve therapeutic dosing (2).

The physiological functions of antibodies are mostly determined by antibody-antigen and antibody-receptor specific interactions. However, the nonspecific interactions between antibodies (i.e., self-association) in the concentrated antibody solutions can also affect their functions. Nonspecific attractive interactions can cause various forms of condensation, including liquid-liquid phase separation, aggregation, and crystallization. Upon such condensation, antibodies lose their solubility, and may lose their biological activity. Particularly, in the pharmaceutical industry, these processes impact storage stability and safety of protein therapeutics thus impeding drug development (3). For example, immunogenicity of some biologics has been attributed to formation of protein aggregates (4). The mechanisms of protein condensation are complex and depend on protein concentration, buffer composition, temperature, etc. Clearly, the factors which affect protein condensation throughout the shelf-life must be understood and controlled to ensure biotherapeutic effectiveness.

One important condensation process is liquid-liquid phase separation (LLPS). In LLPS, a homogeneous protein solution spontaneously separates into two coexisting phases with different protein concentrations. This phenomenon takes place upon changing the temperature or other solution conditions, and is reversible. In contrast to aggregation or crystallization, LLPS, while highly sensitive to the average “net” attractive interaction between proteins, are much less sensitive to the distribution pattern and the nature of the “local” interactions on the protein surface. As a result, LLPS exhibits universal features applicable to a variety of proteins. LLPS is often superseded by aggregation, gelation, or crystallization. In such cases, LLPS can still be important as an underlying metastable phase transition, which substantially affects kinetics of these other condensation processes.

Recently, LLPS of several pharmaceutical antibodies have been reported (5–9). There are five isotypes of mammalian antibodies with distinct Fc regions, including IgA, IgD, IgE, IgG, and IgM. For each isotype, there are also large numbers of idiotypes with different Fab regions. Due to this great variety of antibodies, their condensation may occur at noticeably different conditions. As a cooperative phenomenon, LLPS is sensitive to rather small changes in the average interprotein interaction, and thereby can provide a useful tool to evaluate the propensities of different antibodies to condense.

High concentrations of both monoclonal and polyclonal antibodies also occur in the blood of patients with immunoproliferative disorders associated with a number of diseases, such as multiple myeloma, hepatitis C, and HIV. In these cases, excessive endogenous antibodies (mainly IgG, IgM, and their mixtures) precipitate in blood at temperatures lower than 37 °C. This medical phenomenon is called cryoglobulinemia (10–12). Sometimes, intravascular condensation of antibodies can even occur at body temperature and have adverse physiological consequences such as auto immunogenicity, increase in blood viscosity, and deposition in blood vessels. The cryoglobulinemia is reversible upon raising the temperature, and antibodies may maintain their ability to bind to antigen. These characteristics are consistent with LLPS.

In order to investigate the propensity of antibodies to undergo protein condensation in vivo, both in the case of cryoglobulinemia and in the pharmaceutical applications, the solution conditions of blood serum must be taken into account. Here we report the study of the LLPS of a monoclonal human antibody, which is denoted by IgG2-A as in ref. 5, under solution conditions mimicking those in a blood serum. Specifically, we investigated LLPS at physiological pH (pH = 7.4) in the presence of human serum albumin (HSA), which is the major protein component in blood serum.

The solution conditions, such as protein concentration, composition, temperature, buffer properties, etc., under which LLPS occurs are represented by a phase diagram. The phase diagram may be viewed as a collection of coexistence curves which represent the dependence of phase separation temperature on the protein concentration at various conditions. In this work, we have determined the coexistence curves of a MAb solution in the presence of various concentrations of HSA. Here we show that the MAb solutions have much lower critical concentration and much wider coexistence curve as compared to solution of compact globular proteins. We ascribe this difference to extended Y-like shape of MAb molecules. Further, we find that HSA preferentially partitions into protein-rich phase and lowers phase


The authors declare no conflict of interest.

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components of blood serum.

