

The 2nd JHUPO

The Second Annual Meeting of Japan Human Proteome Organization

Congress Program

Invited Speech

Keynote Speech 1 (1G-KS1) 14:50-15:20, May 19th, 2004

Chair: Kazuyuki Nakamura

Know liver more through proteome, make life better for human
-- Introduction of the Human Liver Proteome Project

Fuchu He^{1),2)} (¹⁾Committee of HUPO Human Liver Proteome Project, ²⁾ China
National Center of Biomedical Analysis)

Keynote Speech 2 (1G-KS2) 16:30-17:00, May 19th, 2004

Chair: Akihiko Takahashi

Human Brain Proteome Project

Helmut E. Meyer (Medical Proteom-Center, Ruhr-University)

Plenary Lecture (2G-PL) 13:00-13:40, May 20th, 2004

Chair: Akira Tsugita

Proteomic analysis of colorectal cancer: strategies for novel biomarker discovery

*Richard J. Simpson¹⁾²⁾³⁾, Robert L. Moritz²⁾³⁾ (¹⁾ President of AOHUPO, ²⁾ Joint Protein Structure Laboratory, Ludwig Institute for Cancer Research (Melbourne Tumor Biology Branch), ³⁾ the Walter and Eliza Hall Institute of Medical Research)

Oral Presentations (May 19, 2004, Grand Hall)

Session 1G1 Proteomics of aging and diseases 9:30-10:50

Chair: Tadashi Yamamoto

1G1-1 Disease Proteomics of adrenal gland in the rdw rat with hereditary hypothyroidism

*Masamichi Oh-Ishi ¹⁾, Makiko Osaka ¹⁾, Mamoru Satoh ¹⁾, Yoshio Kodera ¹⁾, Tadakazu Maeda ¹⁾, Yasuhiro Sakai ²⁾ and Senichi Furudate ³⁾ (¹⁾ Department of Physics, School of Science, Kitasato University , ²⁾ Department of Anatomy, School of Medical., Kitasato University , ³⁾ Department of Exp. Animal, School of Medical, Kitasato University)

1G1-2 Identification of altered protein expression and post-translational modifications in primary colorectal cancer using agarose two-dimensional gel electrophoresis

*Takeshi Tomonaga ¹⁾, Kazuyuki Matsushita ²⁾, Masamichi Oh-Ishi ³⁾, Yoshio Kodera ³⁾, Tadakazu Maeda ³⁾, Hideaki Shimada ²⁾, Takenori Ochiai ²⁾ and Fumio Nomura ¹⁾ (¹⁾ Department of Molecular Diagnosis, Graduate School of Medicine, Chiba University , ²⁾ Department of Academic Surgery, Graduate School of Medicine, Chiba University , ³⁾ Laboratory of Biomolecular Dynamics, Department of Physics, Kitasato University School of Science)

1G1-3 Proteome analysis on heat stress-induce apoptosis of human T lymphoblastic leukemia cells

*Kazuyuki Nakamura ¹⁾, Masanori Fujimoto ¹⁾, Yasuhiro Kuramitsu ¹⁾, Yuji Nagasaka ²⁾, Yuzo Yamasaki ³⁾, Tomoko Kuriki ³⁾, Tosifusa Toda ⁴⁾ and Andre Sobel ⁵⁾ (¹⁾ Department of Biochemistry and Biomolecular Recognition, Yamaguchi University School of Medicine, ²⁾ Department of Human Nutrition, Yamaguchi Prefectural University, ³⁾ Life Science Laboratory, Shimadzu Corporation , ⁴⁾ Proteomics Collaboration Research, Tokyo Metropolitan Institute of Gerontology , ⁵⁾ INSERM U440-Institut du Fer a Moulin)

1G1-4 Proteome analysis of cellular senescence induced by 5-bromodeoxyuridine in HeLa cells

*Ryo Ukekawa ¹⁾, Hisashi Hirano ²⁾ and Dai Ayusawa ¹⁾ (¹⁾ Division of Biochemistry, Kihara Institute for Biological Research, Yokohama City University , ²⁾ Division of Plant Genetic Engineering, Kihara Institute for Biological Research, Yokohama City University)

Session 1G2 Glycomics 10:50-12:10

Chair: Naoyuki Taniguchi

1G2-1 Development of a total system for glycoproteomics

*Jun Hirabayashi (National Institute of Advanced Industrial Science and Technology)

1G2-2 Glycosylation analysis of glycoproteins by LC/MS

*Nana Kawasaki , Akira Harazono , Noritaka Hashii , Satsuki Itoh , Toru Kawanishi and Takao Hayakawa (National Institute of Health Sciences)

1G2-3 Capillary affinity electrophoresis for the analysis of modification of proteins with carbohydrate chains

*Kazuaki Kakehi (Faculty of Pharmaceutical Sciences, Kinki University)

1G2-4 Constructing the basic strategy for glycoproteomics

*Yoshinao Wada ¹⁾ and Michiko Tajiri ²⁾ (¹⁾ MCH Research Institute Osaka , ²⁾ JST Innovation Plaza Osaka)

Session 1G3 Human Liver Proteome 15:20-16:20

Chair: Kazuyuki Nakamura

1G3-1 Proteomic analysis of proteins secreted by HepG2 cells

*Ryo Yamashita ^{1) 2)} , Yuko Fujiwara ¹⁾ , Kazuki Yasuda ¹⁾ and Yasushi Kaburagi ¹⁾ (¹⁾ Department of Metabolic Disorder, Research Institute, International Medical Center of Japan, ²⁾ Department of Endocrinology and Metabolism, Yokohama City University Graduate School of Medicine)

1G3-2 Proteomic Analysis for Hepatocellular Carcinoma Tissues from Patients Infected with Hepatitis C Virus

