Biomolecules in water and water in biomolecules

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ABSTRACT

It is a common understanding that the molecular recognition is an essential elementary process for protein to function. The molecular recognition is a thermodynamic process which is characterized by the free energy difference between two states of a host-guest system, bound and unbound. On the other hand, the time to reach the thermodynamic equilibrium depends on the free energy barrier mainly associated with the conformational fluctuation of protein. Therefore, the molecular recognition is a thermodynamic process conjugated with the conformational fluctuation of protein.

We have been developing a new theory for the molecular recognition by protein based on the statistical mechanics of liquids, or the 3D-RISM/RISM theory. The theory has demonstrated its amazing capability of "predicting" the process from the frist principle. [1] However, what we have investigated so far is an entirely equilibrium process both in protein conformation and solvation.

Recently, we have started to incorporate the conformational fluctuation of protein into the molecular recognition process in two ways. The first of those is a "static" one in which we just shake the protein conformation to find the local minimum of the free energy surface by the combined 3D-RISM/RISM with conformational sampling algorithms, and to see if one can find the distribution of a guest molecule in the recognition site. One example of such studies will be presented in the talk. [2] The other method is to take the "dynamic" fluctuation of protein conformation into account. The process can be described by hybridized 3D-RISM/RISM with the generalized Langevin dynamics theories. The methodology is currently under construction, and some prospective view of the theory will be presented in the lecture.

REFERENCES

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