

ポスター発表リスト Poster Presentation List

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発表時間 (A) October 28 (Tue) 16:00-17:00 & October 29 (Wed) 17:00-18:00
 Presentation Time (B) October 28 (Tue) 17:00-18:00 & October 29 (Wed) 16:00-17:00

発表番号 No.	氏名 Name	所属 Affiliation	演題名 Title of Presentation	発表時間 Poster Time
01.計算化学 (分子計算・分子認識) Computational Chemistry (Molecular Modeling・Molecular Recognition)				
P01-01*	Seita Kawakami	Kagoshima University	A Study on the Improvement of an Antibody Epitope Prediction Method Using Protein-Protein Docking	(A)
P01-02*	Sakura Hyakuta	Kagoshima University	Development of a Method for the Rational Design of Chemical Chaperones and Its Application to Anti-Prion Compounds	(B)
P01-03*	Ayato Mizuno	Graduate school of Pharmacy, Meijo University	Virtual Alanine Scan for Predicting Drug Resistance to SARS-CoV-2 Main Protease Inhibitors	(A)
P01-04*	Chie Motono	National Institute of Advanced Industrial Science and Technology (AIST)	CrypTothML: A Hybrid MD-ML Approach for Cryptic Site Prediction	(B)
P01-05	Takashi Yoshidome	Department of Applied Physics, Graduate School of Engineering, Tohoku University	Deep-learning Model for Fast Computation of Grid Inhomogeneous Solvation Theory	(A)
P01-06	Masatake Sugita	Institute of Science Tokyo	Analysis of membrane permeation processes of cyclic peptides on multiple reaction coordinates based on the Markov state model	(B)
P01-07*	Takeo Tsuga	The University of Osaka	Enhancing Kinase Substrate Specificity Prediction by Integrating Structural and Dynamic Interaction Features	(A)
P01-08*	Takanori Aoki	PeptiDream Inc.	Rotamer Profiling of Non-Canonical Amino Acids for Enhanced Ramachandran Mapping	(B)
P01-09*	Mana Uwatoko	Yokohama City University	Machine Learning Assessment of TCR-pHLA Interactions Using AlphaFold-Based Structural Models	(A)
P01-10*	Hajime Sugiyama	Mitsubishi Chemical Corporation	In Silico Insight into the Structural Basis of Allosteric Inhibitor Selectivity between ERK2 and p38α	(B)
P01-11*	Junyi Yu	The University of Osaka	Protein-protein coupled intrinsic dynamics webtool development and application	(A)
P01-12	Tatsuya Ohyama	Institute of Physical and Chemical Research	The effect of packing on GTP hydrolysis of Ras in crystal	(B)
P01-13*	Teppey Yamada	Okayama University	Asymmetry and Heterogeneity in the Plasma Membrane	(A)
P01-14*	Hiroaki Oheda	yokohama-city University	Collective behavior of the Type 51 R-body predicted by AlphaFold 3	(B)
P01-15*	Hikaru Higuchi	Meiji University	Structure and diffusivity of water coexisting with antithrombogenic polymer	(A)

