

1 Article

2 Reverse coarsening and the control of particle size 3 distribution through surfactant

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9 Featured Application: Generation of monodisperse ensembles of nanoparticles

10 **Abstract:** The minimization of surface area, as a result of the minimization of (positive) surface
11 energy is a well-known driving force behind the spontaneous broadening of (nano)particle size
12 distribution. We show that surfactant molecules binding to particle surfaces effectively decrease
13 the surface energy and may change its sign. In this case, contrary to the expected broadening
14 behaviour, a minimum of free energy is achieved at maximum surface area for all particles, i.e.
15 when the particles are identical. Numerical simulations based on the classical
16 Lifshitz-Slyozov-Wagner theory with surfactant-induced surface energy renormalization confirm
17 the collapse of the particle size distribution. As the particle size evolution is much slower than
18 particle nucleation and growth, the manipulation of surface energy with in-situ replacement of
19 surfactant molecules provides a method for controlling particle size distribution with great
20 potential for creating mono-disperse nanoparticles, a key goal of nanotechnology.

21 **Keywords:** Free energy; surface energy; surfactants; molecular ligands; mono-disperse
22 nanoparticles; particle coarsening

23

24 1. Introduction

25 The generation of identical nanoparticles [1-7] and fine nanostructures [8-10] is a key
26 requirement for self-assembly processes in bottom-up nanotechnology. However, structure
27 coarsening, or Ostwald ripening [11], is a universal phenomenon that stands in the way of forming
28 identical nano-building blocks through quasi-equilibrium methods. Coarsening represents the
29 spontaneous evolution of precipitated particles, during which smaller particles transfer mass to
30 bigger ones thus broadening the particle size distribution (PSD) [12-15]. This is a common
31 phenomenon taking place at the final stages of many first-order phase transformations following
32 nucleation and growth, for example in two-phase mixtures [11], binary alloys [16], clusters on
33 surfaces [17], oil-water emulsions [18], and during epitaxial growth [19-20] and synthesis of
34 nanoparticles [21]. The main driving force behind coarsening is the minimization of interfacial area
35 between the two phases and as such it depends intimately both on the interface energetics and the
36 system temperature. Much effort has been devoted to find ways to inhibit or even reverse coarsening
37 in order to achieve a narrower PSD. Known examples of PSD narrowing discussed in the literature
38 include the so-called digestive ripening [1-3, 22, 23]; inverse ripening [24-27]; and size focusing
39 during production-controlled growth [28, 29]. Some of these processes take place in the presence of
40 surfactants, which are widely used in nanoparticle production mainly to stabilize particles [30-32]
41 and to tune the growth regimes towards production of particles with required shapes and sizes
42 [33-35]. There are also mechanisms of inhibition, or of arresting Ostwald ripening [36-38], which do

43 not permit real narrowing of the PSD but rather preserve it from broadening. Digestive ripening can
 44 be explained by taking into account electric charges on the particle and by including the electrostatic
 45 energy in the free energy analysis [22-23], while inverse ripening has been observed for gold
 46 inclusions in an amorphous SiO₂ matrix irradiated with MeV gold ions [25, 27]. The PSD narrowing
 47 in the latter case is of transient character. It is affected by mechanical stresses and requires
 48 fine-tuning of radiation-annealing cycles. On the other hand, size focusing during
 49 production-controlled growth is predicted for effectively open systems where the material deposited
 50 on particles is continuously reproduced in the bulk of solution [28, 29]. In summary, there is
 51 currently no effective theory describing the phenomenon of PSD narrowing in conservative and
 52 charge-neutral systems.

