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The Competitive Binding of Proteins to Gold Nanoparticles Disclosed by Molecular Dynamics Simulations

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ABSTRACT: This work reports the results of coarse-grained molecular dynamics simulations of citrate-coated gold nanoparticles (AuNP) in interaction with insulin and fibrinogen, two of the most abundant proteins in the plasma. It has been found that: a) the corona of citrate-coated AuNP of 5 nm core diameter is composed by a single layer of proteins comprising a maximum of 20 insulins, whereas only 3 fibrinogens are contemporaneously present; b) the binding site for insulin is specific and independent from the number of insulins considered in the computational simulations, whereas fibrinogen presents different binding modes, as a function of protein concentration and composition. Moreover, fibrinogen is able to accommodate two citrate-coated AuNPs in independent binding sites localized at the ending nodes; c) a competitive process for AuNP binding is observed when insulins and fibrinogens are contemporaneously present in the simulations; d) the overall proteins secondary structure is maintained upon binding to a single citrate-coated AuNP, but small changes in helix and sheet percentages are observed for both proteins; e) a partial unfolding of the α -helix bundle is found for fibrinogen bound to two AuNPs. This may provide a molecular level understanding of the inflammatory response to nanoparticles.

INTRODUCTION

In the last years, the interest in the interaction of nanoparticles (NPs) with biological medium is grown due to the huge number of possible applications in nano-medicine and nano-technology.^{1,2} It is well known that the contact between NPs and biological medium triggers a competition between different biological molecules to adsorb on the surface of the nanoparticles.³

The composition of the protein corona is unique to each NPs⁴, and mediates the interaction of the NP with biological machineries, eliciting the physiological response (i.e. agglomeration, cellular uptake, circulation lifetime, signaling, kinetics, transport, accumulation and toxicity).⁵

The mechanism of formation of the protein corona is still poorly understood^{2,6,7,8} being a complex process that depends on many parameters, such as the physicochemical properties of the NP (size, shape, composition, surface decoration, and surface charges), the nature of the physiological environment (blood, cell cytoplasm, etc.), and the duration of exposure.

Moreover, the effect of the physico-chemical properties of the NP on the native structure of the absorbed protein has been demonstrated as being potentially responsible for abnormal functions bringing to diseases.⁹⁻¹¹

Precious information on these processes can be gained by computer simulations techniques, which proved to be of tremendous help to understand the structure and dynamics of biological macromolecules in different environments.^{2,7,12,13}

In this work, coarse-grained molecular dynamics simulations of citrate-coated gold nanoparticles (AuNP) in interaction with insulin and fibrinogen will be carried out. These two proteins are among the most abundant in the plasma, show very different physico-chemical properties, and their abnormal conformational changes could promote autoimmune diseases and inflammation.¹⁴⁻¹⁷

To our knowledge, this is the first computational study that addresses the effect of protein concentration, protein competition and multiple AuNPs on the binding modalities of two important proteins. To validate the computational results, a wide comparison with the experimental data available in the literature on these or similar systems will be carried out.^{15,17-19} Moreover, potential biological and toxicological implications will also be discussed.

METHODS

Coarse-grained model

The AuNP of 5nm diameter was built using a coarse-grained model previously described,¹² and summarized as follow:

- 48 positively charged beads (+e) were randomly placed on a spherical surface at 2.5nm from the center of the NP, maintaining an uniform distribution of beads.^{20,21} On the center of the bead distribution, a neutral bead associated with a repulsive spherical wall provides a spherical shape to the AuNP and avoids the penetration of citrates and proteins throughout the AuNP surface.
- 100 beads with negative charge (-3e) representing citrate molecules were randomly distributed in the AuNP surroundings.
- A 100ns molecular dynamics simulation was performed on a simplified system formed by the AuNP and 100 citrates in order to determine the maximum number of citrates adsorbed on the AuNP surface. The plateau in the graph “number of bound citrates vs time” was reached after 80ns for 37 citrate molecules.

The last simulation frame was used as input for the protein-AuNP simulations, after deletion of unbound citrates. The extended-diameter of the AuNP after citratre-coating is 5.7nm.

The crystal structures of fibrinogen and insulin were retrieved from the Protein Data Bank (PDB): the fibrinogen 3GHG²² and insulin 4EWZ²³ structures were chosen as they show the best resolution and the highest homology with the wild-type structure among all the structures deposited in the PDB. The proteins were treated with a CG single-bead model: each amino acid was replaced by a single bead with the same mass and total charge of the related amino acid and with the same coordinates of the α -carbon atom. The approach used was necessary to reduce the high computational cost given by the number of proteins involved, and to maintain a good spatial and temporal resolution.²⁴⁻²⁷

The standard protonation states at pH 7 were assigned to the treatable aminoacid residues of the proteins.

Force field

The force field used to model proteins-AuNP interactions¹² is briefly summarized:

$$U = \sum_{i,j} U_{bonded} + \sum_{i,j} U_{non-bonded} \quad (1)$$

where :

$$\sum_{i,j} U_{bonded} = \sum_{i,j} U_{bonds}(i,j) + \sum_{i,j,k} U_{angles}(i,j,k) + \sum_{i,j,k,l} U_{dihedrals}(i,j,k,l) \quad (2)$$

$$\sum_{i,j} U_{non-bonded} = \sum_{i,j} U_{non-bonded}^{local}(i,j) + \sum_{i,j} U_{non-bonded}^{non-local}(i,j) \quad (3)$$

The functional form of the force field comprises a short-terms potential (U_{bonded}) and a long-term potential ($U_{non-bonded}$). The first term describes bonds, angles and dihedrals of proteins. Parameters related to these potentials (R , θ_0 and φ_0) are calculated on the reference structure of proteins. Force field parameters for proteins are reported in ref.s²⁵⁻²⁷. Citrates force field parameters are adapted from Ding *et al.*²⁸ All parameters are described in Table S.1 in the SI.

Non-local non-bonded interactions describe Van der Waals and electrostatic potentials established between the AuNP and the protein and among protein beads. Protein beads that are closer to the cutoff of 8.5Å interact through non-bonded local terms, while beads beyond the cutoff interact with non-local non-bonded terms. The cutoff for the non-local non-bonded terms is set to 30Å in order to take into account interactions with the repulsive spherical wall of the central gold bead.

Proteins-AuNP and citrates-AuNP interactions are accounted for by Van der Waals and electrostatic terms described by Li *et al.*²⁹. VdW interactions describe excluded volume interactions between two beads distant r_{ij} :

$$U_{vdW} = \sum_{i,j} \frac{\sigma^6}{r_{ij}^{12}} \quad (4)$$

where σ is the reference radius set to 3.8Å.

