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Research Interests

- Protein engineering of flavoproteins
- Structure-function relationship of metalloproteins
- Genetics of sulfate-reducing bacteria

Creative Achievements in The Application of New and Existing Science and Technology

(1,2) Flavoproteins and **metalloproteins** are a class of biologically important macromolecules, which have various functions such as electron transfer, oxidation, and reduction. These diverse functions of proteins have been thought to depend on the ligands from amino acid residues, coordination structures, and protein structures in immediate vicinity of flavin derivatives and metal ions. In these projects, I am studying the relationship between the 3-D structure and dissociation constant, redox potential, and cofactor selectivity of FMN-binding protein, flavodoxin, flavoredoxin, rubredoxin, and rubredoxin-like protein. **Various analysis of wild type and mutant proteins clarified the structure-function relationship of these redox proteins. (3)** The sulfate-reducing bacteria of the genus *Desulfovibrio* can perform **anaerobic respiration utilizing sulfate** as terminal electron acceptor. I have been **cloned many genes** from *D. vulgaris* (Miyazaki F) and **constructed expression system of its gene to understand their characters**. However, the 'real' physiological activities of some gene products are still unknown although they may be well-characterized *in vitro*.

Technology (Product, Process, Device, Service etc.) That I Want to Request for Collaboration

- Novel methods to characterize the wild type and mutant flavoproteins and metalloproteins
- Application of novel redox proteins such as an electronic device
- Genetic engineering using sulfate-reducing bacteria such as vector and recombination technique

A List of 5 Key Publications

- Photoinduced electron transfer from aromatic amino acids to the excited isoalloxazine in single mutated flavin mononucleotide binding proteins. Effect of the dimer formation on the rate and the electrostatic energy inside the proteins, N. Nunthaboot, K. Lugsanangarm, A. Nueangaudom, S. Pianwanit, S. Kokpol, F. Tanaka, S. Taniguchi, H. Chosrowjan, T. Nakanishi, M. Kitamura, ***Computational and Theoretical Chem.*** **1108,** 1-9 (2017).
- Structure analysis of the flavoredoxin from *Desulfovibrio vulgaris* Miyazaki F reveals key residues that discriminate the functions and properties of the flavin reductase family, N. Shibata, Y. Ueda, D. Takeuchi, Y. Haruyama, S. Kojima, J. Sato, Y. Niimura, M. Kitamura, Y. Higuchi, ***FEBS J.*** **276,** 4840–4853 (2009).
- Pathway of chymotrypsin evolution suggested by the structure of the FMN-binding protein from *Desulfovibrio vulgaris* (Miyazaki F), E. Liepinsh, M. Kitamura, T. Murakami, T. Nakaya, G. Otting, ***Nature Struct. Biol.*** **4(12),** 975-978 (1997).
- A gene encoding a cytochrome *c* oxidase-like protein is located closely to the cytochrome *c*-553 gene in the anaerobic bacterium, *Desulfovibrio vulgaris* (Miyazaki F), M. Kitamura, K. Mizugai, M. Taniguchi, H. Akutsu, I. Kumagai, T. Nakaya, ***Microbiol. Immunol.*** **39(1),** 75-80 (1995).
- Novel FMN-binding protein from *Desulfovibrio vulgaris* (Miyazaki F) -Cloning and expression of its gene in *Escherichia coli*- M. Kitamura, S. Kojima, K. Ogasawara, T. Nakaya, T. Sagara, K. Niki, K. Miura, H. Akutsu, I. Kumagai, ***J. Biol. Chem.*** **269(8),** 5566-5573 (1994).