Poster Presenters Abstracts

Poster P1-P195

P1 A TISSUE-SPECIFIC GENE EXPRESSION ATLAS OF UNIPARENTAL DUPLICATION AND METHYLATION MUTANT MICE

Reiner Schulz[1], Kathryn Woodfine[1], Trevelyan R. Menheniott[1], Deborah Bourc'his[2], Timothy Bestor[3] and Rebecca J. Oakey[1]

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P2 RETROTRANSPOSITION: A MECHANISM FOR GENERATING NEW IMPRINTED GENES?

Ruth McCole, Andrew J. Wood, Reiner Schulz and Rebecca J. Oakey

Kings College London

P3 PROGRESS TOWARDS INTEGRATION OF MOUSE PHENOME RESOURCES

John Hancock, Mouse Phenotype Database Integration Consortium

MRC Harwell, Harwell, UK

P4 COMPARATIVE ANALYSIS OF THE POLYLEUCINE STRUCTURE IN THE MAMMALIAN TASTE RECEPTOR, T1R1 GENE.

Mitsuru Ebihara

Dept. Food Science, Ishikawa Prefectural University

P5 IF WE COULD TALK TO THE ANIMALS

Mathew W. Wright, Michael J. Lush, Elspeth A. Bruford

HUGO Gene Nomenclature Committee (HGNC)

P6 EVOLUTIONARY CONSERVED CDT2-INTS7 INTERGENIC REGION ACTS AS A BIDIRECTIONAL PROMOTER AND IS ASYMMETRICALLY REGULATED

Kenichi Yoshida

Department of Life Sciences, Meiji University School of Agriculture

P7 COMPARATIVE GENOMIC MAPPING OF THE HUMAN GHRELIN GENE REVEALS NOVELS EXONS GIVING RISE TO ALTERNATIVE SPLICE VARIANTS, INCLUDING NATURAL ANTISENSE TRANSCRIPTS

Inge Seim, Adrian Herington, Lisa Chopin

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P8 EXPLORING THE MOLECULAR BASIS FOR ATHLETIC PERFORMANCE TRAITS IN NORTH SWEDISH TROTTERS

Gabriella Lindgren[1], Ingrid Jacobsson[2], Aneta Ringholm[2], Knut Roed[3], Sofia Mikko[1], Leif Andersson[2]

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P9 MAUSDB: THE GERMAN MOUSE CLINIC OPEN SOURCE PHENOTYPE- AND MOUSE MANAGEMENT SYSTEM

Holger Maier, Christoph Lengger, Ralph Steinkamp, Karlheinz F. Schaeble, Helmut Fuchs, Valerie Gailus-Durner, Martin Hrabe de Angelis

GSF-National Research Center for Environment and Health, Institute of Experimental Genetics, Munich/Neuherberg, Germany

P10 COMPARATIVE FUNCTIONAL ANNOTATION: THE MOUSE PERSPECTIVE

Judith A. Blake, David P. Hill, Mary E. Dolan, Harold J. Drabkin, Li Ni, and Dmitry Solnikov

Mouse Genome Informatics Group, The Jackson Laboratory

P11 REARRANGEMENT EVENTS HAVE SYNCHRONIZED WITH NUCLEOTIDE SUBSTITUTIONS DURING MAMMALIAN EVOLUTIONARY HISTORY

Tsuyoshi Hachiya, Yasunori Osana, Kris Popendorf and Yasubumi Sakakibara
Department of Biosciences and Informatics, Keio University

P12 MURASAKI: LANGUAGE-THEORY BASED HOMOLOGY DETECTION ACROSS MULTIPLE LARGE-SCALE GENOMES

Kris Popendorf, Yasunori Osana, Hacchiya Tsuyoshi, Yasubumi Sakakibara
Keio University

P13 DEVELOPMENT OF INFORMATIONAL INFRASTRUCTURES TO SHARE MOUSE PHENOTYPE AND EXPERIMENTAL PROCEDURES OF PHENOTYPING PLATFORM WITH MULTIPLE INSTITUTIONS

Hiroshi Masuya[1], Sumi Yoshikawa[1], Naohiko Heid[1], Norio Kobayashi[1], Takeshi Arikuma[3], Tetsuro Toyoda[1]., Riichiro Mizoguchi[2], Tetsuo Noda[1], Yoichi Gondo[1], Shigeharu Wakana[1] and Toshihiko Shiroishi[1]
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P14 COMMON AND DIFFERENTIAL RESPONSES TO STEROID HORMONES VIA THEIR COGNATE RECEPTOR-BINDING SITES IN HUMAN GENOME

Kuniko Horie-Inoue[1], Ken-ichi Takayama[1,2], Satoshi Inoue[1,2]
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P15 ANALYSES OF NON-CODING RNAS IN BOVINE GENOME.

Evgeny Glazov, Sean McWilliam, Wes Barris, David Tang, and Brian Dalrymple
CSIRO Livestock Industries

P16 EXPRESSION OF HUMAN CIS NATURAL ANTISENSE TRANSCRIPTS AFFECTED BY THEIR OVERLAPPING ARRANGEMENTS IN THE GENOME

Naoki Osato, Yoshiyuki Suzuki, Kazuho Ikeo, Takashi Gojobori
DNA Data Analysis Laboratory, Center for Information Biology and DNA Data Bank of Japan

P17 MOLECULAR EVOLUTION OF GP25L GENE FAMILY

Shoichi Matsukuma, Mituyo Yoshihara
Kanagawa Cancer Center Research Institute, Division of molecular pathology and genetics

P18 SEQUENCE COMPARISON OF FSH-RECEPTORS AMONG 12 MOUSE STRAINS

Osamu Suzuki
National Institute of Biomedical Innovation

P19 MOUSE GENE NOMENCLATURE: WHERE ARE WE IN GENE NAMING?

