PRESS RELEASE

August 23, 2009 (Sunday), 0900 hrs, Singapore

4th Asian Epigenomics Conference attracts an overwhelming international scientific delegation of over 300 – to be held in Singapore in August 2009

23 August 2009 - The Genome Institute of Singapore (GIS), a research institute under the Agency for Science, Technology and Research (A*STAR), will host the fourth Asian epigenomics conference on 24th and 25th August 2009. The two-day epigenomics conference, which is the first to be held in Singapore, will take place at Biopolis, the nation’s life sciences hub.

The conference, Epigenetics in Development and Diseases Conference: 4th Asian Epigenomics Meeting, will see the coming together of 28 renowned speakers from Asia, Europe and the US, with an expected 350-strong delegation, out of which about 40 percent are from overseas. It will feature scientific sessions covering epigenomics, higher-order genome organization, epigenetics and human disease, and challenges of epigenetic drug discovery.

Epigenetics is a topical and important research area that studies the changes in biological properties associated with the DNA template without alteration of DNA sequences. In addition to the well-studied phenomenon of DNA methylation, histone modifications are involved in the study of epigenetics. These modifications of the chromatin templates have profound effects on gene regulation and other biological processes. Epigenetic mechanisms are known to play critical roles in a wide variety of cellular processes. Deregulation of epigenetic controls can lead to human diseases or developmental defects.
Epigenomics is an emerging frontier of research that addresses the global analyses of epigenetic landscapes at the whole genome level. In the near future, we will witness the leap in knowledge generation in this area, and this research will have an impact on many fields such as cancer and development. In fact, epigenomics has been identified as one of the roadmap initiatives by the National Institutes of Health (USA). Globally, much interest has been shown in the analysis of epigenomes of different model organisms, including that of the human.

Dr Ng Huck Hui, Senior Group Leader at the GIS and one of the founding members of the Asian Epigenome Alliance said, “We expect a very successful meeting and sharing of the minds at the conference. Registrations have exceeded our expectations by 1.5 times, and this is in no small part due to the impressive line-up of international expert speakers.” Dr Ng heads the organising committee for this year’s conference.

“With the increasing investment in biomedical research by the Asian government,” added Dr Ng, “there is no doubt that the research carried out in Asian countries will have increasing impacts in the global scientific arena.

“We are also very pleased to partner with the Lilly Singapore Centre for Drug Discovery during this conference to co-organise a session on Epigenetics in Drug Discovery. During this session, the speakers will discuss the methods to translate research in epigenetics into drug discovery for the treatment of human diseases. Given the importance of epigenetic regulation in human health and diseases, it is not surprising at all that epigenetic drugs are well on the radar screen of pharmaceutical companies. It is also our honour to have Prof Peter Jones, a very distinguished scientist, to speak at this session”.

The previous conferences were held in Seoul (2006), Osaka (2007) and Shanghai (2008).
Notes to the Editor:

**Founding members of the Asian Epigenome Alliance:**

1. Dr Young-Joon Kim, Underwood Distinguished Professor and Director of Yonsei Genome Institute, Yonsei University, Korea
2. Dr Toshikazu Ushijima, Chief of Carcinogenesis Division, National Cancer Centre Research Institute, Japan
3. Dr Jingde Zhu, Shanghai Cancer Institute, China
4. Dr Huck Hui Ng, Senior Group Leader, Genome Institute of Singapore, Singapore

**Speakers' Profiles**

**Hiroyuki ABURATANI**  
*University of Tokyo, Japan*  
Hiroyuki Aburatani, MD, PhD, is currently a Professor of Genome Science at the Research Center for Advanced Science and Technology, the University of Tokyo since 2003. Professor Aburatani studied medicine at Tokyo University and graduated in 1980. After he completed a clinical internship in Tokyo University medical school hospital and took a specialty training for hepatology at Tokyo metropolitan Komagome hospital, he studied plasma lipoprotein gene polymorphisms in relation to cardiovascular diseases at Tokyo University medical school and received his PhD degree in Internal medicine in 1988. He studied cancer genetics at Center for Cancer Research, Massachusetts Institute of Technology from 1988 to 1994. He has been a leading scientist in the study of cancer genomics and the genomic variation in human diseases. He is actively involved in establishing a systemic approach to elucidate mechanisms of human diseases as a member of Laboratory of Systems Biology and Medicine at Research Center for Advanced Science and Technology (RCAST), the University of Tokyo. His research interest is “Genomic medicine”.

