

Conformational change of an α -helix segment of bovine serum albumin adsorbed on graphene

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Abstract

We investigated the adsorption characteristics of an α -helical segment with 12 residues derived from the full protein structure of bovine serum albumin. It was found that the peptide adsorbs onto graphene, leading to significant changes in the helical content. Adsorption onto graphene induces a transition in the peptide, destabilizing the close-packed α -helices to form significant amounts of loose-packed 3_{10} -helices. This is confirmed through comparison of the hydrogen bond formation in the peptide with and without the presence of graphene.

Keywords: Molecular Dynamics, Bovine Serum Albumin, Graphene, Adsorption, Protein Conformation

Introduction

Critical applications of graphene in biotechnology includes biosensing, bio-related nanotechnology, and drug delivery. Biofunctionalization of graphene also promotes its solubility and biocompatibility, while potentially enhancing the properties of biological materials such as proteins and DNA through their immobilization, interaction, and/or catalysis using graphene [Wang et al. (2011)]. Many remarkable applications led to intensive numerical characterizations of the binding and adsorption of proteins on graphene. An important protein is bovine serum albumin (BSA), as conjugation with graphene allows customization of its electronic, chemical, and mechanical properties, leading to good materials for stabilizing and clustering nano-particle assemblies of gold, platinum, palladium, and silver [Liu et al. (2010)]. These conjugates are also soluble with at different pH without aggregating. Covalent attachment of BSA to GO results in a highly water-soluble conjugate, allowing for full exfoliation of GO nanosheets in a manner that can be easily reproduced, scaled, and controlled [Shen et al. (2010)].

Molecular Dynamics Simulation

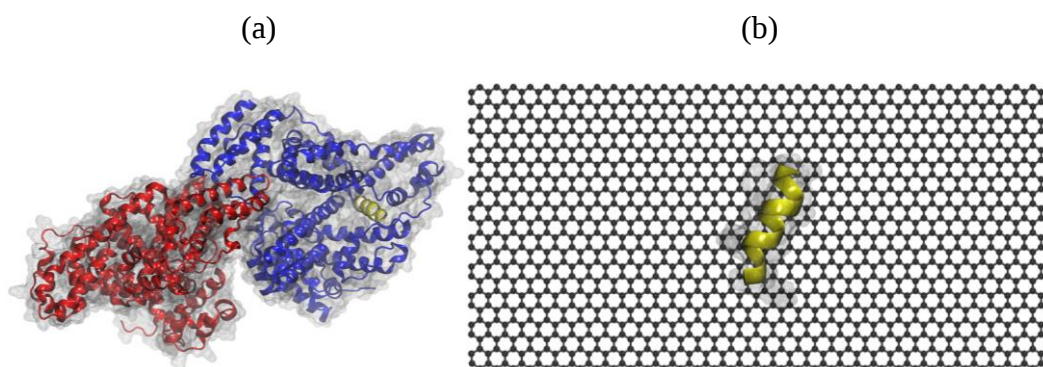


Figure 1. α -helical segment in yellow, (a) selected from the full BSA molecule and (b) placed on top of a graphene monolayer in black

The α -helical BSA segment selected for our simulation consists of 12 residues of chain A, corresponding to the amino acid sequence 208-220 from the corresponding Protein Data Bank (PDB) code: 4F5S. This is depicted in Fig 1a. All simulations were performed in GROMACS [Pronk et al. (2013)] with the Amber99 forcefield [Wang et al. (2000)] at the temperature of 300K and atmospheric pressure of 1 bar, and solvated in TIP3P [Jorgensen et al. (1983)] water. The results were analyzed and visualized using both GROMACS and VMD [Humphrey et al. (1996)]. The root mean square displacement (RMSD), hydrogen bonding, and helical content of the peptide were determined for both BSA only and BSA adsorbed onto graphene.