P01-16*	Matsumoto Hiromu	Kyushu University	Development of Machine Learning Force Fields for Cyclic Peptides: Generating Data with the Fragment Molecular Orbital Method to Explore Applicability	(B)
P01-17*	Masahiro Shimizu	Institute of Science Tokyo	Development of an automatic parameter adjustment method for REST/REUS MD and its application to predicting the membrane permeability of cyclic peptides	(A)
P01-18*	Yuta Kawaura	Kyushu University	Predicting Protein-Ligand Binding Affinity via Markov State Modeling and Fragment Molecular Orbital Analysis	(B)
P01-19	Yoshiki Yugami	Osaka Metropolitan University Graduate School of Science	Experiment-based Structural Ensemble Construction of Linear Diubiquitin Using Multi-scale Simulation and Deep Generative Modeling	(A)
P01-20*	Kenta Omoto	Grad.Sch.Sci., Osaka Metropolitan Univ.	Structural dynamics analysis of actin filament formation using molecular dynamics simulation.	(B)
P01-21	Shinji Amari	MOLSIS Inc.	Development of PLIF Analysis Method Incorporating PIEDA Components from the Fragment Molecular Orbital (FMO) Method	(A)
P01-22*	JIN CHUAN	Institute of Science Tokyo	Predicting cyclization efficiency of cyclic tetrapeptides via molecular dynamics simulations	(B)
P01-23*	Noritaka Inoue	Schrödinger K.K.	Metadynamics-based Approach to Predicting the Membrane Permeability of Drug-like Compounds	(A)
P01-24*	Remii Takahashi	Yokohama City University	Inhibitor Screening of RseP and Elucidation of the molecular basis of substrate selectivity using AlphaFold3	(B)
P01-25	Takashi Amisaki	Tottori University	MM/PB(GB)SA and conformational analyses of hMTH1-nucleotide complexes	(A)
P01-26*	Keisuke Yanagisawa	Institute of Science Tokyo	Quantitative Estimation of Protein-Ligand Substructure Interaction with Inverse Mixed-Solvent Molecular Dynamics Simulation	(B)
P01-27*	Genki Kudo	University of Tsukuba	Exploring Structural Diversity of PROTAC-Mediated Ternary Complexes via Extensive Conformational Search	(A)
P01-28*	Junya Yamagishi	Preferred Networks	Evaluating Performance of Binding Free Energy Perturbation with NNP-driven Custom Force Field	(B)
P01-29*	Hirofumi Watanabe	WithMetis Co., Ltd.	Practical preprocessing and visualization of fragment molecular orbital calculations for drug design	(A)
P01-30	Masao Fujisawa	Dept. of Biotechnological Science, Kindai University	Interaction of cyclic peptide drug with beta-Cyclodextrin	(B)
P01-31*	Tomohiro Sato	RIKEN	Application of the FMO prediction models to 3D protein structures predicted by AlphaFold2 and MD simulations.	(A)
P01-32	Naofumi Nakayama	CONFLEX Corporation	Re-Evaluation of Protein-Peptide Binding Poses by Conformation and Orientation Search of Peptide with All-Atom Model	(B)
P01-33	Takuya Fujie	Institute of Science Tokyo	log Pow Prediction for Cyclic Peptides Using Molecular Simulations	(A)

