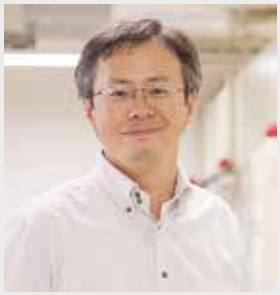
RESEARCH ACTIVITIES

Research Center of Integrative Molecular Systems

The mission of CIMoS is to analyze molecular systems in nature to find the logic behind the sharing and control of information between the different spatiotemporal hierarchies, with the ultimate goal of creating novel molecular systems on the basis of these findings.

The Origin of 24 Hour Period in Cyanobacterial Clock System

Research Center of Integrative Molecular Systems
Division of Trans-Hierarchical Molecular Systems



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2011 Associate Professor, Nagoya University
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Keywords Circadian Clock, Clock Proteins, Cyanobacteria

Circadian (approximately 24 h) clocks are endogenous time-keeping systems encapsulated in living cells, enabling organisms to adapt to daily fluctuation of exogenous environments on the Earth. These time-keeping systems, found ubiquitously from prokaryotes to eukaryotes, share the three characteristics. First, the circadian rhythmicity of the clocks persists even without any external cues (self-sustainability). Second, the period is little dependent on ambient temperature (temperature compensation). Third, the phase of the clock can be reset by external stimuli such as lightning, humidity, or temperature so as to be synchronized to the external phase (synchronization).

KaiC, a core protein of the circadian clock in cyanobacteria, undergoes rhythmic structural changes over approximately 24 h in the presence of KaiA and KaiB (Kai oscillator). This slow dynamics spanning a wide range of both temporal and spatial scales is not well understood, and is central to a fundamental question: What determines the temperature-compensated 24 h period? The Kai oscillator reconstitutable *in vitro* is advantageous for studying its dynamic structure through a complementary usage of both X-ray crystallography and solution scattering, its transient response by using physicochemical techniques, and its molecular motion through a collaborative work with computational groups (Abe *et al. Science* 2015). Our mission is to explore the frontier in molecular science of the circadian clock system from many perspectives.

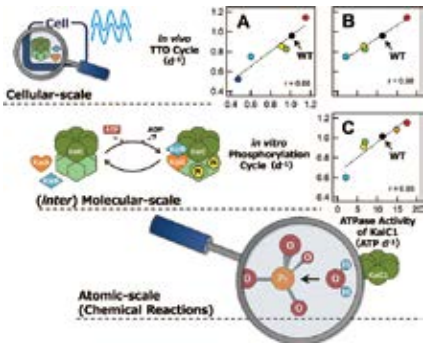

Figure 1. *Trans*-hierarchic nature of the circadian clock system in cyanobacteria. Cross-correlational plots (A–C) among frequency of *in vivo* transcription and translation oscillation (TTO) cycle, frequency of *in vitro* phosphorylation cycle, and ATPase activity of KaiC for cyanobacteria carrying period-modulating KaiC mutants (circles). Fine correlations in three panels indicate regulatory mechanisms of KaiC ATPase as the core basis for *trans*-hierarchic nature of cyanobacterial circadian clock system.

Selected Publications

- Y. Furuike, J. Abe, A. Mukaiyama and S. Akiyama, *Biophys. Physicobiol.* **13**, 235–241 (2016).
- J. Abe, T. B. Hiyama, A. Mukaiyama, S. Son, T. Mori, S. Saito, M. Osako, J. Wolanin, E. Yamashita, T. Kondo and S. Akiyama, *Science* **349**, 312–316 (2015).
- Y. Murayama, A. Mukaiyama, K. Imai, Y. Onoue, A. Tsunoda, A. Nohara, T. Ishida, Y. Maéda, T. Kondo and S. Akiyama, *EMBO J.* **30**, 68–78 (2011).
- S. Akiyama, *Cell. Mol. Life Sci.* **69**, 2147–2160 (2012).
- S. Akiyama, A. Nohara, K. Ito and Y. Maéda, *Mol. Cell* **29**, 703–716 (2008).