*Yasuhiro Kuramitsu ¹⁾ , Motonari Takashima ^{1) 2)} , Yuuichirou Yokoyama ^{1) 3)} , Norio Iizuka ⁴⁾ , Tosifusa Toda ⁵⁾ , Isao Sakaida ³⁾ , Kiwamu Okita ³⁾ , Masaaki oka ²⁾ and Kazuyuki Nakamura ¹⁾ (¹⁾ 1st Biochemistry, Yamaguchi University School of Medicine , ²⁾ 2nd Surgery,

Yamaguchi University School of Medicine ,³⁾ 1st Internal Medicine, Yamaguchi University School of Medicine ,⁴⁾ Bioregulatory Function, Yamaguchi University School of Medicine
⁵⁾ Tokyo Metropolitan Institute of Gerontology)

1G3-3 Proteomic analysis of human intrahepatic calculosis

*Takuji Nabetani ¹⁾ , Yo Tabuse ²⁾ , Akira Tsugita ^{1) 2)} and Jyunichi Shoda ³⁾ (¹⁾ Tokyo Rikakikai Co., Ltd. Proteomics Research Laboratory ,²⁾ NEC Proteomics Research Center, ³⁾ Tsukuba Univ. Med. School)

Session 1G4 Human Brain Proteome 17:00-18:20

Chair: Akihiko Takahashi

1G4-1 Proteomics in Alzheimer,s disease

*Teruyuki Tsuji , Aiko Shiozaki , Masahiro Aoki and Shun Shimohama (Department of Neurology, Graduate School of Medicine, Kyoto University)

1G4-2 Phosphoproteomics of human brain tissue and human neuroblastoma SH-SY5Y cells

*Tosifusa Toda ¹⁾ , Norie Araki ²⁾ , Hisashi Hisatomi ^{1) 3)} , Katsumi Kawano ³⁾ , Hiraku Morisawa ¹⁾ and Mikako Hirota ¹⁾ (¹⁾ Proteomics Collaboration Research, Tokyo Metropolitan Institute of Gerontology ,²⁾ Graduate School of Medical Sciences, Kyushu University ,³⁾ SRL, Inc.)

1G4-3 Proteomic analysis of hippocampus proteins related to the ischemic neuronal apoptosis using p53 gene knockout mice

*Norie Araki¹⁾, Keiko Cho¹⁾ Joe Hirano²⁾ Satoshi Ono²⁾ Kazuchika Furuishi³⁾ Katsumi Kawano⁴⁾ Tosifusa Toda ⁵⁾ Tomohiro Araki ⁶⁾ Akira Tsugita ⁷⁾ and Kohji Fukunaga⁸⁾ Hideyuki Saya¹⁾ ,¹⁾ Dept. Tumor Gen. and Biol., Grad. Sch. Med. Sci., Kumamoto Univ.,²⁾ Amersham Bio. KK,⁴⁾ Applied Bio. Japan Ltd,⁵⁾ Proteomics Collaboration Research Group, Tokyo Metropolitan Institute of Gerontology ,⁶⁾ Biosci. Sch. Agric. Kyushu Tokai University ,⁷⁾ Proteomics Research Lab.)

1G4-4 Detection of soluble N-glycosylated proteins in aged-rat brain with 2D-PAGE

*Yuji Sato¹⁾, Sayaka Shimazaki²⁾, Masami Ishida²⁾, Tosifusa Toda³⁾, Haruhiko Yamamoto²⁾ and Tamao Endo¹⁾ (¹⁾ Glycobiology Research Group, Tokyo Metropolitan Institute of Gerontology, ²⁾ Kanagawa University, Faculty of Science, ³⁾ Proteomics Collaboration Research Group, Tokyo Metropolitan Institute of Gerontology)

Oral Presentations (May 19, 2004, Second Hall)

Session 1S1 Informatics and databases 9:30-10:50

Chair: Hiroshi Mizushima

1S1-1 Development of IT platform for proteomics research

*Seiji Okuizumi¹⁾, Akihisa Kenmochi¹⁾, Masao Satoh¹⁾, Yoko Takaki¹⁾, Ken'ichi Kamijo¹⁾ and Akira Tsugita^{1) 2)} (¹⁾ Proteomics Research Center, Fundamental and Environmental Research Laboratories, NEC Corporation, ²⁾ Tokyo Rikakikai Co., Ltd. Proteomics Research Laboratory)

1S1-2 Collaborative proteomics framework with XML databases and an integrated XML viewer for 2DPAGE

*Hiraku Morisawa¹⁾, Hisashi Hisatomi^{1) 2)}, Mikako Hirota¹⁾ and Tosifusa Toda¹⁾ (¹⁾ Proteomics Collaboration Research Group, Tokyo Metropolitan Institute of Gerontology, ²⁾ Analytical Center for Medical Science, SRL Inc.)

1S1-3 Proteomics of normal human kidney glomerulus: 2-DE profiling and construction of XML-based database

*Yutaka Yoshida¹⁾, Bo Xu¹⁾, Ying Zhang¹⁾, Kenji Miyazaki²⁾, Masao Sato²⁾, Seiji Okuizumi²⁾, Akihisa Kenmochi²⁾, Ken'ichi Kamijo²⁾, Akira Tsugita²⁾, Tetsuo Osawa³⁾, Eishin Yaoita¹⁾ and Tadashi Yamamoto¹⁾ (¹⁾ Division of Structural Pathology, Institute of Nephrology, Niigata Graduate School of Medical and Dental Sciences, ²⁾ Proteomics Research Center, Fundamental and Environmental Res.Lab., NEC Corp., ³⁾ Department of Urology, Niigata City General Hospital)