P01-34*	Masaki Mishina	Grad. Sch. BOST KINDAI Graduate School of Biology- Oriented Science and Technology Major in Biological Systems Engineering	Dynamics and Interaction of the Novel Anticoagulant AFS Warhead-Endowed Covalent Aptamer TBA4 with Thrombin, a Key Target in Blood Coagulation	(B)
P01-35*	Nanami Matsumoto	Grad. Sch. of KINDAI Univ.	Molecular dynamics simulation study of PET Tracer PBB3 and TMEM Fibril interactions	(A)
P01-36*	Koki Yano	Graduate school of science and technology , Keio university	Investigating the Allosteric Inhibition Mechanism of the Target Protein for Type 1 Diabetes Using Molecular Dynamics Simulation	(B)
P01-37	Yuki Miyaguchi	MOLSIS Inc.	MOE Interface Development for MD Calculation Software "GENESIS"	(A)
P01-38*	Ryusei Kumatani	Nihon University	Structural dynamics and conformational behavior of aptamer binding to AML1 protein	(B)
P01-39*	Hiroimitsu Shimoyama	The Noguchi Institute	Structural and Interaction Analysis for Understanding the Specificity of the O -Glycoprotease IMPa	(A)
02.データサイエンス Data Science				
P02-01*	So Ukiyama	CHUGAI PHARMACEUTICAL CO., LTD.	Integrated Analytical Platform to Accelerate Scientist- Driven CMC Research	(B)
P02-02*	Koh Sakano	Institute of Science Tokyo	Natural Product-likeness Prediction with Chemical Language Models	(A)
P02-03*	Shota Gunji	Institute of Science Tokyo	Machine Learning-Based Discovery of Narrow- Spectrum Antibiotics	(B)
P02-04*	Takamasa Suzuki	Institute of Science Tokyo	Development of a de novo molecular generative model using decoupled setting in multi-objective Bayesian optimization	(A)
P02-05*	Chisato Hayakawa	Department of Regulatory Science, Faculty of Pharmaceutical Sciences, Nagoya City University	A Chemical Structure-Based Machine Learning Model for Semi-quantitative Prediction of Human Acetylcholinesterase Inhibitory Activity	(B)
P02-06*	Rintaro Yashiro	Science Tokyo	Exploring Structured Biological Pathways in Context with Retrieval-Augmented Generation	(A)
P02-07*	Yusuke Tateishi	Kumamoto University	Interpretable Activity Prediction of SGLT2 Inhibitors using Dynamics- and Electronic-Structure-Augmented Graph Attention Networks	(B)
P02-08*	Takafumi Nishii	Yokohama National University	Efficient Discovery of Ferroptosis Inhibitors in the Biphenol Space via Synthetic Feasibility Prediction using Positive-Unlabeled Machine Learning	(A)
P02-09*	Yuto Matsumoto	Yokohama National University	Compound Embeddings from Textual Data and Fingerprints by Doc2Vec and Classification and Interpretability Using Them	(B)
P02-10*	Yuki Sato	Science Tokyo	Study on Feature Extraction Models for Protein 3D Structures Using AlphaFold2-based Neural Networks	(A)

P02-11	Shun Uratani	Graduate School of Creative Science and Engineering, Waseda University	Sensitivity Analysis of Tumor Angiogenesis and Growth Based on 3D Computational Modeling of Cell Activity and Vital Energy	(B)
P02-12*	Yi-An Chen	National Institutes of Biomedical Innovation, Health and Nutrition	BAIKINMINE, a mine of integrated microbiome knowledge	(A)
P02-13*	Rina Hirahara	INSTITUTE for PROTEIN RESEARCH THE UNIVERSITY OF OSAKA	Construction of a machine learning model to predict compounds targeting G-quadruplexes formed by ALS/FTD-related C9orf72 hexanucleotide repeats	(B)
P02-14*	Yixuan Sui	Keio University	Enhancing the Predictive Performance of PPI Inhibitory Activity Models through Data Imbalance Correction	(A)
P02-15	Kikuko Kamisaka	RIKEN	Recent Developments of FMO DB in 2025: Enhancing FMO Data Accessibility through Visualization Tools	(B)
P02-16*	Nobuaki Yasuo	Science Tokyo	TRACER: reaction-based molecular optimization using conditional transformer and Monte-Carlo tree search	(A)
P02-17*	Sosuke Asano	Graduate School, Keio University	An Unsupervised Deep Learning Method to Identify Characteristic Amino Acid Residues from Molecular Dynamics Simulation by Comparing Similar Systems	(B)
P02-18*	Tsubasa Nagae	Yokohama City University	Development of an Integrated Machine Learning Model for the Design and Prediction of PPI Modulators	(A)
P02-19*	Kenta Sumitomo	The university of tokyo	Prediction of antibody non-specificity and identification of antibody candidates using machine learning with NGS data from selection experiments	(B)
P02-20*	Takuho Ri	The University of Tokyo	Compressing the Uncurated PubChem-120M: A Universal Chemical Latent Space trained on SMILES denoising	(A)
P02-21*	Yoshinobu Igarashi	RIKEN	Toward Multimodal Foundation Models: Assessment of Encoders for Compounds, Sequences, Expression, and Language	(B)
P02-22*	Seiji Matsuoka	RIKEN	Implementation of a Chemical Structure Database System Bridging Open Science and Drug Discovery	(A)