1. Atomic-Scale Origins of 24 Hour Period in Cyanobacterial Clock System[1,2)]

The cyanobacterial circadian clock can be reconstructed *in vitro* by mixing three clock proteins (KaiA, KaiB, and KaiC) and ATP. As shown in Figure 2, KaiC ATPase activity exhibits a robust circadian oscillation in the presence of KaiA and KaiB. Astonishingly, the temporal profile of KaiC ATPase activity exhibited an attenuating and oscillating component even in the absence of KaiA and KaiB. A detailed analysis revealed that this signal had a frequency of 0.91 d^{-1}, which approximately coincided with the 24 h period. KaiC is thus the source of a steady cycle that is in tune with the Earth's daily rotation.

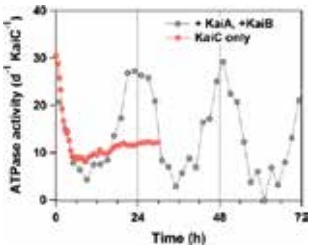

Figure 2. Time-course of KaiC ATPase activity.

To identify the structural origins of slowness encoded in KaiC (Figures 1B & 1C), its N-terminal ATPase domain was analyzed using high-resolution x-ray crystallography. A water molecule is prevented from attacking into the ideal position (a black dot in Figure 3) for the ATP hydrolysis by a steric hindrance near ATP phosphoryl groups. In addition, this hindrance is surely anchored to a spring-like structure derived from polypeptide isomerization. The ATP hydrolysis, which involves access of a water molecule to the bound ATP and reverse isomerization of the polypeptide, is expected to require a significantly larger amount of free energy than for typical ATP hydrolysis. The atomic structure discovered by us explains why the ATPase activity of KaiC is so much lower (by 100- to 1,000,000-fold) than that of typical ATPase molecules.

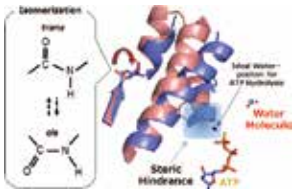

Figure 3. Structural basis for steady slowness. The steric barrier prevents access of a water molecule to the catalytic site (indicated by a black dot).

2. *Trans*-Hierarchic Nature of Cyanobacterial Circadian Clock System[3)]

How is the intra-molecular slowness encoded in KaiC (Figures 2 and 3) transmitted to the inter-molecular interactions with other Kai proteins? Protein-ligand interactions are often discussed whether a structural change of the protein comes before or after the ligand binding (Figure 4). The conformational selection (CS) scheme predicts that the protein first undergoes a structural change to form a specific intermediate. The ligand is then recognized specifically through the intermediate state to form a tight ligand-protein complex. On the other hand, in the induced-fit (IF) scheme, the ligand and protein form an encountered complex without meaningful structural changes, and then both the ligand and protein undergo structural changes to form the tight protein-ligand complex. Under the ligand-saturating conditions, the rate of forming the protein-ligand complex differs between CS (k_f) and IF ($k_f + k_b$) schemes (Figure 4).

A tryptophan residue was introduced in the N-terminal ring of KaiC as the fluorescent probe for KaiBC complex formation.[3)] Our detailed analysis of the kinetic data indicated that KaiB exclusively selects the post-ATP-hydrolysis state of KaiC to form the KaiBC complex. The CS mechanism is elegantly designed in KaiC so that the slow intra-molecular reaction (k_f: The slow rate of ATPase) in KaiC can be the rate-liming step of the overall KaiBC complex formation.

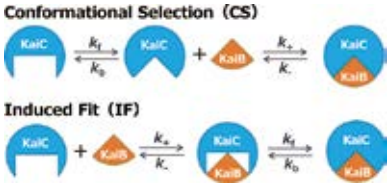

Figure 4. Conformational selection and induced-fit schemes.

3. Instrumentation for Studying Biological Clock Systems[4)]

We have improved stability over time, signal-to-noise ratio, time resolution, temperature control, automated high-throughput measurements each for fluorescence tracking system,[3)] auto-sampling device,[4)] HPLC,[1)] FTIR, and small-angle x-ray scattering (SAXS). The developed devices were utilized in identifying the core process of generating circadian periodicity in cyanobacterial circadian clock.[2,3)]

4. Bio-SAXS Activity in IMS[5)]

We have supported SAXS users so that they can complete experiments smoothly and publish their results.[5)]

References

1) S. Akiyama, A. Mukaiyama, J. Abe and Y. Furuike, *Biological Clocks: With Reference to Suprachiasmatic Nucleus*, 73–77 (2017).
2) J. Abe, T. B. Hiyama, A. Mukaiyama, S. Son, T. Mori, S. Saito, M. Osako, J. Wolanin, E. Yamashita, T. Kondo and S. Akiyama, *Science* **349**, 312–316 (2015).
3) A. Mukaiyama, Y. Furuike, J. Abe, E. Yamashita, T. Kondo and S. Akiyama, *Sci. Rep.* **8**, 8803 (2018).
4) Y. Furuike, J. Abe, A. Mukaiyama and S. Akiyama, *Biophys. Physicobiol.* **13**, 235–241 (2016).
5) Submitted.

