1SAP-07 新規光受容体群シアノバクテリオクロムの吸収波長調節メカニズム
Color tuning mechanism of novel photoreceptors
cyanobacteriochrome
Rei Narikawa 1,2 (Univ. of Tokyo, Dept. of Life Sci., 1 JST, PRESTO)

Cyanobacteriochromes (CBCRs) are cyanobacterial tetrapyrrole-binding photoreceptors that are distantly related to red/far-red light sensing phytochromes and cover the visible and near-ultraviolet regions of spectrum. CBCRs include many photoconversion types such as violet/green, blue/green, green/red and red/green reversible photoconversions. Many biochemical and spectral studies have identified that the diverse spectral properties are due to different chromophore species and different photoconversion mechanism. Recently, structures of chromophore-binding domains of red/green-type AnPixJ and blue/green-type TePixJ were determined. In this presentation, I introduce the color tuning mechanism of the diverse CBCRs based on this structural information.

1SBP-01 1細胞解析のための１分子シーケンシングシステムの開発
Development of Single Molecule Sequencing System for Single Cell Analysis
Sotaro Uemura (BIKEN Center for Life Science Technologies)

Recent transcriptome studies have shown that gene expression number of steps and precise quantification. Current single-cell techniques require several numbers of critical steps of preparation, such as cDNA synthesis or amplification steps. However these steps introduce multiple biases and significant sample loss that hardly reflect the original molecular counts of transcripts at single cell level. To solve these issues we are developing all in one direct single cell analysis system at single molecule detection, which contributes for minimization of number of steps and precise quantification.

1SBP-02 REAL-TIME MONITORING OF BIOMOLECULES IN ZERO-MODE WAVEGUIDES: DNA SEQUENCING AND BEYOND
Paul Peluso (Pacific Biosciences)

At Pacific Biosciences, we have developed a technology that observes individual biomolecules at work in real time. ZMWs are nanostructures that drastically reduce the effective optical observation volume, thereby permitting the use of higher concentrations of fluorescently tagged molecules for single-molecule studies. This technological advance provides the ability to monitor the speed, processivity, and efficiency of the enzyme to be exploited for new capabilities. The power of SMRT (Single Molecule, Real-Time) Sequencing technology - characterized by long read lengths and fast run times - is highlighted through examples such as finishing genomes, characterizing full-length transcript diversity, rapid pathogen sequencing, and the direct detection of epigenetic markers.

1SBP-03 タンパク質翻訳伸長過程の実時間ダイナミクス計測
Dynamics of translation elongation in real time
Joseph Puglisi, Albert Tsai, Jin Chen, Guy Kornberg, Magnus Jonasson, Alexey Petrov, Sean O’Leary, Capece Mark (Department of Structural Biology, Stanford University School of Medicine)

Translation of proteins by the ribosome is a highly dynamic process, requiring coordination of mRNA, tRNA, protein factors and ribosomal conformation to drive the process with high speed and fidelity. We have applied a variety of single-molecule fluorescence approaches to observe conformational and compositional dynamics at each codon of an mRNA in real time. Our results have revealed the basic mechanisms of elongation and the dynamic origins of rare elongation events such as stalling, frameshifting and drug inhibition.

1SBP-04 Single Molecule Electrical Sequencing of DNA and microRNA
Masateru Taniguchi (The Institute of Scientific and Industrial Research, Osaka University)

Two paradigm shifts in DNA sequencing technologies, from bulk to single molecules and from optical to electrical detection, are expected to realize label-free, low-cost DNA sequencing. Here we report on single-molecule electrical sequencing of DNA and microRNA by a hybrid method of identifying single-base molecules via tunneling current and random sequencing. Our method reads short DNA and let-7 microRNA sequences. We have developed the method to control the translocation speed of single-DNA molecules passing through a nanopore, in an effort to obtain high accuracy and throughput in reading out sequences. The translocation speed can be controlled using gate voltage, in order to control electro-osmotic flow within a nanopore.

1SBP-05 類似配列の高速な全ペア列挙に基づく NGS データの解析手法
NGS data analyses based on ultra-fast all pairs similarity search
Kana Shimizu (Computational Biology Research Center, National Institute of Advanced Industrial Science and Technology)

Recent progress in sequencing technology calls for efficient computational methodologies for analyzing huge amount of DNA sequence fragments. In our recent study, we developed ultra-fast algorithm for evaluating sequence similarity of next generation sequencing (NGS) data. The algorithm, named SlideSort, finds all similar pairs from a set of NGS data, and serves as a building block for various important analyses including clustering analyses and identification of frequently appeared sequence patterns. In this talk, I will give a brief introduction of the algorithm and will show some application studies as well as further direction of our study.