03.量子構造生命科学

Quantum-Structural Life Science

P03-01*	Mayu Kitano	Osaka Metropolitan University	Crystal structures of the staurosporine complexes provide a basis for developing highly selective MAP2K4 and MAP2K6 inhibitors.	(B)
P03-02*	Yusuke Takashima	National Institutes of Biomedical Innovation, Health and Nutrition	Refinement of RNA Tertiary Structures via Distance-Map Correction and Machine Learning	(A)
P03-03*	Keiichi Kimura	AOI Biosciences Inc.	Novel Allosteric Drug Discovery Platform based on Quantum-Inspired Optimization Solutions "SQBM+"	(B)
P03-04*	Shuhei Miyakawa	The University of Osaka	Can Fragment Molecular Orbital Calculations Explain Ligand Binding Characteristics? A Comprehensive Study Using PDB from BindingDB	(A)

P03-05*	Ryoya Kawabata	Osaka Metropolitan University	Electron Density Topography (EDT) Based on Middle-Angle X-ray Scattering Data Reveals Novel Structural Insights into MAP2K6 and p38 α MAPK in solutions.	(B)
04.ADME・毒性 ADMET				
P04-01*	Motohiro Kato	DMPK academy	Top-down approach for prediction of drug-drug interactions using physiologically based pharmacokinetic model	(A)
P04-02*	Kiyoshi Hasegawa	TECHNOPRO R&D company	New Molecular Design Using PBPK Simulations and Machine Learning Models	(B)
P04-03*	Koji Jojima	National Institute of Health Sciences	Evaluating Pre-trained Transformer Models for Toxicity Prediction Task: Effectiveness and Performance for Hepatotoxicity.	(A)
P04-04*	Takuya Suzuoka	Institute of Science Tokyo	Integrating Pharmacokinetic Principles into Deep Learning for Reliable ADMET Profiling	(B)
P04-05*	Yohei Ohto	Graduate School of Pharmaceutical Sciences, The University of Tokyo	Validity and application of temporal information extracted from patent information	(A)
P04-06*	Kotaro Suzuki	Graduate School of Pharmaceutical Sciences, Nagoya City University	<i>In Silico</i> Prediction of Gapmer Antisense Oligonucleotides-induced ALT Elevation	(B)
P04-07	Tsuyoshi Kato	Gunma University	Biology-Driven Gene Selection Improves RNA-Seq-Based Toxicity Prediction in StemPanTox Beta	(A)
P04-08*	Ryoko Terada	Institute for Protein Research, Osaka University	Application of K_m and V_{max} -Based Prediction Models to Assessing the Influence of CYP2C9 Polymorphisms on Pharmacokinetics	(B)
P04-09*	Soyoka Tanihata	Tottori University	Modeling Ethnic Differences in Drug Clearance via Predicted Pharmacokinetics from Chemical Structures	(A)
P04-10*	Ayane Takamatsu	Institute for Protein Research, The University of Osaka	Predicting substrates for transporters involved in the drug transfer into breast milk	(B)
P04-11	Tomoya Aoyagi	Graduate School of Advanced Science and Engineering, Waseda University	Metabolomic Analysis Driven Search for Biologically Active Marine Natural Products from the Mixture of Dredge Bycatch	(A)
05.バイオインフォマティクス Bioinformatics				
P05-01*	Sachiko Kawano	POLA CHEMICAL INDUSTRIES, INC.	XGBoost-Based Gene Expression Profiling of Senile lentigo Using Skin Transcriptomic Data Collected by Microbiopsy	(B)
P05-02	Chiaki Handa	Kissei pharmaceutical. Co., Ltd.	Bayesian Network Analysis for Disease Mechanism Estimation and Drug Target Discovery	(A)
P05-03*	Yajie Hu	Osaka University, Institute for Protein Research (IPR)	Comparing Structural and Dynamic Differences Among Globin-like Proteins	(B)