1S1-4 New approaches to network analysis using KeyMolnet

*Hiromi Sato , Miki Fukuda , Makoto Shigetaka , Yohko Wakamatsu , Yoko Inoue , Yoshinobu Mizoguchi , Nobuo Tomioka and Akiko Itai (Institute of Medicinal Molecular Design, Inc. (IMMD))

Session 1S2 Structural and functional proteomics 10:50-12:10

Chair: Masaru Tanokura

1S2-1 Structural genomics on development and differentiation of organisms and replication and repair of DNA

*Masaru Tanokura (Department of Applied Biological Chemistry, Graduate School of Agricultural and Life Sciences, University of Tokyo)

1S2-2 Structural Proteomics to Drug Discovery

*Akiko Tanaka ¹⁾ and Shigeyuki Yokoyama ^{1) 2) 3)} (¹⁾ RIKEN Genomic Sciences Center, ²⁾ RIKEN Harima Institute, ³⁾ University of Tokyo)

1S2-3 Structure and function of water and ion channels analysed by cryo-electron microscopy

*Yoshinori Fujiyoshi ^{1) 2)} (¹⁾ Graduate School of Science, Kyoto University, ²⁾ Structural Analysis team, BIRC/AIST)

1S2-4 Participation of SecA in the membrane protein localization in *Bacillus subtilis*

*Keigo Bunai ¹⁾, Manabu Nozaki ¹⁾, Tadashi Nemoto ²⁾ and Kunio Yamane ¹⁾ (¹⁾ Institute of Biological Sciences, University of Tsukuba, ²⁾ National Institute of Advanced Industrial Science and Technology)

Session 1S3 Protein interaction and protein complexes 14:50-16:30

Chair: Hisashi Hirano and Tohru Natsume

1S3-1 Analysis of biomolecular Interactions by multiplexed capillary electrophoresis instrument

*Kiyohito Shimura ¹⁾, Takuma Waki ²⁾, Masaki Okada ²⁾, Tosifusa Toda ³⁾ and Ken-ichi Kasai ¹⁾ (¹⁾ Department of Biological Chemistry, Faculty of Pharmaceutical Sciences, Teikyo University, ²⁾ Quantum Design Japan, ³⁾ Proteomics Collaboration Research Group, Tokyo Metropolitan Institute of Gerontology)

1S3-2 Analysis of proteins interacted with gel-resolved proteins by a novel protein chip and mass spectrometry.

*Hisashi Hirano ¹⁾, Jian-zhong Tan ²⁾, Nobutake Suzuki ¹⁾ and Mikiko Arima ¹⁾ (¹⁾ Division of Plant Genetic Engineering, Kihara Institute for Biological Research, Yokohama City University, ²⁾ Tottori University)

1S3-3 Beyond the Structural Proteomics: A New Method for Intermolecular Interaction Analysis by Non-empirical Molecular Orbital Calculations.

*Tadashi Nemoto ¹⁾, Dimtri Fedorov ¹⁾, Yuto Komeiji ¹⁾, Kenji Kanazawa ¹⁾, Masami Uebayasi ¹⁾ and Kazuo Kitaura ¹⁾ (¹⁾ National Institute of Advanced Industrial Science and Technology)

1S3-4 Protein interaction network topology analysis for drug target discovery

*S.J. Lynden¹⁾, O.C. Idowu¹⁾, P. Periorellis¹⁾, M.P. Young²⁾, P. Andras¹⁾ (¹⁾ School of Computing Science, Newcastle University, UK., ²⁾ School of Biology, Newcastle University, UK.)

1S3-5 Systematic analysis of protein interactions using human full length cDNA

*Tohru Natsume (National Institute of Advanced Industrial Science and Technology (AIST))

Session 1S4 New technologies in Proteomics 16:30-18:30

Chair: Hiroshi Nakanishi and Keiichi Hosokawa

1S4-1 Application of the Chemical Inkjet Printer to Microscale Proteomics

*Masaru Furuta (Life Science Laboratory, Shimadzu Corporation)

1S4-2 Comparison of methods in phosphoproteomics

*Ken Oofusa ^{1) 2)}, Akira Yamagata ^{1) 2)} and Katsutoshi Yoshizato ^{2) 3)} (¹⁾ Prophenix Co., Ltd.,²⁾ JST, Innovation Plaza, Hiroshima, ³⁾ Graduate School of Science, Hiroshima University)

1S4-3 C-terminal sequencing method for protein in polyacrylamide gel

*Kenji Miyazaki ¹⁾, Ken'ichi Kamijo ¹⁾ and Akira Tsugita ^{1) 2)} (¹⁾Proteomics Research Center, Fundamental & Environmental Research Laboratories, NEC corp.,²⁾Tokyo Rikakikai Co., Ltd. Proteomics Research Laboratory)

1S4-4 New method of peptide sequencing by modification with Fluorescent reagent using MALDI-TOF-MS PSD method

*Hiroshi Nakanishi and Masatoshi Nakagawa (Biological Information Research Center, National Institute of Advanced Industrial Science and Technology)

1S4-5 Bridging signals using internal standard with cultured isotope tags (BISCUIT) for quantitative tissue proteome

*Yasushi Ishihama , Yoshiya Oda , Tsuyoshi Tabata , Norimasa Miyamoto , Koji Sagane , Toshitaka Sato and Takeshi Nagasu (Laboratory of Seeds Finding Technology, Eisai Co.,Ltd)

1S4-6 Analysis for Epigenetic Modification of Histones in Liver

*Keiichi Hosokawa ¹⁾, Jialing Gao ¹⁾, Takuji Nabetani ¹⁾, Akira Tsugita ^{1) 2)}, Kenji Miyazaki ²⁾ and Kenichi Kamijo ²⁾ (¹⁾ Proteomics Research Laboratory Tokyo Rikakikai Co. Ltd. , ²⁾ Proteomics Research Center, Fundamental and Environmental Research Laboratories, NEC Corp)

Oral Presentations (May 20, 2004, Grand Hall)

Session 2G1 Human Plasma Proteome 9:00-10:20

Chair: Tadashi Kawai

2G1-1 A Fully Automated Multi-dimensional Protein Profiling System in Large-scale

Proteome Analysis for Human Plasma Proteomics

*Kiyonaga Fujii and Toshihide Nishimura (Clinical Proteome Center, Tokyo Medical University)

2G1-2 Multidimensional Fractionation and Analysis of the Human Plasma Proteome

*Michael H. Simonian and Betgovargez Edna (Molecular Development Center, Beckman Coulter, Inc.)

