The 18th Symposium
of Japan Consortium for Glycobiology and Glycotechnology

Reboot Glycoscience to Further Height

December 7 – 8, 2021 Online Meeting

Program on December 7 (Tue), 2021

Opening Address
Shinya Fushinobu (University of Tokyo)

President Address
Tamao Endo (JCGG President)

Tamio Yamakawa Award Lecture and Award Ceremony

Chair: Tamo Endo (JCGG President)
Kevin P, Campbell (HHMI / University of Iowa)
Structural basis of LARGE 1-mediated elongation of matriglycan on dystroglycan

Dystroglycan is a widely expressed plasma membrane protein that requires extensive post-translational processing and glycosylation to function as a receptor for laminin-G-like (LG) domain extracellular matrix (ECM) proteins including laminin, agrin and perlecan. Matriglycan is a linear repeating disaccharide of alternating xylose and glucuronic acid that is synthesized by the like-acetylglucosaminyltransferase-1 (LARGE1) on α-dystroglycan and binds LG domain ECM proteins. Addition of matriglycan enables α-dystroglycan to serve as the predominant ECM receptor in skeletal muscle and brain. Abnormalities in the post-translational processing of α-dystroglycan that result in an absence or reduction of matriglycan cause various forms of muscular dystrophy, known as dystroglycanopathies, with or without brain and eye involvement.

Session 1 Let's Start 2021 Glycobiology

Chair: Tadashi Suzuki (RIKEN)

Regulation of the Notch intercellular signaling pathway by *O*-glucosylation
Hideyuki Takeuchi (University of Shizuoka)

Notch signaling is an evolutionarily conserved signaling pathway that regulates cell fate decisions in metazoan. The Notch receptor is a type-I transmembrane protein with epidermal growth factor-like (EGF) repeats in its extracellular region. The EGF domain undergoes *O*-fucose, *O*-glucose, and/or *O*-GlcNAc modifications[1]. We demonstrated that POGLUT1/rumi is a protein O-glucosyltransferase essential for Notch signaling in flies and mice. *O*-Glucose is converted into a trisaccharide structure (Xylα1-3Xylα1-3Glc1β-) by two xylosyltransferases and another xylosyltransferase, XXYLT1. Crystal structures of XXYLT1 complexed with substrates revealed that its retaining mechanism is SNi-like[2]. Recently, we found patients with limb-girdle muscular dystrophy with mutations in POGLUT1[3]. They showed a decrease in the number of satellite cells, a decrease in Notch signaling, and hypoglycosylation and decreased laminin-binding capacity of muscle-derived dystroglycan. Future work will focus on the molecular mechanisms by which *O*-glucosylation regulates Notch receptor activation and the full picture of Notch glycosylation in vivo.

References

1) Saiki W, Ma C, Okajima T, Takeuchi H. Current views on the roles of *O*-glycosylation in controlling Notch-ligand interactions. Biomolecules 11(2): 309 (2021)

2) Yu H, Takeuchi M, LeBarron J, Kantharia J, London E, Bakker H, Haltiwanger RS, Li H, Takeuchi H. Notch-modifying xylosyltransferase structures support an SNi-like retaining mechanism. Nat. Chem. Biol. 11(11): 847-854 (2015)

3) Servian-Morilla E*, Takeuchi H*, Lee TV*, Paradas C et al. A POGLUT1 mutation causes a muscular dystrophy with reduced Notch signaling and satellite cell loss. EMBO Mol. Med. 8(11): 1289-1309 (2016) (*:Co-first)

Development and application of ultra-sensitive glycome analysis method using capillary electrophoresis
Takayuki Kawai (Kyushu University)

The glycomic profiling of small population of cells is essential for the development of next-generation medicine for targeting abnormal glycosylation associated with pathogenesis. We developed an ultra-sensitive glycome analysis

method using capillary electrophoresis coupled with laser-induced fluorescence (CE-LIF) and mass spectrometry (CE-MS). By coupling large-volume sample stacking and transient isotachophoresis techniques, a new dual stacking method named “large-volume dual preconcentration by isotachophoresis and stacking (LDIS)” was developed, which could enhance sensitivity by approximately 2,000-fold, with a limit of detection around 65 fM (91 zmol) for 8-aminopyrene-1,3,6-trisulfonic acid-labeled oligosaccharides. This technique was finally applied to trace *N*-glycome analysis. Unique profiles were observed from ~100 cultured cells in different cell lines. Trace *N*-glycans were also successfully profiled from laser-microdissected tissue sections. Thus, this work contributes to the progress of glycomic research for next-generation medicine.