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and aggregation of the antibody molecules. All these condensation
signifies attractive interactions between the antibody molecules
observed critical concentration, is at least twice as large as the
highly nonspherical shape of antibody molecules. This value
value of the critical volume fraction of MAb reflects the extended,
particle interaction varies from infinity to zero (14). The small
fraction varies from 13% to 23% as the spatial range of the inter-

(13), we find that the critical concentration corresponds to a
coexistence curve specifies the concentrations of the two coexist-
phase for all concentrations. For temperatures below \(T_c\), the MAb solution remains in a stable homogeneous

Liquid-Liquid Phase Separation of MAb-Water Binary Solution at Physiological
pH. We have measured the temperature for phase separation, \(T_{ph}\), of our MAb as a function of antibody concentration, \(c_1\), and obtained the coexistence curve shown in Fig. 1. In a binary solution, the maximum temperature occurs at the critical point. Thus, in Fig. 1 we observe that the critical temperature, \(T_c\), is equal to \(-0.6 \pm 0.1^\circ\text{C}\), and the critical concentration, \(c_c\), is \(90 \pm 9\) mg/mL. For temperatures greater than the critical temperature, the MAb solution remains in a stable homogeneous phase for all concentrations. For temperatures below \(T_c\), the coexistence curve specifies the concentrations of the two coexisting liquid phases corresponding to that temperature.

Using the value of 0.71 mL/g for the protein specific volume (13), we find that the critical concentration corresponds to a critical volume fraction of 6.3%. This value is quite small considering that in solutions of spherical particles the critical volume fraction varies from 13% to 23% as the spatial range of the interparticle interaction varies from infinity to zero (14). The small value of the critical volume fraction of MAb reflects the extended, highly nonspherical shape of antibody molecules. This value implies that the volume of a spherical particle, which matches the observed critical concentration, is at least twice as large as the actual volume of the antibody molecule.

The phenomenon of separation into coexisting liquid phases signifies attractive interactions between the antibody molecules (14). Such attractive interactions can also lead to crystallization and aggregation of the antibody molecules. All these condensation phenomena of pharmaceutical or endogenous antibodies can have serious pathophysiological consequences in vivo such as immunogenicity, increase in blood viscosity, and deposition in blood vessels. From this perspective it is important to investigate how the condensation of antibodies can be affected by other components of blood serum.

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<td>98</td>
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<td>(\frac{\partial T_{ph}}{\partial c_1})</td>
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<td>(\frac{T_{ph}}{\text{°C} \cdot \text{mL/g}})</td>
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Liquid-Liquid Phase Separation of MAb-HSA-Water Ternary Solutions.

In view of the fact that HSA is a major component of blood serum, we have measured the effect of HSA on the phase separation of MAb in aqueous solutions at physiological pH. We find that, regardless of MAb concentration, the addition of HSA lowers the phase separation temperature in direct proportion to the HSA concentration, \(c_2\). We list in Table 1 the values of \(\frac{\partial T_{ph}}{\partial c_2}\), at fixed MAb concentration, \(c_1\), and have the average value: \(-0.24 \pm 0.03\) °C · mL/mg. Therefore, at the typical concentration of HSA in blood of \(-40\) mg/mL (15), HSA reduces the phase separation temperature by \(-9^\circ\text{C}\). Thus, HSA may have a significant role in preventing condensation of antibodies in blood at body temperature.

The values in Table 1 were found by measuring the decrease in phase separation temperature upon adding HSA at fixed MAb concentration. \(T_{ph}\) decreases linearly with increase of \(c_2\) as shown in Fig. 2A at two representative values of \(c_1\). (See Fig. S1 in SI Appendix for the entire dataset). In Fig. 2B we plot the coexistence curves (\(T_{ph}\), \(c_1\)) at several values of HSA concentration, \(c_2\). We see that the entire coexistence curve shifts downwards as \(c_2\) increases. Fig. 2A and B represent two cross sections of a phase diagram, which describes the solution conditions required for LLPS of MAb in the presence of HSA. Due to the diversity of antibodies, the critical temperatures, \(T_c\), of different antibodies may vary widely. Indeed, in the case of cryoglobulinemia, antibodies form condensates even at body temperature. Thus, the phase diagram can become a clinically important representation of the conditions under which pathophysiological protein condensation can occur in blood.