2G1-3 Purification and Identification of two Ovarian Cancer Biomarkers from Human Serum: Transthyretin and Transferrin

Kathy Kozak , Feng Su, Kym Faull, Srinivasa Reddy and *Robin Farias-Eisner (Department of Obstetrics and Gynecology, UCLA School of Medicine, University of California-Los Angeles)

2G1-4 Analysis for sera of ovarian cancer patient using Surface-Enhanced Laser Desorption/Ionization (SELDI) ProteinChip®

*Masakatsu Fujinoki ¹⁾ , Tetsu Kamemori ²⁾ , Ichio Fukasawa ²⁾ , Makiko Furuno ²⁾ , Tatsuo Yamazaki ²⁾ , Fujiyuki Inaba ²⁾ , Kun Zhu ²⁾ , Nobuaki Kousaka ²⁾ , Yoriko Ota ²⁾ and Noriyuki Inaba ²⁾ (¹⁾ Department of Physiology, Dokkyo University School of Medicine, ²⁾ Department of Obstetrics and Gynecology, Dokkyo University School of Medicine)

Session 2G2 Clinical applications of differential proteomics 14:15-15:35

Chair: Tadashi Kondo

2G2-1 Cancer proteomics for biomarker development

*Tadashi Kondo ¹⁾ , Tetsuya Okano ¹⁾ , Masayo Yamada ¹⁾ , Hiromitsu Hatakeyama ¹⁾ , Tatsuhiko Kakisaka ¹⁾ , Yoshiyuki Suehara ¹⁾ , Tesshi Yamada ¹⁾ and Setsuo Hirohashi ¹⁾ (¹⁾ Cancer Proteomics Project, National Cancer Center Research Institute)

2G2-2 Study of human brain tumors by the proteomic and transcriptomic differential approach using cleavable ICAT, 2D-DIGE, and DNA array

*Norie Araki¹⁾, Keiko Cho¹⁾ Tosifusa Toda²⁾ Kazuchika Furuishi³⁾ Joe Hirano⁴⁾ Satoshi Ono⁴⁾ Hiromi Sato⁵⁾ Tomohiro Araki⁶⁾ Hideo Nakamura⁷⁾ Hideyuki Saya¹⁾ (¹⁾ Dept. Tumor Gen. and Biol., Grad. Sch. Med. Sci., Kumamoto Univ.,²⁾ Tokyo Metro. Inst. Gerontol.,³⁾ Applied Bio. Japan Ltd,⁴⁾ Amersham Bio.KK,⁵⁾ IMMD Inc. ,⁶⁾ Biosci. Sch. Agric. Kyushu Tokai Univ. ,⁷⁾ Dept. Neurosurgery, Grad. Sch. Med. Sci., Kumamoto Univ.)

2G2-3 Identification of a colon cancer marker from human cancer cell panel using the SELDI ProteinChip Platform

*Mieko Shiwa¹⁾ , Yukiko Nishimura²⁾ , Rumi Wakatabe¹⁾ , Hirotohi Ota³⁾ , Yo Kato⁴⁾ and Takao Yamori²⁾ (¹⁾ CIPHERGEN Biosystems KK, ²⁾ Division of Molecular Pharmacology, Cancer Chemotherapy Center, Japanese Foundation for Cancer Research, ³⁾ Department of Surgery, Cancer Institute Hospital, Japanese Foundation for Cancer Research, ⁴⁾ Department of Pathology, Cancer Institute, Japanese Foundation for Cancer Research)

2G2-4 Molecular classification and chemosensitivity prediction in human gliomas based on the proteome analysis

*Yasuo Iwadata¹⁾, Tsukasa Sakaida^{1), 2)}, Takaki Hiwasa²⁾, Masaki Takiguchi²⁾, Shuichi Fujimoto³⁾, Akira Yamaura¹⁾ (¹⁾Departments of Neurological Surgery, Chiba University Graduate School of Medicine, ²⁾Departments of Biochemistry & Genetics, Chiba University Graduate School of Medicine, ³⁾Division of Chemotherapy, Chiba Cancer Center Research Institute)

Oral Presentations (May 20, 2004, Second Hall)

Session 2S1 Peptidomics 9:00-10:20
Chair: Naoto Minamino

2S1-1 Disease Peptidome

*Yoshio Koderia¹⁾ , Toshiyuki Fukutomi¹⁾ , Tomihisa Kogo¹⁾ , Sen-ichi Furudate²⁾ , Akira Omori³⁾ and Tadakazu Maeda¹⁾ (¹⁾ School of Science, Kitasato University ²⁾ School of Medicine, Kitasato University ³⁾ Mitsubishi Kagaku Institute of Life Sciences)

2S1-2 Peptidomics-based Discovery of Peptide Tumor Markers

*Kazuki Sasaki (National Cancer Center)

2S1-3 Combining Proteomics, Peptidomics and MALDI Imaging for the Investigation of the Pathophysiology of Experimental Parkinson's Disease