References
1) Ohtsubo K et al. Nat. Med. 2011, 17, 1067
2) Kawai T et al. J. Chromatogr. A 2018, 1565, 138
3) Kawai T et al. Anal. Chem. 2019, 91, 10564

Tools and databases in glycoscience

Issaku Yamada (The Noguchi Institute)

We have been developing GlyTouCan, an International Glycan Structure Repository to store glycan structure data with unique numbers. In the process, we have developed the WURCS notation for describing glycan structures and tools for converting glycan structures to WURCS. In addition, GlyCosmos, a portal site for glycoscience, has developed GlyComb to store structural data of glycoconjugates and GlycoPOST and UniCarb-DR to store mass spectrometry data. In addition, the GlyCosmos database integrates various data related to glycoscience, such as genes, proteins, glycans, and diseases, and is linked with other databases. We are also preparing manuals on how to use the various tools and databases.

References
1) Fujita A et al., The international glycan repository GlyTouCan version 3.0. Nucleic Acids Res. 2021 Jan 8;49(D1):D1529-D1533. doi: 10.1093/ nar/gkaa947. PMID: 33125071
2) Matsubara M et al. WURCS 2.0 update to encapsulate ambiguous

carbohydrate structures. J. Chem. Inf. Model. 2017;57(4):632-637. doi: 10.1021/acs.jcim.6b00650. PMID: 28263066
3) Yamada I et al. The GlyCosmos Portal: a unified and comprehensive web resource for the glycosciences. Nat. Methods 2020 Jul;17(7):649-650. doi: 10.1038/s41592-020-0879-8. MID: 32572234.

Session 2 Short Presentation of Sponsor Corporations

Chair: Eriko Hagiya

Tokyo Chemical Industry Co., FUSHIMI Pharmaceutical Co., Novozymes Japan, Agilent Technologies, GlycoTechnica Ltd., and GlyTech Inc.

Session 3 Glycoscience Expanding from the Discovery of Enzymes

Chair: Kaoru Takegawa (Kyusyu University)

Functional identification of plant glycosyltransferases by reverse biochemistry

Takeshi Ishimizu (Ritsumeikan University)

Plants contain much amount and type of glycans than mammals. The plant genome encodes about three times as many carbohydrate-related enzyme genes as the mammalian genome. However, due to the complexity of glycan structures and the degree of gene duplication, conventional biochemical, genetic, and reverse genetic methods are often not applicable for gene identification of carbohydrate-related enzymes in plants. We have recently identified the function of glycosyltransferases by using a "reverse biochemistry" approach combined with an omics-based gene expression analysis method. I will present two examples of functional identification of plant glycosyltransferases; the plant cell wall polysaccharide pectin RG-I:rhamnosyltransferase and the specialized metabolite glycoside apiin apiosyltransferase.

References

1) Takenaka et al. Nature Plants 4, 669-676 (2018)
2) Wachananawat et al. Front. Plant Sci. 11, 997 (2020)
3) Fujimori et al. Carbohydr. Res. 477, 20-25 (2019)

Discovery of the degradative enzymes for the D-arabinan components of *Mycobacterium* cell wall.

Kiyotaka Fujita (Kagoshima University)

D-Arabinofuranose (Araf) exists in the D-arabinan parts of the lipoarabinomannan (LAM) and arabinogalactan in the cell wall fraction of *Mycobacteria*. The D-arabinan structure is commonly constituted by α-1,5-D-Araf backbone with some α-1,3-D-Araf branching, and is terminated by β-1,2-Araf structure. We have been cloned and characterized D-arabinan degrading enzymes such as endo-D-arabinase, exo-α-D-arabinofuranosidase, and exo-β-D-arabinofuranosidase from *Mi. arabinogalactanolyticum*. D-Arabinan structure was completely degraded to D-Ara by these enzymes. In this talk, I would like to explain some difficulties for the finding of novel D-arabinan degrading enzymes.