53 Besides the quasi-equilibrium fabrication methods when the system is thermodynamically
 54 driven, narrow PSDs are also successfully generated using discrete size selection by undercooling
 55 [39-41] and dewetting [42-43] in non-equilibrium regime. Here, we study the role of surfactants, or
 56 surface binding molecular ligands [44-50] in controlling PSDs. We present a thermodynamic
 57 mechanism for particle size stabilization and narrowing of a PSD by surfactant molecules binding to
 58 particle surfaces. This process is illustrated by considering a simple dilute solution of two species
 59 (referred to here as *molecules*) in a neutral solvent in the presence of precipitated aggregates (called
 60 *particles*) of one of the components. Based on a free energy analysis, we demonstrate that there exists
 61 a range of parameters at which reverse coarsening (RC) occurs, and consequently, smaller
 62 precipitated particles grow at the expense of bigger ones. This regime is spontaneous, i.e. it is
 63 thermodynamically driven and converts any initial distribution of particles into an array of almost
 64 identical particles [51]. Notably, the transition into this regime can be obtained by varying the
 65 surfactant concentration and/or the system's temperature.

66 3. Results and discussion

67 Thermodynamic theory of reverse coarsening

68 Following the classical approach [13-15], we use a mean-field approximation in our analysis.
 69 This approximation assumes that the particles are sufficiently far from each other so that they only
 70 interact through the averaged characteristics of the solution, and that their occupied volume is
 71 negligible compared to the entire volume of the system. First, we analyze the thermodynamic
 72 stability of a single particle in the solution with a given concentration of indential molecules (we
 73 call them *A-molecules*) in the presence of surfactant molecules (*B-molecules*). Then, by writing the
 74 molecular chemical potential as a function of particle size we obtain the conditions for RC by
 75 considering the mass exchange between particles in an ensemble. Second, we confirm our prediction
 76 of RC by direct numerical simulations of the particle ensemble evolution using Kinetic Monte Carlo
 77 technique.

78 3.1. Isolated particle in a binary solution

79 In our thermodynamic analysis we consider a conservative system consisting of a dilute binary
 80 A-B solution and a precipitated spherical A-particle of radius R measured in the units of typical
 81 intermolecular distance and containing $N_p = 4\pi R^3 / 3$ molecules. The system contains M_A
 82 molecules of material A, M_B molecules of material B and M_L molecules of a solvent. For simplicity we
 83 assume that a molecule A can bind only one molecule B and vice versa with characteristic energy
 84 ε_{AB} . This binding results in the formation of N_C number of A-B complexes (dimers) in the solution,
 85 and in concentration n_S of B-molecules on particle surfaces. The free energy of the system is

$$86 \quad G = -\varepsilon N_p + \gamma S_p (1 - n_S) - \varepsilon_{AB} n_S S_p + T S_p \cdot [n_S \ln(n_S) + (1 - n_S) \ln(1 - n_S)] \\ 87 \quad - \varepsilon_{AB} N_C + T \cdot (N_C \ln(N_C) + N_A \ln(N_A) + N_B \ln(N_B) + N_L \ln(N_L) - M_\Sigma \ln(M_\Sigma)), \quad (1)$$

87 where $\varepsilon > 0$ and $\gamma > 0$ are the cohesive and surface energies per A-molecule in the particle,
 88 respectively, T is the temperature in energy units (eV), $S_p = 4\pi R^2$ is the number of molecules on

89 the particle surface, $N_A = M_A - N_P - N_C$, $N_B = M_B - S_P n_S - N_C$, $R \ll 1$ and
 90 $M_\Sigma = N_A + N_B + N_C + M_L$. In Eq. (1) we neglected possible interactions between B-molecules (see
 91 Appendix A for details) and assumed a simple form for the entropy, which provides a lower limit
 92 estimate [52].

93 The minimization of the free energy G with respect to the independent variables
 94 N_P, N_C and n_S in the limit of a dilute solution with $M_L \gg N_A + N_B + N_C$ yields (see Appendix
 95 B)