*Per E Andren¹⁾; Marcus Svensson¹⁾; Karl Sköld¹⁾, Anna Nilsson¹⁾ Helena Nordvarg²⁾ and Per Svenningsson³⁾ (¹⁾ Laboratory for Biological and Medical Mass Spectrometry, Uppsala University, ²⁾Amersham Biosciences, ³⁾ Karolinska Institute)

2S1-4 Peptidome database construction for the pig and mouse brain peptides

*Naoto Minamino¹⁾, Hiromiki Kuwahara¹⁾, Yasuko Matsui¹⁾, Junko Isoyama-Tanaka¹⁾, * Takahiro Kihara¹⁾, Masami Matsubae^{2) 1)}, Toshifumi Takao²⁾ and Masaharu Isoyama³⁾ (¹⁾ National Cardiovascular Center Research Institute, ²⁾ Institute for Protein Research, Osaka University, ³⁾ Protein Research Foundation)

Session 2S2 Pharmacoproteomics 14:15-15:35

Chair: Yoshiya Oda

2S2-1 Using Functional Proteomics to Develop Non-invasive Vaccines: Application of Proteomics in Biodefense and Human Infectious Diseases

*Eric Huang (University of Alabama at Birmingham)

2S2-2 Chemical Proteomics for Drug Discovery

*Yoshiya Oda (Eisai, Laboratory of Seeds Finding Technology)

2S2-3 New approach to chemical biology using affinity beads

*Tadashi Wada and Hiroshi Handa (Graduate School of Bioscience & Biotechnology, Tokyo Institute of Technology)

2S2-4 Reduction of Nonspecific Binding protein on Affinity Matrices

*Akito Tanaka, Masayuki Haramura and Akira Yamazaki (Reverse Proteomics Research Institute Co., Ltd.)

Poster Presentations (May 19, 2004, Exhibition Hall) 13:00-14:20

Chair: Yutaka Yoshida, Norie Araki

1P-1 Proteomic analysis of tumor progression : Differential expression of intracellular protein between murine fibrosarcoma progressor and regressor

*Eiko Hayashi ^{1) 2)}, Yasuhiro Kuramitsu ¹⁾, Masanori Fujimoto ¹⁾, Xiulian Zhang ¹⁾, Norio Iizuka ³⁾, Futoshi Okada ⁴⁾, Masanobu Kobayashi ⁴⁾, Yoshiya Ueyama ²⁾ and Kazuyuki Nakamura ¹⁾ (¹⁾ Department of Biochemistry and Biomolecular Recognition, ²⁾ Department of Oral and Maxillofacial Surgery, ³⁾ Department of Bioregulatory Function, ⁴⁾ Division of Cancer Pathobiology)

1P-2 Curative effect of thyroxine treatment on hereditary hypothyroidism as evaluated by normalization of pancreatic proteome of the rdw rat

*Mamoru Satoh ¹⁾, Eri Satoh-Haruta ¹⁾, Akira Omori ²⁾, Masamichi Oh-Ishi ¹⁾, Yoshio Koderia ¹⁾, Sen-Ichi Furudate ³⁾ and Tadakazu Maeda ¹⁾ (¹⁾ Laboratory of Biomolecular Dynamics, Department of Physics, School of Science, Kitasato University, ²⁾ Laboratory of Biopolymer Conformation Analysis, Mitsubishi Kagaku Institute of Life Sciences, ³⁾ Department of Laboratory Animal Science, School of Medicine, Kitasato University)

1P-3 Administration effects of phthalate ester (DBP and DEHP) as plastic additives on estrus cycle and proteome analysis of pituitary gland in rats.

*Yasushi Sakamoto ¹⁾, Narumi Hirosawa ¹⁾, Yuuko Suzuki ¹⁾ and Kazuyuki Yano ²⁾ (¹⁾ Department of Biomedical Research Center Division of Analytical Science, Saitama Medical School, ²⁾ Department of Chemistry, Saitama Medical School)

1P-4 Analysis of DNA damage and apoptosis in leukemic cells treated with bisphenol A

*Shinji Oikawa, Ayako Furukawa, Saeko Tada-Oikawa and Shosuke Kawanishi (Department of Environmental and Molecular Medicine, Mie University School of Medicine)

1P-5 High Molecular Mass Proteome of Androgen Independent Prostate Cancer

*Hidetoshi Kuruma ¹⁾, Shin Egawa ¹⁾, Masamichi Oh-Ishi ²⁾, Yoshio Koderu ²⁾, Mamoru Satoh ²⁾, Weigiang Chen ¹⁾, Shiro Baba ¹⁾ and Tadakazu Maeda ²⁾ (¹⁾ Department of Urology, Kitasato University School of Medicine, ²⁾ Department of Physics, Kitasato University School of Science)

1P-6 Two-dimensional electrophoretic profiling of normal human kidney: differential protein expression in the glomerulus, cortex and medulla

*Bo Xu ¹⁾, Yutaka Yoshida ¹⁾, Ying Zhang ¹⁾, Eishin Yaoita ¹⁾, Tetsuo Osawa ²⁾ and Tadashi Yamamoto ¹⁾ (¹⁾ Division of Structural Pathology, Institute of Nephrology, Niigata Graduate School of Medical and Dental Sciences, ²⁾ Department of Urology, Niigata City General Hospital)

1P-7 Proteomic Signatures of TT2F Mouse Embryonic Stem Cells Containing a Single Human Chromosome 21 in Neuronal Differentiation