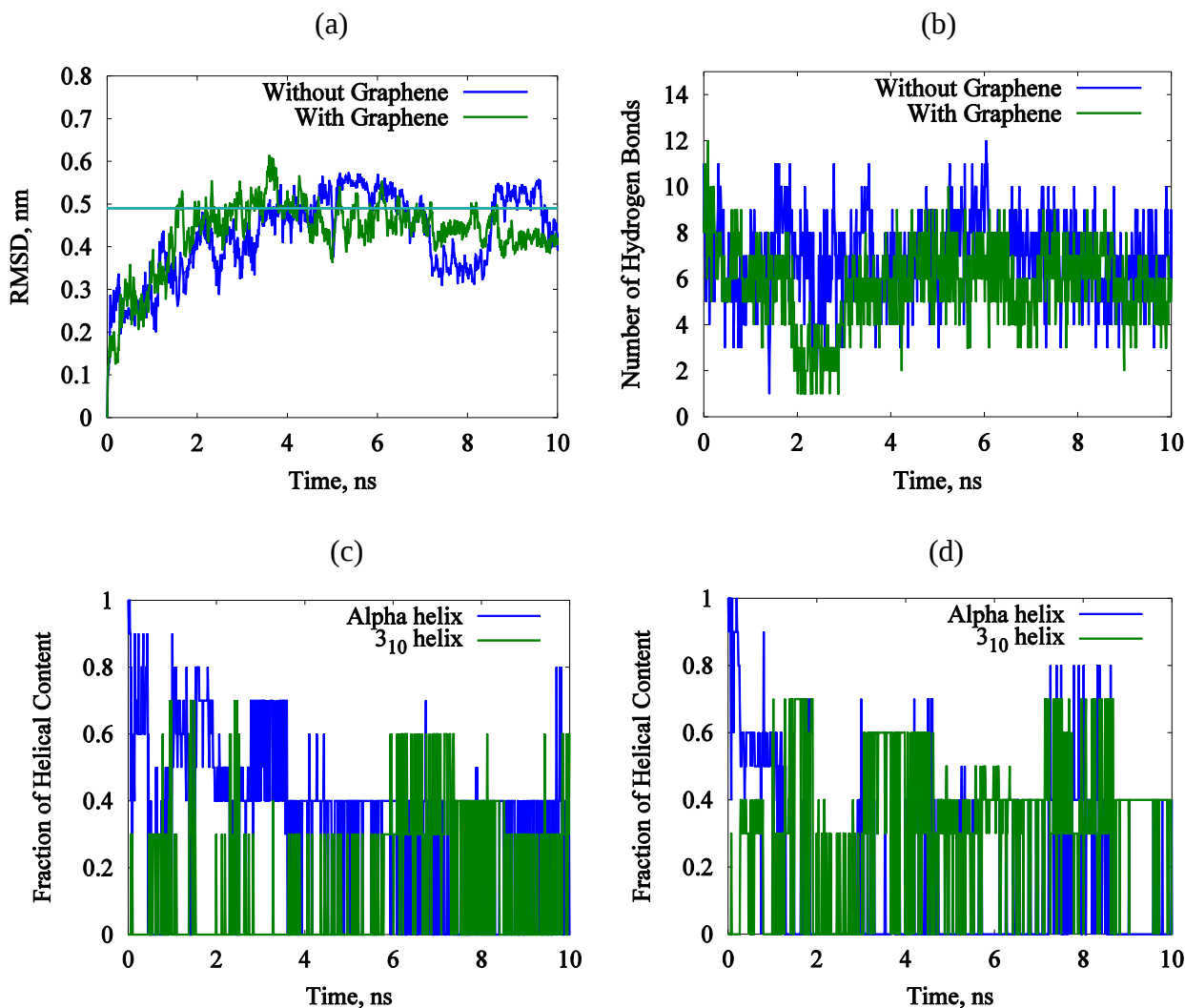


Figure 2. (a) RMSD, (b) number of hydrogen bonds, and (c), (d) helical content as a fraction of the original α -helical content for BSA only and BSA with graphene respectively

From Fig. 2a, it is observed that the BSA peptide is well equilibrated for both cases within 10ns of simulation time. Fig. 2b shows hydrogen bonds breaking in the presence of graphene within 2ns of simulation time, and reforming again after that. This can be attributed to the destabilization of the α -helix of BSA due to adsorption onto graphene, leading to a transition from a close-packed α -helix structure to a loose-packed 3_{10} -helix structure. Comparison of Figs. 2c and 2d shows significant increases in the 3_{10} -helical content as a fraction of the initial α -helical content if graphene is introduced. This is likely to be due to strong interaction energies between the BSA peptide and graphene, as well as the influence of π - π stacking of the sidechain of the tryptophan residue with graphene, as depicted in Fig. 3.

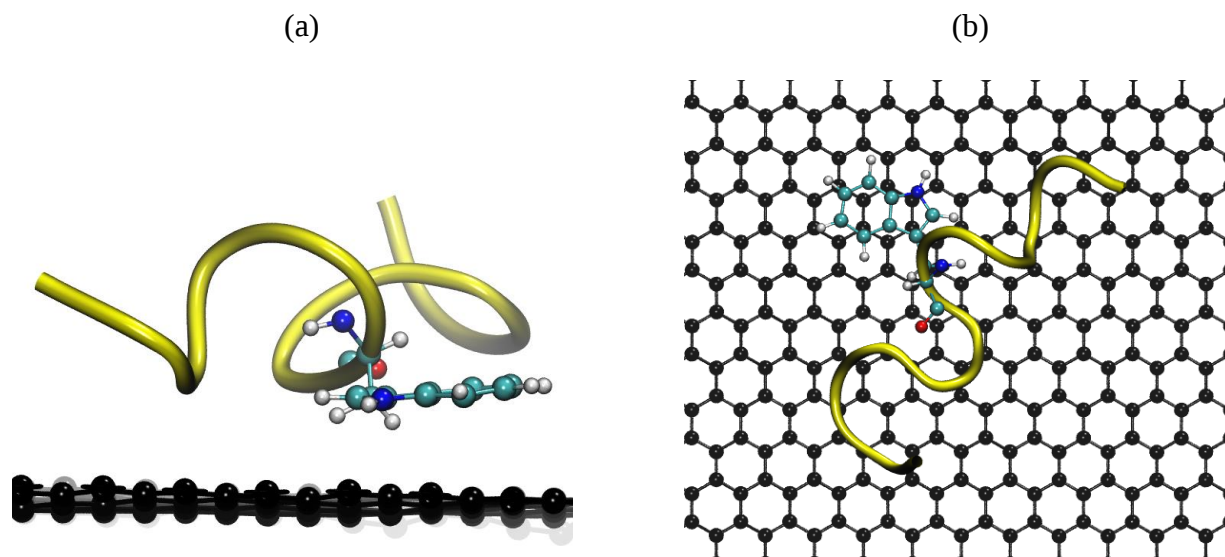


Figure 3. (a), (b) Side and top view of the π - π stacked sidechain (coloured beads and chains) of the tryptophan residue of BSA (yellow) with graphene (black beads and chains) respectively

Conclusions

Conformational changes of an α -helical BSA segment can be induced upon adsorption onto graphene. The presence of graphene induces the formation of 3_{10} -helices through destabilization of the α -helices, verified through comparison of the hydrogen bond breakage and formation in the peptide with and without the presence of graphene. These changes could be due to the influence of strong interactions between the peptide and graphene, as well as the effects of π - π stacking of the sidechain of the tryptophan residue with graphene.

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