

## University of Tsukuba | Center for Computational Sciences

# **Biological Sciences on HA-PACS/T2K**

## QM/MM Studies on Reaction Mechanisms

Nitric Oxide Reductase (NOR)









Nitric Oxide Reductase (NOR) is a transmembrane protein which catalyzes a reduction of nitric oxide (NO) to nitrous oxide (N<sub>2</sub>O). This is a critical step for the denitrification process in the anaerobic respiration. In 2010, first x-ray structure of NOR was reported at the atomic resolution (2.7 Å). It was revealed that the catalytic site is constituted by a non-heme iron FeB and a heme b3, but the reaction mechanism of NOR has not been fully elucidated.

We have investigated the NOR reaction mechanism by using a quantum mechanical/ molecular mechanical (QM/MM) method [1]. Intermediate states and the reaction energy profile were determined to clarify the catalytic reaction mechanism.

[1] M. Shoji et al., *Mol. Phys.* 2013.



DNA topoisomerase (topo) is a DNA-binding enzyme which catalyzes interconversions of the different topological forms of DNA. This enzyme forms a covalent intermediate in which catalytic tyrosine residue is covalently bonded to the DNA backbone phosphate, after and before cleavage and religation reactions. Recently, one crystal structure of the covalent intermediate of yeast topo II in complexed with single DNA was solved at the 3.0Å resolution, as shown in Figure. Using the x-ray structure as the initial coordinate, we performed MD (molecular dynamics) simulations and QM/MM calculations. We revealed a new reaction mechanism, named Substrate Mediated Proton Relay (SMPR) mechanism, for the DNA religation reaction in topo II.

[2] K. Hanaoka, et al., J. Biomol. Struct. Dyn. 2013.

#### Astrobiology

**Chirality Formation of Amino Acids in the Early Solar System** 



#### The naturally-occurring amino acids in terrestrial life are all the levorotatory (L-) form, none of the D-form. The origin for its selectivity still remains a

### **GPU Accelerated Molecular Orbital Calculation**







big mystery. One of the possible scenarios is that the chiral induction of amino acids is formed on meteorites in the early solar systems [3]. In order to validate the hypothesis, we have investigated the mechanisms of photo-induced chirality formation by using the TDDFT method. Circular dichroism and UV- absorbance spectrum were calculated for amino acids and plausible chiral induction mechanisms were discussed.

[3] J. R. Cronin et. al., Science 275, 951 (1997); M. H. Engel et. al., Nature 389, 265 (1997).

GPU accelerated Fock matrix preparation of a Hartree-Fock (HF) calculation routine, which is a basic and common process in various ab initio molecular orbital (MO) calculations, has been implemented into the FMO program [4]. With overlapping mixed calculation of CPU and GPU, total elapsed time was remarkably reduced. Figure shows timing results for HF/6-31G(d) calculation of 126 atomic molecule (1,282 AO) with four CPU cores (Intel E5 Sandy Bridge-EP, 2.6GHz) and one GPU (NVIDIA M2090). Here, integral types with red legend text were assigned to GPU.

[4] http://www.openfmo.org/OpenFMO/

http://www.ccs.tsukuba.ac.jp/