References

1) Kotani S et al. Biken J. 14, 379-387 (1971)
2) Fujita K, Suda Y. P2019-017358A

Discovery of novel phosphorylases and creation of oligosaccharides library

Hiroyuki Nakai (Niigata University)

Various oligosaccharides possessing multiple functional bioactive properties such as prebiotic effects, antibacterial effects, and immunopotentiative action have been recently reported and widely used as food additive and pharmaceutical materials. The functions depend on their constituent carbohydrates and linkage types. Therefore, it is valuable to establish synthetic methods for a wide variety of oligosaccharides by practical enzymatic synthesis. Phosphorylases are one group of carbohydrate active enzymes involved in the cleavage and formation of glycosidic linkages. Noticeably, the phosphorolysis is reversible, making phosphorylase suitable catalyst for efficient synthesis of particular oligosaccharide. Although utilization of phosphorylase for oligosaccharide synthesis had been limited because only few different phosphorylases had been known. In this time, we report about the screening of novel phosphorylases that are useful for chemoenzymatic synthesis of oligosaccharides, practical

production of the oligosaccharides, and functional evaluation by microbiological, immunological, and food scientific methods, in particular for development of next generation prebiotics.

A consideration from the search history of new starch-related enzymes by old biotechnology

Tomoyuki Nishimoto (HAYASHIBARA CO., LTD)

In this lecture, I would like to share the results of considering the search method based on my experience of being involved in the search for new starch-related enzymes.

Hayashibara Co., Ltd. has discovered many new enzymes by searching with old biotechnology that does not depend on genetic information[1-4]. On the other hand, is New Biotechnology, based on genetic information that has become mainstream in recent years, a shortcut for discovering new enzymes? I find it difficult to make a complete transition.

The point is how to build the best system for continuous discovery by fusing the good points of both. And above all, it goes without saying that we will continue to input information to determine novelty / usefulness. Searching for new enzymes is an attractive field, where you can compete against the world without special equipment if you have a little luck

Reference

1) 茶圓博人, 等：細菌における二つの新規なトレハロース生成系, 応用糖質科学, 43, 213-221 (1996).

2）河野正樹, 森哲也, 西本友之：澱粉から生成する環状オリゴ糖に関する研究の進展 微生物がもたらす不思議な糖, 化学と生物, 57, 679-691 (2019)

3) Chaeb H et al. Two novel pathways for the enzymatic synthesis of trehalose in bacteria. Oyo Toshitsu Kagaku : J. Appl. Glycosci. 43, 213-221 (1996)

4) Kohno M, Mori T, Nishimoto T. Development of research on cyclic oligosaccharides derived from starch: Mysterious saccharides created by microorganisms, Kagakutoseibutsu 57, 679-691 (2019)

Program on December 8 (Wed), 2021

Session 4 Design and Function of Glycan Materials

Chair: Kazunari Akiyoshi (Kyoto University)

Gene delivery system using polysaccharide-based nanoparticles

Toshinori Sato (Keio University)

Polysaccharides with excellent biodegradability and biocompatibility have been developed as non-viral vectors. The pDNA/chitosan complex was efficiently taken up into cells and showed high gene expression activity[1]. Gene delivery with improved cell affinity was achieved using lactose and mannose-modified chitosan. Furthermore, ternary complexes in which the surface of the cationic pDNA/chitosan complex was coated with chondroitin sulfate[2] or hyaluronic acid[3] have been developed. Tumor growth was suppressed in vivo by using ternary complexes containing the suicide gene pTK. In the gene delivery system, it is possible to efficiently transfer the gene into cells and tumor tissues by selecting appropriate polysaccharides.

References

1) Sato T, Ishii T, Okahata Y. Biomaterials 22, 2075-2080 (2001)
2) Hagiwara K, Nakata M, Koyama Y, Sato T. Biomaterial 33, 7251-7260 (2012)
3) Sato T, Nakata M, Yang Z, Torizuka Y, Kishimoto S, Ishihara M. J. Gene Med. 19, e2968 (2017)

Preparation and applications of cyclodextrin supramolecular structures

Toshiyuki Kida (Osaka University)

Cyclodextrins (CDs) have a sub-nanometer-sized cavity into which guest molecules with the appropriate size and shape can be incorporated. In addition, CDs can form supramolecular assemblies such as cage-type, channel-type, and layer-type assemblies by utilizing hydrogen bonds between the hydroxyl groups on the wider and narrower rims of the ring or host–guest interactions with guest molecules. In this lecture, I will introduce the results of our research on the preparation of supramolecular structures composed of regular CD assemblies and their applications.