Electrostatic interactions between two beads of charge z_i and z_j at a distance r_{ij} are given by the Debye-Hückel potential:

$$U_{elec} = \sum_{i,j} \frac{z_i z_j e^2}{4\pi\epsilon_0\epsilon_r r_{ij}} e^{-\frac{r_{ij}}{l_D}} \quad (5)$$

where l_D is the Debye length defined as $l_D = (8\rho l_b I)^{-\frac{1}{2}}$ and l_b is the Bjerrun length at room temperature which is set to 7Å. The ionic strength (I) is set to an ion concentration of 150 mM, and the dielectric constant, ϵ , is set to 10 to maximize the speed of the corona formation process and to avoid very long computational times.

Notwithstanding the significant approximations made in codifying the attracting forces, this force field showed to be able to represent the corona formation in reasonable agreement with the available experimental data.^{12,30}

Molecular dynamics

Molecular dynamics simulations were performed using the DL_POLY_2.20 software.³¹ The temperature of the system was maintained constant at 300K using the Berendsen thermostat. The time-step used is 1fs and. Each trajectory is 50ns long; this is the time required to reach the a stable number of proteins is adsorbed on the AuNP surface. Three independent simulations have been performed for each system by changing the initial starting velocities in order to increase the statistics of the production runs.

Two kinds of simulations were performed:

1. The two systems AuNP-insulins and AuNP-fibrinogens were simulated separately by changing the number of proteins in the simulations in order to study the effect of protein concentration on the maximum number of adsorbed proteins. Simulations were performed with 10, 20, 34, 50, 70 and 100 insulin proteins and with 1, 2, 4 and 8 fibrinogen proteins. The AuNP was fixed at the center of a cubic box with boundary periodic conditions. The citrate molecules were free to move.
2. To observe the competitive binding of the two proteins, computational simulations at different insulin/fibrinogen ratio (10:1, 20:2, 34:4) were carried out.

Electrostatic potential surfaces

The electrostatic potential surfaces of insulin and fibrinogen are calculated using the built-in plugin of the Swiss-Pdb Viewer³² using the same parameters as used in molecular dynamics simulations, that is, a ionic strength I of 150 mM and a dielectric constant ϵ of 10.

Contact probability between Proteins and citrate-coated AuNP

The contact probability for each amino acid residue is defined as the ratio of the amount of time in which the distance of a given amino acid residue of the protein X from the NP surface is less than a given cutoff (6.5 Å), and the amount of time in which the protein X remains adsorbed on the NP surface. These values are normalized in order to obtain the sum of all probabilities equal to 1.¹²

Insulins are considered adsorbed on the AuNP if the distance between the center of mass of the protein and the AuNP surface is closer than 19Å. This value is estimated by considering the center of mass of insulin at 10Å from its surface plus a bonding distance of 9Å in order to take into account insulins bonded to citrates on the AuNP surface besides the insulins directly adsorbed on the AuNP surface. The shape and compact structure of this protein justify this approximation.

Due to its elongated shape, the procedure described above is not suitable for fibrinogen. In this case, the number of fibrinogens bound to the AuNP are simply counted by visualization of the trajectory of the simulations using the VMD software.³³

Proteins conformational changes

Atomistic representations of each coarse-grained protein were re-mapped using the MaxSprout webserver.³⁴ The backbone dihedral angles of each reconstructed structure were calculated using the built-in Ramachandran plot tool.³²

Conformational changes of the protein upon binding to the citrate-coated AuNP were computed on the last configuration reached by each adsorbed protein. Free proteins were not used for calculations.

Protein binding energy

The total energy of the systems considered can be defined as follows:

$$E_{tot} = E_{citrate-AuNP} + \sum_n \dot{A} E_{prot} + E_{interaction} \quad (6)$$

where $E_{citrate-AuNP}$ is the total energy of the citrate-coated AuNP, and $\sum_n \dot{A} E_{prot}$ is the summation over

the internal energy of all proteins in the system. Moreover,

$$E_{interaction} = E_{prot-prot}^{interaction} + E_{binding}^{all} \quad (7)$$

where $E_{prot-prot}^{interaction}$ refers to the interaction energy among all the proteins in the simulation box, and

$E_{binding}^{all}$ is the binding energy of the adsorbed proteins with the citrate-coated AuNP. By replacing the

interaction energy term, $E_{interaction}$, in eq (6), and simplifying:

$$E_{binding}^{all} = E_{tot} - E_{citrate-AuNP} - \sum_n \dot{A} E_{prot} - E_{prot-prot}^{interaction} \quad (8)$$

The summation of the total internal energy of proteins and the interaction energy between proteins is calculated as the total energy of all proteins, E_{prot}^{total} .

All energy terms were obtained by averaging four energy minimized configurations sampled at 42ns, 45ns, 48ns and 50ns, when the maximum number of adsorbed proteins is reached. A 100 steps minimization procedure was performed for each selected configuration before energy computation in order to remove unphysical contacts without changing significantly the system conformation.

The binding energy for each protein, $E_{binding}$, is obtained dividing the overall binding energy, $E_{binding}^{all}$, by the number of adsorbed proteins in each simulation.

It is worth underlining that, although the maximum adsorption capacity for the computational simulation with 10 insulins is six, the calculation of $E_{binding}$ has been performed by sampling configurations containing only four adsorbed proteins on the AuNP, since the last two insulins adsorb only in the late stage of the computational simulations.

Interaction of Fibrinogen with two AuNPs

The interaction of a single fibrinogen molecule with two AuNPs has also been investigated. In this case, one molecule of fibrinogen was positioned in a cubic box with two citrate-coated AuNPs having a gold core of 5nm diameter (extended-diameter, after citrates coating: 5.7nm) positioned at approximately 30nm from its center of mass. In order to explore multiple configurations the fibrinogen and the two citrate-coated AuNPs were allowed to move freely.

Harmonic potentials with constant of 5000Kcal/mol and a cutoff of 1nm were applied to the AuNP beads in order to maintain the nanoparticle structure rigid. The total mass of the AuNP is partitioned among the gold beads.

RESULTS AND DISCUSSION

The results obtained by coarse-grained molecular dynamics simulations of different amounts of insulins and fibrinogens interacting with a citrated-coated AuNP of core diameter 5 nm are described in the following in terms of corona formation and composition, proteins binding sites, structural changes upon binding, competitive proteins adsorption, and multiple NP binding.

Insulin and fibrinogen are among the most abundant proteins in the plasma and show very different structural characteristics.