Lois J. Maltais, Monica McAndrews-Hill, Judith A. Blake, Carol J. Bult, Janan T. Eppig, Mouse Genome Informatics (MGI) Staff
The Jackson Laboratory

P20 APPLICATION OF SNP GENOTYPING ASSAY FOR TYPING OF HUMAN MITOCHONDRIAL DNA CONTROL REGION IN TAIWAN

Shiao-ping Huang, and Jing-Jing Lai
Department of Medical Technology, Fooyin University

P21 FROM PHENOTYPE TO GENE USING THE MOUSE GENOME INFORMATICS DATABASE

Carol Bult, Judith Blake, Janan Eppig, James Kadin, Joel Richardson, Martin Ringwald, and the Mouse Genome Informatics Group
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P22 EVOLUTION OF THE SCHLAFEN GENES, A GENE FAMILY POSSIBLY INVOLVED IN EMBRYONIC LETHALITY, MEIOTIC DRIVE, IMMUNE SYSTEM DEVELOPMENT AND POXVIRUS VIRULENCE

Saijal Naik, Olivia Bustos, Gayle Ayers, Aaly Meheraly, Ellen Pritham and Elena de la Casa-Esperon
Department of Biology. University of Texas at Arlington. USA

P23 GENETIC CHARACTERIZATION OF THE WILD-DERIVED HOUSE MICE IN EAST ASIA

Jun J. Sato[1], Yasunori Yamaguchi[1], Junpei Ueta[1], Hitoshi Suzuki[2], Wang Chunyan[3], Alexei P. Kryukov[4], Kazuyuki Mekada[5], Naoyuki Takahata[6], Kazuo Moriwaki[5]
[1]Fukuyama University, [2]Hokkaido University, [3]Lanzhou Institute of Biological Products, [4]Russian Academy of Sciences, [5]RIKEN BRC, [6]Gtraduate School of Advanced Studies

P24 A MATHEMATICAL MODEL FOR AFFYMETRIX GENECHIP PROBE LEVEL DATA BASED ON FUNCTIONAL STATES OF GENE - ON/OFF

Keiko Otani[1], Megu Ohtaki[2], Keiko Hiyama[2], Eiso Hiyama[2], Kenichi Satoh[2], Takeshi Shimamoto[2], Dokki Mohamad [2], Masataka Andoh[2], Tetsuji Tonda[2], Masahiko Nishiyama[2]
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P25 A COMPARATIVE STUDY OF THE ABCG2 GENE IN MILK PRODUCTION

Jerry Wei, Julie A. Cavanagh, Mehar S. Khatkar, Lisa G. Riley, Paul A. Sheehy, Herman W. Raadsma and Peter Williamson
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P26 PREDICTION OF NUCLEAR LOCALIZATION PROTEINS WITH CHARGE PERIODICITY OF 28 RESIDUES

Noriyuki Sakiyama, Runcong Ke and Shigeki Mitaku
Department of Applied Physics, Graduate School of Engineering, Nagoya University

P27 A GENOME-WIDE MAP OF 8.27 MILLION SNPs IN THE LABORATORY MOUSE GENOME

B. Karlak[1], K. Frazer[1], C. Wade[2,3], M. Bogue[4], D. Hinds[1], E. Beilharz[1], R. Gupta[1], J. Montgomery[1], M. Morenzoni[1], G. Neilsen[1], S. Osborn[1], C. Pethiyagoda[1], L. Stuve[1], F. Johnson[5], M. Daly[2,3], D. Cox[1]
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P28 cSNP MINING FROM 3,210 FULL-LENGTH ENRICHED cDNA SEQUENCES OF KOREAN NATIVE PIGS

Vijaya Dirisala, Juhyun Kim, Kwangha Park, Nameun Kim, Younshin Oh, Hojun Choi and Chankyu Park
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P29 IDENTIFICATION OF EVOLUTIONALLY CONSERVED FAT REGULATORY GENES USING COMPARATIVE GENOMIC APPROACH

Ken Yagi, Itoshi Nikaido, Yosuke Mizuno, Yasushi Okazaki
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P30 THE STATE OF ANNOTATION IN HAVANA

Laurens Wilming, J Almeida, C Amid, I Barnes, D Carvalho Silva, S Donaldson, A Frankish, R Gibson, E Hart, R Kinsella, G Laird, J Loveland, J Mudge, A Mujica, J Rajan, H Sehra, E Sheridan, C Steward, M-M Suner, M Thomas, Jennifer Harrow and Tim Hubbard
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P31 POSMED: A WEB DATABASE EXPLORING THE OMIC SPACE BASED ON LITERATURE MINING

Norio Kobayashi, Yoshikazu Hasegawa, Naohiko Heida, Satomi Matsushita, Keith Player, Yoshiki Mochizuki, Manabu Ishii and Tetsuro Toyoda
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P32 GMV: A COMPARATIVE GENOME BROWSER FOR MURASAKI

Yasunori Osana, Kris Popendorf, Yasubumi Sakakibara
Keio University

P33 SHOE: PROMOTER ANALYSIS TOOL

Natalia Poluliakh[1,2], Harada Hajime[1], Wataru Fujibuchi[1], Martin Frith[1], Paul Horton[1]
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P34 THE MOUSE GENOME ASSEMBLY AND MOUSE RESOURCES AT NCBI

Valerie A. Schneider, Deanna M. Church and the NCBI annotation team
National Center for Biotechnology Information, NIH, Bethesda, MD, U.S.A.

P35 ASSESSING EXPRESSION TECHNOLOGIES AND THEIR APPLICATION TO COMPLEX LOCI.

Alistair M. Chalk, Matthew Anderson, Ryan Wolski, Nick Matigian, Alan Mackay-Sim and Christine Wells
National Center for Adult Stem Cell Research,Eskitis Institute for Cell and Molecular Therapies, Griffith University

P36 CASIMIR; TOWARDS A STRATEGY FOR COORDINATION AND SUSTAINABILITY OF MOUSE INFORMATICS RESOURCES

Paul Schofield[1], Vassilis Aidinis[2], Ewan Birney[3], Steve Brown[4], Duncan Davidson[5], Michael Gruenberger[1], Anne-Marie Mallon[4], Glenn Proctor[3], Eli Reuveni[6], Nadia Rosenthal[6], Klaus Schughart[7], Glauco Tocchini-Valentini[8], Tom Weaver[9], John Hancock[4]
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P37 A GENOME-WIDE ANALYSIS OF TRANSCRIPTION REGULATION IN MACROPHAGE, THE ACTIVITY IN THE GNP-ECW/FANTOM4

Harukazu Suzuki and The GNP-ECW/FANTOM4 consortium
Laboratory for Genome Exploration Research Group, RIKEN GSC, Yokohama, Japan

P38 PREPARATION OF DEEP-CAGE LIBRARIES FOR 454 AND SOLEXA SEQUENCERS.