*Ryuichi Nishigaki ^{1) 2) 3)}, Mitsutaka Kadota ^{1) 2)}, Yasuhiro Kazuki ⁵⁾, Tosifusa Toda ³⁾, Chi Chiu Wang ⁴⁾, Yasuaki Shirayoshi ⁵⁾ and Mitsuo Oshimura ⁶⁾ (¹⁾ Department of Human Genome Science (Kirin Brewery), Graduate School of Medical Science, Tottori University, ²⁾ Department of Molecular and Cell Genetics, Graduate School of Medical Science, Tottori University, ³⁾ Proteomics Collaboration Research Group, Tokyo Metropolitan Institute of Gerontology, ⁴⁾ Department of Obstetrics & Gynaecology, The Chinese University of Hong Kong, ⁵⁾ Department of Molecular and Cell Genetics, Life Science Division, Faculty of Medicine, Tottori University, ⁶⁾ Department of Biomedical Science, Regenerative Medicine and Biofunction, Graduate School of Medical Science, Tottori University)

1P-8 Proteomic analysis of virus infection using 2D DIGE and MALDI-ToF MS

*Tetsuji Noda ¹⁾, Minako Iwama ²⁾, Ryo Hasegawa ¹⁾, Joe Hirano ¹⁾, Junichi Inagawa ¹⁾, Yuichi Ishizuka ¹⁾ and Kiyohisa Mizumoto ²⁾ (¹⁾ Amersham Biosciences K.K. Proteomics, ²⁾ Kitasato University, School of Pharmaceutical Sciences, Laboratory of Biochemistry and Molecular Biology)

1P-9 A Case of Cushing's Syndrome with Adrenocortical Benign Adenoma, which is suspected cancer before an adrenalectomy, and characteristic protein expression patterns using Two-dimensional Map of Human Adrenal Gland Protein

*Takanori Ebisawa¹⁾, Hisashi Hisatomi^{2),3)}, Tuyoshi Isaka¹⁾, Kanta Taniguchi¹⁾, Tosifusa Toda³⁾,

Kiminobu Sasano⁴⁾, Katsuyoshi Tojo¹⁾ and Naoko Tajima¹⁾ (¹⁾ Division of Diabetes, Metabolism and Endocrinology, Department of Internal Medicine, Jikei University School of Medicine, ²⁾ Analytical Center for Medical Science, SRL, Inc., ³⁾ Proteomics Collaboration Research Center, Tokyo Metropolitan Institute of Gerontology, ⁴⁾ Division of Pathology, Tohoku University)

1P-10 Changes in spinorphin and dipeptidyl peptidase III in human cerebrospinal fluid from patients with rheumatoid arthritis and osteoarthritis

*Yukio Yamamoto ¹⁾, Yoshiko Akita ¹⁾, Shigeyuki Tai ²⁾, Susumu Fukasaku ³⁾, Teruhide Yamaguchi ⁴⁾, Tadashi Oshizawa ⁴⁾, Kazuko Yamaoka ¹⁾, Mariko Shimamura ¹⁾ and Tadahiko Hazato ¹⁾ (¹⁾ Tokyo Metropolitan Institute of Medical Science, ²⁾ Tokyo Metropolitan Boktoh Hospital, ³⁾ School of Medicine, Juntendo University, ⁴⁾ National Institute of Health Sciences)

1P-11 Proteomic analysis of the plasma membrane fraction from 3T3-L1 adipocytes

*Toshiyuki Mikami ¹⁾, Akane Tsujimoto ¹⁾, Hiroyuki Sato ¹⁾, Chihiro Higuchi ¹⁾, Shinichi Kojima ¹⁾ and Mitsuru Hashiramoto ²⁾ (¹⁾ Genomic Science Laboratories, Sumitomo Pharmaceuticals, ²⁾ Department of Diabetology and Clinical Laboratory Medicine, Ehime University School of Medicine)

1P-12 Searching for genes involved in arteriosclerosis: proteomic analysis of cultured human umbilical vein endothelial cells undergoing replicative senescence.

Hiroki Kamino ¹⁾, Masaharu Hiratsuka ^{2) 3)}, Tosifusa Toda ⁴⁾, *Ryuichi Nishigaki ^{3) 1) 4)}, Mitsuhiro Osaki ^{6) 6)}, Hisao Ito ⁵⁾ and Mitsuo Oshimura ⁶⁾ (¹⁾ Department of Molecular and Cell Genetics, Graduate School of Medical Science, Tottori University, ²⁾ Department of Molecular and Cell Genetics, Life Science Division, Faculty of Medicine, Tottori University, ³⁾ Department of Human Genome Science (Kirin Brewery), Graduate School of Medical Science, Tottori University, ⁴⁾ Proteomics Collaboration Research Group, Tokyo Metropolitan Institute of Gerontology, ⁵⁾ Division of Organ Pathology, Department of Microbiology and Pathology, Faculty of Medicine, Tottori University, ⁶⁾ Department of Biomedical Science, Regenerative Medicine and Biofunction, Graduate School of Medical Science, Tottori University University)

1P-13 Human chromosome 21q22.2-qter carries a gene(s) responsible for downregulation of mlc2a

Yasuhiro Kazuki ¹⁾, *Ryuichi Nishigaki ¹⁾, Motoshi Kimura ²⁾, Yoshiteru Kai ²⁾, Satoshi Abe ²⁾, Chiga Okita ²⁾, Yasuaki Shirayoshi ⁵⁾, Kazunori Hanaoka ⁴⁾, Kazuma Tomizuka ⁵⁾ and Mitsuo Oshimura ²⁾ (¹⁾ Department of Molecular and Cell Genetics, Graduate School of Medical Science, Tottori University, ²⁾ Department of Biomedical Science, Regenerative Medicine and Biofunction, Graduate School of Medical Science, Tottori University, ³⁾ Department of Molecular and Cell Genetics, Life Science Division, Faculty of Medicine, Tottori, ⁴⁾ Laboratory of Molecular Embryology, Department of Bioscience, Kitasato University School of Medical Science, Tottori, ⁵⁾ Pharmaceutical Research Laboratory, KIRIN Brewery Co., Ltd.)