Insulin is a small protein, which promotes the adsorption of glucose to skeletal muscles and it is responsible for lipid storage in fat tissue. It is a dimer made by two chains (A, and B), respectively of 21 and 30 amino acids, linked via two disulfide bonds with a compact round-shape tertiary structure and a molecular weight of 5.808 kDa.²³

Fibrinogen is a rod-shaped protein, converted by thrombin into fibrin during the blood coagulation process. It has a molecular weight of 340kDa and comprises three different polypeptide chains (α , β

and γ), arranged as a dimer. The elongated structure is approximately 45 nm long, and diameter ranges from 1.7nm to 4.55nm.²²

Corona formation

In the first series of computational simulations, the formation of the corona has been investigated by varying the total number of insulin proteins (10, 20, 34, 50, 70 and 100) in the simulation box.

The number of proteins absorbed as a function of time for different protein concentrations is reported in **Figure 1a**. As expected, the number of absorbed insulins depends on the protein concentration considered. The maximum adsorption capacity of the citrate-coated AuNP with an extended diameter of 5.7nm is 20, and it is reached after 40 ns, when 70 and 100 proteins are included in the simulation box.

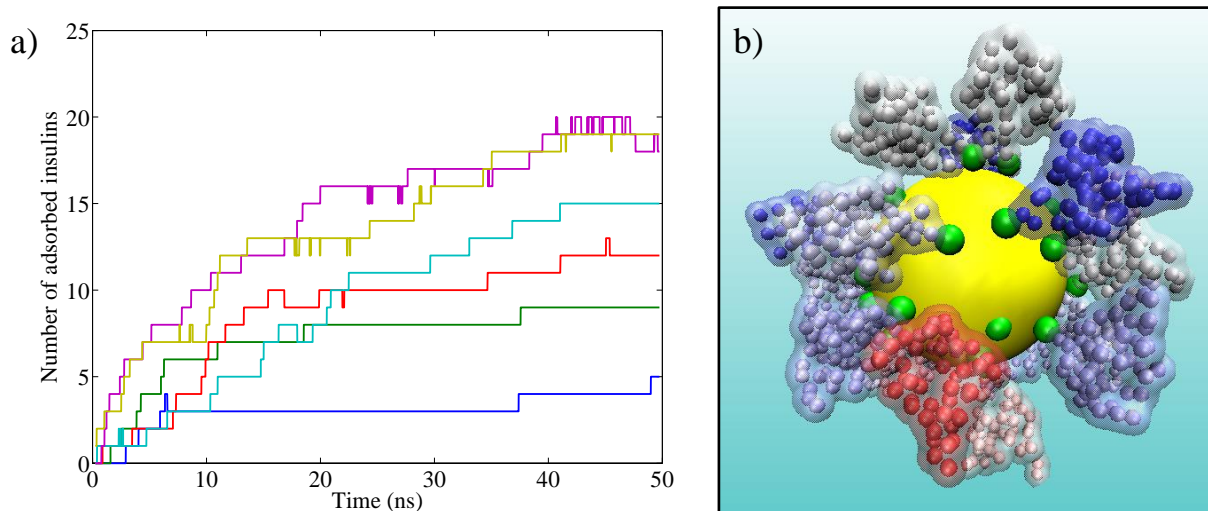


Figure 1. a) Moving average of the number of insulin proteins bound to the citrates-coated AuNP during the computational simulation for different protein concentrations: 10 insulins in blue, 20 in green, 34 in red, 50 in cyan, 70 in purple and 100 in brown. The moving average is performed over 25 timesteps in order to smooth out short-term fluctuations. b) Snapshot of the protein corona around the citrate-coated AuNP made by 20 insulins. The snapshot has been taken from the computational simulation with 70 insulins at 45ns, the insulins non-interacting with the AuNP are omitted for clarity

reason. The coarse-grained models of the proteins are represented different colors; citrates are represented in green.

In all cases, the corona is composed by a single layer of proteins (see **Figure 1b**, and **Figure S1** in **SI**). In fact, at variance with the results obtained for other proteins such as ubiquitin¹², only a limited tendency for aggregation of insulin proteins is highlighted in this study. The formation of a few dimers with a lifetime ranging from 1 to 3.5ns is observed only occasionally, and, in simulations with 100 insulins two clusters made of three insulins, linked by a citrate molecule are found.

The results of the series of computational simulations carried out with the fibrinogen proteins show that the maximum number of proteins that can bind to the citrate-coated AuNP is 3. Moreover, the probability of finding 1 or 3 proteins interacting contemporaneously with the AuNP is similar, i.e. 43%, and 37.5%, respectively. This unexpected result (fibrinogen is 45nm long, i.e. ten times the AuNP diameter) is due to the binding modalities of fibrinogen, that will be described in details in paragraph 2.2.

Several numerical methods for the estimation of the adsorption capacity of a nanoparticle of given size have been published^{4,35,36}, they mainly differ for the approximations made to consider the protein size and shape (see paragraph S.3 in SI for details).

Table 1 lists the results obtained with the methods of Calzolari *et al.*³⁵, Dell'Orco *et al.*⁴ and Wang *et al.*³⁶, together with the results obtained from the computational simulations carried out in this work.

Table 1. Maximum number of proteins that can bind to a gold nanoparticle (N_{\max}) with a gold core diameter of 5nm, calculated according to different numerical methods, and from the computational simulations carried out in this work for insulins and fibrinogens.

N_{\max}			
Calzolari ³⁵	Wang ³⁶	Dell'Orco ⁴	This work

Insulin	12	25	36	20
Fibrinogen	1 (1.4)	1 (0.7)	7 (6.7)	3

The values $R_{\text{protein}}(\text{insulin})=1.25\text{nm}$, $R_{\text{protein}}(\text{fibrinogen})=8\text{nm}$, $R_{\text{gyra}}(\text{insulin})=0.995\text{nm}$ and $R_{\text{gyra}}(\text{fibrinogen})=5.97\text{nm}$ have been used to compute data listed in the first three columns.

From the analysis of the data, the limitations of the approximation at the basis of the numerical methods considered is evident. In fact, a good agreement with the results of the computational simulations is obtained only for insulins in the case of the method of Wang et al.³⁶, which takes into account the radius of gyration of the protein.

The marked discrepancy with the number of adsorbed fibrinogens computed with the method of Dell'Orco *et al.*⁴ is mainly due to the crude approximation of the protein shape to a sphere of radius 8nm, and to the differences in the dimension of the NP considered (35 nm in ref. ⁴).

Proteins conformational changes upon binding

The Ramachandran plots reported in **Figure 2** show that the binding of the proteins to the citrate-coated AuNP induces a degree of disorder in their three-dimensional structure, although the overall conformation of both proteins is maintained.