In LLPS, the concentrations of MAb as well as the concentrations of HSA are different in the two coexisting phases. The actual partitioning of these two proteins depends on the magnitude and the sign of the interprotein interactions between pairs of MAb-MAb, MAb-HSA and HSA-HSA. These interprotein interactions are also responsible for the suppression of LLPS temperature of MAb solutions upon the addition of HSA. Therefore, it is important to measure quantitatively the actual compositions of MAb and HSA in the two coexisting phases.

Partitioning of MAb and HSA in the Coexisting Phases. At any fixed temperature beneath \(T_c\), the concentration of each protein in each coexisting phase depends upon the initial concentrations of the two proteins in the starting solution. We measured the concentrations of MAb and HSA in pairs of coexisting phases at fixed temperature. In Fig. 3 we present our results for two different temperatures. In Fig. 3, each pair of two data points representing the two coexisting phases are connected by a so-called “tie-line.” Fig. 3 shows that the concentration of HSA in the MAb-rich phase is higher than that in the MAb-poor phase, i.e., HSA preferentially partition into the protein-rich phase. This observation implies that the interprotein interaction between

Fig. 1. Liquid-liquid phase separation of MAb solutions in 0.1 M Tris HCl buffer at pH 7.4. The eye guide for the LLPS boundary is indicated by the dashed line. The crossed square is the critical point determined at the maximum of the phase boundary.

Fig. 2. (A) Decrease of LLPS temperature, \(T_{ph}\), vs. the HSA concentration, \(c_2\), at fixed MAb concentration, \(c_1\). Linear fitting of \(T_{ph}\) vs \(c_2\) at each \(c_1\) is shown by the dashed line. (B) LLPS boundaries at fixed temperature as HSA concentration, \(c_2\), increases (The data were obtained by interpolation of the data in SI Appendix; Fig. S1).
MAB and HSA is attractive. In part this attraction may be attributed to the electrostatic interaction between MAB and HSA. Indeed, the isoelectric point of MAB is $pI = 8.8$ and that of HSA is $pI = 5.7$ (calculated using www.expasy.org). Thus, at the physiological pH 7.4, MAB and HSA carry charges of opposite sign.

In Fig. 3, we also designate the binodal curve ($c_1$, $c_2$) at constant temperature by fitting data from both partitioning measurement and $T_{cp}$ measurement. Using the method of analysis described previously (16), we also estimated the positions of the critical points of the MAB-HSA-water ternary solution. In Fig. 3, we show that $c_1$ at the critical points are equal to $105 \pm 10$ mg/mL at both measured temperatures. The critical concentration of MAB in the ternary solution is equal to that found for the pure MAB solution, within experimental error.

Discussion

In this work, we report the observation of LLPS of an IgG2 monoclonal antibody at physiological pH, as well as in the presence of human serum albumin. While LLPS in solutions of globular proteins is well documented (16, 18–21), it is often preempted by aggregation or crystallization. Recently, reports have appeared of such LLPS in solutions of antibodies (5–9, 22). Antibodies can be present in blood at relatively high concentrations. Furthermore, antibodies are widely and increasingly used in concentrated solutions as pharmaceutical drugs. In view of these facts, it is very important to quantitatively investigate phase separation phenomena for these proteins. Indeed the loss of homogeneity due to the formation of droplets of condensed phases can have adverse effects both physiologically, and in the manufacturing and storage of MAB-based therapeutics.

Phase Diagram of MAB Aqueous Solutions. As is the case with other proteins, the MAB phase diagram provides a comprehensive delineation of the solution conditions under which phase separation can occur. Theoretical analysis of this diagram can provide insights into the intermolecular interactions responsible for the condensation of the protein. In previous studies of globular proteins, the main features of the coexistence curve such as the critical temperature, critical concentration, and the width of the coexistence curve were successfully explained in terms of the effective magnitude, range and anisotropy of the interprotein interactions (14, 23). However, these previous theoretical studies were predicated on the model of proteins as spherical particles (14, 23). We shall see here that such theories may have limited applicability to the phase behavior of Y-shaped antibody molecules.