P05-04*	Kouki Maebara	Nagoya City University	Development of a Predictive Model for Chemically Induced Rat Liver Cell Necrosis Using Visualized Transcriptome Data	(A)
P05-05*	Kodai Miyazaki	School of Pharmaceutical Sciences, University of Shizuoka	Identification of Cancer-Associated Fibroblast Subtypes That Promote HCC Progression and Their Differentiation Programs	(B)
P05-06*	Yulong Gou	Institute for Protein Research, The University of Osaka	A Mechanism-based Prediction Model of P-glycoprotein Compound Efflux	(A)
P05-07*	Akira Shinohara	Department of Computer Science, School of Computing, Institute of Science Tokyo	Compound Retrosynthesis Analysis Using Consensus Estimate	(B)
P05-08*	Wen Tao Wu	Osaka University IPR	Machine Learning-Guided Design of Thermostable Proteins: Leveraging Bayesian Optimization for Efficient Mutational Scanning	(A)

06.創薬応用

Drug Discovery Application

P06-01*	Akimi Hori	JAPAN TOBACCO INC.	Building a system to support a data-driven drug discovery DMTA cycle	(B)
P06-02*	Seisuke Takimoto	JAPAN TOBACCO INC.	Initiatives for predict-first DMTA cycle in JT	(A)
P06-03*	Kairi Furui	Institute of Science Tokyo	ALLM-Ab: Active Learning-Driven Antibody Optimization Using Fine-tuned Protein Language Models	(B)
P06-04*	Apakorn Kengkanna	Institute of Science Tokyo	CatDRX: Reaction-Conditioned Generative Model for Catalyst Design and Optimization	(A)
P06-05*	Sho Masunaga	Institute of Science Tokyo	GraphBioisostere: General Bioisostere Prediction Model with Deep Graph Neural Network	(B)
P06-06*	Masami Sako	Institute of Science Tokyo	DiffPharma : A Conditional Diffusion Framework for Interaction-Constrained 3D Molecular Design	(A)
P06-07*	Yuta Kikuchi	Institute of Science Tokyo	Binding Interaction Analysis of Anticancer Saponin OSW-1 with Oxysterol-binding Proteins	(B)
P06-08	Masataka Kuroda	National Institutes of Biomedical Innovation, Health and Nutrition	Analysis of hydration related to double-strand stability of nucleic acid medicines	(A)
P06-09	Hiroto Terada	Grad. Sch. Sci., Osaka Metropolitan Univ.	Discovery of novel inhibitor candidate compounds using accurate <i>in silico</i> screening protocol	(B)
P06-10*	Yuki Murakami	Yokohama City University	Data-driven Design of PROTAC Linkers to enhance Cell Membrane Permeability	(A)
P06-11*	Yunoshin Tamura	Preferred Networks, Inc.	Application of Relative Binding Free Energy Perturbation (RBFEP) to Multiple Compounds Bound to One Binding Site Simultaneously	(B)
P06-12	Kohei Ohta	Medical and Biological Laboratory Co., Ltd.	Design and Optimization of Anti-FGFR4 Minibinders by Integrating Machine Learning and Computational Chemistry	(A)