1P-14 Proteomic analysis of lipid raft components during T-cell activation

*Michimoto Kobayashi ¹⁾, Joe Hirano ²⁾ and Seisuke hattori ¹⁾ (¹⁾ Division of Cellular Proteomics, Institute of Medical Science, University of Tokyo, ²⁾ Amersham Biosciences K.K.)

1P-15 Comprehensive analysis of targets of anti-endothelial cell antibodies

*Tomohiro Kato ¹⁾, Rie Karasawa ^{2) 1)}, Seido Ooka ²⁾, Taichi Sekine ¹⁾, Hiroyuki Nishimura ³⁾, Nobuyuki Nukina ⁴⁾, kenn-ichi mitsui ⁴⁾, Shoichi Ozaki ²⁾ and Kusuki Nishioka ¹⁾ (¹⁾ Institute of Medical Science, St. Marianna University School of Medicine, ²⁾ Department of Rheumatology, St. Marianna University School of Medicine, ³⁾ Toin Human Science and technology Center, Toin University of Yokohama, ⁴⁾ Riken Brain Science Institute)

1P-16 Proteomic profiling of human SH-SY5Y neuroblastoma cells under oxidative stress induced by 6-hydroxydopamine

*Megumi Nakamura ¹⁾, Takako Ohsawa ²⁾, Hiraku Morisawa ¹⁾, Yoko Sakurai ¹⁾ and Tosifusa Toda ¹⁾ (¹⁾ Proteomics collaboration research group, Tokyo Metropolitan Institute of Gerontology, ²⁾ Cellular Signaling Research Group, Tokyo Metropolitan Institute of Gerontology)

Poster Presentations (May 20, 2004, Exhibition Hall) 10:30-11:50

Chair: Tadashi Nemoto, Mitsuo Takayama

2P-1 Analysis of Sulfo- and Phospho-Peptides as tetrabutylammonium Salts by Matrix

Assisted Laser Desorption/Ionization Mass Spectrometry

Masaaki Ueki and *Miyuki Yamaguchi (Faculty of Science, Tokyo University of Science)

2P-2 Parallel Purification of Serum Peptides for Mass Spectrometry

*Kazuhiya Kameyama ¹⁾, Elena Chernokalskaya ²⁾, Mark Kavonian ²⁾, Heather Glazebrook ²⁾, Sara Gutierrez ²⁾, Aldo Pitt ²⁾ and Jack Leonard ²⁾ (¹⁾ Nihon-Millipore KK, ²⁾ Millipore Corporation)

2P-3 Digestion of Complex Protein Samples in 2,2,2-Trifluoroethanol (TFE) Yield Increased Sequence Coverage and Protein Identifications by Mass Spectrometry Analysis

*John A Chakel , Jose E Meza , Christine A Miller and Steven M. Fische (¹⁾ Agilent Technologies, Santa Clara, CA)

2P-4 Comprehensive approach to generate and to evaluate anti-mKIAA antibodies.

*Kiyoko Shimada ^{1) 2)}, Mihoko Nagano ^{1) 2)}, Yasuhiro Hara ^{1) 2)}, Hiroshi Kohga ^{1) 2)}, Osamu Ohara ^{3) 4)}, Shigeki Yuasa ⁵⁾, Takahiro Nagase ³⁾, Noriko Okazaki ³⁾ and Hisashi Koga ^{1) 2) 3)} (¹⁾ CREATE, ²⁾ Chiba Industry Advancement Center, ³⁾ Kazusa DNA Research Institute, ⁴⁾ RIKEN Research Center for Allergy and Immunology, ⁵⁾ National Institute of Neuroscience)

2P-5 Development of efficient in-gel digestion system

*Hiroyuki Katayama , Haruna Saito , Yasushi Ishihama , Tsuyoshi Tabata , Yoshiya Oda , Toshitaka Sato and Takeshi Nagasu (Laboratory of Seeds Finding Technology , Eisai Co., Ltd.)

2P-6 Novel proteomic analysis platform for post translation modification, protein phosphorylation: combination of DIGE, PMF by MALDI-ToF MS and MS/MS analysis by ESI-IT MS.

Tetsuji Noda ¹⁾, Yuichi Ishizuka ¹⁾, Noriko Oshima ¹⁾, Masayuki Kubota ²⁾, Junko Kimata ²⁾ and *Joe Hirano ¹⁾ (¹⁾ Amersham Biosciences K.K., ²⁾ Thermo Electron K.K.)

2P-7 n-gel detection of protein carbonyls by Cy-hydrazide

*Takeshi Ueno , Yusuke Kawashima , Yoshio Koderu , Masamichi Oh-Ishi and Tadakazu Maeda (Kitasato University Graduate School of Fundamental Life Science)

2P-8 Characterization of three different mass spectrometry instruments for efficient proteome analysis.

*Haruna Saito , Hiroyuki Katayama , Yasushi Ishihama , Tsuyoshi Tabata , Yoshiya Oda , Toshitaka Sato and Takeshi Nagasu (Laboratory of Seeds Finding Technology, Eisai Co., Ltd.)

2P-9 Tags for oxidized proteins, TOP, induced by reactive oxygen species

*Yoshio Koderu , Mamoru Satoh , Yusuke Kawashima and Tadakazu Maeda (School of Science, Kitasato University)

2P-10 A cryodetector mass spectrometer with mass independent sensitivity and energy resolution for quantitative analysis of very large biopolymers.