**Edwin CHEUNG**  
*Genome Institute of Singapore, Singapore*  
Edwin Cheung, PhD, Senior Research Scientist, Genome Institute of Singapore. Dr. Cheung’s work is focused on elucidating the molecular basis by which steroid hormones control the development and progression of human cancers. Specifically, he is interested in applying modern biological approaches to define the rules governing signal-regulated gene expression by steroid hormones (estrogen and androgen), their cognate receptors and associated cofactors. Dr. Cheung received his bachelor’s degree from UC Berkeley. He then obtained his Ph.D. degree from University of Manchester. After his Ph.D., Dr. Cheung received a Susan G. Komen Breast Cancer Foundation postdoctoral fellowship and an NIH postdoctoral fellowship to perform his postdoctoral research at Cornell University. Following his postdoctoral work, he moved to Singapore and started his own group at the Genome Institute of Singapore.

**Job DEKKER**  
*University of Massachusetts Medical School, USA*  
Job Dekker is an Associate Professor in the Program of Gene Function and Expression and the Department of Biochemistry and Molecular Pharmacology at the University of Massachusetts Medical School. His group studies the spatial organization of genomes in relation to gene regulation. Dr. Dekker developed the Chromosome Conformation Capture technology (3C) that is used to detect long-range interactions between genomic elements. More recently his laboratory developed high-throughput methods based on 3C that employ deep-sequencing to map the spatial organization of entire chromosomes at unprecedented resolution.
Sam EL-OSTA
Baker IDI Institute, Australia

Associate Professor Sam El-Osta is a Senior Research Fellow, Head of the Epigenetics in Human Health and Disease Laboratory, and, Preclinical Head of the Diabetes Division at the Baker IDI Heart and Diabetes Institute. He is Head of the Epigenomics Profiling Facility and is an Associate Professor of Medicine, Monash University. He also has dual appointments at the Department of Medicine at Monash University and at the Department of Pathology at the University of Melbourne. His ongoing research is currently funded with a number of international and national grants. Dr El-Osta has recently identified a pathway for sustained activation of genes and proteins implicated in diabetic vascular disease involving effects on epigenetic change. Despite major advances in treatment methods, diabetes is still the leading cause of new blindness in people 20 to 74 years old, the leading cause of end-stage renal failure, and the leading cause of non-traumatic limb amputation. His research specifically demonstrates that transient hyperglycemia causes profound epigenetic changes associated with the persistent activation of genes implicated in diabetic vascular disease. These observations have profound implications for diabetes treatment. Therapies, which minimize transient hyperglycaemic excursions, should significantly reduce the enormous burden of diabetic complications. Characterizing the regulatory complex responsible for persistent epigenetic change and improving pharmacological inhibitors to restrain continual increases induced by hyperglycaemia will provide new targets for generating end-organ protective agents for clinical problems associated with diabetic vascular complications. Dr El-Osta's increasing international profile and research independence, is exemplified by the AMGEN Society “Australian Medical Researcher of the Year” 2006 award and more recently awarded the inaugural “Juvenile Diabetes Research Foundation/Macquarie Group Foundation Diabetes Research Innovation Award” 2008 for innovative basic research by exceptional researchers in Australia contributing to the search for the prevention and/or a cure for type 1 diabetes and its complications.

Ernesto GUCCIONE
Institute of Molecular and Cellular Biology, Singapore

I obtained my Master's degree in Medical Biotechnology in 2000 from Bologna University and my PhD in 2004 from the International Center for Genetic Engineering and Biotechnology (ICGEB), Trieste, Italy. I then did my postdoctoral work at the European Institute of Oncology (Milan, Italy) where I studied the role of chromatin in defining c-Myc target site recognition. I also identified PRMT6, a member of the Protein Arginine Methyltransferase family, as an important enzyme in controlling transcriptional repression. During my postdoctoral training, I spent four months as an EMBO fellow in the laboratory of J.LaBaer at Harvard Institute of Proteomics. I joined IMCB in August 2008 as a Principal Investigator.