Mitsuyoshi Murata, Sachiko Ishikawa. Yoshiko Hayashida. Kengo Hayashida. Hiromi Nishiyori. Hiromi Sano. Akira Hasegawa. Michihira Tagami. Shiro Fukuda. Shinji Kondo. Lassmann Timo. Arner Erik. Daub Carsten. Piero Carninci. Yoshihide Hayashizaki
RIKEN

P39 NEXT GENERATION SEQUENCER DATA PROCESSING AND MANAGEMENT SYSTEM FOR DEEP CAGE AND SHORT RNA SEQUENCES

Jessica Severin, Timo Lassmann, Ryoko Ishihara, Shintaro Katayama, Hideya Kawaji, Yoshihide Hayashizaki, Carsten Daub
Riken

P40 MOUSE PHENOME DATABASE: SELECTED UPDATES (OCT 2007)

Terry Maddatu, Stephen Grubb, Carol Bult, Molly Bogue
The Jackson Laboratory

P41 THE CENTER FOR GENOME DYNAMICS RESEARCH OVERVIEW

Randy Smith, The Center for Genome Dynamics*, Gary Churchill
The Jackson Laboratory

P42 Evola: ORTHOLOG DATABASE OF ALL HUMAN GENES IN H-InvDB WITH MANUAL CURATION OF PHYLOGENETIC TREES

Ryuichi Sakate[1], Akihiro Matsuya[1,2], Yoshihiro Kawahara[1], Yoshiharu Sato[1], Takashi Gojobori[3,4], Takeshi Itoh[3,5], Tadashi Imanishi[3]
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P43 ONTOLOGICALDISCOVERY.ORG: A WEB RESOURCE FOR THE EMPIRICAL DISCOVERY OF PHENOTYPIC RELATIONS ACROSS SPECIES AND EXPERIMENTAL SYSTEMS

Erich J. Baker[1], Zuopan Li[2], Jeremy Jay[2], Vivek Philip[3], Yun Zhang[2], Michael A. Langston[2,3], Elissa J. Chesler[3,4]
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P44 DIFFERENCES IN MICRORNA EXPRESSION ACROSS COMMON MOUSE INBRED STRAINS USING TAQMAN RT-PCR

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P45 TRANSCRIPTS AND THEIR EXPRESSION PATTERNS IN THE REGION CONTAINING THE HYBRID STERILITY 1 GENE

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P46 IDENTIFICATION OF NOVEL TRANSCRIPTOME SIGNATURES CHARACTERISTIC OF ERYTHROPOIETIC RESPONSE BY HIGH-RESOLUTION PROFILING OF MOUSE BLOOD USING SOLEXA 1G SEQUENCING TECHNOLOGY

Matthew N. Fedoruk, Jim L. Rupert
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S1-7/P47 AN ENU-INDUCED MUTATION OF A MIRNA ASSOCIATED WITH PROGRESSIVE HEARING LOSS

Morag Lewis[1], Elizabeth Quint[2], Agnieszka Rzadzinska[1], Anne Kent-Taylor[1], Helmut Fuchs[3], Martin Hrabé De Angelis[3], Cordelia Langford[1], Stijn Van Dongen[1], Anton Enright[1], Nick Redshaw[4], Tamas Dalmay[4], Karen P Steel[1,2]
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P48 ANALYSIS OF MICRO RNAS INVOLVED IN OSTEOBLASTIC DIFFERENTIATION

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P49 GLOBAL ANALYSIS OF MICRORNA AND GENE EXPRESSION IN HUMAN CELL LINES

Yoshinao Ruike[1], Atsuhiko Ichimura[1], Soken Tsuchiya[2], Kazuharu Shimizu[2], Ryo Kunimoto[3], Yasushi Okuno[3] and Gozoh Tsujimoto[1]
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P50 MULTIPLEX CDNA QUANTIFICATION METHOD BY DNA ENCODING TECHNOLOGY

Osamu Gotoh[1], Atsushi Kameda[1], Yasufumi Murakami[2], Akira Suyama[1]
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P51 CAGE-TSSCHIP; PROMOTER-BASED EXPRESSION PROFILING USING THE 5'-LEADING LABEL OF CAPPED TRANSCRIPTS

Shintaro Katayama[1], Mutsumi Kanamori-Katayama[1], Yuki Tsujimura[1], Noriko Ninomiya[1], Kazumi Yamaguchi[1,2], Piero Carninci[1,3], Yoshihide Hayashizaki[1,3]
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P52 GENETIC CONTROL OF GENE EXPRESSION AND GENE NETWORK IN THE HIPPOCAMPUS OF LXS MICE

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P53 HIDDEN LAYERS OF HUMAN SMALL RNAS

Hideya Kawaji[1], Mari Nakamura[2], Yukari Takahashi[1], Albin Sandelin[3], Shintaro Katayama[2], Carsten Daub[2], Shiro Fukuda[2], Chikatoshi Kai[2], Jun Kawai[2], Jun Yasuda[1], Carninci Piero[4], Yoshihide Hayashizaki[1,2,4]
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P54 DEVELOPMENT OF 454-CAGE METHOD FOR MONITORING DYNAMIC GENE EXPRESSION CHANGE

Norihiro Maeda[1], Hiromi Nishiyori[1], Mari Nakamura[1], Tika Kawazu[1], Mitsuyoshi Murata[1], Hiromi Sano[1], Kengo Hayashida[1], Shiro Fukuda[1], Michihira Tagami[1], Akira Hasegawa[1], Kayoko Murakami[1], Kate Schroder[2], Katharine Irvine[2], David Hume[2], Piero Carninci[1], Harukazu Suzuki[1], Yoshihide Hayashizaki[1]
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P55 MATRIX RNAI AS A TOOL FOR DEPICTING A HUMAN INTER-TRANSCRIPTION FACTOR REGULATORY NETWORK

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P56 TRANSCRIPTOME ANALYSIS BY 5'-3' DITAGS.

Miki Kojima, Hiromi Nishiyori, Yoshiko Hayashida, Yuki Tsujimura, Hiromi Sano, Akira Hasegawa, Shiro Fukuda, Takahiro Suzuki, Atsutaka Kubosaki, Carsten Daub, Jun Kawai, Harukazu Suzuki, Yoshihide Hayashizaki, Piero Carninci
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P57 LOGIC OF REPEAT ELEMENTS TRANSCRIPTION

Piero Carninci[1,2], Yasumasa Kimura[2], Timo Lassman[2], Carsten Daub[2], Kazunori Waki[2], Geoffrey Faulkner[3], Sean Grimmond[3], David Hume[3,4], Valerio Orlando[5], Nadine Horning[5], Yoshihide Hayashizaki[1,2]
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P58 DECIPHERING THE PROMOTOME OF PURIFIED CELL TYPES WITH LONGER CAGE TAGS.

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P59 BIOINFORMATICS APPROACH TO IDENTIFICATION OF GENES INVOLVED IN MULTIPLE PITUITARY HORMONE DEFICIENCY: NOTCH SIGNALING AND ORTHODENTICLE RELATED TRANSCRIPTION FACTORS

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P60 A GENETIC ANALYSIS OF MELANOCORTIN 1 RECEPTOR (MC1R) GENE AND ITS RELATIONSHIP TO COAT COLOR IN A "MELANIC" VOLE (Eothenomys melanogaster)

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Institute of Zoology and Department of Life Science, National Taiwan University

P61 THE NATIONAL BIO RESOURCE PROJECT FOR THE RAT IN JAPAN - AN UPDATE

Birger Voigt, Tomoji Mashimo, Akiko Takizawa, Ryoko Okajima, Ken-ichi Yamasaki, Satoshi Nakanishi, Takashi Kuramoto and Tadao Serikawa
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P62 GENOMIC ANALYSIS OF GASDERMIN A (GSDMA) AND GASDERMIN C (GSDMC) LOCI IN THE MAMMALIAN GENOME

Tamura M., Tanaka S., Fujii T., Kato Y. and Shiroishi T.
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P63 ANALYSIS OF GENE EXPRESSION RELATED TO THE ONE CARBON METABOLIC PATHWAY AND DNA METHYLATION STATUS IN THE RAT LIVER DURING VITAMIN B-12-DEFICIENCY.