*Tsuyoshi Karasawa¹⁾, R.Chalk²⁾, G. Hayn²⁾, L. Schultheis²⁾, U. Matter²⁾, S. Alves³⁾ and R. Zenobi³⁾ (¹⁾ SCBioSciences Corporation, ²⁾ COMET AG, Analytics, ³⁾ ETH Zurich, Dep. Of Chemistry)

2P-11 An algorithm for the MS analysis of successive C-terminal amino acid truncation reaction

*Hiroaki Torii ¹⁾, Kenji Miyazaki ¹⁾, Ken'ichi Kamijo ¹⁾ and Akira Tsugita ¹⁾²⁾ (¹⁾ Proteomics Res. Center, Fundamental and Environmental Res. Labs., NEC Corp, ²⁾ Tokyo Rikakikai Co., Ltd. Proteomics Research Laboratory)

2P-12 2D PAGE / MALDI ToF or Mud LC / ESI-IT. Which should we choose for plasma proteome analysis?

*Takeshi Kawamura ¹⁾, Yuichi Ishizuka ²⁾, Kiyonaga Fujii ¹⁾, Junichi Inagawa ²⁾, Masato Kikkawa ²⁾, Tetuji Noda ²⁾, Joe Hirano ²⁾ and Toshihide Nishimura ¹⁾ (¹⁾ Tokyo Medical University, Clinical Proteome Center, ²⁾ Amersham Biosciences K.K)

2P-13 Development of a purification method for phosphoproteins with immobilized metal affinity chromatography (IMAC) and its application to phosphoproteome analysis.

*Mitsuyo Machida ¹⁾, Hidetaka Kosako ¹⁾, Masato Ushiyama ^{1) 2)}, Junichi Inagawa ^{1) 2)}, Joe Hirano ²⁾, Eisuke Nishida ³⁾ and Seisuke Hattori ¹⁾ (¹⁾ Division of Cellular Proteomics (BML), Institute of Medical Science, University of Tokyo, ²⁾ Amersham Biosciences, K. K., ³⁾ Department of Cell and Developmental Biology, Graduate School of Biostudies, Kyoto University)

2P-14 Disease peptidomics: Its development and application to a diabetes model mouse

*Toshiyuki Fukutomi ¹⁾, Yoshio Kodera ¹⁾, Tomihisa Kogo ¹⁾, Sen-ichi Furudate ²⁾, Akira Omori ³⁾ and Tadakazu Maeda ¹⁾ (¹⁾ Department of Physics, School of Science, Kitasato University, ²⁾ Department of Laboratory Animal Science, School of Medicine, Kitasato University, ³⁾ Mitsubishi Kagaku Institute of Life Science (MITILS))

2P-15 ISOLATION OF LIPID FRACTION AND ANALYSES OF FATTY ACIDS IN BIOTECHNOLOGICAL PROCESSING OF BIOMASS *Rhodobacter Capsulatus*

* Sani Salisu (Moscow Academy of Fine Chemical Technology)

2P-16 2D-PAGE Based Proteomics and Protein Analysis - Unravelling Biological Networks- Detailing Individual Protein Function

* Thomas Pohl (Brigitte Wittmann-Liebold)

2P-17 Reduction of streaking in the first-dimensional isoelectric focusing by a convenient prevention of re-oxidation of proteins

*Hisashi Hisatomi ^{1) 2)}, Megumi Nakamura ¹⁾, Yoko Sakurai ¹⁾, Hiraku Morisawa ¹⁾, Mikako Hirota ¹⁾, Kohji Nomura ¹⁾, Katsumi Kawano ^{1) 2)} and Tosifusa Toda ¹⁾ (¹⁾ Proteomics Collaboration Research Group, Tokyo Metropolitan Institute of Gerontology, ²⁾ Analytical Center for Medical Science, SRL Inc.)

Technical Presentations

Grand Hall 14:20-14:50, May 19, 2004

1G-TP Advanced proteome analysis of human serum and CSF after immunodepletion

of high abundance proteins

Rudolf Grimm (Agilent Technologies Inc.)

Second Hall 14:20-14:50, May 19, 2004

1S-TP 2D PAGE Approaches for Differential Protein Expression Analysis and Biomarker Discovery

John Randall, Ph.D. (Protein Function Division, Life Science Group, Bio-Rad Laboratories)

Grand Hall 13:45-14:15, May 20, 2004

2G-TP Two ways for Clinical Proteome

Hideki Sasaki (Amersham Bioscience KK)

Second Hall 13:45-14:15, May 20, 2004

2S-TP CIPHERGEN's SELDI Expression Difference Mapping (EDM) and Interaction Difference Mapping (IDM) Platforms: A technical overview of how serum biomarkers are discovered and identified using SELDI.

Rebecca Caffrey, Ph.D. (Ciphergen Biosystems Inc.)

Joint Workshop Yoikuin Memorial Hall

Chair: Toshihide Nishimura, Mitsuo Takayama

JW-1 JASCO International Co.,Ltd. 16:00-17:00, May 20, 2004

Introduction of MALDI micro

Teruaki Yamazaki (JASCO International Co.,Ltd.)

New technology for proteome analysis using Q-TOF MS

Kyoko Sasaki (JASCO International Co.,Ltd.)

Study for site specific glycosylation analysis - the next step in proteomics

Akihiro Sato (JASCO International Co.,Ltd.)

JW-2 Shimadzu Corporation 17:00-18:00, May 20, 2004

AccuSpot for MALDI plate spotting

Morimasa Hayashi (Shimadzu Corporation)

Advantage of MALDI-QIT-TOF MS in Glycoprotein Analysis

Yoshinao Wada (MCH Research Institute Osaka)

JW-3 Applied Biosystems Japan 18:00-19:00, May 20, 2004

Use of Novel Tagging Chemistries to Study Protein-Protein Interactions and Protein
Expression Profiling from Affinity Pull-Downs

Kazuchika Furuishi, Ph.D. (Applied Biosystems Japan Ltd.)

Protein Expression Profiling: Targeted Proteomics Techniques for Studying
Cytochrome P450 Enzymes

Takuichi Tsubata, Ph.D. (Applied Biosystems Japan Ltd.)