* IMS International Internship Program

Protein Design Using Computational and Experimental Approaches

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Keywords Structural Biology, Protein Folding, Protein Design for Structure and Function

Protein molecules spontaneously fold into unique three-dimensional structures specified by their amino acid sequences from random coils to carry out their functions. Many of protein studies have been performed by analyzing naturally occurring proteins. However, it is difficult to reach fundamental working principles of protein molecules only by analyzing naturally occurring proteins, since they evolved in their particular environments spending billions of years. In our lab, we explore the principles by computationally designing protein molecules completely from scratch and experimentally assessing how they behave.

Protein design holds promise for applications ranging from catalysis to therapeutics. There has been considerable recent progress in computationally designing proteins with new functions. Many of protein design studies have been conducted using naturally occurring protein structures as design scaffolds. However, since naturally occurring proteins have evolutionally optimized their structures for their functions, implementing new functions into the structures of naturally occurring proteins is difficult for most of cases. Rational methods for building any arbitrary protein structures completely from scratch provide us opportunities for creating new functional proteins. In our lab, we tackle to establish theories and technologies for designing any arbitrary protein structures precisely from scratch. The established methods will open up an avenue of rational design for novel functional proteins that will contribute to industry and therapeutics.

Selected Publications

- N. Koga, R. Tatsumi-Koga, G. Liu, R. Xiao, T. B. Acton, G. T. Montelione and D. Baker, "Principles for Designing Ideal Protein Structures," *Nature* **491**, 222–227 (2012).
- Y.-R. Lin, N. Koga*, R. Tatsumi-Koga, G. Liu, A. F. Clouser, G. T. Montelione and D. Baker*, "Control over Overall Shape and Size in De Novo Designed Proteins," *Proc. Natl. Acad. Sci. U. S. A.* **112**, E5478–E5485 (2015).

1. Principles for Designing Ideal Protein Structures

Understanding the principles for protein folding is complicated by energetically unfavorable non-ideal features—for example kinked α-helices, bulged β-strands, strained loops and buried polar groups—that arise in proteins from evolutionary selection for biological function or from neutral drift. Here, we uncovered the principles for protein folding by designing "ideal" protein structures, which are stabilized by completely consistent local and non-local interactions. We discovered a set of rules relating local backbone structures (secondary structure patterns) to tertiary motifs (Figure 1 left), which were identified using a combination of folding simulations and analyses of naturally occurring proteins. Building backbone structures according to the rules (Figure 1 top right) and placing side chains stabilizing the backbone structures, we can readily design the proteins that have funnel-shaped folding energy landscapes leading into the target folded state.

Using this approach, we designed sequences predicted to fold into ideal protein structures consisting of α-helices, β-strands and minimal loops, using the Rosetta program. Designs for five different topologies were found to be monomeric and very stable and to adopt structures in solution nearly identical to the computational models (Figure 1 bottom right). These results suggest that the local backbone structures determine the tertiary folded structures rather than the details of amino acid sequences.

2. Control over Overall Shape and Size in De Novo Designed Proteins

To achieve fine control over protein shape and size within a particular topology, we have extended the design rules by systematically analyzing the codependences between the lengths and packing geometry of successive secondary structure elements and the backbone torsion angles of the loop linking them. We demonstrate the control afforded by the resulting extended rule set by designing a series of protein with the same fold but considerable variation in secondary structure length, loop geometry, β-strand registry, and overall shape. Solution NMR structures of four designed proteins for two different folds show that protein shape and size can be precisely controlled within a given fold. These extended design principles provide the foundation for custom design of protein structures performing desired functions.