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P64 TRANSCRIPTIONAL NETWORK ANALYSIS OF THE GLUCOCORTICOID RECEPTOR BASED ON THE HIERARCHICAL GENOMIC APPROACH

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P65 A NOVEL PEROXISOMAL PROTEASE TYSND1 IS REGULATED BY PPAR AGONIST AND PROCESSES PTS1- AND PTS2-CONTAINING ENZYMES INVOLVED IN *ß*-OXIDATION OF FATTY ACIDS

Igor V. Kurochkin[1], Yumi Mizuno[2], Ken Yagi[2], Yuichi Ninomiya[2], Akihiko Konagaya[1], Yoshiyuki Sakaki[1], Christian Schönbach[1] and Yasushi Okazaki[2]
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P66 EXPLORATION OF ADIPOSE TISSUE TRANSCRIPTOME NETWORK TRIGGERED IN VIVO BY AN INSULIN SENSITIZING AGENT, PIOGLITAZONE

Yoshinori Ochiai, Yi-Qiang Liang, Masakuni Serizawa, Naoko Birukawa, Sabrina Jesmin, Norihiro Kato
International Medical Center of Japan

P67 CLONING, SEQUENCING AND QUANTIFICATION OF BCL-2 AND BAX GENES FROM LAGOSTOMUS MAXIMUS (Rodentia)

Jensen CF, Ostermann K, Vitullo AD, Vollmer G
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P68 THE RAT GENOME DATABASE: INTEGRATING BIOLOGICAL INFORMATION INTO THE GENOMIC CONTEXT

Mary Shimoyama, George Kowalski, Stan Laulederkind, Rajni Nigam, Victoria Petri, Jennifer Smith, Jeff dePons, Dawei Li, Simon Twigger, Anne Kwitek, Howard Jacob
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P69 CELL DEATH WITH EXCESSIVE AUTOPHAGY OCCURS IN SERINE PROTEASE INHIBITOR KAZAL TYPE 3 DEFICIENT ACINAR CELLS

Masaki Ohmuraya, Kimi Araki and Ken-ichi Yamamura
Institute of Molecular Embryology and Genetics, Kumamoto University

P70 AUTOPHAGY DELIVERS TRYPSINOGEN TO THE LYSOSOME IN ACUTE PANCREATITIS

Masaki Ohmuraya, Kimi Araki and Ken-ichi Yamamura
Institute of Molecular Embryology and Genetics, Kumamoto University

P71 DEVELOPMENTAL DEFECTS OF KIDNEY IN FSTL1 GENE TARGETING MICE

Jingye Xu, Haibo Sha, Mingyan Yu and Xiang Gao
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P72 MOUSE KIDNEY PROXIMAL TUBULE-CELL SPECIFIC ABLATION MEDIATED BY HUMAN DIPHTHERIA TOXIN RECEPTOR

Michiko Sekine[1], Chouji Taya[1], Kunie Matsuoka[1], Sumiyo Takahama[1], Yoshiko Akita[1], Satomi Yamada[1], Toshiaki Monkawa[2], Akemi Suzuki[3] and Hiromichi Yonekawa[1]
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P73 EPITHELIAL-SPECIFIC BLOCKAGE OF THE MYD88-DEPENDENT TLR SIGNALING PATHWAY CONTRIBUTES TO SPONTANEOUS INTESTINAL INFLAMMATION

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P74 EMMA - THE EUROPEAN MOUSE MUTANT ARCHIVE

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P75 FBXO11, MUTATED IN OM MOUSE MUTANT MODEL JEFF, BINDS THE SMAD3/SMAD4 ANCHOR PROTEIN SPECTRIN BETA II

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P76 WHICH C57BL/6 SUBSTRAIN IS USED FOR THE BACKGROUND STRAIN OF YOUR MOUSE?

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P77 LASER-ASSISTED IVF - AN ALTERNATIVE APPROACH FOR SUCCESSFUL CRYOPRESERVATION OF MUTANT MOUSE LINES ON C57BL/6 BACKGROUND

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P78 SCREENING FOR DYNEIN COMPLEX MUTATIONS IN AN ENU MOUSE LIBRARY

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P79 DEAFNESS MOUSE MUTANTS WITH HAIR CELL IMPAIRED CALCIUM-SIGNALING GENERATED BY THE RIKEN ENU MUTAGENESIS PROGRAM

Osamu Minowa, Maki Inoue, Hiromi Motegi, Hideaki Toki, Yoshiyuki Sakuraba, Shigeharu Wakana, Yoichi Gondo, Toshihiko Shiroishi, Tetsuo Noda
RIKEN GSC

P80 THE JACKSON LABORATORY REPOSITORY: RESOURCE FOR INDUCIBLE AND CONDITIONAL MUTATION MOUSE STRAINS FOR MODELING HUMAN DISEASE

David Bergstrom, Bo Chang, Muriel Davisson, Leah Rae Donahue, Ken Johnson, Cathy Lutz, Steve Murray, Laura Reinholdt, Mike Sasner, Steve Rockwood and the Repository Team
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P81 A MOUSE MODEL FOR JUVENILE HYDROCEPHALUS

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P82 GENE TARGETING IN C57BL/6 ES CELL LINES: EFFECTS OF GENETIC VARIATION AND CHROMOSOMAL INSTABILITY

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P83 MOUSE EMBRYO/SPERM BANK AT THE CENTER FOR ANIMAL RESOURCES AND DEVELOPMENT (CARD), KUMAMOTO UNIVERSITY

Naomi Nakagata, Takehito Kaneko, Yukie Haruguchi, Tomoko Kondo, Hiromi Machida, Kiyoko Fukumoto, Yoshiko Nakagawa, Mika Koga, Shuuji Tsuchiyama, Naoko Nakamura, Satomi Yoshizumi, Mari Koga, Toru Urano and Ken-ichi Yamamura
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P84 NOVEL MOUSE MODELS OF DIABETES MELLITUS GENERATED BY THE RIKEN ENU MUTAGENESIS PROJECT

