Interaction between Human Serum Albumin and Toxic Free, PEG-InP/ZnS QDs using Multi-Spectroscopic Study: Excellent Alternate to Heavy Metal Based QDs

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Introduction

To date most explored and applied core shell semiconductor nanocrystals (CdSe/ZnS, CdSe/ZnSe, CdSe/CdS, CdS/PbS, CdS/HgS, ZnSe/ZnS, ZnS/CdS, HgS/CdS, PbS/ZnS) exhibits toxicity[1]. Greener, heavy metal and toxic free semiconductor nanocrystals are the most interested segment of the current bio-nanotechnology. In the present paper, structural changes of human serum albumin (HSA) due to its interaction with toxic free poly ethylene glycol ligand coated InP/ZnS QDs (PEG-InP/ZnS QDs) was probed by employing multi-spectroscopic tools.

Materials and Methods

Various concentrations of PEG-InP/ZnS QDs (2 nM-10 nM) were prepared in double distilled water and HSA samples of 1µM concentration were prepared in Phosphate buffer saline at pH-7.0. Later such samples were used in steady state, temperature dependent fluorescence, synchronous fluorescence spectral and time resolved measurements. Then SFS scans for HSA-InP/ZnS Qs were performed at $\Delta\lambda$=15 and 60 nm corresponds to tyrosine and tryptophan residues, respectively.

Results and Discussion

Experimentally calculated $K_{SV} = 0.48\times10^{8} M^{-1}$ and $k_q = 8.14\times10^{15} M^{-1}s^{-1}$ fluorescence quenching constants from Fig. 1 for HSA-QDs conjugates are much greater compared to the values obtained for biological macromolecules due to the collision mechanism[2]. A close examination of Fig.2 reveals that reduction in HSA synchronous fluorescence intensity after conjugation with PEG-InP/ZnS QDs is more and uniform for $\Delta\lambda$= 60 nm which showed PEG-InP/ZnS QDs binds predominantly to Trp-214 residue.

Figure 1: Stern-Volmer Plot.

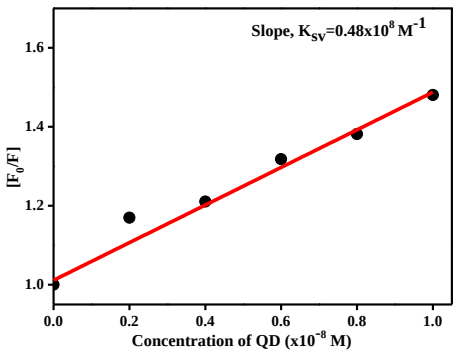
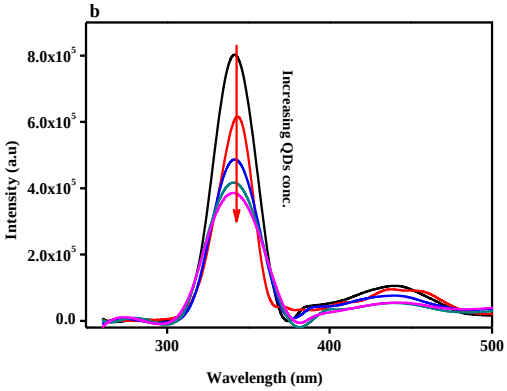


Figure 2: SFS spectra of HSA-QDs at Δλ=60 nm.



Conclusion

At higher temperatures these bioconjugates are unstable and static quenching mechanism shifts towards collisional quenching phenomenon. Binding and synchronous fluorescence analysis showed PEG-InP/ZnS QDs binds predominantly to Trp-214 residue through hydrophobic forces. Observed blue shift from 343 to 338 nm in PL spectra of indicates conformational deformation around Trp-214. The E_T, K_T and R_0 were all calculated for HSA and PEG-InP/ZnS QDs system from FRET studies. The -ΔG, +ΔH, +ΔS implied, HSA-InP/ZnS QDs bioconjugation is spontaneous, endothermic, entropy driven. Hill coefficient (n≅1) and binding affinities (k_b) confirmed strong binding of HSA to QDs surface through 'non-cooperative interactions'.

Bibliography

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