課題番号	研 究 課 題	国際共同研究員 氏名	所属機関国名	蛋白質研究所 担当研究室
1	Semi-synthesis of post-translationally modified proteins using peptidyl asparaginyl ligases	Liu Chuan Fa	Singapore	蛋白質有機化学研究室
2	Development of a new method to conjugate the defensin peptide to the carrier protein P64K using a MeOGly strategy	Garay-Pérez Hilda Elisa	Cuba	蛋白質有機化学研究室
3	Structure determination for beta-glycosidases including accessory domains	Cairns James Robert Ketudat	Thailand	蛋白質結晶学研究室
4	Crystallization and X-ray diffraction analysis of halophilic cellulase (CelGH5) from Indonesia local isolate	Puspaningsih Ni Nyoman Tri	Indonesia	蛋白質結晶学研究室
5	Structural and functional study on the survival-essential factors from bacterial pathogens for the development of novel antibiotics which induce suicide effect (phase IV)	Lee Bong-Jin	Korea	超分子構造解析学研究室
6	Crystal structure of glucose-6-phosphate 1-dehydrogenase	Chen Chun-Jung	Taiwan	超分子構造解析学研究室
7	Structural analysis of Immune System Proteins based on Ligand recognition	Hwang Kwang Yeon	Korea	超分子構造解析学研究室
8	Crystallographic fragment screening and structure determination for anticancer target proteins (Phase V)	Kim Hyoun Sook	Korea	超分子構造解析学研究室
9	Three-dimensional structure determination of metallo-hydrolase from Bacillus sp., carboxylic acid reductase from Mycobacterium phlei, and carboxylesterase from Anoxybacillus geothermalis D9.	Mohamad Ali Mohd Shukuri	Malaysia	超分子構造解析学研究室
10	Structures of an aminopeptidase P and N-recognins for the Pro/N-degron pathway	Song Hyun Kyu	Korea	超分子構造解析学研究室
11	Structural study of Cell penetrating peptides	Lee Soo Jae	Korea	超分子構造解析学研究室
12	Does the KSR scaffold control dose-responses to RAF and MEK inhibitors and their combinations in RAS mutant cells?	Kholodenko Boris	Ireland	細胞システム研究室
13	Computational modelling of EML4-ALK signaling pathway	SAMPSON IOSIFINA	UNITED KINGDOM	細胞システム研究室
14	A systems biology approach to overcoming treatment resistance in B-cell malignancies.	Mitchell Simon	United Kingdom	細胞システム研究室
15	Artificial Intelligence-guided discovery of novel quorum sensing inhibitors as next-generation therapeutics against Pseudomonas aeruginosa infection	Kumar Rajnish	India	計算生物学研究室
16	Determining the protein structure of TBX1 variants by ultra-high magnetic field NMR spectroscopy	Hiroi Noboru	USA	高磁場NMR分光学研究室
17	Characterizing allostery in proteins upon peripheral membrane-binding using elastic network models	Reuter Nathalie	Norway	生体分子動態モデリング研究室
18	Quantifying the role of chromatin remodelers in meiotic recombination using 1D southern hybridization.	Gunjan Deepakkumar Mehta	India	ゲノム-染色体機能研究室