References

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3) N. Koga, R. Tatsumi-Koga, G. Liu, R. Xiao, T. B. Acton, G. T. Montelione and D. Baker*, *Nature* **491**, 222–227 (2012).
4) J. Fang, A. Mehlich, N. Koga, J. Huang, R. Koga, M. Rief, J. Kast, D. Baker and H. Li*, *Nat. Commun.* **4**, 2974 (2013).
5) Y.-R. Lin, N. Koga*, R. Tatsumi-Koga, G. Liu, A. F. Clouser, G. T. Montelione and D. Baker*, *Proc. Natl. Acad. Sci. U. S. A.* **112**, E5478–E5485 (2015).
6) Y.-R. Lin, N. Koga, S. M. Vorobiev and D. Baker*, *Protein Sci.* **26**, 2187–2194 (2017).

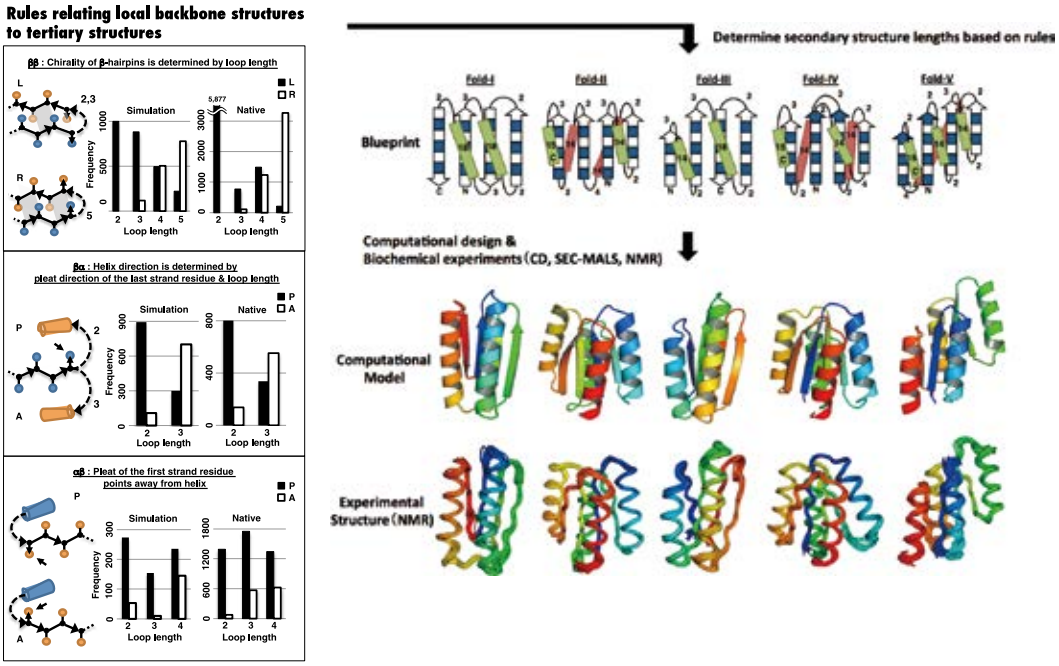

Figure 1. Left: Rules relating local backbone structures to tertiary motifs. Right: De novo designed protein structures.

Award

KOGA, Nobuyasu; Morino Foundation for Molecular Science (2018).

Open up Future Electronics by Organic Molecules

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Keywords Molecular Conductors, Organic Superconducting Transistors, Supramolecular Nanowires

Organic molecules are attracting recent attention as new ingredients of electronic circuits. Their functionalities have been developed considerably, but are still to be explored and advanced. Our group focuses on a development of organic electronics in the next era by providing new mechanism and concepts of the device operation and fabrication. For example, an electronic phase transition is utilized for the ON/OFF switching of our field-effect-transistor (FET). This special FET is called an organic Mott-FET, where the conduction electrons in the organic semiconductor are solidified at the OFF state because of Coulomb repulsion among carriers. However, these solidified electrons can be melted by applying a gate voltage, and show an insulator-to-metal transition so-called Mott-transition to be switched to the ON state. Because of this phase transition, a large response of the device can be achieved, resulting in the highest device mobility ever observed for organic FETs. At the same time, Mott-transition is known for its relevance to superconductivity. Not only in organic materials but also in inorganic materials such as cuprates, Mott-transition is frequently associated with superconducting phase at low temperature. Indeed, our organic FET shows an electric-field-induced superconducting transition at low temperature.