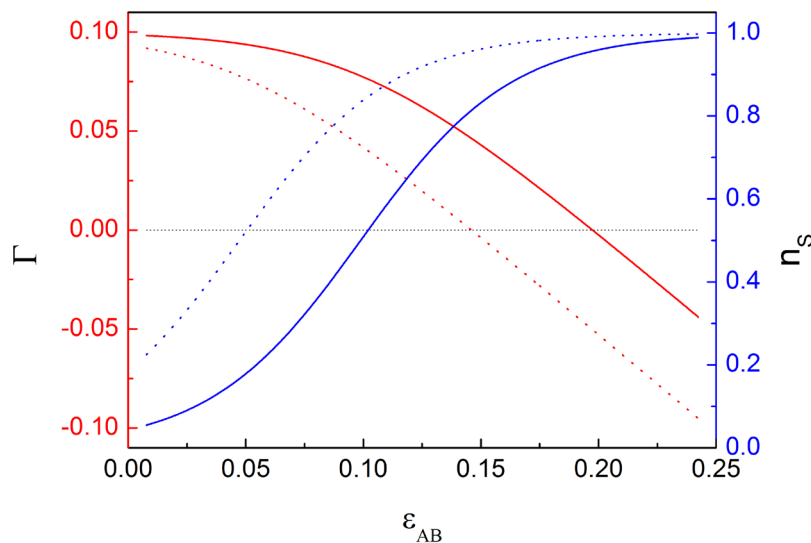
$$T \ln(n_A) = -\varepsilon + \frac{2}{R} \cdot \Gamma, \tag{2}$$

$$n_C = E_0 \cdot n_A \cdot n_B,$$

$$n_S = E_1 \cdot n_B \cdot (1 + E_1 \cdot n_B)^{-1}$$

97 where $E_0 = \exp(\varepsilon_{AB}/T)$, $E_1 = \exp((\gamma + \varepsilon_{AB})/T)$, and $\Gamma = \gamma - T \cdot \ln(1 + n_B E_1)$ is the renormalized
 98 surface energy of A-particle, $n_{A(B)} = N_{A(B)} / M_\Sigma$ and $n_C = N_C / M_\Sigma$ are the number concentrations
 99 of corresponding species in the solution. The first equation in Eq. (2) is a statement of the equality of
 100 chemical potentials for A-molecules in the solution $\mu_A(sol) = T \ln(n_A)$ and in the particle
 101 $\mu_A(R) = -\varepsilon + 2\Gamma / R$ of radius R . The second and third equations of Eq. (2) give the equilibrium
 102 concentrations of A-B complexes in the solution and of B-molecules on the particle surfaces,
 103 respectively. Note that the surfactant B-molecules always reduce the surface energy, as $\Gamma < \gamma$ due
 104 to $\ln(1 + n_B E) > 0$. For high enough values of ε_{AB} , the effective surface energy Γ can become
 105 negative (see Fig. 1) resulting in a narrowing of the size distribution for an ensemble of particles in
 106 solution. The same figure also shows the surface concentration of surfactant n_S as a function of
 107 ε_{AB} illustrating an increase in surface concentration n_S and a decrease in Γ with increasing bulk
 108 concentration n_B of the surfactant molecules.

109 The effect of surface energy renormalization by A-B bonding can be obtained by considering the
 110 molecular chemical potential $\mu_A(R) = -\varepsilon + 2\Gamma / R$ for a particle of radius R in solution containing
 111 other A-particles. The case of positive Γ corresponds to ordinary coarsening when A-molecules are
 112 transferred from smaller particles to bigger ones until a single big particle remains. If $\Gamma = 0$ the
 113 molecular chemical potential according to the first line in Eq. (2) becomes independent of R hence
 114 the PSD should also be time-independent. More interestingly, if $\Gamma < 0$ the molecular



116 **Figure 1.** Effective surface energy Γ (red) and concentration n_s of surfactant molecules (B) on
 117 particle surface (blue) as functions of A-B bonding ε_{AB} for two values of the bulk concentration of
 118 surfactant $n_b = 0.002$ (solid) and $n_b = 0.01$ (dotted) plotted according to Eqs (2) for $\gamma = 0.1$ eV
 119 and $T = 0.032$ eV .