Maki Inoue, Hiromi Motegi, Yoshiyuki Sakuraba, Hideaki Toki, Shigeharu, Wakana, Yoichi Gondo, Osamu Minowa, Toshihiko Shiroishi, Tetsuo Noda
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P85 A NOVEL PHEX MUTATION WITH DEFECTIVE GLYCOSYLATION CAUSES HYPOPHOSPHATEMIA AND RICKETS IN MICE

Xiwen Xiong, Xiang Gao
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P86 A BREEDING SCHEME FOR THE FUNCTIONAL ANALYSIS OF THE MOUSE X CHROMOSOME

Frank J Probst, Andrew S Salinger, Monica J Justice
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P87 CHARACTERIZATION AND MAPPING OF BARTHEZ, A NEW MOUSE MUTATION WITH A COMPLEX PHENOTYPE THAT INCLUDES ALOPECIA

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P88 ENU-INDUCED RANDOM MUTAGENESIS SCREEN FOR IMMUNE OR ALLERGIC DISEASE MODEL IN THE MOUSE

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P89 ICST IS A MOUSE MODEL FOR GLAUCOMA

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P90 EGTC, DATABASE FOR THE EXCHANGEABLE GENE TRAP CLONES; RESOURCE OF MOUSE AND ES CELL LINES FOR THE FUNCTIONAL ABALYSIS OF THE MOUSE GENOME

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P91 THE MASK MUTATION REVEALS THE FUNCTION OF TRANSMEMBRANE SERINE PROTEASE 6 (TMPRSS6), WHICH REGULATES HEPCIDIN AND CONTROLS ABSORPTION OF DIETARY IRON

Xin Du[1], Terri Gelbart[2], Pauline Lee[2], Ellen She[3], Navjiwan Mann[1], Sosathya Sovath[1], Ernest Beutler[2], Bruce Beutler[1]
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P92 A DOMINANT-NEGATIVE MUTATION IN GDF5 GENERATED BY ENU MUTAGENESIS IMPAIRS JOINT FORMATION AND CAUSES OSTEOARTHRITIS (OA): A NOVEL MOUSE MODEL FOR OA

Tatsuya Furuichi[1], Hiroshi Masuya[2], Keiichiro Nishida[3], Gen Nishimura[4], Hidehiko Kawabata[5], Shigeharu Wakana[2], Toshihiko Shiroishi[2] and Shiro Ikegawa[1]
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P93 A NOVEL *PTGIS* GENE MUTATION SPONTANEOUSLY FOUND IN AN ICR CLOSED COLONY MOUSE

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P94 G3 RECESSIVE SCREENS FOR LOCI CONTROLLING MOUSE DEVELOPMENT

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P95 A NOVEL SPONTANEOUS STERILE MOUSE THAT WAS FOUND IN ICR CLOSED COLONY IS CAUSED BY *SMC1B* GENE MUTATION.

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P96 CHARACTERIZATION OF A NEW DWARFING MUTATION, PEEWEE, IN THE MOUSE

Bokryeon Lee[1], Kiyoshi Kano[1], Sachi Kume[1], Takuma Shimaoka[1], James Young[2], Pasty Nishina[2], Jurgen Naggert[2], Simon John[2], Kunihiko Naito[1]
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P97 SEARCHING FOR SOD1 ALS MODIFIERS IN THE MOUSE

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P98 IDENTIFYING GENES THAT MODIFY HUNTINGTON'S DISEASE IN THE MOUSE

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P99 NMR BASED METABOLIC DISEASE MODEL MOUSE SCREENING IN ENU MUTAGENESIS PROGRAM

Hiromi Motegi[1], Yuuri Tsuboi[2], Jun Kikuchi[3,4,5], Takashi Hirayama[2,4,5], Shigeharu Wakana[1], Toshihiko Shiroishi[1,6], Yoichi Gondo[1], Tetsuo Noda[1,7]
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P100 DEVELOPMENT OF DATABASE FOR EXPERIMENTAL PARAMETERS OF REPRODUCTIVE TECHNOLOGIES

Hideki Kaneda[1], Hiroshi Masuya[1], Kenji Mochida[2], Atsuo Ogura[2], Toshihiko Shiroishi[1], Naomi Nakagata[3], Ken-ichi Yamamura[4], Yuichi Obata[2] and Shigeharu Wakana[1]
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P101 MUTANT MODELS FOR ESOPHAGEAL CARCINOGENESIS IN RIKEN MOUSE ENU-MUTAGENESIS PROJECT

Hideaki Toki[1], Yuriko Saiki[3], Noriko Yamamoto[3], Yoshiyuki Sakuraba[2], Hiromi Motegi[1], Maki Inoue[1], Hideki Kaneda[1], Osamu Minowa[1], Shigeharu Wakana[1], Yoichi Gondo[2], Toshihiko Shiroishi[1,4], Tetsuo Noda[1,3]
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P102 ANALYZING MULTIPLE MOUSE LINES POSSESSING POINT MUTATION ON BETA-CATENIN (CTNNB1) GENE

Takuya Murata, Kumiko Karouji, Ai Nakahara, Taichi Yamaguchi, Emi Nakayama, Norie Uemura, Yoshiyuki Sakuraba, Ryuutaro Fukumura, Hideki Kaneda, Shigeharu Wakana, Tetsuo Noda, Toshihiko Shiroishi, Yoichi Gondo
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P103 RIKEN BRC TO ESTABLISH MOUSE RESOURCES OF THE HIGHEST GLOBAL STANDARDS

Atsushi Yoshiki, Fumio Ike, Noriko Hiraiwa, Hatsumi Nakata, Kazuyuki Mekada, Yasuyuki Kitaura, Keiji Mochida, Masayo Kadota, Ayumi Murakami, Maiko Fujita, Megumi Ohkawa, Atsuo Ogura, Kuniya Abe, Kazuo Moriwaki, Yuichi Obata
RIKEN BRC

P104 EVALUATION OF ENU-INDUCED MUTATION SCREENING SYSTEM BY NON-FLUORESCENT TILLING METHOD

Ryutaro Fukumura, Yoshiyuki Sakuraba, Naomi Fujimoto, Takuya Murata, Shigeharu Wakana, Tetsuo Noda, Toshihiko Shiroishi, Yoichi Gondo
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P105 ESTABLISHMENT OF EMBRYONIC STEM CELL LINES DERIVED FROM MSM/MS STRAIN ORIGINATED FROM MUS MUSCULUS MOLOSSINUS.