Indeed, one of the striking features of the coexistence curve of pure MAB is the very small value of the critical concentration, $c_c$, or critical volume fraction, $\phi_c = c_c v_p$, where $v_p = 0.71 \text{ mL/g}$ is the specific volume of protein molecules (13). In Table 1, we compare the critical volume fractions found theoretically for spherical particles in the limit of very short and very long range of attraction, as well as the experimentally observed critical volume fractions for various proteins. We believe that the small critical volume fraction of antibodies is a consequence of its extended, Y-like shape.

In Fig. 4, we show several coexistence curves plotted using the scaled variables $T/T_c$ and $c/c_c$. Curve 1 shows the mean-field prediction for a solution of attractive hard spheres with a Carnahan-Starling approximation for the entropy. We may quantify the width, $w$, of each coexistence curve by fitting the curve in the

Quasielastic Light-Scattering (QLS) Study of the MAB-HSA Mixture Solution. We have measured the apparent diffusion coefficients, $D$, of protein molecules in pure MAB solutions and in MAB-HSA mixtures containing 30% (w/w) HSA, as a function of total protein concentration (Fig. S2 in SI Appendix). We deduced the apparent diffusion coefficient, $D^*$, of proteins for infinitely dilute pure and mixed solutions. Using these $D^*$s, we calculated that the apparent hydrodynamic radius, $R_h^*$, of pure MAB solutions is equal to $5.9 \pm 0.1 \text{ nm}$. Similarly, we have found the $R_h^*$ for pure HSA monomers to be equal to $4.1 \pm 0.2 \text{ nm}$. In the MAB-HSA mixture, the apparent $R_h^*$ is equal to $5.7 \pm 0.3 \text{ nm}$. This value indicates that no heterodimerization or other strong interactions between MAB and HSA takes place. The apparent diffusion coefficients decrease with the total protein concentration both in pure MAB solutions and in MAB-HSA mixtures. The negative value of $\partial D^*/\partial c$ is indicative of attractive interactions. The value of the normalized slope, $d(D/D^*)/dc$, is less negative for the mixture than that for the pure MAB solution, which implies that HSA diminishes the effective interprotein attraction. This observation is in accord with the suppression of LLPS upon the addition of HSA.

\[\text{Fig. 3. Partitioning of MAB and HSA upon LLPS at fixed temperature (a) } T = -2.2°C, \text{ and (b) } T = -4.2°C. \text{ The points representing the two coexisting phases are connected by the solid lines, i.e., the tie lines. Dashed lines are eye guides for the binodal curves fitted from both cloud-point measurements (open triangles) and partitioning measurements (solid circles). The critical points are represented by the crossed square.}\]
The values are taken from refs. 14, 16, 24, and 18. The value listed for (IgG2-A) is taken from Fig. 1 and is consistent with data reported for other immunoglobulins in refs. 6 and 7.

The values are taken from ref. 14.

The values are taken from ref. 16.

The values are taken from ref. 18.

The values are taken from ref. 6.

The values are taken from ref. 7.

effectively spherical, have limited applicability in the description of used model free energies, which assume a spherical shape of and possibly from its flexibility. Thus, it appears that currently these characteristics of the MAb coexistence curve result that these nearly spherical proteins follow coexistence curves similar which is much wider than curve 1. The data points shown for curve 1, the width is w = 6.15. Curve 2 shows the theoretical fit (20) of the data for bovine γB crystallin taken from ref. 18. Because of the short range and highly anisotropic (aeolotopic) interactions (14, 23), this coexistence curve has width w = 27 which is much wider than curve 1. The data points shown for other nearly spherical proteins follow coexistence curves similar to curve 2 (16, 24). Interestingly, the coexistence curve for our MAb (curve 3) is even wider than that observed for nearly spherical, and is asymmetrical: being much wider on the high concentration side than on the low concentration side. For curve 3, w = 120. Coexistence curves of other reported MAb’s also share similar broad and asymmetrical shapes (6, 7). We believe that these characteristics of the MAb coexistence curve result from the highly nonspherical Y-like antibody shape (25, 26), and possibly from its flexibility. Thus, it appears that currently used model free energies, which assume a spherical shape of protein molecules, have limited applicability in the description of the thermodynamic properties of solutions of antibody.