120 chemical potential is lower for smaller particles and energy minimization requires the A-molecules
 121 to be transferred from bigger to smaller particles. This process of reverse coarsening (“size
 122 focusing”) results in a mono-disperse (for thermodynamic limit see [51]) particle ensemble with the
 123 equilibrium particle radius R_{eq} determined by the initial PSD function $f(R)$ and the particles’ total
 124 volume as

$$125 \quad R_{eq} = \left[\frac{\int_0^{\infty} R^3 f(R) dR}{\int_0^{\infty} f(R) dR} \right]^{1/3} \quad (3)$$

126 For instance, if the initial PSD is a Gaussian $f(R) = \frac{1}{\sqrt{2\pi} \cdot \sigma} \exp\left(-\frac{1}{2\sigma^2}(R - \langle R \rangle)^2\right)$ with a
 127 mean radius $\langle R \rangle$ significantly higher than the variance σ , then the value of R_{eq} is very close
 128 (within a few percents) to $\langle R \rangle$ and does not depend on ε_{AB} .

129 3.2. Simulation of reverse coarsening in the particle ensemble

130 The value of R_{eq} given by Eq. (3) is a good estimate if the PSD before collapse is close to the
 131 initial PSD. This estimate implicitly assumes that the surface energy γ does not depend on the
 132 particle radii or shapes. In reality the shape of small particles may deviate from spherical, which in
 133 context of our theory means that γ would increase with R . In turn, this dependence on the radius
 134 implies that $\Gamma > 0$ for small enough particles (depending on ε_{AB} and T) which will dissolve and
 135 transfer their mass to bigger particles with $\Gamma < 0$. Such mass transfer modifies the initial PSD and
 136 shifts the mean radius, hence R_{eq} , towards higher values.

137 To confirm this effect, we conduct numerical simulations using Kinetic Monte Carlo technique
 138 [53]. We start with a distribution of spherical particles nucleated and grown so that their evolution is
 139 only possible by exchange of molecules between particles. This initial configuration is chosen so that
 140 the vast majority of A-molecules are bound in particles. The particle surfaces are covered with
 141 B-molecules, which significantly slows down an exchange of A-molecules between particles and
 142 solution. Therefore, it is reasonable to assume that the molecular diffusion in solution is the fastest
 143 process and the coarsening process is limited by the attachment-detachment events with effective
 144 reaction rate constant K . Then, the evolution of the i -th particle’s radius R_i (measured in the units of
 145 inter-atomic distance) within this Wagner approximation [15] can be described by

$$146 \quad \frac{dR_i}{dt} = K \cdot (n - n_{GT}(R_i)), \quad (4)$$

147 where $n_{GT}(R_i)$ is the Gibbs-Thomson concentration (equilibrium concentration) for the i -th
 148 particle and n is the mean field concentration of free A-molecules in solution. The latter is
 149 determined using mass conservation for all particles (valid because of our earlier assumption about
 150 the dominant fraction of A-molecules contained in particles)

$$151 \quad \frac{d}{dt} \sum_{i=1}^N \frac{4}{3} \pi R_i^3 = \sum_{i=1}^N 4\pi R_i^2 \frac{dR_i}{dt} = \sum_{i=1}^N 4\pi K R_i^2 \cdot (n - n_{GT}(R_i)) = 0 \rightarrow n = \frac{\sum_{i=1}^N R_i^2 \cdot n_{GT}(R_i)}{\sum_{i=1}^N R_i^2} \quad (5)$$

