# Molecular Dynamics Study of Hydration Water Behavior in Blue Copper Protein

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Blue copper proteins are categorized into three types (type1, type2, and type3) by their structures and functions. Azurin is one of the type 1 blue copper protein. The structure consists of eight $\beta$ strands and an $\alpha$ helix with 128 residues. Azurin has the functionality of electron transfer because of their prominent reactivity. The active site of azurin consists of a copper ion and five ligand residues(His46, Cys112, His117, Gly45, and Met121). In previous studies, we investigated physical and chemical properties of azurin concern with the active site using molecular dynamics (MD) simulation and density functional theory (DFT) calculations[1, 2]. In these studies, we found the geometrical structure of azurin in solution and studied there electronic structures[2]. Physical properties of protein surface hydration water are also interesting. Inter molecular hydrogen bonds between water molecules, which is observed in hydration water surrounding protein, has been investigated[3]. Moreover, glasslike behavior of water molecules near the protein surface has been also observed[4].

In this study, we carry out MD simulation using AMBER99 force field in room and some lower temperatures. In these simulations, we adopt the crystal structure of oxidized *Pseudomonas aeruginosa* azurin at pH5.5 (PDBID:4AZU) as an initial coordinate. The cutoff radii for nonbond interactions are 8 Å. The SHAKE algorithm is performed the bonds involving hydrogen. Azurin puts in explicit solution model with 3351 TIP3P balk waters (Fig. 1.). All simulations are carried out under NPT ensemble non periodic condition.

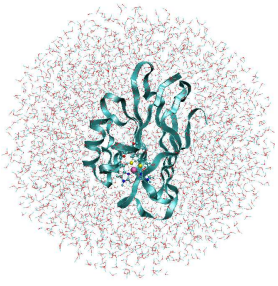

Figure 1: Secondary structure of azurin in solution model with 3351 TIP3P balk waters

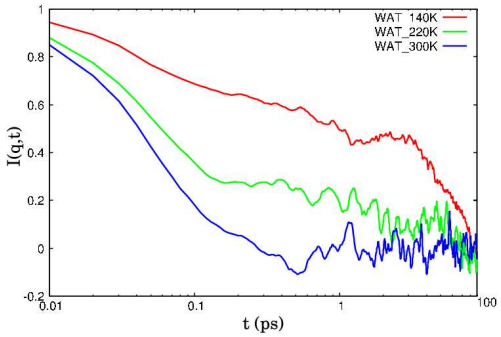


Figure 2: Intermediate scattering function in each temperature (q=1.8Å$^{-1}$)

From the results of these simulations, we have analyzed the hydration water behavior. In some temperatures, we calculated the intermediate scattering function at q=1.8Å$^{-1}$ defined by equation (1):

$$I(q,t) = \frac{1}{3N}\langle \sum_{i=1}^{N} \mathbf{exp}[i\mathbf{q}\cdot(\mathbf{R_i(t)} - \mathbf{R_i(0)})]\rangle. \quad (1)$$

where $N$ is the number of water hydrogen atoms and $\mathbf{R}$ is the position vector of the $i$ th atom. *I(q,t)* at low temperature are decay slowly as shown in Fig. 2. Moreover, we calculated the incoherent dynamical structure factor $S(q,\omega)$, which is obtained by time Fourier Transform of *I(q,t)*. We found the low frequency corresponding to the behavior of the hydration waters from $S(q,\omega)$. From these simulations and analysises, we found protein surface hydration water is less diffusibility than waters far from the protein and behavior of them strongly depends on system temperature.

## References

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