The **insulin** protein (**Figure 2a**) shows a decrease in both the α -helix and β -sheets content upon binding with respect to the X-ray structure. However, this conformational change seems not to be due to the citrate-coated AuNP but to the dynamics of the protein at room temperature, since it is also observed in solution (NMR structure, pdb code 1HLS³⁷). In fact, the % of α -Helices and β -Sheets content is: 40.9 ± 10.2 and 2.1 ± 6.4 in the MD simulation, 47 and 0 in the NMR structure, 48.9 and 10.6 in the X-ray (4EWZ²³) structure, respectively.

The Ramachandran plot of fibrinogen reported in **Figure 2b** shows differences in the secondary structures elements with respect to the starting configuration (crystal structures 3GHG²²: blue stars)

of the fibrinogen. However, on average, the variation in the α -helices and β -sheets content is in the order of the 2% and 3%, respectively.

These findings are in agreement with circular dichroism (CD) and fluorescence observations on the interaction between gold NPs of different diameters and common blood proteins: in general, small NPs better retain native-like protein structure and function in comparison with larger NPs.³⁸

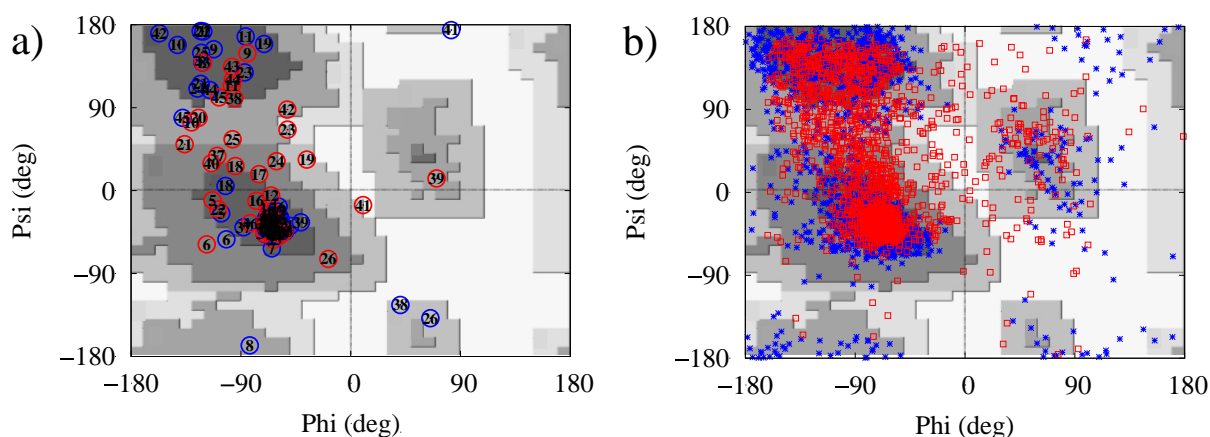


Figure 2. Ramachandran plot of a) insulin, and b) fibrinogen. In blue data from the X-ray structure and in red the data obtained, from the computational simulations, as mean of the dihedral angles computed on the adsorbed proteins. In b) numbers refer to the dihedral angle involved, while in a) labels are omitted for clarity.

Protein binding site

The protein binding site can be identified by the analysis of the contact probability of each amino acid residue with the surface of the citrate-coated AuNP. The results for the insulin proteins are reported in **Figure 3**.

As demonstrated in a previous study on the interaction between ubiquitins and AuNPs of different sizes¹², the area of the protein more suitable for the interaction is characterized by the presence of

both positive and negative charges that can interact respectively with citrates and gold beads of the AuNP.

The electrostatic potential surface of insulin (reported in **Figure 3b**) shows that the region in the last half of the B chain (represented in red in **Figure 3a**) possesses this characteristic. In particular, the most significant contacts with the positive gold charged beads are made by E42 and the C-terminal of chain A (N21), whereas R43 and K50 interact with the negative citrates beads bonded to the AuNP (**Figure 3d**).

These residues are spatially close together, (**Figure 3c**) and define a specific contact probability area in line with the experimental results of SERS evaluation of the insulin-AuNP interactions, which showed that many functional groups, predominantly the carboxy groups, participate in bonding to the surface.¹⁴