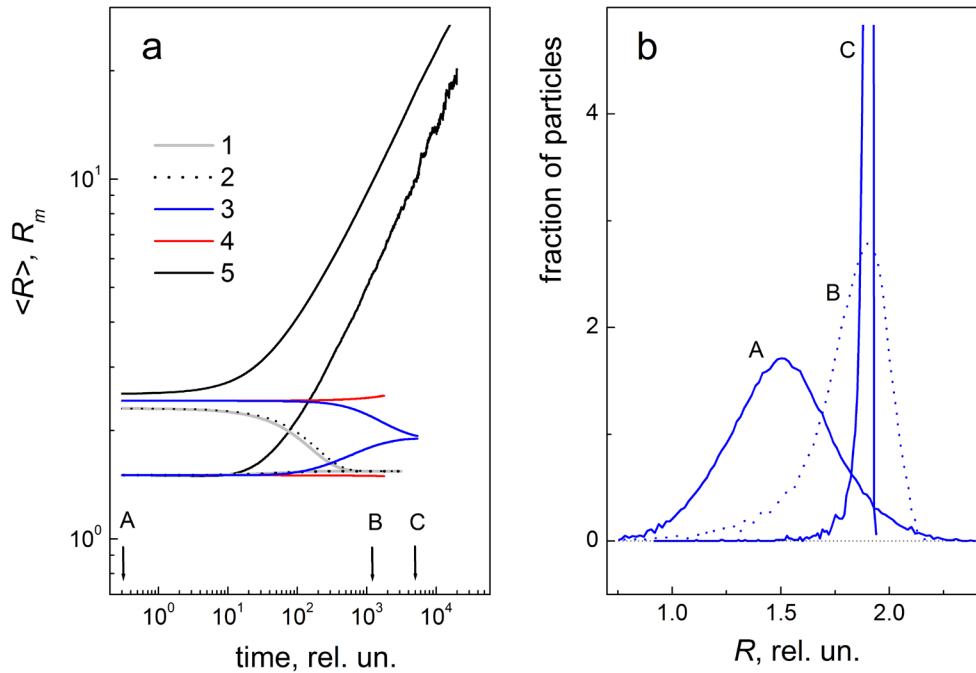
152 The Gibbs-Thomson concentration is given by the equality of molecular chemical potentials in
 153 the particle and solution $T \ln(n_{GT}) = -\varepsilon + 2\Gamma / R$ (see Eq. (2)) taking a more realistic expression for
 154 surface energy γ . This expression is obtained considering the generic expression for particle energy
 155 $\varepsilon(N)$ as a function of the number N of atoms/molecules it contains [54-57]

$$156 \quad -\varepsilon(N) = -\varepsilon + \varepsilon_S \cdot N^{-1/3} + \varepsilon_C \cdot N^{-2/3} + \varepsilon_E \cdot N^{-1} \quad (6)$$

157 where $\varepsilon > 0$ is the bulk contribution to energy (cohesive energy), $\varepsilon_S > 0$ is the contribution of
 158 facets' surfaces, $\varepsilon_C > 0$ is the contribution of edges, and ε_E defines the energy origin (reference
 159 point). Adopting this expression for the generic case of spherical particles with radius R and
 160 neglecting the small energy origin ε_E we use $N \sim R^3$ in Eq. (6) so that the energy per molecule in
 161 a particle (or molecular chemical potential) takes the form $-\varepsilon(R) = -\varepsilon + 2\gamma(R)/R$ with
 162 $\gamma(R) = \gamma_0 + \frac{\gamma_1}{R}$. Both parameters γ_0 and γ_1 are positive, as the former corresponds to true surface
 163 energy for $R \gg 1$, while the latter takes into account non-sphericity effects according to Eq. (6).
 164 With such a generic form, this equation can effectively account also for the contributions to the
 165 surface energy coming from possible roughness of particle surfaces. Therefore, the surface energy
 166 $\gamma(R)$ decreases with increasing particle radius making larger particles relatively more stable. With
 167 this surface energy, the Gibbs-Thomson concentration is now

$$168 \quad n_{GT}(R) = \exp \left[-\frac{\varepsilon}{T} + \frac{2\gamma_0}{T \cdot R} + \frac{2\gamma_1}{T \cdot R^2} - \frac{2}{R} \cdot \ln(1 + n_B E_1) \right] \quad (7)$$

169 Using Eqs (4)-(7) we introduced molecular absorption and emission probabilities by the particle (Eqs
 170 (16)-(17) in Ref [51]) and implemented them in the original Fortran code to simulate the evolution of
 171 10^4 particle ensemble. For illustration purposes we considered two values of γ_1 : 0 and 0.01 eV. The
 172 results shown in Fig. 2 correspond to some realistic values of known model parameters, chosen for
 173 illustrative purpose. We see that both the mean $\langle R \rangle$ and maximum R_m radii continuously grow
 174 with time for $\varepsilon_{AB} = 0.18$, which is characteristic for ordinary coarsening. In contrast, for
 175 $\varepsilon_{AB} > 0.197$ eV the evolution displays reverse coarsening, as the radii $\langle R \rangle$ and R_m both converge
 176 to the same value R_{eq} predicted by Eq. (3), which for $\gamma_1 = 0$ gives the value of R_{eq} very close to
 177 $\langle R \rangle$ of the



