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

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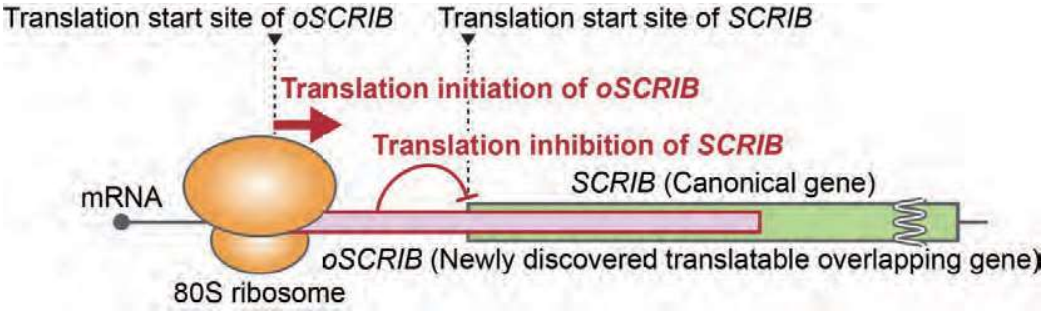
Our unit provides high quality structural characterization methods to the field of biological science, aiming to further understand the mechanism and action of biological molecules. We manage specialized and technical instruments including protein chemical analyses, mass spectrometry. Our challenge to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

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

Research Results

- We discovered a microprotein-coding overlapping gene of Hippo-YAP/TAZ signaling effector *SCRIB* by human proteogenomic analysis.
- We found that methytaion enzyme the methylase METTTL9 modifies histidine residues of proteins.
- We performed proteome analysis of co-precipitates with STING and showed that the COP-I complex is involved in the transport of STING to the ER.



Translational repression of a canonical gene *SCRIB* by a newly discovered translatable overlapping gene *oSCRIB*. Our study revealed that the translation initiation of *oSCRIB* results in the translational inhibition of the downstream gene *SCRIB*, which will contribute to non-excessive expression of *SCRIB* as a Hippo-YAP/TAZ signaling effector gene in human cells.

主要論文 / Publications

Nomura, Y., Dohmae, N.
Discovery of a small protein-encoding cis-regulatory overlapping gene of the tumor suppressor gene Scribble in humans.
Commun. Biol. **4**,1098 (2021)

Davydova, E. *et al.*
The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes.
Nat. Commun. **12**, 891. (2021)

Mukai, K. *et al.*
Homeostatic regulation of STING by retrograde membrane traffic to the ER.
Nat. Commun. **12**, 61. (2021)

生命分子解析ユニット
Biomolecular Characterization Unit

TP

タンパク質の構造を調べて、生命現象の謎にせまります

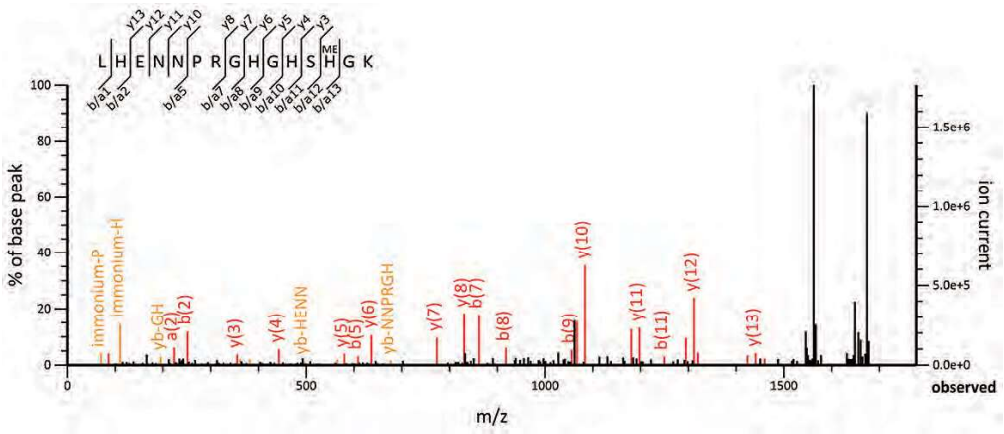
当ユニットは、生命現象の解明に向け、生体成分構造解析法の開発や構造解析の応用研究を行っている。生体成分の中でも特にタンパク質は生命現象の源であり、さまざまな生物活性がある。そのタンパク質の構造を詳細に調べることで、活性と遺伝子との対応、生物学的活性のメカニズムや活性の制御機構を解明する。また、装置ならびに設備の設置や管理、解析方法に関する情報の整備をすることで研究支援を行っている。

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

研究成果

- ヒトのプロテオゲノミクス解析によりHippo-YAP/TAZシグナルエフェクター*SCRIB*のオーバーラップ遺伝子がマイクロタンパク質へと翻訳されていることを発見した。
- メチル化酵素METTL9は、タンパク質のヒスチジン残基を修飾することを明らかにした。
- STINGと共沈するタンパク質のプロテオーム解析を行い、COP-I複合体がSTINGのERへの輸送に関与していることを示した。



MALDI TOF-TOF mass spectrum of S100A9-derived peptides from WT and Mettl9 KO mouse neutrophils. As a result of comparison between WT and Mettl9 KO mouse neutrophils, we found that His109 of S100-A9 is methylated with METTL9.

2021年度メンバー / FY2021 Members

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