References

1) Harata K. Structural aspects of stereodifferentiation in the solid state. Chem. Rev. 1998, 98, 1803–1828
2) Kida T, Marui Y, Miyawaki K, Kato E, Akashi M. Unique organogel formation with a channel-type cyclodextrin assembly. Chem. Commun. 2009, 3889-3891
3) Kida T, Teragaki A, Kalaw J, Hajime S. Supramolecular organogel formation through three-dimensional α-cyclodextrin nanostructures: Solvent chirality-selective organogel formation. Chem. Commun. 2020, 56, 7581–7584

Polysaccharide ester derivatives and their marine biodegradability

Tadahisa Iwata (University of Tokyo)

The increasing environmental and economic concerns on the utilization of petrochemicals have led researchers to rely on plant biomass as a feedstock for the synthesis of polymeric materials. Furthermore, biodegradable plastics that are completely degraded into CO_2 and water by the action of microorganisms to solve marine microplastic pollution are strongly desired. Recently, our group succeeded in synthesizing new thermoplastics from polysaccharides such as xylan, glucomannan, curdlan, pullulan, etc by esterification and found interesting thermal, mechanical, and optical properties. More recently, we succeeded in synthesizing the unnatural-type polysaccharide, α-1,3-glucan, by enzymatic polymerization.

In this paper, we introduce various thermal and mechanical properties obtained from various polysaccharide ester derivatives, and their molecular and crystal structures were investigated by using wide-angle X-ray diffraction. Furthermore, the possibility for various utilization as injection molding, melt-spun fibers, high transparent films, etc. will be presented.

Session 5 Industry-Academy-Public Institution Joined Seminar

Chair: Shinya Fushinobu

Separation techniques of supercritical fluid chromatography for study on sphingoglycolipids

Hiroaki Takeda (RIKEN)

Electrospray ionization mass spectrometry (MS) is a first choice for detecting low abundance lipids in biological samples. Recently, supercritical fluid

chromatography (SFC) has attracted attention for overcoming problems about structural diversity and quantification. By using stationary phases with high polarity, various lipid classes (e.g. diacylglycerols, phospholipids and sphingolipids) were separated within 20 min while maintaining sharp peak shapes. SFC also separated some isomeric lipids such as positional isomers of lyso-phospholipids (e.g. 1-acyl vs 2-acyl types) and diastereomeric glycolipids (e.g. β-glucosylceramide vs β-galactosylceramide). Although lipid molecules within the same class were not separated, the individual lipid levels of structural isomers with different fatty acid side chains were monitored by fatty acyl-based MS/MS fragments. By adding internal standards for each lipid class, each molecule was analyzed within an appropriate quantification. In my presentation, I want to talk about the advantage of lipid separation using SFC system and the potential for glycolipids study.

References
1) Takeda H et al. J. Lipid Res. 59. 1283-1293 (2018)
2) Takeda H et al. J. Lipid Res. 60. 1465-1474 (2019)

Possibilities and the latest technologies of Supercritical Fluid Chromatography

Shinnosuke Horie (Shimadzu Corporation)

Supercritical Fluid Chromatography (SFC) utilizes carbon dioxide (CO_2) as main mobile phase. CO_2 is nonpolar, however, compatible with various kinds of solvents from alcohols though hydrocarbons. It produces a new separation mode like a combination of nonpolar solvent and nonpolar stationary phase. Therefore, it provides wider range of selectivity compared to HPLC. CO_2 should be supercritical phase conceptually, however, subcritical and/or liquid phase of CO_2 are also available in actuality.
Here, I introduce possibilities of SFC including the latest technologies, LC-SFC switching and fractionation.

Studies of syntheses and mass analyses for polysaccharide and glycopeptides

Hiroki Shimizu (AIST)

Although polysaccharides could be synthesized in these days, analysis of them is not easy but matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) is promising. Meanwhile, glycopeptides can be synthesized by solid-phase peptide synthesis (SPPS), we should consider reactivity and cost of glycoamino acid synthons and stability and purification difficulties for synthesized glycopeptides. Also, analysis of glycopeptides is difficult but again MALDI- MS is promising. We will, here, present our academia-industry cooperation activities, namely developing microwave assisted glycopeptide synthesizer GPS (EYELA) and usefulness of MALDImini-1 (Shimadzu Co.) for glycopeptides and polysaccharides.