178

179 **Figure 2.** a) Time evolution of the mean $\langle R \rangle$ and maximum R_m radii calculated for ensemble of
 180 10^4 particles with Gaussian initial distribution ($\langle R \rangle = 1.5$ and standard deviation $\sigma = 0.25$) obtained
 181 via numerical solution of Eqs (4) - (7) for $T=0.032$ eV (100° C), $\gamma_0=0.1$ eV, $\varepsilon=0.4$ eV and
 182 $n_B \approx 0.002$. The values of ε_{AB} and γ_1 , respectively are (eV units): 1) 0.24 and 0; 2) 0.21 and 0; 3) 0.21
 183 and 0.01; 4) 0.196 and 0; 5) 0.18 and 0. b) PSD corresponding to the curves 3) at the time moments
 184 indicated by arrows in a).

185 initial PSD. For $\gamma_1 = 0.01$ eV, the value of R_{eq} is larger than the average radius $\langle R \rangle$ of the initial
 186 PSD. As discussed, this effective increase in $\langle R \rangle$ in the early stages is due to the mass transfer from
 187 the smaller particles with $\Gamma > 0$ to the bigger particles with $\Gamma < 0$. Clearly, there is a threshold
 188 value for ε_{AB} above which the system displays reverse coarsening. This threshold is determined by
 189 the requirement $\Gamma = 0$ and depends on the surfactant concentration n_B , the molecular-surfactant
 190 interaction energy ε_{AB} , the temperature T , and the size dependence of the surface energy
 191 determined by γ_1 . In the case of $\gamma_1 \approx 0$ the threshold value ε_{AB}^* is estimated for the values in Fig. 1
 192 as

$$193 \quad \Gamma = \gamma_0 - T \cdot \ln(1 + n_B E_1) \approx 0 \rightarrow \varepsilon_{AB}^* \approx 0.197. \quad (8)$$

194 Choosing a surfactant with $\varepsilon_{AB} \approx \varepsilon_{AB}^*$ preserves the initial PSD (see curves 4 in Fig. 2). The
 195 evolution of the PSD is relatively slow (mind the log scale for x-axis in Fig. 2), therefore replacing the
 196 surfactant molecules with those having $\varepsilon_{AB} \approx \varepsilon_{AB}^*$ or $\varepsilon_{AB} > \varepsilon_{AB}^*$ allows to stop or reverse it,
 197 respectively, providing a great opportunity for thermodynamic control of the PSD for generated
 198 nanoparticles. It is worth noting that the values of ε_{AB} generating reverse coarsening must also
 199 have an upper limit, as at values $\varepsilon_{AB} > \varepsilon$, the A-molecules would rather form molecular-surfactant
 200 complexes in the solution than stay bound together as a particle. Therefore, in our case the inequality
 201 $\varepsilon_{AB} < \varepsilon$ must hold. The value of ε_{AB}^* in our simulations is chosen for illustration purpose without

reference to any particular material's surface or binding molecule. Determining ε_{AB}^* in practice is difficult, as it requires measuring the particle's surface energy γ in solution. In our case it is reasonable to demand that ε_{AB}^* is low enough for the surfactant molecules not to affect the particle shape during its growth or dissolution [58]. Note that the fine tuning of the coarsening process, which is determined by the value of the effective surface energy Γ , can be easier achieved by varying the bulk concentration of surfactant molecules n_B and the system temperature T rather than ε_{AB} using different surfactant molecules.

From our simulations, we conclude that the main signature of reverse coarsening is the dissolution of the largest particles in the ensemble. While both the mean and the maximum particle radii increase in ordinary coarsening, the maximum radius in reverse coarsening will, at some point in time, decrease indicating partial dissolution of the biggest particles. This feature is crucial for experimental identification of the reverse coarsening process.