P06-13*	Masayoshi Shimizu	Institute of Science Tokyo	COFFEE-PRESC: a fast pre-screening method using chemical compound retrieval by fragment pose pairs	(B)
P06-14*	Mio Yokoyama	Kumamoto University	Discovery and Optimization of Natural Product-Derived GLS1 Inhibitors via Quantum Chemical Analysis	(A)
P06-15*	Satoshi Yoneyama	Institute of Science Tokyo	Construction of representative fragment sets based on mutual 3D structural similarity and docking feasibility for fragment-based virtual screening	(B)
P06-16*	Kaho Akaki	Institute of Science Tokyo	Enhancing virtual screening accuracy by refining docking calculation scoring with mixed-solvent molecular dynamics	(A)
P06-17*	Masahito Ohue	Institute of Science Tokyo	Computational Design of Monoclonal Antibodies Using Protein Language Models, Structure Prediction, and Physics-Based Evaluation: Application to Human TIGIT Targeting	(B)
P06-18*	Asato Yamauchi	Institute of Science Tokyo	Integrating Antibody and Payload Information for Predicting the Drug-to-Antibody Ratio of Antibody-Drug Conjugates via Machine Learning	(A)
P06-19*	Ryoya Nakano	Institute of Science Tokyo	Improvement of fragment-based protein-ligand docking using the Quantum Annealer	(B)
P06-20*	Chiharu Konda	OpenEye, Cadence Molecular Sciences	Predicting affinity: 3D QSAR and its interplay with RBE by NES	(A)
P06-21*	Kei Sato	Graduate School of Advanced Science and Engineering, Waseda University	LC/MS-based metabolomic analysis of marine sponge species of genus <i>Petrosia</i> and the identification of a new polyacetylene	(B)
P06-22*	Yusuke Ihara	Ajinomoto Co., Inc.	Development of a Novel 3D Molecular Representation for Odorants: Toward Predictive Modeling of Olfactory Receptor Activity and Odor Perception	(A)
P06-23	Kotaro Osaki	Department of Surgery, School of Medicine, Tottori University Faculty of Medicine	Evaluation of a Docking-Based Prediction Method from Apo Structures Using CDK2 Inhibitors	(B)

07.臨床インフォマティクス
Clinical Application

P07-01	Taro Oshiro	JAPAN TOBACCO INC.	Predicting the biological pathways activated by cigarette or heated tobacco product use: a proof-of-concept study	(A)
P07-02*	Genki Masuda	Institute of Science Tokyo	Computational Identification of Antigen-Specific Sequences from BCR Repertoires Using an Antibody Language Model	(B)
P07-03*	Hayato Nakahara	Tottori university	Development and Evaluation of a Machine Learning Model for Classifying Neurodegenerative Diseases from Transcriptomic and GO Data	(A)

08.分子ロボティクス
Molecular Robotics

P08-01*	HISASHI TADAKUMA	ShanghaiTech University	Development of DNA origami nanodevices to capture and analyze expressome	(B)
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P08-02*	Shogo Kinugawa	Department of Applied Chemistry, Graduate School of Engineering, Mie University	Shape-transformable DNA origami tubes for programmable stacking-mediated self-assembly	(A)
P08-03*	Reo Toho	Department of Applied Chemistry, Graduate School of Engineering, Mie University	DNA Origami Nanoactuators for Stimulus-Responsive and Programmable Liposome Shape Control	(B)
P08-04*	Cancelled			
P08-05	Shin-ichiro Nomura	Graduate school of Engineering, Tohoku University	Development of Multicellular-Type Molecular Robots with Nucleic Acid Sensors for MPS Applications	(B)
P08-06*	Ren Nobusawa	Graduate School of Medical Life Science, Yokohama City University	Development of a Soft Robotics-Based Physical Simulator Reproducing the Motion Mechanism of V ₁ -ATPase	(A)
P08-07*	Seiichi Ishida	Sojo University	Advancing Microphysiological Systems for Non-Animal Drug Testing: Trends in Technical Considerations and their Solutions with Molecular Robotic Technologies	(B)
09.健康科学 Health Sciences				
P09-01*	Yuai Fukuzawa	Institute of Science Tokyo	Microbiome as biomarkers of ICI in esophageal cancer patients	(A)
10.AI創薬 AI Drug Discovery				
P10-01*	Kosuke Takeuchi	DAIICHI SANKYO CO., LTD.	Development and Enhancement of NITER: Expanding Access to Multi-Billion-Scale Compound Libraries and Public Data Sources	(B)
P10-02*	Akitoshi Okada	Daiichi Sankyo Co., Ltd.	Boltz2 benchmark on in-house dataset: thinking of how to effectively use in drug discovery campaigns	(A)
P10-03*	Reiji Teramoto	Chugai pharmaceutical, Co., Ltd.	Enhancing ADME Property Prediction with Ensemble C-Mixup TabPFN in a low data regime.	(B)
P10-04*	Yasunobu Yamashita	The University of Osaka	Deep Learning-Aided Drug Discovery via the Latent Space Visualization of Deep Neural Networks	(A)
P10-05*	Calvin Davey	TechnoPro, Inc. TechnoPro R&D Company	Assessing Generative AI Embeddings for Predicting Drug Response from scRNA-Seq	(B)
P10-06*	Shogo Nakamura	Institute of Science Tokyo	Learning Chemical Reaction Trajectories with Transformer and GFlowNet for Molecular Optimization	(A)
P10-07*	Koshiro Aoki	Institute of Science Tokyo	Contrastive Learning on Protein Binding Structures for Drug-Target Interaction Prediction	(B)
P10-08*	Victoire Cachoux	Iktos K.K.	Synthesis-driven GenAI for Molecule Design: Growing and Linking Optimizers	(A)
P10-09*	Yiming Zhang	Graduate School of Frontier Sciences, The University of Tokyo	Leveraging LLM and Bayesian Optimization for Multi-Objective Lead Optimization	(B)