Phase Diagrams of MAb-HSA Aqueous Solutions. There are two important features of the phase diagrams of MAb-HSA-water ternary solutions: the reduction of $T_{ph}$ upon addition of HSA and the preferential partitioning of HSA into the concentrated MAb phase. In the following discussion, we will connect these two features to the “effective energies” of MAB-HSA interactions and to the excluded volume entropies for both of these molecules. In the limit of a small mole fraction of HSA, $x = N_2 / N_1 \ll 1$, where $N_1$ and $N_2$ are the numbers of molecules of MAB and HSA respectively, the HSA-HSA interaction is negligible. Hence, we may write the Helmholtz free energy as: $F = F^0 + N_2kT\ln(\phi_2/\alpha) + N_2E_{21}$. Here, $F^0(\phi_1, T)$ is the Helmholtz free energy of a pure MAB solution. The remaining terms, linear in $N_2$, represent the entropic and energetic contributions of HSA. The entropic term is written as the entropy of an ideal solution of HSA in the volume, $V_{eff}$, accessible to it. Thus, the quantity $\alpha(\phi_1, T)$ represents the fraction of the total volume accessible to HSA, i.e., $\alpha = V_{eff}/V$. The energetic component, per HSA molecule, due to the MAB-HSA interaction is denoted as $E_{12}(\phi_1, T)$. In the high temperature approximation, both $\alpha$ and $E_{12}$ are independent of $T$.

The Reduction of the Phase Separation Temperature of MAB Solutions in the Presence of HSA. We now examine the factors, which determine the change of $T_{ph}$ in a MAB solution, $\Delta T_{ph}$, upon addition of a small mole fraction, $x$ ($x < 1$) of HSA. Using the equilibrium condition, $\mu_1 = \mu_2$, and general thermodynamic relations (27), we have derived $\Delta T_{ph}$ at constant volume fraction of MAB, $\phi_1$ (see SI Appendix):

$$\Delta T_{ph} = \frac{dT_{ph}/d\phi_1}{\partial\Pi/\partial\phi_1} \left[ -kT_{ph}(\phi_1^2/\phi_1^1 - \phi_1^1/\phi_1^1) - \left( \frac{\partial E_{12}}{\partial \phi_1} \right)_{T, \phi_1} \right]$$

[1]