5. Conclusions

We have presented a free-energy analysis and simulation studies of a dilute binary molecular solution with precipitated particles of one component and the other component acting as a surface passivating surfactant. Our analysis predicts that for certain component concentrations and strength of molecular-surfactant interaction, the system of precipitated particles evolves towards equilibrium in such a way that the PSD spontaneously narrows, leading eventually to a mono-sized array of particles. The narrowing of the size distribution is mainly due to a strong enough surface passivation of particle surfaces by surfactant molecules, which renders the effective surface energy of particles negative. The effect is confirmed by direct simulations of the PSD evolution in a large ensemble of poly-dispersed particles. This reverse coarsening effect is a new paradigm for the thermodynamically controlled solution-processed generation of mono-sized nano-particulate arrays of various materials.

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Appendix A

The role of interaction between B-molecules

The above analysis is based on an assumption that the interaction between B-molecules can be neglected. This interaction if high enough may significantly affect the coverage of particle surfaces by B-molecules. In particular, a significant B-B interaction ε_{BB} could promote formation of large B-clusters on the particle surface and even cause complete coverage if the B-cluster grows over its critical size. To illustrate the effect consider the simplified situation of the critical 2D cluster formation of B-molecules on a flat surface of A-crystal. The condition for the critical cluster formation is given by the equivalence of chemical potentials of B-molecules in the surface gas phase of concentration n_s and in the critical cluster of radius r_c , namely $T \ln(n_s) = -\varepsilon_{BB} + \gamma_B / r_c$, where γ_B is the energy per B-molecule on the cluster perimeter. For the critical radius we then obtain $r_c = \gamma_B / (\varepsilon_{BB} + T \ln(n_s))$. Using this one can easily obtain the critical cluster nucleation barrier Δ_c

$$\Delta_c = (-\varepsilon_{BB} - T \ln(n_s)) \cdot \pi r_c^2 + \gamma_B 2\pi r_c = \pi \frac{\gamma_B^2}{(\varepsilon_{BB} + T \ln(n_s))} \quad (\text{A1})$$

Eq. (A1) shows that for the ε_{BB} values such low that $\varepsilon_{BB} + T \ln(n_s) \leq 0$ no critical cluster can be formed therefore the interaction between B-molecules can be disregarded.

Appendix B

Derivation of main equations

To provide details on the derivation of Eqs (2), consider the free energy of the system

$$G = -\varepsilon N_p + \gamma S_p (1 - n_s) - \varepsilon_{AB} n_s S_p + TS_p \cdot [n_s \ln(n_s) + (1 - n_s) \ln(1 - n_s)] - \varepsilon_{AB} N_C + T \cdot (N_C \ln(N_C) + N_A \ln(N_A) + N_B \ln(N_B) + N_L \ln(N_L) - M_\Sigma \ln(M_\Sigma)) \quad (\text{A2})$$

where $\varepsilon > 0$ and $\gamma > 0$ are the cohesive and surface energy per A-molecule, respectively, T is the temperature in energy units (eV), $N_p = 4\pi R^3 / 3$ and $S_p = 4\pi R^2$ (particle radius R is measured in the units of typical intermolecular distance) is the total number of molecules in the A-particle and the number of molecules on particle surface, respectively, N_C , N_B and N_L are the numbers of A-B complexes, B-molecules and solvent molecules, respectively, in the solution, n_s is the concentration of B-molecules on the surfaces of A-particle, which are assumed to be in a gas-type phase. Introduce the total numbers of molecules M_i such that

$$N_A = M_A - N_p - N_C, N_B = M_B - S_p n_s - N_C, M_\Sigma = N_A + N_B + N_C + M_L = M_A - N_p - N_C + M_B - S_p n_s + M_L, M_L = N_L \quad (\text{A3})$$

