

2025年度 国際共同研究 採択課題一覧

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	Development of on-resin synthetic methodologies for the preparation of cell-permeable cyclic peptides containing dithiolanes	Gloria Lourdes Serra Lemes	Uruguay	蛋白質有機化学研究室
2	Discovery of cyclic peptide-based antibiotics targeting bacterial lipid A or peptidoglycans, part I	Wei-Chieh Cheng	Taiwan	蛋白質有機化学研究室
3	Structural analysis of a plant glucosyl ceramidase(GBA2)-like enzyme from Arabidopsis thaliana	James Robert Ketudat Cairns	Thailand	蛋白質結晶学研究室
4	Crystallization and X-ray analysis of a thermostable glycoside hydrolase family 43 β -xylosidase (GbtXyl43B) from Geobacillus thermoleovorans IT-08	Ni Nyoman Tri Puspaningsih	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)	Bong-Jin Lee	Republic of Korea	超分子構造解析学研究室
6	Structural analysis of Ca ²⁺ -binding proteins from Schistosoma mansoni	Kwang Yeon Hwang	Republic of Korea	超分子構造解析学研究室
7	Crystal structure determination enzymes for industrial, agricultural and medical applications	Mohd Shukuri Mohamed Ali	Malaysia	超分子構造解析学研究室
8	Phase II Structural Investigation of Anticancer Target Proteins and Their Complexes with Therapeutic Inhibitors	Hyoun Sook Kim	Republic of Korea	超分子構造解析学研究室
9	Structural study of Cell penetrating peptides	Lee Soo Jae	South Korea	超分子構造解析学研究室
10	Crystal structure of aminoimidazole ribonucleotide synthetase with co-factor and inhibitor complex	Chun-Jung Chen	Taiwan	超分子構造解析学研究室
11	Mathematical modelling of EML4-ALK-bound adaptor proteins in condensates	SAMPSON IOSIFINA	UNITED KINGDOM	細胞システム研究室
12	In silico modelling of S. aureus' impact on human keratinocyte NF- κ B homeostasis and the skin's innate immunity	Ahmad Abdullah Mannan	United Kingdom	細胞システム研究室
13	Using single-cell genomics to investigate the progression of hepatocellular carcinoma	Haswanth Vundavilli	India	計算生物学研究室
14	Computational Exploration of the Conformational Landscape Underlying the Function of the FABD-like Domain in HEV Polyprotein	Thibault Michel Joseph Tubiana	France	生体分子動態モデリング研究室
15	Elucidation of residue network working for allostery in Bacillus subtilis PyrR, using Molecular Dynamics, Thermodynamics and Machine Learning	Shubhra Ghosh Dastidar	India	生体分子動態モデリング研究室
16	Deep learning for capturing signal-dependent enhancer heterogeneity at the single cell level	Ken Murakami	Austria	細胞システム研究室
17	To study the role of 15N-dynamics on cognate DNA recognition of two transcription factors with diverse modes of DNA interaction.	Sulakshana Pradyot Mukherjee	India	高磁場NMR分光学研究室