Here, $T_{ph}$ is the phase separation temperature of the pure MAB solution, $\Pi$ is the osmotic pressure of the solution, and $\Omega_2$ is the volume of one HSA molecule. The slope of the coexistence curve of pure MAB solution, $dT_{ph}/d\phi_1$, is positive at $\phi_1$ smaller than the critical volume fraction $\phi_c$ and is negative at $\phi_1$ larger than $\phi_c$. The osmotic incompressibility in a pure MAB solution, $d\Pi/\partial\phi_1$, is always positive in a stable phase. Because experimentally $\Delta T_{ph}$ is negative for all values of $\phi_1$, it follows that the bracketed term in Eq. 1 must have opposite signs on the two sides of the coexistence curve. The first term in the brackets describes the effect of HSA partitioning. The experimentally observed partitioning of HSA is small (Fig. 3): $\phi_c^2 \approx \phi_c^1$. This observation is actually remarkable because the condensed phase has much less free volume, $V_{eff}$, to accommodate the HSA than has the dilute phase. When $\phi_1^1 = \phi_c^1$ the partitioning term in Eq. 1 becomes equal to $-kT_{ph}(\phi_1^1/\phi_1^1)$. The second term in the bracket characterizes the change of osmotic pressure upon addition of HSA. Using $\Pi = -(\partial F/\partial V)_{N_1, N_2, T}$, and our expression for the Helmholtz free energy, it follows that $\left( \frac{\partial E_{12}}{\partial \phi_1} \right)_{T, \phi_1} = kT_{ph}\Omega_2 + \phi_1(\partial E_{12} - kT_{ph}\ln\alpha(\phi_c^1)/\partial\phi_1)$. The first term here represents the ideal (van’t Hoff) contribution to the osmotic incompressibility. Under the conditions of no partitioning ($\phi_1^1 = \phi_c^1$), this contribution cancels the first term in the brackets in Eq. 1. This cancellation reflects the fact that adding an ideal, noninteracting solute should produce no change in the coexistence curve. The second term: $\phi_1(\partial E_{12} - kT_{ph}\ln\alpha(\phi_c^1)/\partial\phi_1)$, represents the nonideal contribution of HSA to the osmotic incompressibility. This term involves two elements: the MAB-HSA interaction energy $E_{12}$ and the excluded volume entropy $-kT_{ph}\ln\alpha$. Using a Monte Carlo simulation and a three-sphere model for the Y-shaped MAB molecule (see SI Appendix), we have evaluated the free volume fraction $\alpha$ as a function of $\phi_1$. A graph of $\partial(\ln\alpha)/\partial\phi_1$ vs. $\phi_1$ is shown in (Fig. S6 in SI Appendix). This excluded volume contribution is positive and monotonically increases with $\phi_1$. At the critical point, this derivative is equal to 10. Because $\phi_1(\partial E_{12} - kT_{ph}\ln\alpha(\phi_c^1)/\partial\phi_1)$
changes sign at the critical point, it follows that there $\partial E_{12}/\partial \phi_1 = -10kT_{ph}$. The energy $E_{12}$ is a smooth monotonic function of $\phi_1$, thus $\partial E_{12}/\partial \phi_1$ is not expected to vary dramatically. Indeed, in the mean-field approximation, $E_{12} = e_{12}\phi_1$, this derivative would be constant, $e_{12} = -10kT_{ph}$ over the entire range of $\phi_1$, and $E_{12}$ will be $-1.4kT_{ph}$ at the critical point. The negative value of this energy is consistent with an attractive MAb-HSA interaction. This significant attraction compensates for the low entropy of HSA in the protein-rich phase and produces the nearly equal values of HSA volume fractions in the two phases.

**Partitioning of MAb and HSA.** As has been seen above, the partitioning of HSA into the two coexisting phases is closely connected with the magnitude and sign of the change in $T_{ph}$ (Eq. 1). The partitioning of HSA is controlled by its chemical potential: $\mu_2 = (d\phi_2/dx)_{N, V, T}$. Using the expression for Helmholtz free energy, we derived that: $\mu_2 = kT\ln(\phi_2/\alpha) + E_{12}$. The partitioning of HSA between the two phases, i.e., the relation between $\phi_2$ and $\phi_1$, is determined by the equilibrium condition, $\mu_2 = \mu_1^0$, which has the form:

$$kT_{ph}\ln(\phi_1^{0II}/\phi_2^{0II}) = E_{12}(\phi_1^{0II}) - E_{12}(\phi_1).$$

This equation connects the ratio of HSA volume fractions in the two phases to the excluded volume entropies and the MAB-HSA interaction energies. With $\alpha(\phi_1)$ determined by Monte Carlo simulation, Eq. 2 provides an alternative way to evaluate $E_{12}$. Using the simulation results and the experimental data from five tie-lines (Fig. 3), we have deduced $\Delta E_{12} = E_{12}(\phi_1^{0II}) - E_{12}(\phi_1)$ and found that this quantity ranged from $-1.8kT_{ph}$ to $-1.1kT_{ph}$. The negative value of $\Delta E_{12}$ implies an attractive interaction between MAb and HSA. This attraction is the driving force for the partitioning of HSA. In the mean-field approximation, $E_{12} = e_{12}\phi_1$, then $e_{12} = \Delta E_{12}/(\phi_1^{0II} - \phi_1)$ has a value ranging from $-14.0kT_{ph}$ to $-13.8kT_{ph}$. Considering the approximations involved, this result is quite consistent with the estimation above, $e_{12} = -10kT_{ph}$, based on the shift of the coexistence curve upon adding HSA.