Taking into account Eqs (A3) we can choose three independent variables: N_p , N_C and n_s . The free energy given by Eq. (A2) is expressed in these variables as

$$G = -\varepsilon N_p + \gamma S_p (1 - n_s) - \varepsilon_{AB} n_s S_p + TS_p \cdot [n_s \ln(n_s) + (1 - n_s) \ln(1 - n_s)] - \varepsilon_{AB} N_C + TN_C \ln(N_C) + T \cdot (M_A - N_p - N_C) \ln(M_A - N_p - N_C) + T \cdot (M_B - S_p n_s - N_C) \ln(M_B - S_p n_s - N_C) + TM_L \ln(M_L) - T \cdot (M_A - N_p - N_C + M_B - S_p n_s + M_L) \ln(M_A - N_p - N_C + M_B - S_p n_s + M_L) \quad (\text{A4})$$

Minimization of G means that $dG = \frac{\partial G}{\partial N_p} \delta N_p + \frac{\partial G}{\partial n_s} \delta n_s + \frac{\partial G}{\partial N_C} \delta N_C = 0 \rightarrow \frac{\partial G}{\partial N_p} = \frac{\partial G}{\partial n_s} = \frac{\partial G}{\partial N_C} = 0$.

Applying this minimization to Eq. (A4) gives

$$\begin{aligned} \frac{\partial G}{\partial N_p} &= -\varepsilon + \frac{2}{R} (\gamma (1 - n_s) - \varepsilon_{AB} n_s + T [n_s \ln(n_s) + (1 - n_s) \ln(1 - n_s)]) + \\ &+ T \ln \left(\frac{M_A - N_p - N_C + M_B - S_p n_s + M_L}{M_A - N_p - N_C} \right) - T n_s \frac{2}{R} \ln \left(\frac{M_B - S_p n_s - N_C}{M_A - N_p - N_C + M_B - S_p n_s + M_L} \right) = 0 \\ \frac{\partial G}{\partial n_s} &= -(\gamma + \varepsilon_{AB}) S_p + TS_p \ln \left(\frac{n_s}{1 - n_s} \right) - S_p T \ln \left(\frac{M_B - S_p n_s - N_C}{M_A - N_p - N_C + M_B - S_p n_s + M_L} \right) = 0 \\ \frac{\partial G}{\partial N_C} &= -\varepsilon_{AB} + T \ln \left(\frac{N_C \cdot (M_A - N_p - N_C + M_B - S_p n_s + M_L)}{(M_A - N_p - N_C) \cdot (M_B - S_p n_s - N_C)} \right) = 0 \end{aligned} \quad (\text{A5})$$

Suppose that $M_L \gg N_A + N_B + N_C$, $M_A \gg N_p + N_C$. Then, after simplification, we have

$$\begin{aligned}
 & -\varepsilon + \frac{2}{R} \left(\gamma(1-n_s) - \varepsilon_{AB}n_s + T \left[n_s \ln \left(\frac{n_s}{n_B} \right) + (1-n_s) \ln(1-n_s) \right] \right) - T \ln(n_A) = 0 \\
 266 \quad & -(\gamma + \varepsilon_{AB}) + T \ln \left(\frac{n_s}{(1-n_s)n_B} \right) = 0 \quad (A6) \\
 & -\varepsilon_{AB} + T \ln \left(\frac{n_C}{n_A \cdot n_B} \right) = 0
 \end{aligned}$$

267 These equations represent the equality of chemical potentials of A-molecules in solution and in the
 268 particle (first line), of B-molecules in solution and on the particle surfaces (second line), and of the
 269 dimers and unbound A- and B-molecules in the solution (third line). The solution to the second and
 270 third equations is given by

$$271 \quad n_C = n_A n_B E_0, \quad E_0 = \exp \left(\frac{\varepsilon_{AB}}{T} \right), \quad n_s = \frac{n_B E_1}{1 + n_B E_1}, \quad E_1 = \exp \left(\frac{\gamma + \varepsilon_{AB}}{T} \right) \quad (A7)$$

272 Substituting n_s into the first of Eqs (A6), we obtain

$$273 \quad T \ln(n_A) = -\varepsilon + \frac{2}{R} \cdot \Gamma, \quad \Gamma = \gamma - T \ln(1 + n_B E_1) \quad (A8)$$

274 Combining Eqs (A7) and (A8) gives Eqs (2).

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