Another approach to the future electronics is a three-dimensional (3D) patterning of molecular devices using crystal engineering. Because each molecule can be designed to show different functionalities, it should be attractive to construct nano-structured devices by self-assembly. We are especially focusing on a development of supramolecular nanowires that allow 3D periodic wiring in nano-scale. By encapsulating a 1D array of conducting molecules in a channel formed inside 3D supramolecular network, it is possible to construct a sheathed nanowires aligned in a periodic order as shown in Figure 1.

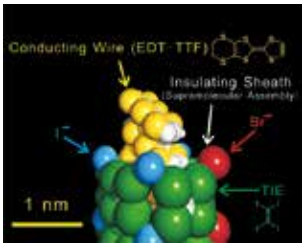

Figure 1. Crystal structure of supramolecular nanowire.

Selected Publications

- Y. Kawasugi, K. Seki, Y. Edagawa, Y. Sato, J. Pu, T. Takenobu, S. Yunoki, H. M. Yamamoto and R. Kato, "Electron–Hole Doping Asymmetry of Fermi Surface Reconstructed in a Simple Mott Insulator," *Nat. Commun.* **7**, 12356 (8 pages) (2016).
- M. Suda, R. Kato and H. M. Yamamoto, "Light-Induced Superconductivity Using a Photo-Active Electric Double Layer," *Science* **347**, 743–746 (2015).
- H. M. Yamamoto, M. Nakano, M. Suda, Y. Iwasa, M. Kawasaki and R. Kato, "A Strained Organic Field-Effect Transistor with a Gate-Tunable Superconducting Channel," *Nat. Commun.* **4**, 2379 (7 pages) (2013).
- H. M. Yamamoto, "Sheathed Nanowires Aligned by Crystallographic Periodicity: A Possibility of Cross-Bar Wiring in Three-Dimensional Space," *CrystEngComm* **16**, 2857–2868 (2014).

1. Light-Induced Superconductivity in an Organic Mott-FET[1,2)]

κ-(BEDT-TTF)Cu[N(CN)$_2$]Br (κ-Br) is an organic Mott-insulator at room-temperature, but turns into metallic and superconducting states at low temperature. (BEDT-TTF = bis(ethyelenedithio)tetrathiafulvalene) In our previous works, a tensile strain from FET substrate altered κ-Br's ground state into a Mott-insulating state, when its thin (*ca.* 100 nm) crystal was laminated on top of SiO_2/Si^{++} substrate and cooled down to low temperature. In those experiments the electronic state at low temperature became completely insulating because of the large tensile strain that originates in mismatching of thermal expansion coefficients between κ-Br (30 ppm/K) and Si (2 ppm/K). However, one can anticipate from the *T*–*P* (temperature *vs*. pressure) phase diagram that mixed electronic state between superconducting and Mott-insulating states will be realized when the tensile strain is much weaker. To achieve such a mixed state (or, percolate-superconducting state), Nb-doped $SrTiO_3$ is used as a back-gate substrate because of its larger thermal expansion coefficient (*ca.* 10 ppm/K) than Si. An aluminum oxide layer was grown by atomic layer deposition technique to form a gate dielectric on the substrate to form a FET device structure. With this type of FET substrate, we have achieved an electric-field-induced superconductivity in κ-Br.

Recently, we have inserted a photochromic self-assembled monolayer (SAM layer: Figure 2, right panel) into this device in order to make it photo-active. We have employed a photochromic molecule 'spiropyran' whose UV-converted isomer 'merocyanin' is known to exhibit zwitter-ionic structure. Because the photochromic molecules are aligned in the same direction in the SAM, a strong electric field can be generated by photo-irradiation, when the spiropyran is converted into the merocyanin form. Thus, excess carriers can be injected to the FET interface due to the strong dipole moment of merocyanin.

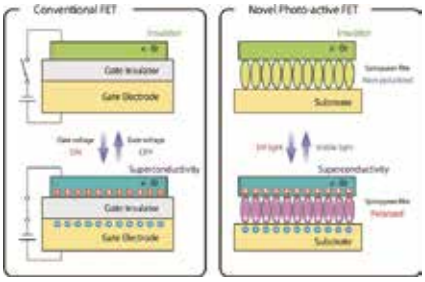

Figure 2. Device schematic for conventional superconducting FET (left) and our photo-active FET (right).
This figure shows p-type doping by molecular dipole-moment.