Glycosylation analysis using benchtop MALDI-MS
Takashi Nishikaze (Shimadzu Corporation)

Mass spectrometry (MS) with soft ionization methods is now recognized as an indispensable tool for fragile biomolecule analysis. In the glycan/glycosylation analysis fields, due to its rapidity and simplicity, matrix-assisted laser desorption/ ionization (MALDI) MS is commonly used, as well as electrospray MS. Shimadzu Corporation has put two-types of true benchtop MALDI-MS lineup on the market, MALDI-8020 and MALDImini™-1. MALDI-8020 is a simple linear-type TOF (time-of-flight) MS, allowing rapid and semi-quantitative analysis. MALDImini-1 employs Shimadzu-original digital ion trap technology that enables structure-informative MS^n analysis with light and compact instrument shape. furthermore, we recently released a novel reagent kit “SialoCapper™-ID Kit”. This reagent kit was developed for glycan pre-treatment prior to MS analysis. The chemical modification by the reagent kit not only stabilizes sialic acids on glycans, but also discriminates linkage isomers of sialic acids. Here, the unique concept of our benchtop MS and the reagent kit will be presented with glycosylation analysis-related applications.

Session 6 The Next Generation Created by Glycan Synthesis

Chair: Kiichiro Totani (Seikei University)

Synthesis of useful glycosides utilizing boron-mediated aglycon delivery
Daisuke Takahashi (Keio University)

1,2-cis Glycosides are frequently found in various biologically active natural products, pharmaceuticals, and functional materials. However, the stereoselective synthesis of these glycosides is still difficult due to the lack of neighboring group participation. Therefore, the development of efficient synthetic methods has been required. In this context, we have recently developed novel 1,2-cis-stereoselective glycosylations using 1,2-anhydroglycosyl donors and boronic or boronic acid catalysts, namely, “Boron-Mediated Aglycon Delivery (BMAD)”. In this presentation, I wish to report mainly on the efficient synthesis of biologically active glycosides using a BMAD method and their biological activities.

References
1) 高橋大介: 有機合成化学協会誌, 2020, 78, 221-231
2) Tanaka M, Nakagawa A, Nishi N, Iijima K, Sawa R, Takahashi D, Toshima K. J. Am. Chem. Soc. 2018, 140, 3644-3651
3) Nishi N, Seki K, Takahashi D, Toshima K. Angew. Chem. Int. Ed. 2021, 60, 1789-1796

Carbohydrate research in Tottori University

Toshiki Nokami (Tottori University)

A variety of carbohydrate research has been carried out in Tottori University targeting glucosamino glycans, lipopolysaccharides, chitin/chitosan, and their oligosaccharides. Among these research projects synthetic study of oligosaccharides is one of the major approaches to reveal their properties and those of the corresponding polysaccharides. In this talk oligosaccharide synthesis based on the electrochemical method will also be introduced to discuss how to contribute to the research area.

References
1) a) Isoda Y, Sasaki N, Kitamura K, Takahashi S, Manmode S, Takeda-Okuda N, Tamura J, Nokami T, Itoh T. Beilstein J. Org. Chem. 2017, 13, 919. b) Manmode S, Kato M, Ichiyanagi T, Nokami T, Itoh T. Asian J. Org. Chem. 2018, 7, 1802
2) a) Yano K, Itoh T, Nokami T, Carbohydr. Res. 2020, 492, 108018. b) Morimoto Y, Takahashi S, Isoda Y, Nokami T, Fukamizo T, Suginta W, Ohnuma T. Carbohydr. Res. 2021, 499, 108201. c) 矢野君晟, 佐々木紀彦, 伊藤敏幸, 野上敏材: 有機合成化学協会誌 2021, 79, 839

Chemical synthesis of derivatives of arabinofuranoside and its application to the analysis of arabinan degrading enzymes

Akihiro Ishiwata (RIKEN)

Mycobacterial arabinan consists of only D-form of arabinofuranoside (Araf) residues found in arabinogalactan and lipoarabinomannan. The degrading enzymes of arabinan which should be as a novel target for the antimycobacterial agents have not been well studied mainly due to the limited supply of pure arabinan substrate. Our synthetic study for the arabinan and the probes led us to investigate the substrate specificity and the mechanistic insight of endo-arabinanase and exo-α-arabinofuranosidase. In addition, bifidobacterial homologues were found to accept D-fructofuranosides as the substrate. The probes of an enantiomeric L-Araf-containing plant glycan were also applied to the study on the novel bifidobacterial L-arabinofuranosidases.