Furthermore, it is interesting to examine the relative partitioning of $\phi_{Q\text{pEMA}}$ and $\phi_{pEpEMA}$, $\phi_{Q\text{pEMA}}$ and $\phi_{pEpEMA}$ are identical in shape and signal and are different at only one amino acid position. For these “similar” proteins, the difference between the molar ratios of $\phi_{Q\text{pEMA}}$ to $\phi_{pEpEMA}$, $x$, in the two coexisting phases, is solely determined, when $x$ is small, by the difference of the molar entropy of $\phi_{Q\text{pEMA}}$-$\phi_{Q\text{pEMA}}$ like-unlike interaction, $\Delta E_{12}$, and that of $\phi_{pEpEMA}$-$\phi_{pEpEMA}$ like-like interaction, $\Delta E_{11}$, in these two phases. We have previously shown (16) that this relative partitioning of similar proteins can be described by: $kT_{ph}(\ln x - \ln x^{0II}) = \Delta E_{12} - \Delta E_{11}$, where $\Delta E_{12} = E_{12}(\phi_1^{0II}) - E_{12}(\phi_1)$ and $\Delta E_{11} = E_{11}(\phi_1^{0II}) - E_{11}(\phi_1)$. The driving force for the relative partitioning of $\phi_{Q\text{pEMA}}$ is: $\Delta E_{12} = \Delta E_{11}$. Using the experimental data in Table S1 in SI Appendix, we can deduce $\Delta E_{12} - \Delta E_{11} \approx -0.1kT$. The negative value of $\Delta E_{12} - \Delta E_{11}$ suggests that the partitioning $\phi_{Q\text{pEMA}}$-$\phi_{pEpEMA}$ is attractive stronger than the $\phi_{pEpEMA}$-$\phi_{pEpEMA}$ attraction. The magnitude of $\Delta E_{12}$ is larger than that of $\Delta E_{11}$ by one tenth of the thermal energy $kT$. This change in interaction energy is caused by the alteration of a single amino acid residue. While the small difference between $\Delta E_{12}$ and $\Delta E_{11}$ is expected to have a small effect on the phase separation temperature, this difference produces an observable partitioning of these similar proteins. In vivo, as well as in biopharmaceutical production we frequently encounter mixtures of various antibody isoforms. The case of $\phi_{Q\text{pEMA}}$ and $\phi_{pEpEMA}$ provides an important example of phase separation partitioning in such mixtures of closely related antibody variants.

In conclusion, we have observed LLPS of a monoclonal antibody, IgG2-A, at physiological pH. The phase diagram of our MAb solution is distinctly different from that of nearly spherical globular proteins. Our experiments, together with the data available for other antibodies (5–9), show that: the immunoglobulins have a markedly lower critical concentration and a much broader, asymmetric coexistence curve. We believe that these features are associated with the highly nonspherical shape of an IgG molecule, i.e., the Carnahan-Starling form for excluded volume entropy of hard spheres is unsuitable for thermodynamic analysis of antibody solutions. We have also examined the effect of HSA, the major protein component in blood, on the LLPS of MAbs. We have found that the phase separation temperature decreases as HSA concentration increases. This result is remarkable as it implies that HSA may play a significant role in maintaining the stability of antibodies in blood. By applying a general thermodynamic analysis, we have attributed the reduction of phase separation temperature of MAb solutions in the presence of HSA to the attractive interaction between MAb and HSA. This phenomenon shows the role of the protein-additive interaction in tuning the phase separation temperature of the protein solution. Furthermore, the partitioning of HSA (or any other excipient) also depends on the energy of MAb-additive interaction. In a special case of $\phi_{Q\text{pEMA}}$, a minor antibody isoform, we have given a further analysis of the relative partitioning, and conclude that the $\phi_{Q\text{pEMA}}$-$\phi_{pEpEMA}$ MAb attraction is stronger than the $\phi_{pEpEMA}$-$\phi_{pEpEMA}$ attraction.