A κ-Br thin crystal is mounted on the SAM/Al_2O_3/Nb-$SrTiO_3$ substrate, and cooled down to low temperature. The resistance of the device showed weakly insulating temperature dependence, suggesting a percolate-superconducting state. Upon irradiation of UV-light, the resistivity at 5 K went down quickly and low-resistance state was observed after 180 sec. Temperature dependence of resistivity showed sudden drop around 7 K, confirming superconducting transition after the UV-light irradiation. Reverse photo-reaction by visible light led the phase transition back to the insulating state again. The switching of this device seems to originate from the light-induced formation of internal dipole moment in the SAM-layer, which resulted in a hole-doping at the FET interface. This speculation was confirmed by dual-gate experiment of this device, where gate-induced hole carriers worked cooperatively with the light-induced carriers. This result is the first example of light-induced superconductivity in FET devices, and allows remote control of superconducting device without direct wiring.

One can invert the direction of the molecule and its related electric field by designing a photochromic SAM molecule with different geometry. By such a strategy, we were able to achieve n-type light-induced superconductivity as shown in Figure 3. In this device, the threshold gate voltage for superconducting transition was shifted in the negative direction, as the UV irradiation proceeded. This implies that the light-induced carrier is an electron. These photo-active devices pave the way for new type of photo-electronics.

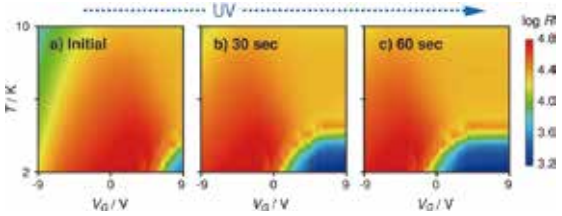

Figure 3. Emergence of n-type superconductivity by UV-irradiation. At the initial state (a), the device shows a normal ambipolar transistor behavior. After the UV-irradiation, superconducting region (blue) appears from electron-doped side (panels b and c).

References

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2) M. Suda, N. Takashina, S. Namuangruk, N. Kungwan, H. Sakurai and H. M. Yamamoto, *Adv. Mater.* **29**, 1606833 (2017).

Awards

SUDA, Masayuki; The 12th Condensed-Matter Science Prize (2017).
SUDA, Masayuki; The Commendation for Science and Technology by the Minister of Education, Culture, Sports, Science and Technology The Young Scientists' Prize (2018).

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Development of Graphene Molecules as Organic Semiconductors

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Keywords Organic Synthesis, Organic Semiconductor, Graphene Molecule

Graphene and curved graphenes have been extensively investigated by both chemists and physicists because of their unique structures and properties. C_{60} fullerene is spherical and has the positive Gaussian curvature. Carbon nanotubes (CNTs) have the cylindrical structures with the zero Gaussian curvature. The introduction of curvatures to graphene changes the dimensionality and electronic properties. For example, graphene is a two-dimensional zero-gap semiconductor with the ambipolar character (both p- and n-types). C_{60} is a zero-dimensional n-type semiconductor, and CNTs are one-dimensional p-type semiconductors or metals. Three-dimensional graphenes with the negative Gaussian curvature were proposed as shown in Figure 1. It is interesting to see how the curvature influences the structure and properties of the graphene molecule.

Perfluorination is a simple method to prepare an n-type semiconductor with the same molecular symmetry. It is important to understand the impact of perfluorination on the solid-state structures and charge transport properties. We are currently working on the synthesis of new perfluorinated aromatic compounds.

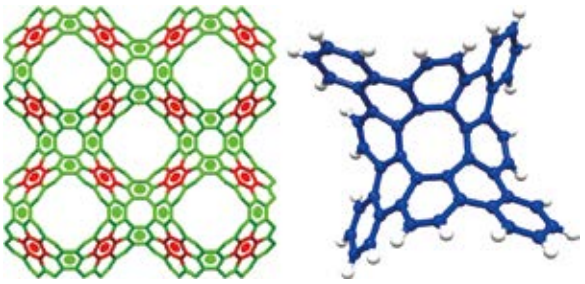

Figure 1. Schwarzite P192 (left) as a hypothetical 3D graphene with the negative Gaussian curvature. Tetrabenzo[8]circulene (right) as a repeating molecular unit for Schwarzite P192.