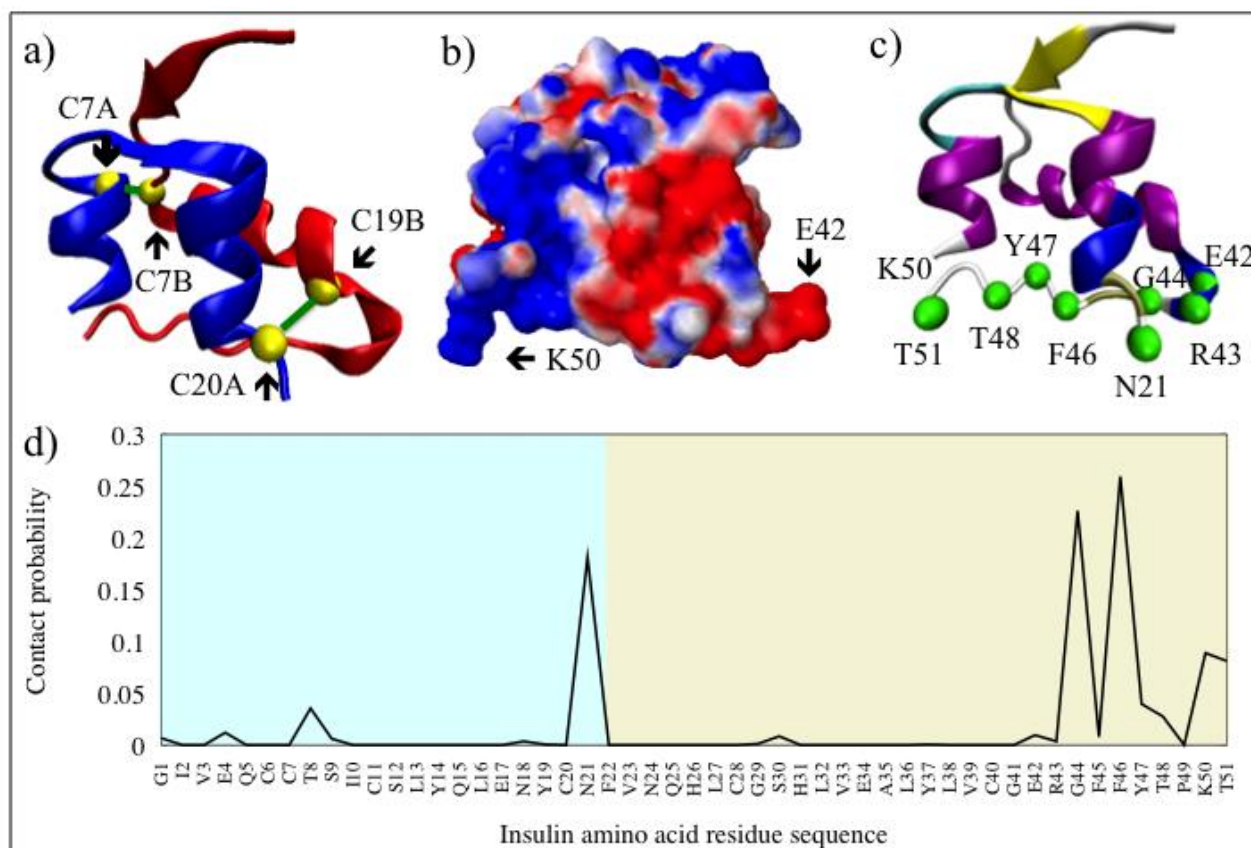


Figure 3. a) cartoon representation of the CG model of insulin (PDB ID: 4EWZ): chain A is colored in red and the chain B in blue. Aminoacids forming disulfide bonds are highlighted in yellow. b) Electrostatic potential surface of insulin (atomistic level) where red areas represent negative potential and blue areas represent positive potential. c) Cartoon representation of the CG model of insulin colored according to its secondary structure. Green beads represent the residues with high contact probability. d) Contact probability of insulins amino acid residues with the citrate-coated AuNP surface: cyan area represents the chain A and the beige area the chain B. A bead is considered to be in contact with the AuNP if its mean contact probability is greater than 0.001.

The interaction established by these amino-acid residues with the citrate-coated AuNP appears to be independent from the number of insulins considered in the computational simulations (and from the number of bound protein), as shown by the analysis of the binding energy per protein (E_{binding}), computed according to eq. 8, and listed in **Table 2**. Indeed, while cooperative binding was observed experimentally for absorption of insulin to 100 nm NPs, little influence was observed on subsequent adsorption events to smaller nanoparticles (5nm).³⁸

Table 2. Binding energies as a function of the concentration of adsorbed proteins.

Insulins					
N_{tot} (N_{bound})	E_{tot}	$E_{\text{citrates-AuNP}}$	$E_{\text{prot}}^{\text{total}}$	E_{binding}	$\pm DE_{\text{binding}}$
10 (4)	-1885.0	-1521.0	-321.3	-10.7	8.7
20 (9)	-2270.2	-1551.5	-633.0	-9.5	1.4
34 (12)	-2840.2	-1609.7	-1060.7	-14.1	1.3
50 (15)	-3363.0	-1584.7	-1542.7	-15.7	3.0
70 (20)	-3870.7	-1543.7	-2136.0	-9.82	2.2
100 (19)	-4866.7	-1611.0	-3090.5	-8.7	2.1
Fibrinogens					
N_{tot} (N_{bound})	E_{tot}	$E_{\text{citrates-AuNP}}$	$E_{\text{prot-prot}}^{\text{interaction}}$	E_{binding}	$\pm DE_{\text{binding}}$
1 (1)	-5926	-1450	-3696	-780	17
2 (1)	-10420	-1615	-7950	-855	35
4 (1)	-18355	-1584	-16065	-706	56
8 (3)	-33448	-1589	-32227		

N_{tot} refers to the total number of proteins in simulation, while (N_{bound}) to the number of adsorbed proteins in simulation and $\pm DE_{\text{binding}}$ is the absolute error of the binding energy. Energies are expressed in Kcal/mol.

Visual inspection of the trajectories reveals that the orientation of the insulins in an upright position on the AuNP surface with the N-terminal of the second chain upward is maintained in all the computational simulations, and the variation in the binding energies depends mainly on the rearrangement of the citrates on the AuNP surface upon protein binding, that takes place in approximately 1-2ns.

Nonspheroid or fibrous proteins, such as fibrinogen (**Figure 4a**), can interact with a surface in a number of configurations (**Figure 4c**). Both side-on and end-on binding of fibrinogen to different substrates have been described in the literature.^{39,40} The electrostatic potential surface of **fibrinogen** is much less polarized with respect to the one of insulin, and shows small negative and positive areas disseminated over the whole molecule, (**Figure 4b**). In general, the molecular surface in the region comprising the boundary between the α -nodule and the β -nodule seems to possess the best characteristics required for the interaction with the citrate-coated AuNP. In fact, the most probable contacts are established with amino acid residues belonging to the α - and β -nodules (end-on-1 configuration), as highlighted in **Figure 4c** and **4d**. However, being the binding less specific with respect to the insulin protein, the overall contact probability is lower.