Darryl IRWIN
Sequenom Asia Pacific

Dr Darryl Irwin was awarded his undergraduate degree from the Queensland University of Technology and PhD from the University of Queensland. Darryl's PhD focused on developing techniques for non-invasive prenatal diagnosis by multiplexed genotyping of single fetal cells from the cervix. Darryl has previously worked at Agen Biomedical (3 years) developing an Elisa based diagnostic for D-Dimer, a blood clot breakdown product. Also Darryl spent 2 years in a clinical genetics laboratory at the Mater Mothers Hospital as well as 3 years as the Genotyping Business Unit Manager at the Australian Genome Research Facility where he managed the Sequenom, Affymetrix and microsatellite genotyping teams. Darryl is now Manager – Applications and Technology for Sequenom Asia Pacific. Darryl’s specific interests include structural variations, clinical diagnostics and agricultural applications.
Ricky JOHNSTONE  
Peter MacCallum Cancer Center  
Associate Professor Ricky Johnstone is a cancer researcher who has utilized genetic mouse models of hemopoietic malignancies and solid tumors to decipher the molecular events underpinning cancer cell death by drugs such as histone deacetylase inhibitors (HDACi). A true understanding of how HDACi kill tumor cells has provided a molecular rationale for the development of unique combination anti-cancer therapies using HDACi and other novel targeted therapeutics. Dr Johnstone completed his BSc.(Hons.) degree from the University of Melbourne in 1988 with a double major in Pathology and Immunology. In 1990 he accepted an Australian Postgraduate Award and started work on his PhD at the Austin Research Institute that was completed in 1993. In 1994, he was awarded a C.J. Martin Fellowship from the National Health and Medical Research Council of Australia (NHMRC) to perform postdoctoral studies in the Department of Pathology at Harvard University Medical School in Boston, USA in the laboratory run by Prof. Yang Shi, studying the regulation of transcription by the WT1 tumor suppressor protein. In 1999, he was awarded an R.D. Wright Research Fellowship from the NHMRC and in 2000, won a Wellcome Trust Senior International Research Fellowship. He moved to the Peter MacCallum Cancer Institute in February 2000 to establish the Gene Regulation Laboratory within the Cancer Immunology Program and was appointed as Pfizer Australia Senior Research Fellow and an NHMRC Senior Research Fellow (Honorary) in 2005. He has won prestigious scientific prizes including the 2003 AMGEN Prize for Excellence in Translational Medical Research and the 2005 Australian Academy of Science Gottschalk Medal that recognises outstanding research in the medical sciences. He has published over 100 peer-reviewed manuscripts. In 2008 Dr Johnstone and Dr Grant McArthur established the Cancer Therapeutics Program within the Peter MacCallum Cancer Centre to bring together a critical mass of researchers with the aim to translate fundamental research findings into clinical outcomes that will benefit cancer patients. In 2008 Dr Johnstone was appointed as an Assistant Director of Research at the Peter Mac and will play a key role in defining the strategic direction of the research division over the coming years.

Peter JONES  
University of Southern California, Los Angeles  
Dr. Peter A. Jones, Director of the University of Southern California/Norris Comprehensive Cancer Center and Distinguished Professor of Urology and Biochemistry & Molecular Biology, at the Keck School of Medicine University of Southern California, is known for his studies on the molecular biology cancer and of basic mechanisms of DNA methylation and its role in cancer and differentiation. His laboratory discovered the effects of 5-azacytidine on DNA methylation and linked this process to the activation of silenced genes.

Dr. Jones was born in South Africa, raised and attended school in Rhodesia (now Zimbabwe), and received his Doctor of Philosophy Degree from the University of London in 1973. He joined the USC in 1977, attaining the rank of Professor in 1985, and became Director of the Cancer Center in 1993. In 1983 he won the USC Associates Award for Creativity in Research and Scholarship. He is the author of more than 250 journal publications and book chapters, and serves on several national and international committees, panels, and editorial boards. He is the past President of the American Association for Cancer Research. He has received a variety of honors, including the Outstanding Investigator Grant from the National Cancer Institute and the Kirk A. Landon Award for Basic Cancer Research for the AACR.
Jae-Bum KIM  
Seoul National University, Korea  
Dr. Jae Kim is a professor of School of Biological Sciences, Seoul National University. He received his BS and MS from Seoul National University and Ph. D from Harvard University in 1996. After his postdoctoral fellowship at Harvard Medical School and MIT, he joined the faculty of School of Biological Sciences, Seoul National University in 2000. Dr. Kim’s group has been working on the regulation of gene expression and signal transduction for the understanding of “lipid and glucose metabolism”, which is crucial to resolve the prevailing health issues such as obesity and diabetes. In addition, his group has been investigating to elucidate the underlying mechanism for certain cell type differentiation such as adipocytes and osteoblasts from mesenchymal stem cells.