Selected Publications

- T. Iwamoto, Y. Watanabe, Y. Sakamoto, T. Suzuki and S. Yamago, "Selective and Random Syntheses of [*n*]Cycloparaphenylenes (*n* = 8–13) and Size Dependence of their Electronic Properties," *J. Am. Chem. Soc.* **133**, 8354–8361 (2011).
- Y. Sakamoto and T. Suzuki, "Tetrabenzo[8]circulene: Aromatic Saddles from Negatively Curved Graphene," *J. Am. Chem. Soc.* **135**, 14074–14077 (2013).
- Y. Kuroda, Y. Sakamoto, T. Suzuki, E. Kayahara and S. Yamago, "Tetracyclo(2,7-carbazole)s: Diatropicity and Paratropicity of Inner Regions of Nanohoops," *J. Org. Chem.* **81**, 3356–3363 (2016).
- Y. Sakamoto and T. Suzuki, "Perfluorinated and Half-Fluorinated Rubrenes: Synthesis and Crystal Packing Arrangement," *J. Org. Chem.* **82**, 8111–8116 (2017).

1. Perfluorination of Rylene Compounds for Electronics and Optoelectronics

Perfluorination of aromatic compounds is a simple method of exchanging all hydrogen with fluorine, and it is possible to convert a p-type semiconductor to an n-type one.[1] Although the molecular weight greatly increases, the melting point, sublimation temperature, and stability do not change so much. Therefore, perfluorinated aromatic compounds can be handled under similar conditions. As seen in pentacene ($C_{22}H_{14}$) and perfluoropentacene ($C_{22}F_{14}$), the size and symmetry of the hydrogen molecule and the fluorine form are comparable. Because of this advantage, comparative study is easy and contributes to a deep understanding of molecular properties. In this research, we decided to fluorinate the rylene compound as a new target.

The rylene compound is an oligomer in which the 1,8 and 4,5 positions of naphthalene ($C_{10}H_8$) are connected.[2] Perylene (dimer, $C_{20}H_{12}$), terrylene (trimer, $C_{30}H_{16}$), and quarterrylene (tetramer, $C_{40}H_{20}$) have been known for a long time. Oligomers up to octamer have been reported as derivatives with solubilizing groups. Rylene compounds are interesting in the following three points. (1) High efficiency singlet fission (SF) can be expected. (2) Perylene derivatives such as diindenoperylene (DIP, $C_{32}H_{16}$) and dibenzotetraphenylperiflanthene (DBP, $C_{64}H_{36}$) have been frequently used for organic solar cells, and reports on organic thin films have increased. (3) Polyrylene corresponds to an armchair-type graphene nanoribbon (GNR) with the minimum width.

In collaboration with the Momiyama group, we synthesized some fluorinated naphthalene monomers and are working on perfluorinated perylene.

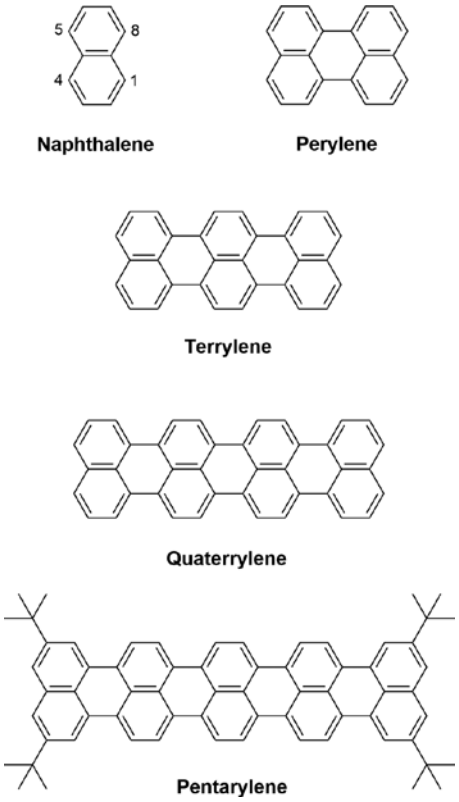

Figure 2. Chemical structures of naphthalene to pentarylene.

References

1) Y. Sakamoto and T. Suzuki, *J. Org. Chem.* **82**, 8111–8116 (2017).
2) J. T. Markiewicz and F. Wudl, *ACS Appl. Mater. Interfaces* **7**, 28063–28085 (2015).