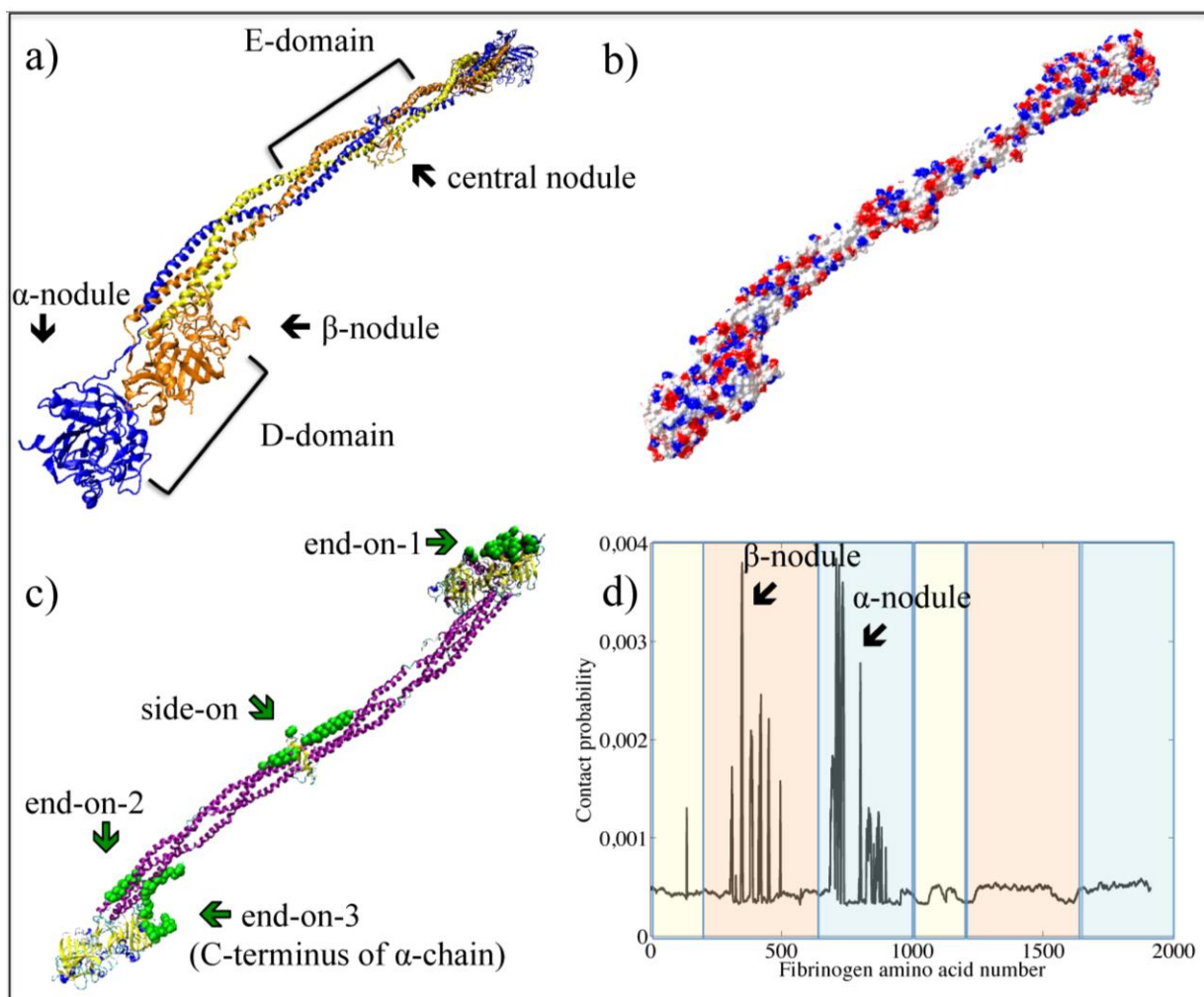


Figure 4. a) cartoon representation of the CG model of fibrinogen (PDB ID: 3GHG) where each nodule is labeled: the α -chain is coloured in yellow, the β -chain in orange and the γ -chain in blue; b)

electrostatic potential surface of fibrinogen (atomistic level) where red areas represent negative potential and blue areas represent positive potential. c) Cartoon representation the CG model of fibrinogen colored according to its secondary structures. Green beads represent the residues with high contact probability with the citrate-coated AuNP (binding regions). d) Contact probability of fibrinogens with the AuNP surface. Different colored areas represent the three distinct fibrinogen chains: α -chain in yellow, β -chain in orange and γ -chain in blue. A bead is considered to be in contact with the AuNP if its mean contact probability is greater than 0.0007.

In the computational simulations carried out with 8 fibrinogens, three fibrinogens are interacting contemporaneously with the AuNP. Differences in the contact areas of each fibrinogen can be appreciated among the three molecules. Besides the area between the α - and β -nodules described formerly (end-on configuration, named end-on-1 in **Figure 4c**), the ending part of the β -nodule (end-on-2 in **Figure 4c**), and the region between the β -nodule and the α -helix (end-on-3 in **Figure 4c**) are also involved in the interaction (**Figure 4c**).

An exception to this general interacting behaviour mainly involving the β -nodule and surrounding regions is observed in the computational simulation with 4 fibrinogens. In this case, only one molecule interacts with the AuNP, and the interacting site is localized on the central nodule (side-on) (**Figure 4c**).

The energetic consequences of the different binding modes are described in **Table 2**. In the first two computational simulations, with 1 and 2 fibrinogens respectively, the binding mode and kinetic is almost the same (end-on-1, **Figure 4**) and the binding energies differ mainly for the citrate rearrangement on the AuNP surface. The interaction of fibrinogen via its central nodule (side-on, **Figure 4**) is less favoured. In the simulation with 3 bound fibrinogens, the computed binding energy (not reported in **Table 2**) is positive due to steric hindrance among the three proteins. However, visual

inspection of the trajectories shows that the proteins remain persistently bound to the AuNP through the citrate molecule.

The results obtained for fibrinogens are in contrast with the experimental observations of little effect on competitive or cooperative fibrinogen binding to small nanoparticles (5nm)³⁸, probably because the high curvature of the NP increases the deflection angle between adsorbed proteins, decreasing protein–protein interactions.⁴¹

Competitive binding of insulins and fibrinogens

A number of computational simulations has been carried out with different amount of insulin and fibrinogen proteins contemporaneously present in the simulation box in order to get some light into the mutual effect of the two proteins on their binding modalities. In particular, the relative concentrations of insulin/fibrinogen of 10:1, 20:2, 34:4 have been considered. The results obtained, listed in **Table 3** show a competition of these two kinds of proteins for binding with the citrate-coated AuNP. The presence of fibrinogens in the computational simulation box significantly reduce the number of insulins, which bind the citrate-coated AuNP.

Table 3. Number of proteins adsorbed on the AuNP when both proteins are present in the computational simulation box.

Proteins	Insulin						Fibrinogen			
N of Proteins in the simulation box	10	20	34	50	70	100	1	2	4	8
N of Proteins Adsorbed (after 50ns)	5	9	12	15	20	19	1	1	1	3

Proteins	Insulin + Fibrinogen								
N of Proteins in the simulation box	10	+	1	20	+	2	34	+	4
N of Proteins Adsorbed (after 50ns)	3	+	1	1	+	0	2	+	0

The dynamics of the interaction is explained in **Figure 5**. In the computational simulation concerning the 10:1 protein ratio (**Figure 5a**), two insulins adsorb before the binding of fibrinogen, which occurs at around 20 ns of the dynamic run. A rearrangement of the proteins on the citrate-coated AuNP surface allows a third insulin molecule to be adsorbed after ~8ns. The four proteins remain contemporaneously bounded to the nanoparticle for ~15ns, then a steric repulsion occurs between the fibrinogen and the first molecule of insulin bounded, forcing the insulin dissociation. When the relative concentration of insulins and fibrinogens is 20:2 (**Figure 5b**), only one insulin adsorbs onto the AuNP surface after 30 ns of the computational simulation. At approximately 45ns a fibrinogen approaches the AuNP through its α -helix coiled coil region, but electrostatic repulsions with the adsorbed insulin occurs. Therefore, the fibrinogen moves away, whereas the insulin remains bounded to the nanoparticle. In the computational simulation with 34 insulins and 4 fibrinogens (**Figure 5c**), up to three insulins adsorb on the AuNP surface after 20 ns. These remain absorbed for 40 ns, and then a fibrinogen approaches the nanoparticle, interacts with an adsorbed insulin, and, being rejected, moves away provoking the dissociation of the insulin itself. After the first contact that provoked insulin desorption, insulin and fibrinogen move away from the nanoparticle independently.

