# 3 次元 DNA ナノ構造体を用いた $CO_2$ 固定化酵素の集積化

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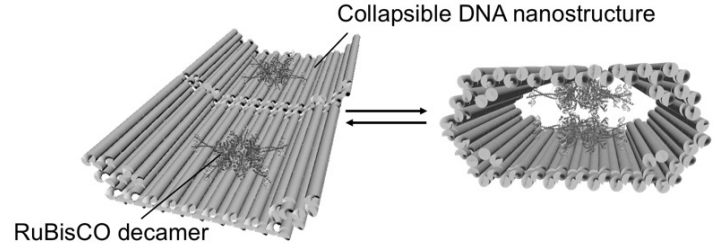
Construction of a $CO_2$ fixing enzyme assembly on 3D DNA nanostructure ([1]*Graduate School of Energy Science, Kyoto University*, [2]*Institute of Advanced Energy, Kyoto University,* [3]*Graduate School of Engineering, Kyoto University*) ○Hiroaki Konishi[1], Dinh Huyen[2], Eiji Nakata[1, 2], Haruyuki Atomi[3], Takashi Morii[1, 2]

Enzymes in living cells are known to be spatially restricted in a specific manner, such as the oligomeric states of enzymes and the arrangement of sequential enzymes in compartments. It is thought that metabolic enzymes are also organized in such a way to control the concentration of intermediates and the efficiency of cascade reactions. Ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO), which is involved in carbon fixation reactions in many autotrophic organisms, forms multimers and fills up the protein compartment carboxysome with carbonic anhydrase[1)], but the effect of enzyme cluster is not clear. By construction of a packed condition of RuBisCO complexes in vitro, we can analyze the mechanism of efficient metabolic reactions in vivo. In this study, we investigated the method of assembling RuBisCO derived from the thermophilic archaeon *Thermococcus kodakarensis* (*Tk*-RuBisCO)[2)] on DNA nanostructures constructed by DNA origami method[3)] via DNA-binding proteins[4)].
*Keywords：DNA nanostructure, RuBisCO, protein adaptor*

生体細胞内での酵素は、単一の酵素が多量体を構築したり、複数の酵素が区画内で連続して配置され組織を形成することで、反応物や中間体の濃度を制御して反応の効率化を実現していると考えられる。独立栄養生物内に存在する酵素 RuBisCO は二酸化炭素固定化反応を担う酵素であり、区画の中で多量体が集合して高効率な反応を進める系が存在する [1)] が、集積化による影響は不明である。このような酵素複合体を試験管内で再現することで、生体内での高効率な代謝反応の機構を解析できる。本研究では、ホモ十量体からなる好熱性古細菌由来の RuBisCO (*Tk*-RuBisCO)[2)] に着目し、DNA オリガミ法 [3)]で構築した DNA ナノ構造体上に、DNA 結合性タンパク質由来のタンパク質アダプター[4)] を介して集積させる方法を検討した。



**Construction of an artificial RuBisCO assembly on DNA nanostructure**

1) Bonacci, W. *Proc. Natl. Acad. Sci. U.S.A.* 2012, **109**, 478-483. 2) Kitano K.; Maeda N.; Fukui T.; Atomi H.; Imanaka T.; Miki, K.; *Structure* 2001, **9**, 473-481. 3) P. W. K. Rothemund, *Nature* 2006, **440** , 297-302. 4) Ngo, T. A.; Nakata, E.; Saimura, M.; Kodaki, T.; Morii, T. *Methods* 2014, **67**, 142-150.