This investigation along with other recent findings (5–9) suggests that LLPS may be a ubiquitous phenomenon in antibody solutions. This fact is of obvious importance for biotechnological and pharmaceutical applications and for understanding the origin of cryoglobulinemia which is a condition observed in a number of human diseases. The present work provides a conceptual experimental and theoretical framework for further studies in this emerging field.

**Materials and Methods**

**Preparation and Purification of MAb and HSA.** MAb, IgG2-A, was produced at Amgen Inc. The original MAb solution contained $\phi_{Q\text{pEMA}}$ and $\phi_{pEpEMA}$ isoforms corresponding to partial and complete cyclization of the heavy chain N termini (Fig. S3 in SI Appendix). The two isoforms were identified by peptide mapping coupled with mass-spectrometry (performed at Amgen Inc.). HSA was purchased from Sigma. The dimers and oligomers of HSA were removed using a preparative chromatographic system (AKTA prime plus, Amersham Biosciences) and a size-exclusion column (Superdex 200, GE Healthcare).

**Solution Preparation.** The purified MAb and HSA proteins were dialyzed exhaustively into Tris HCl buffer (0.1 M, pH 7.4). Solutions containing dilute MAb and HSA in Tris HCl buffer were concentrated by ultrafiltration (Amicon, 10 kDa) and Centrifugation (Amicon Ultra, 10 kDa). The concentrations of MAb and HSA in the mixture solutions were determined using HPLC with a CEX column (pack bare, Phenomenex) and a size-exclusion column (Superdex 200, 10/7.8, Amersham Biosciences).

**Measurement of $T_{ph}$.** A test tube containing the sample was placed in a thermostated light-scattering stage, whose temperature was initially set above the phase separation temperature so that the solution was transparent. The transmitted intensity of a 4-mW He-Ne laser was recorded by a photodiode. The temperature of the sample was then step wise lowered by 0.1 K every 5 min. At a well defined temperature, $T_{cloud}$, the sample became visibly cloudy. The temperature was then step wise raised by 0.1 K every 5 min. The minimum temperature at which the solution became clear again was denoted by $T_{clarity}$. The phase separation temperature $T_{ph}$ is estimated as
the average of $T_{\text{quinty}}$ and $T_{\text{cloud}}$. The difference between $T_{\text{quinty}}$ and $T_{\text{cloud}}$ is hysteresis which reflects the nucleation rate (19). Because hysteresis depends on kinetic processes, all the cooling and heating steps were set with a standard time interval (5 min).

**Measurement of MAb-HSA Partitioning.** The solutions having known $c_1$ and $c_2$ were quenched to a temperature below $T_\mu$, in a thermostated water bath. After an incubation time of one week, a sharp interface formed between two liquid phases. The formation of the sharp interface was taken as an indication that equilibrium was reached. The MAb and HSA in both phases were separated and their concentrations were measured using precalibrated CEX HPLC at pH 6.

**QLS.** All protein samples were filtered through a 0.1 μm Millipore filter and placed in a test tube. QLS experiments were performed on a light-scattering apparatus using a PD2000DLS PLUS correlator (Precision Detectors) and a Coherent He-Ne laser (35 mW, 632.8 nm; Coherent Radiation). The measurements were performed at a scattering angle of 90°. The measured correlation functions were analyzed by the Precision Deconvolve 5.5 software (Precision Detectors). The correlation functions were used to calculate the apparent diffusion coefficients, $D$, of proteins in solutions with given total protein concentration, $c$, at different HSA weight fraction, $\omega = 0\%$, $30\%$, and $100\%$. $D(c = 0)_\omega$ were obtained by extrapolating $D(c)_\omega$ to $c = 0$. The hydrodynamic radii, $\bar{R}_D$, of proteins in solutions with fixed $\omega$ were calculated from $D(c = 0)_\omega$ using Stokes-Einstein relation.

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