References
1) Fujita K, Suda Y. P2019-017358A
2) Ishiwata A, Ito Y. J. Am. Chem. Soc. 2011, 133, 2275
3) Maruyama S et al. Glycobiology 2021, accepted

A multi-faceted system for differential glycoprotein analysis: toward the "design drawings" of glyco-targets for the highly specific antibody drug development

Atsushi Kuno (AIST)

Membrane glycoproteins are known to alter their glycosylation sites and glycan structures along with the change of cell status and environments related to diseases, which is expected to be used as molecular targets for developing more effective antibody drugs with fewer side-effect. In this project, we constructed a new multi-faceted glycosylation analysis system that would be adopted in a seamless discovery pipeline for glyco-target molecules. We used more than 600 tissue specimens of 12 diseases to make the list of glyco-target candidates in 9 diseases. Based on the lists, we confirmed disease-specific glycan alteration on each target using lectin microarray. Twenty-five molecules were analyzed by in-depth GlycoRIDGE, and some of them were provided as the

"design drawings" for making immunogen. Finally, pathological and biochemical validation confirmed the antibodies with glycopeptide-recognizing ability. We expect that the developed technology contributes to new medicine development by expanding the repertoire of drug targets.

References
1) Wagatsuma T et al. Discovery of pancreatic ductal adenocarcinoma-related aberrant glycosylations: A multilateral approach of lectin microarray-based tissue glycomic profiling with public transcriptomic datasets. Front. Oncol. 10, 338 (2020)
2) Sakata-Matsuzawa M et al. Glycans unique to the relapse-prone subset within triple-negative breast cancer as revealed by lectin array-based analysis of surgical specimens. PLoS ONE 16, e0250747 (2021)
3) Noro E et al. N-Glycan structures of Wisteria floribunda agglutinin-positive Mac2 binding protein in the serum of patients with liver fibrosis. Glycobiology in press

Development of a glycoproteomics platform for the identification of diagnostic/therapeutic targets for colorectal cancer

Daisuke Takakura (Yokohama City University)

Aberrant glycosylations in cancer are candidates for diagnostic markers and therapeutic targets. A groundbreaking *O*-glycoproteomics platform was developed with the support of “Project for utilizing glycans in the development of innovative drug discovery technologies”, which identified cancer-specific *O*-glycopeptides from various clinical specimens such as the lung and renal cancers. In this study, comparative *O*-glycosylation analysis was performed using colorectal cancer specimens. We identified some cancer-specific *O*-glycoproteins in the serum and tissue. In this presentation, practical method for the use of the platform and a portion of these data are presented.

References
1) Takakura et al. Selective glycopeptide profiling by acetone enrichment and LC/MS. J Proteomics. 101: 17-30 (2014)

Pharmaceutical application of SKM9-2, a glycopeptide-recognizing antibody

Shoutaro Tsuji (Gunma University Health Welfare)

Malignant mesothelioma is a fatal tumor. Medical treatment and diagnosis were difficult because specific markers for mesothelioma had not been found. We found a highly specific marker for mesothelioma, sialylated HEG1, and isolated the anti-sialylated HEG1 monoclonal antibody, SKM9-2. The specificity and sensitivity of SKM9-2 to mesothelioma reach 99% and 92%, respectively; therefore, SKM9-2 is a marker antibody that can be a standard marker for diagnosis of mesothelioma. In addition, SKM9-2 is a unique antibody that recognizes HEG1 peptide sequences along with two glycans. This time, I will talk about the application of humanized SKM9-2 to pharmaceutical drug.

References

1) Tsuji S et al. Sci. Rep. 7:45768, 2017
2) Naso JR et al. Am. J. Surg. Pathol. 44:1143–1148, 2020
3) Matsuura R et al. Sci. Rep. 8:14251, 2018

Closing Remarks

Shinya Fushinobu (University of Tokyo)