

Number	Title and outline	Organizers	Country
Workshop 2	Evolution of real-time cell imaging and in vivo recording systems: recent advance and new applications to physiological analysis of live-cell and free-moving animals	Masaaki Ikeda Toru Takumi	JAPAN JAPAN
	The aim of this symposium is to overview the recent advance of real-time imaging, in vivo recording of MUA (multiunit activity) and the applications of these systems to physiological analysis of live-cells and freely moving animals. The symposium is consisted of overview of the techniques, the application of multicolor luciferase system for visualization of multiple gene expression, the application of FRET-based imaging to visualize interaction of gene products, electrophysiological activity of brain from freely moving animals, and the application of newly developed luciferases to live-cell imaging.		
Workshop 3	Bio-logging workshop: physiological and biomechanical measurements on wild animals in nature	Katsufumi Sato Nubuaki Arai	JAPAN JAPAN
	Bio-logging science may be defined as “investigation of phenomena in or around free-ranging organisms that are beyond the boundaries of our visibility or experience”. Especially in aquatic environments, where it is almost impossible to directly observe individual animals, animal-borne data loggers are crucial to studying the ecophysiology and biomechanics of animals under natural conditions. Bio-logging lies at the interface between scientific inquiry and technological feasibility. Instrumentation has improved in terms of the data loggers themselves, with increasing memory capacity, and with the availability of new sensors, methods of data recovery, and new techniques for data analysis. The aim of this workshop is to introduce recent advances in this field. We hope to exchange ideas and share information among researchers in the biological, engineering, and information sciences.		
Workshop 4	Structure biology	Da-Neng Wang Yoshinori Fujiyoshi	USA JAPAN
	A biological cell regulates a cell signaling at the front mainly through membrane proteins. For understanding their functions, structure analysis is inevitable. The number of determined structures of proteins including membrane proteins is increasing dramatically mainly because X-ray crystallography is powerful for structure determination of proteins. For example, a G-protein-coupled receptor, human β 2 adrenergic receptor was recently analyzed by X-ray crystallography. Another candidate to study membrane proteins might be electron crystallography. It has been expected that electrons, which interact with matter about 10,000 times stronger than X-rays, could be used for the structural analysis of membrane proteins at an atomic resolution, because helical arrangement of bR was analyzed to a resolution of 7.0 Å in 1975. Henderson and co-workers could actually present an atomic model of bR at a resolution of 3.5 Å. Kuehlbrandt et al. succeeded to make an atomic model of LHC-II. The structure of a typical water channel, AQP1 was also analysed. Based on structural study by the methods, functional details of membrane proteins can be discussed effectively. We organize this symposium because we believe a new era of structure analysis based on X-ray and electron crystallography is dawning.		
Workshop 5	Stem Cell Technology Workshop	Ray Rodgers Eimei Sato	AUSTRALIA JAPAN
	Stem cells underpin the development, repair and or maintenance of organs and tissues in the body. They are increasingly being used in regenerative medicine and for in vivo studies of organs and cells after transplantation of in vitro-prepared stem cells. The technology is currently focusing on identifying and studying stem cells in many organs, and understanding and controlling their cell fates. As the technology progresses the emphasis of the research addresses how best they will be deployed in a physiological setting. The tutorial will cover a number of these aspects using examples from different organs.		