P10-10*	Tomoya Nabetani	Yokohama city university	Enhancing Protein-Protein Interaction Affinity Prediction with TabPFN and Rosetta-Based Structural Descriptors	(A)
P10-11*	Ryo Ogawa	Institute of Science Tokyo	Quantum-informed AI for drug discovery: enhancing generalizability in compound-protein interaction prediction	(B)
P10-12*	Shinya Kawano	Gifu pharmaceutical university	Evaluating Deep Learning Predictions and Score Integration for Drug Discovery	(A)
P10-13*	Taichi Ishikawa	Institute of Science Tokyo	Predicting Protein Allosteric Site based on Atomistic Energy-Weighted Graphs	(B)
P10-14*	Shota Takahashi	Mitsui Knowledge Industry	QAEmap: A deep learning-based method for evaluating ligand coordinate validity in protein-ligand complex structures	(A)
P10-15*	Takashi MATSUMOTO	Institute of Science Tokyo	Conditional Molecular Generation Using 3D Pocket and Interaction Features	(B)
P10-16*	Haris Hasic	Elix, Inc.	kMoL: An Open-source Machine and Federated Learning Library for Drug Discovery	(A)
P10-17*	Taiyo Toita	Graduate School of Medical Life Science, Yokohama City University	Activity prediction-driven optimization of a V-ATPase inhibitor using molecular generative AI	(B)
P10-18	Kohtaro Yuta	In Silico Data,Ltd.	Challenges in Integrating Chemistry and AI for Drug Development	(A)
P10-19*	Tatsuya Yoshizawa	Graduate School of Medical Life Science, Yokohama City University	Molecule Generation with Boltz-2: A Case Study on Kinase Inhibitor Design	(B)
P10-20	Jinzhe Zhang	Preferred Networks Inc	ML-Boosted Virtual Screening at Billion-Compound Scale with Uni-Dock	(A)
P10-21*	Yuki Satoh	ONO PHARMACEUTICAL CO., LTD	REINVENT4 Ecosystem and LLM-Powered Patent Analysis Tool: OSS Implementation with Case Studies	(B)
P10-22*	Takuto Koyama	Graduate School of Medicine, Kyoto University	Empowering Federated Learning for Robust Compound-Protein Interaction Prediction across Heterogeneous Cross-Pharma Domains	(A)
P10-23*	Yasuhiro Yoshikai	The University of Tokyo Graduate School of Pharmaceutical Sciences	Evaluating Mamba as a backbone for language-based foundation models for ligand generation	(B)
11.その他 Others				
P11-01*	Miho Irie	Cross-Industrial Data Science Labs	Buildig a Pipeline for Designing Novel Drug Candidates using Quantum Annealing	(A)
P11-02*	Kimiko Kitamura	National Institute of Health Sciences	The performance characteristics of the commercially available blood brain barrier (BBB)-model installing human induced pluripotent stem cell (hiPSC)-derived BBB cells	(B)