Kimi Araki[1], Naoki Takeda[2], Atsushi Yoshiki[3], Gen Yamada[2], Naomi Nakagata[2], Toshihiko Shiroishi[4], Kazuo Moriwaki[3] and Ken-ichi Yamamura[1]
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P106 ENU-BASED GENE-DRIVEN MUTAGENESIS IN THE MOUSE: MUTATIONS IN CODING/NONCODING AND TRANSCRIBED/NONTRANSCRIBED SEQUENCES

Yoshiyuki Sakuraba, Ryo Takahasi, Ryutaro Fukumura, Takuya Murata, Shigeru Makino, Naomi Fujimoto, Keiko Tsuchihashi, Hiroshi Masuya, Hideki Kaneda, Osamu Minowa, Shigeharu Wakana, Tetsuo Noda, Toshihiko Shiroishi, Yoichi Gondo
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P107 HAIR MORPHOLOGICAL MUTANTS GENERATED IN THE RIKEN MUTAGENESIS PROJECT

Miura I[1], Tanaka S[2], Yokoyama H[1], Shinogi A[1], Kobayashi K[1], Kaneda H[1], Toyoda T[1], Yoshiki A[3], Yonekawa H[4], Kikkawa Y[5], Kunieda T[6], Tamura M[2], Masuya H[1], Wakana S[1], Shiroishi T[1,2]
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S1-3/P108 IDENTIFICATION OF A NOVEL LOSS-OF-FUNCTION MISSENSE MUTATION IN THE RANKL GENE USING ENU MUTAGENESIS

Eleni Douni, Eleni Makrinou and George Kollias
Biomedical Sciences Research Center Alexander Fleming

P109 IDENTIFICATION OF GENETIC MODIFIERS USING RANDOM MUTAGENESIS IN MODELED RHEUMATOID ARTHRITIS AND INFLAMMATORY BOWEL DISEASE

Eleni Douni, Eleni Makrinou and George Kollias
Biomedical Sciences Research Center Alexander Fleming

P110 ESTABLISHMENT OF ENU-INDUCED DOMINANTLY INHERITED RETINAL DEGENERATION IN MICE

Tomohiro Suzuki[1], Hajime Sato[2], Kyoko Ikeda[1], Hiroshi Masuya[1], Haruka Yokoyama[1], Hideki Kaneda[1], Ikuo Miura[1], Kimio Kobayashi[1], Yoichi Gondo[1], Tetsuo Noda[1], Koji Nishida[2], Shigeharu Wakana[1], Toshihiko Shiroishi[1]

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P111 MICE OF ALL TYPES: INTEGRATING PHENOTYPIC DATA FOR SCREENS, MODELS, AND COMPLEX GENOTYPES

Janan Eppig, Cynthia Smith, Susan Bello, Howard Dene, Anna Anagnostopoulos, Monika Tomczuk, Hiroaki Onda, Jill Lewis, James Kadin

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P112 WHERE IN THE WORLD? USING IMSR TO FIND MOUSE RESOURCES

Janan Eppig, Beverly Richards-Smith, Peter Frost, Sharon Cousins, Mark Airey

The Jackson Laboratory

P113 EXAMINATION OF THE SPATIAL AND TEMPORAL EXPRESSION OF SICKLE TAIL (SKT) GENE IN NOTOCHORDAL CELLS.

Kei Semba[1,2], Takashi Andou[1,2], Kyushima Fumie[1,2], Hiroshi Mizuta[2], Masatake Araki[3], Kuniya Abe[4], Kimi Araki[1], and Ken-ichi Yamamura[1]

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P114 GENE-DRIVEN SCREEN OF AN ENU ARCHIVE OF MOUSE DNA AND SPERM.

Zuzanna Tymowska-Lalanne, Mohamed Mohideen Quwailid, Anne Southwell, Debra Brooker, Sian Polley, Amanda Pickard, Martin Fray, Emma Coghill, Roger D. Cox, Paul Denny and Steve D.M. Brown.

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P115 AN E3 UBIQUITIN LIGASE, RNF41, IS ASSOCIATED WITH ANXIETY-LIKE BEHAVIOR, MAJOR DEPRESSION, AND BETA-CARBOLINE-INDUCED SEIZURE

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P116 PROTEOMIC ANALYSIS REVEALS MITOCHONDRIAL DYSFUNCTION IN NEURODEGENERATION-PRONE MICE LACKING MAHOGUNIN RING FINGER-1

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P117 EFFECT OF FLUOXETINE ON THE BEHAVIOR OF MICE WITH ANXIOUS DEPRESSION UNDER PREVENTIVE AND THERAPEUTICAL ADMINISTRATION

Irina L. Kovalenko, Damira F. Avgustinovich, Nataliya N. Kudryavtseva

P118 CHROMOSOMAL ASSIGNMENT OF QTLs INFLUENCING MOUSE ANXIETY-RELATED BEHAVIOR IN THE MODIFIED HOLE BOARD USING CONSOMICS

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P119 GENETIC DISSECTION OF MOUSE ANXIETY-RELATED BEHAVIOR

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P120 A GENETIC ANALYSIS OF ENU INDUCED MOUSE MUTANT THAT SHOWS ADHD LIKE BEHAVIOURAL PHENOTYPES

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P121 MUTATION OF THE NADPH OXIDASE COMPONENT, P22PHOX/NMF333, RESULTS IN BOTH IMMUNOLOGICAL AND VESTIBULAR DEFICITS

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P122 ANALYSES ON LEARNING AND MEMORY IN MICE CARRYING mtDNA WITH A LARGE-SCALE DELETION.

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P123 SYSTEMATIC ANALYSIS OF BEHAVIORAL TRAITS USING CONSOMIC MOUSE STRAINS ESTABLISHED FROM C57BL/6J AND WILD-DERIVED MSM

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P124 MODELING PARKINSON'S DISEASE IN MICE

Deborah Cabin, Dan Zou, Leah Schwandt
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P125 mRNA-LIKE NON-CODING RNAs INVOLVED IN CELL FATE SPECIFICATION OF NEURONAL STEM CELLS

Shiro Tochitani[1,2], Tsugumi Kawashima[2], Shohei Noma[2], Mami Kishima[2], Kengo Hayashida[2], Chihiro Sakaba[2], Eriko Shibazaki[1,2], Yoshihide Hayashizaki[1,2,3]
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P126 TRANSCRIPTOME PROFILES OF A SMALL NUMBER OF IDENTIFIED NEURONS BY COMBINING LASER CAPTURE MICRODISSECTION AND nanoCAGE-ILLUMINA-SOLEXA TECHNOLOGY.