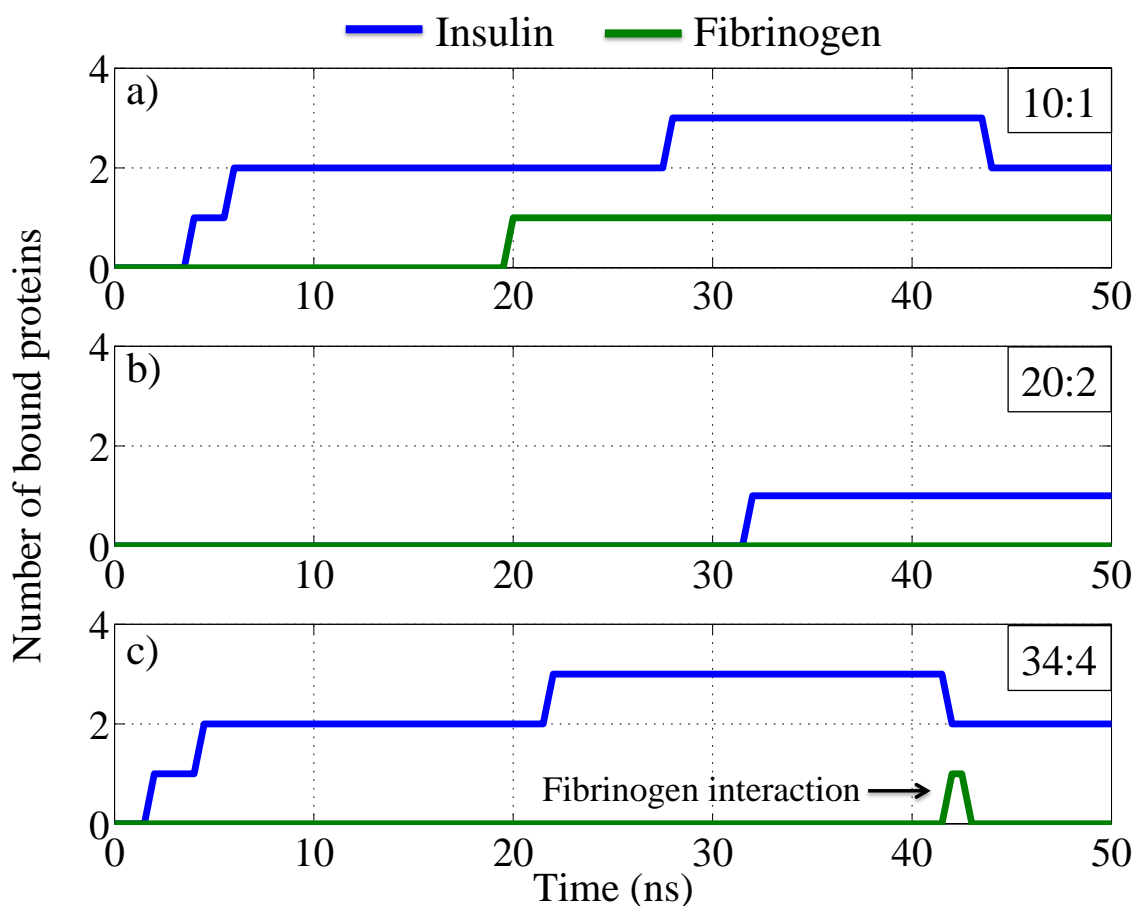


Figure 5. Number of proteins adsorbed on the citrate-coated AuNP as a function of time for the ratio Insulin:Fibrinogen of 10:1 (a), 20:2 (b), 34:4 (c). The blue line represents the number of insulins, and the green line the number of fibrinogens adsorbed on the AuNP during the computational simulation time.

The binding site of insulin in all the computational simulations with fibrinogens is the same as reported in Section 2.2, whereas the fibrinogen adsorbs mainly via the α -helix bundle close to the β -nodule. Insulin-fibrinogen interactions are not observed during the computational simulations.

Unfortunately, only the results of experimental determination of binding constants and the degree of cooperativity of single protein-NP³⁸ are available, whereas there is no other study that explores competitive or cooperative binding effects among different proteins.

Fibrinogen interaction with two AuNPs

The results of an experimental characterization of the molecular interaction between fibrinogen and negatively charged poly(acrylic acid)-coated AuNP of different size, suggested that a single fibrinogen can bind up to two AuNPs with a core diameter of 5.7 nm.¹⁷

In this line, a molecular dynamics simulation of a single fibrinogen in a cubic box with two citrate-coated AuNPs with a 5nm core diameter (extended-diameter citrates and AuNPs, is 5.7nm) was carried out.

After 50ns the two AuNPs bind to fibrinogen in two distinct ways, both localized in the ending nodes of the protein, in agreement with the two independent binding sites found by Deng *et al.*^{17,42} on the basis of the measured Hill coefficient for the binding kinetics. As shown in **Figure 6a**, the first AuNP binds to the end surface of the α -nodule (end-on-1), and the second one to a region between the β -nodule and the α -chain (end-on-3). The first binding topology is the same observed as the most probable in the computational simulations carried out on 1 fibrinogen and 1 citrate-coated AuNP (Section 2.3). This is in agreement with the model proposed by Deng *et al.*,¹⁷ based on the complementarity of the charge surfaces.¹⁶ The second binding topology is the same observed in the computational simulations carried out on 2 and 8 fibrinogens and 1 citrate-coated AuNP (Section 2.3), and reproduces the binding of fibrinogen in the end-on configuration, usually evocated in the literature^{17,16} when fibrinogen proteins bind large NP (31.5 and 64.5 nm diameter).

