

生命分子解析ユニット

Biomolecular Characterization Unit

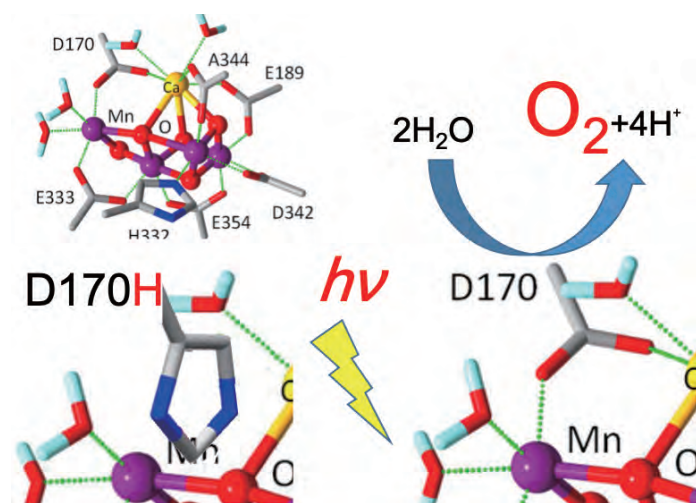


タンパク質の構造を調べて、 生命現象の謎にせまります

研究テーマ

- 生体分子の翻訳後修飾を含めた詳細な構造解析
- 生体分子の定量的解析法の開発
- RNAの質量分析

当ユニットは、生命現象の解明に向け、生体成分構造解析法の開発や構造解析の応用研究を行っている。生体成分の中でも特にタンパク質は生命現象の源であり、さまざまな生物活性がある。そのタンパク質の構造を詳細に調べることで、活性と遺伝子との対応、生物学的活性のメカニズムや活性の制御機構を解明する。また、装置ならびに設備の設置や管理、解析方法に関する情報の整備をすることで研究支援を行っている。



PSII Mutants Regain Oxygen-Evolving Capacity upon Light Irradiation
Oxygen-evolving ability of PSII active center mutants were restored by photoirradiation. We revealed that this mechanism is due to post-translational conversion of amino acids by mass spectrometry.

To resolve the mystery of biological phenomena, we examine the protein structure

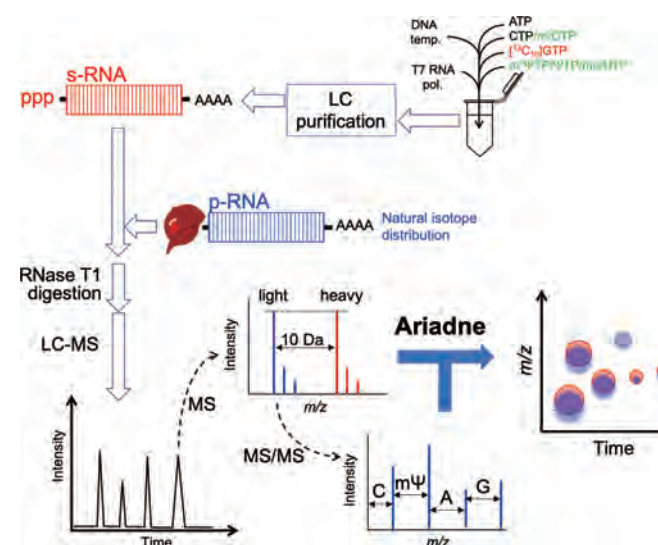
Research Subjects

- Development and application of analytical methods for structural details on biological molecules
- Development of quantitative analysis of biomolecules
- Identification and characterization of RNA by mass spectrometry

Our unit provides high quality structural characterization methods to the field of biological science, aiming to further understand the mechanism and action of biological molecules. We manage specialized and technical instruments including protein chemical analyses, mass spectrometry. Our challenge to research, develop and fine-tune novel characterization methods for biological molecules, is an endless yet rewarding process.

研究成果

- PSII変異体の酸素発生能の復元メカニズムの解析と光合成酸素発生の起源を提唱した。
- mRNA医薬品の特性解析に資する同位体希釈質量分析法を開発した。
- 質量分析とBioID法によるリソソーム膜タンパク質と相互作用するタンパク質の同定法を開発した。



Schematic of quality assessment of mRNA pharmaceuticals
The proposed method has allowed one to quantitatively characterize structures that play critical roles in mRNA's function, i. e. 5'-Capping, modified nucleosides on internal sequence, and poly(A) tail, even for more-than-megadalton mRNA.

Research Results

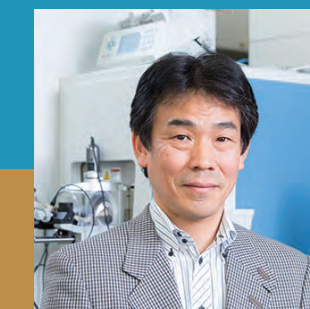
- We found the mechanism of restoration of oxygen-evolving capacity in PSII mutants and proposed the a possible origin of photosynthetic oxygen evolution.
- We have developed the isotope-dilution mass spectrometry method for characterizing mRNA pharmaceuticals.
- We have developed a method to identify proteins that interact with lysosomal membrane proteins using mass spectrometry and BioID.

主要論文 / Publications

Shimada, Y. *et al.*
Post-translational amino acid conversion in photosystem II as a possible origin of photosynthetic oxygen evolution.
Nat Commun. **13**, 4211 (2022)

Nakayama, H., Nobe, Y., Koike, M., Taoka, M.,
Liquid Chromatography-Mass Spectrometry-Based Qualitative Profiling of mRNA Therapeutic Reagents Using Stable Isotope-Labeled Standards Followed by the Automatic Quantitation Software Ariadne.
Anal. Chem. **95**, 1366-1375 (2023)

Nguyen-Tien, D.*, Suzuki, T.*, Kobayashi, T., Toyama-Sorimachi, N., Dohmae, N.
Identification of the interacting partners of a lysosomal membrane protein in living cells by BioID technique.
STAR Protoc. **3**, 101263 (2022) *equal contributor



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