Roberto Simone[1], Christina Vlachouli[1], Dejan Lazarevic[1], Pascarella Giovanni[1], Charles Plessy[2], Yoshihide Hayashizaki[3], Piero Carninci[2] and Stefano Gustincich[1]
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P127 GENETIC DETERMINATION OF LEPTIN, ADIPONECTIN, INSULIN AND IGF-1 LEVELS IN THE BERLIN FAT MOUSE INBRED 860 LINE

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P128 CONSOMIC STRAINS AS A TOOL FOR DISSECTION OF REGULATORY NETWORKS

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P129 EFFECTS OF COMPLETE DEFICIENCY AND C-TERMINAL DELETION OF ADAMTS13 ON HEMOSTATIC FUNCTION IN MICE

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P130 GENOME-WIDE SEARCH FOR GENES WHICH MODULATE INFLAMMATORY ARTHRITIS CAUSED BY ALI18 MUTATION IN MICE

Koichiro Abe[1], Matthias Klaften[2], Thilo Jakob[3], Akira Narita1, Kenji Imai[1], Isabel Rubio-Aliaga[2,4], Sibylle Wagner[2], Martin Hrabe de Angelis[2]
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P131 REVERSE GENETIC STUDIES ON PATHOGENESES OF MITOCHONDRIA-RELATED MALE INFERTILITY

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P132 A COMPREHENSIVE QTL ANALYSIS ON THE SERUM CHOLESTEROL LEVEL BEFORE AND AFTER A HIGH-CHOLESTEROL DIET IN SHRSP

Yuji Harada[1], Tomoji Mashimo[2], Hiroshi Ogawa[3], Zong-Hu Cui[1], Kohei Kawakami[1], Junichi Masuda[3], Yukio Yamori[4], Toru Nabika[1]
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P133 FINE MAPPING OF ADIPOSITY QTL ON MOUSE PROXIMAL CHROMOSOME 2 BY SUBCONGENIC ANALYSIS

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P134 MEIOTIC ARREST IN MALES OF THE B6.CHRXMSM CONSOMIC STRAIN

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P135 GENETIC SUSCEPTIBILITY TO PORPHYROMONAS GINGIVALIS-INDUCED ALVEOLAR BONE LOSS IN MICE

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P136 GENETIC DISSECTION OF QUANTITATIVE TRAIT LOCI AFFECTING MULTIPLE PHENOTYPES IN HETEROGENEOUS STOCK MICE

William Valdar, Jen Taylor, Binnaz Yalcin, Richard Mott, Jonathan Flint
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P137 EXPRESSION OF PLA2G2A PREVENTS TUMORIGENESIS IN AZOXYMETHANE-TREATED C57BL/6 MICE; GENE EXPRESSION STUDIES REVEAL PLA2G2A TARGET GENES IN MOUSE COLON

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P138 IDENTIFICATION OF A NEONATAL GROWTH GENE CANDIDATE USING INTEGRATIVE GENOMICS

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P139 GENETIC DISSECTION OF AN ICR CLOSED COLONY OF THE MOUSE

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P140 HIGH-RESOLUTION FULL COLOR DIGITAL MOUSE ANATOMY BY THREE-DIMENSIONAL INTERNAL STRUCTURE MICROSCOPY

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P141 LYMPHOMA SUSCEPTIBILITY AFFECTS THE DEVELOPMENT OF CLONALLY GROWING PRE-LYMPHOMA CELLS

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P142 FINE MAPPING OF AHL3 AFFECTING BOTH AGE-RELATED AND NOISE-INDUCED HEARING LOSS

Yuka Morita,Sachiko Hirokawa, Hitoshi Okumura,Yoshiaki Kikkawa,Hiromichi Yonekawa, Ryo Kominami
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P143 GENOMIC COPY NUMBER AND EXPRESSION VARIATION WITHIN THE C57BL/6J INBRED MOUSE STRAIN

Dawn Watkins-Chow and William J Pavan
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P144 FINE MAPPING OF LOCI THAT MODIFY SUSCEPTIBILITY TO N-METHYL-N-NITROSOUREA (MNU)-INDUCED T-CELL TUMORS

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P145 ANALYSIS OF SKTS-FP1 LOCUS FOR SKIN TUMOR SUSCEPTIBILITY IN DOMINANT RESISTANT BACKCROSS

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P146 Idd1a, Idd1b, Idd1c and Idd1d EXERT THEIR FUNCTIONS FROM 2 DAYS OLD THROUGH 14 DAYS OLD IN THE NEONATAL INDUCTION OF DIABETES BY DIABETOGENIC CD4+BDC2.5 T CELL CLONES

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P147 SEARCH FOR GENES CONTRIBUTING TO COLON CANCER SUSCEPTIBILITY

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P148 MORPHOMETRIC AND MOLECULAR ANALYSIS OF BXD RECOMBINANT INBRED STRAINS

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P149 HYPOTHYROIDISM-INDUCED DEAFNESS IS ASSOCIATED WITH POOR INNERVATION, REDUCED POTASSIUM CHANNEL GENE EXPRESSION, AND GENETIC MODIFIERS

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P150 NOVEL C-KIT MUTATION KASUMI (KA) CAUSING STEM-CELL DEFICIENCY AND MODIFYING TESTICULAR AND OVARIAN TERATOCARCINOGENESIS IN KA-CONGENIC MICE

Motoko Noguchi[1], Yukiko Fukui[1], Mami Tsume[1], Hatsumi Ikuma[1], Toshinobu Tokumoto[1], Shuji Takabayashi[2], Hideki Kato[2]
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P151 SYSTEMS GENETICS APPROACH TO GENE-ENVIRONMENT INTERACTIONS

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P152 MULTI-DIMENSIONAL BEHAVIORAL, ALCOHOL AND DRUG ADDICTION PHENOTYPE ANALYSIS IN BXD RI MICE

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P153 EXPLORATION OF COMPLEX EPISTATIC GENETIC CONTROL OF NASAL BONE SHAPE IN THE MOUSE USING INTERSPECIFIC RECOMBINANT CONGENIC STRAINS

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P154 INTERSPECIFIC RECOMBINANT CONGENIC STRAINS BETWEEN C57BL/6 AND MICE OF THE MUS SPRETUS SPECIES: A POWERFUL TOOL TO DISSECT GENETIC CONTROL OF COMPLEX TRAITS

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P155 PHENOTYPIC ANALYSIS OF A SET DOMAIN-TRUNCATED MUTATION OF MOUSE ASH1

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P156 REVERSIBLE CONTROL OF METASTASIS BY A PATHOGENIC mtDNA MUTATION

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P157 CANCER GENETIC STUDY FROM MOUSE TO HUMAN: CANCER RISK ASSOCIATED POLYMORPHISMS IN THE AURORA-A GENE

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P158 ANALYSIS OF CALCIUM OSCILLATION OF OOCYTES BY ARTIFITIAL MUTANTS OF SPERM-SPECIFIC PHOSPHOLIPASE C zeta IN THE MOUSE

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P159 PROTEOMIC ANALYSIS OF EARLY DEVELOPMENT IN MICE

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P160 CHROMOSOME SEGREGATION IN MOUSE MEIOSIS

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P161 WHIRLIN COMPLEXES WITH p55 AT THE STEREOCILIA TIP DURING HAIR CELL DEVELOPMENT