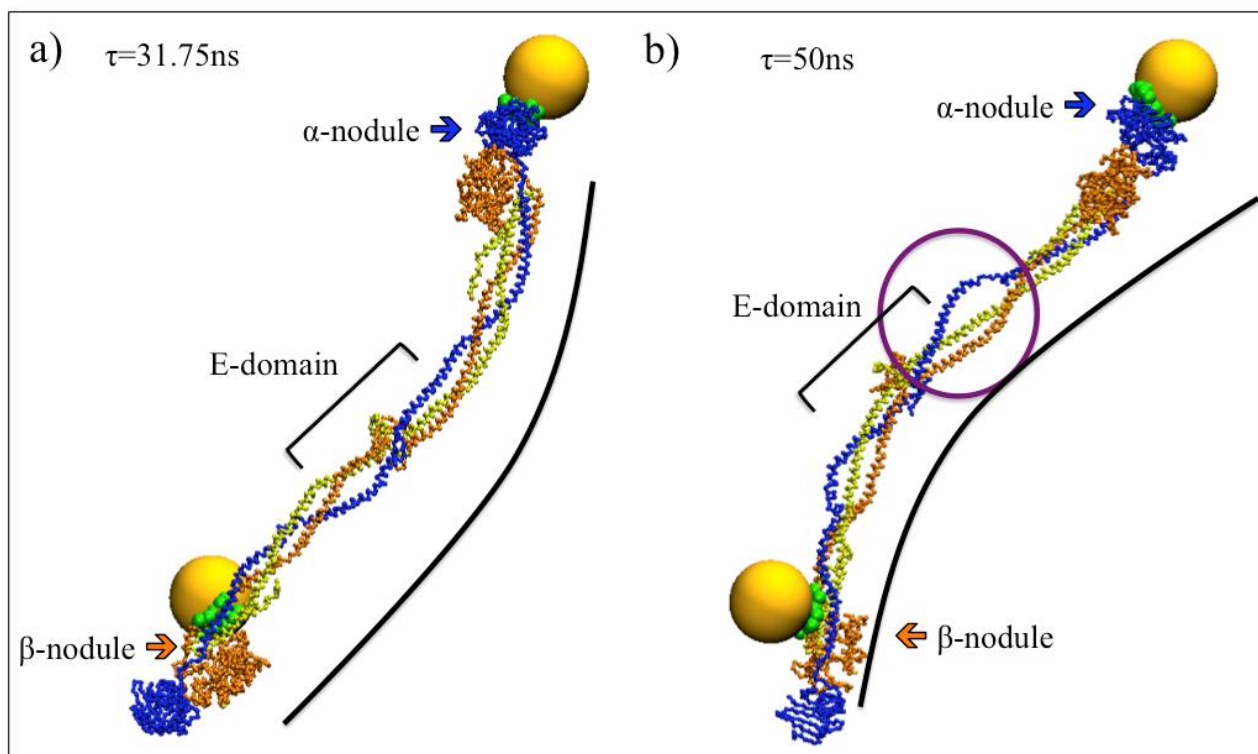


Figure 6. Snapshots of fibrinogen, at CG level, bonded to two citrate-coated AuNPs taken at two different timesteps (31.75ns and 50ns) during the dynamics simulation. Green beads represent amino-acids in contact with AuNPs. Black line shows the bending of fibrinogen along its principal axis. In b) the purple circle shows the partial unfolding of the α -helix bundle near the central nodule.

It is worth noting that fibrinogen shows a propensity to bend along its principal axis when both the citrate-coated AuNPs are adsorbed. The bending originates at the central E-domain, as shown in **Figure 6**. Indeed, this is in line with the results of electron microscopy studies which depict the fibrinogen as a relatively flexible molecule: most molecules exhibit a θ value of 0.5° , while a few could bend as much as 90° , the average angle of bend (θ) at the E-domain being 22° .⁴³

The average angle of bend (θ) at the E-domain in the computational simulations carried out in this work is in agreement with the experimental value ($\sim 20^\circ$), and is almost the same before and after the binding of the 2 citrate-coated AuNP. However, the distribution of the θ angle values found during the computational simulations is narrower after AuNP adsorption, indicating a restricted mobility of the protein (see **Figure S2** in SI).

Moreover, a partial unfolding of the α -helix bundle near the central nodule, highlighted with the purple circle in **Figure 6b**, is observed in the last part of the dynamics run. A loss of α -helical content upon bounding 11-mercaptoundecanoic acid-functionalized AuNPs of different sizes (5.6 and 14.2 nm diameter) was also highlighted by the results of far UV-CD spectroscopy.⁴²

This phenomenon has relevant biological implication since it involves the exposition of a cryptic peptide located in the C-terminus of the fibrinogen γ -chain, which specifically interacts with the integrin receptor, Mac-1. Activation of this receptor increases the NF- κ B signalling pathway, resulting in the release of inflammatory cytokines.¹⁶

CONCLUSIONS

The results of coarse-grained molecular dynamics simulations of insulins and fibrinogens interacting with citrate-coated AuNPs of 5nm core diameter have furnished a detailed description of the process of corona formation.

Several effects have been explored: a) the physico-chemical characteristics and concentrations of each kind of protein with respect to NP adsorption; b) the mutual competition of insulin and fibrinogen on the NP binding process; c) the binding of two NPs to fibrinogen; and d) the protein conformational changes upon NP binding.

A maximum of 20 insulins can bind to citrate-coated AuNP of 5 nm core diameter, whereas only 3 fibrinogens are able to make persistent interactions with the AuNP, contemporaneously. In all cases, the corona is composed by a single layer of proteins, only a limited tendency for aggregation being highlighted in this study.

The binding site for insulin is specific and constituted mainly by the C-terminal residues of the two dimer-chains, in line with experimental results; moreover, it is independent from the number of insulins considered in the computational simulations, as showed also by the computed binding energies per proteins. The binding site for fibrinogen is less specific, in general it is located at the

boundary between the α -nodule and the β -nodule (end-on-1 configuration), however, the ending part of the β -nodule (end-on-2), the region between the β -nodule and the α -helix (end-on-3), and the central nodule (side-on) are also involved in the interaction.

When insulins and fibrinogens are simulated together with the AuNP, a competitive binding process is observed. In particular, the number of adsorbed proteins shows a marked decrease with respect to the single proteins simulations. The binding site of insulin in all the computational simulations with fibrinogens is the same as observed for insulin alone, whereas the fibrinogen adsorbs mainly via the α -helix bundle close to the β -nodule (end-on-3 binding mode). Insulin-fibrinogen interactions are not observed during the computational simulations.

In agreement with experimental observations, fibrinogen is able to accommodate two citrate-coated AuNP in two independent binding sites localized in the ending nodes of the proteins.

The overall proteins secondary structure is maintained upon binding to a single citrate-coated AuNP, but changes in helix and sheet content percentages are observed for both proteins. Interesting is the propensity of fibrinogen to bend at the E-domain, and the restricted mobility of the chain observed in the computational simulations carried out with two AuNPs. This triggers a partial unfolding of the α -helix bundle near the central nodule. Since the conformational state of fibrinogen is critical to leukocyte activation, this phenomenon may provide a molecular level understanding of the inflammatory response to nanoparticles.

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Supporting Informtaion Available

Force-field parameters, number of bound insulins, AuNP adsorption capacity and fibrinogen bending angle. This information is available free of charge via the Internet at <http://pubs.acs.org>.

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TOC

Coarse-grained molecular dynamics simulations of competitive binding of insulins and fibrinogens on citrate-capped gold nanoparticles.