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P162 NEURAL CREST DEFICIT OCCURS IN DOWN SYNDROME MICE AND IS ASSOCIATED WITH SONIC HEDGEHOG MITOTIC RESPONSE DEFICIT

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P163 MITOCHONDRIAL BOTTLENECK DUE TO THE REDUCTION OF MTDNA CONTENT IN THE FEMALE GERMLINE DOES NOT OCCUR IN MICE

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P164 CHANGE OF PATHOGENIC MUTANT mtDNA WITH AGE IN MITOCHONDRIAL DISEASE MODEL MICE (MITO-MICE)

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P165 SCREENING OF METASTASIS RELATED NON-CODING RNA IN MOUSE CELL LINES

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P166 ABNORMAL ASSEMBLY OF KERATIN INTERMEDIATE FILAMENTS IN MOUSE MUTATIONS OF TYPE I INNER ROOT SHEATH KERATIN

Shigekazu Tanaka[1], Ikuo Miura[2], Atsushi Yoshiki[3], Yoriko Kato[1], Haruka Yokoyama[2], Akiko Shinogi[2], Hiroshi Masuya[3], Shigeharu Wakana[2], Masaru Tamura[1], Toshihiko Shiroishi[1,2]

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P167 WHOLE GENOME MAPPING OF HISTONE H3 LYS4 AND 27 TRIMETHYLATIONS REVEALS DISTINCT GENOMIC COMPARTMENTS IN HUMAN EMBRYONIC STEM CELLS

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P168 MOUSE EMBRYOS LACKING SFRP1 AND SFRP2 EXHIBIT ABNORMALITIES OF MALE SEXUAL DEVELOPMENT

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P169 X CHROMOSOME REACTIVATION INITIATES IN NASCENT PRIMORDIAL GERM CELLS IN MICE

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P170 DEVELOPMENTAL ABNORMALITIES OF SPERM IN PCD MUTANT MICE IS ACCOMPANIED BY INSUFFICIENT NUMBER OF SERTOLI CELLS IN THE TESTIS

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P171 IMMUNOHISTOCHEMICAL AND FUNCTIONAL ANALYSIS OF PROTEIN 4.1 IN THE INNER EAR HAIR CELL

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P172 ANALYSIS OF DIFFERENTIALLY METHYLATED REGIONS AMONG VARIOUS TISSUES AND DURING SKIN CARCINOGENESIS IN C57BL/6J MICE

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P173 FUNCTIONAL ANALYSIS OF microRNAs IN HUMAN LUNG CANCER CELL LINE

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P174 USE OF THE SMART-AMPLIFICATION PROCESS FOR RAPID DETECTION OF EGFR MUTATIONS IN LUNG CANCER

A. Lezhava, K. Hoshi, H. Takakura, Y. Mitani, K. Tatsumi, N. Momiyama, Y. Ichikawa, S. Togo, T. Miyagi, Y. Kawai, T. Kikuchi, P. Cidziel, N. Ogawa, T. Arakawa, H. Shimada, Y. Hayashizaki
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P175 A NODAL-INDEPENDENT LEFT-RIGHT ASYMMETRIC GENE MAY PROVIDE A DIRECT READ OUT OF NODAL FLOW

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P176 MAPPING OF ALLELIC IMBALLANCES IN MURINE OSTEOSARCOMA USING WHOLE GENOME MD SNP ARRAYS REVEALES A NEW POTENTIAL TUMOR-SUPPRESSOR-LOCUS ON MMU 13

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P177 HUMAN FCR-LIKE B CELL-SPECIFIC RECEPTORS: LIGAND SEARCHING

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P178 A MICROARRAY BASED APPROACH FOR THE IDENTIFICATION OF GENES INVOLVED IN RESISTANCE/SUSCPTIBILITY TO H. PARASUIS INFECTION

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P179 MICROBIAL DIVERSITY IN INTESTINAL TRACTS OF TWO SPECIES OF RODENTS IN MONTANE AREAS IN TAIWAN

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P180 ESTABLISHMENT OF AN EOSINOPHIL-LESS MOUSE LINE BY TRECK METHOD

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P181 CONDITIONAL GENE TARGETING OF CYP51 (LANOSTEROL 14a-DEMETHYLASE)

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S1-5/P182 QUANTITATIVE TRAITS FOR THE TAIL SUSPENSION TEST: AUTOMATION, OPTIMISATION AND BXD RI MAPPING

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S2-4/P183 MAPPING AND CHARACTERIZING ENU-INDUCED MUTANT MOUSE MODELS OF THROMBOCYTOPENIA

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P184 HYPOTHYROIDISM-INDUCED DEAFNESS IS ASSOCIATED WITH POOR INNERVATION, REDUCED POTASSIUM CHANNEL GENE EXPRESSION, AND GENETIC MODIFIERS

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S1-4/P185 PHENOTYPIC EFFECTS OF THE "MINI-MUSCLE" ALLELE IN A LARGE HR x C57BL/6J MOUSE BACKCROSS

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S1-1/P186 UNFOLDING POPULATION STRUCTURE AND ANALYSING GENETIC VARIABILTY OF ZALAWADI, GOHILWADI AND SURTI GOAT BREEDS OF GUJARAT(INDIA) USING MICROSATELLITES

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S2-6/P187 PSTPIP2 IS MUTATED IN THE FIREWALKER MOUSE TO CAUSE AN AUTOIMMUNE DISEASE

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P188 GENETIC DISSECTION OF MOUSE ANXIETY-RELATED BEHAVIOR

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P189 GENETIC POLYMORPHISM STUDY OF IGF-I GENE IN DAIRY BUFFALOES OF GUJARAT (INDIA).

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S2-3/P190 AN N-ETHYL-N-NITROSOUREA MUTAGENESIS SCREEN IN MOUSE IDENTIFIES A CANDIDATE REGION FOR CARDIOMYOPATHY IN THE PROXIMAL END OF CHROMOSOME 1

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S2-1/P191 GEMIN2 PLAYS AN IMPORTANT ROLE IN STABILIZING THE SURVIVAL OF MOTOR NEURON COMPLEX

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S2-5/P192 HAIR-LOSS MUTATION (DEP) CAUSED BY A MUTATION IN PALMITOYL TRANSFERASE ZDHHC21

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S2-2/P193 TRANSCRIPTION REGULATORY CASCADES IN RETINOIC ACID-INDUCED GROWTH ARREST OF HEPG2 CELLS.

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S1-6/P194 IDENTIFICATION OF CONSERVED DNA REGIONS AND A SET OF TRANSCRIPTION FACTORS INVOLVED IN COMBINATORIAL REGULATION OF SEVERAL HUMAN LIVER-ENRICHED TRANSCRIPTION FACTOR GENES

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S1-2/P195 GENOME-WIDE ANALYSIS ON ABNORMAL H3K9 ACETYLATION IN ADULT CLONED MICE

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