Young-Joon KIM  
Yonsei University, Korea  
Underwood Distinguished Professor and Director of the Yonsei Genome Institute. Dr. Kim’s work is focused on the regulatory mechanism of mouse innate immune system as well as epigenetic regulation of disease-associated gene expressions.

Dr. Kim received his BS degree from Seoul National University, and his Ph.D. degree from Stanford University. Following his postdoctoral research at the Roger Kornberg’s laboratory at the Stanford University, he joined the faculty of Samsung Biomedical Research Institute in 1994, and moved to the Yonsei University in 2000 where he rose to the rank of Full Professor.

Dr. Kim established the Yonsei Genome Institute in 2007. Dr. Kim received numerous awards and honors, including the The Life Science Research Award from Korean Molecular and Cell Biology Society (2006). He has served on the AACR international human epigenome taskforce team (2004-2005), Review committee (2003-2008) and Council of Scientists (2008-2012) of Human Frontier Science Foundation. He also organized several international congresses as the Chair of the Academic Program Committee in the Federation of Asian and Oceanian Biochemistry and Molecular Biology Conference (2007), and International Cell Biology Congress (2008).

Yutaka KONDO  
Aichi Cancer Center Research Institute, Japan  
Yutaka Kondo is a Section Head in Division of Molecular Oncology, Aichi Cancer Center Research Institute. His work is focused on the regulation of gene expression by histone modifications and DNA methylation in human cancers, and the clinical implications of these aberrant changes. Dr. Kondo obtained his M.D. and Ph.D. degree from Nagoya City University Medical School in Japan. After his postdoctoral research in the Department of Leukemia at the University of Texas, MD Anderson Cancer center, he joined the faculty of MD Anderson Cancer center in 2004. Dr. Kondo moved to Aichi Cancer Center Research Institute in Japan in 2005. His works accomplished to date highlight the importance of histone modifications in cancers, their relationship with aberrant DNA methylation and gene silencing, and the potential in gene discovery. Now his interest is in epigenetic mechanisms in tumor-propagating cells.

Edison LIU  
Genome Institute of Singapore, Singapore  
Dr. Edison Liu (B.S. Chemistry and Psychology, Stanford University 1973 and M.D. in 1978). He received his residency training in internal medicine at Washington University, St. Louis, and clinical cancer fellowships at Stanford University (Oncology), and at the University of California at San Francisco (Hematology). He then pursued post-doctoral studies as a Damon-Runyan Cancer Research Fellow at the University of California. In 1987, he joined the faculty of Medicine at the University of North Carolina at Chapel Hill where he was director of UNC’s Specialized Program of Research Excellence (SPORE) in Breast Cancer. In 1996, he joined the NCI as the Director of the Division of Clinical Sciences. In 2001, Dr. Liu assumed the position of...
Executive Director, Genome Institute of Singapore. His current scientific research investigates the dynamics of gene regulation on a genome scale that can explain biological states in cancer. Dr. Liu’s awards include the Leukemia Society Scholar (1991-1996), the Brinker International Award for basic science research in Breast Cancer (1996), the Rosenthal Award from the American Association for Cancer Research (2000), the President’s Public Service Medal for his work in helping Singapore resolve the SARS crisis, and a Doctor of Medicine Sciences honoris causa (2007). In 2007, Dr. Liu was elected the President of the Human Genome Organization.

Alex MEISSNER
Broad Institute, USA
Alex Meissner recently joined Harvard University as assistant professor in the department of stem cell and regenerative biology. He is also a member of the Harvard Stem Cell Institute and an associate member of the Broad Institute.

During his Ph.D. in Rudolf Jaenisch’s laboratory, Alex trained in developmental biology, nuclear transfer, and stem cell technology using the mouse as a model system. In addition, he worked extensively on developmental- and disease-related aspects of DNA methylation. Alex was author and co-author of several papers that demonstrated the conversion of fibroblasts into pluripotent cells through overexpression of defined transcription factors. This field of induced pluripotent stem cells has received wide attention and raises the prospects of generating patient-specific stem cells without the need for embryos.

Along with his colleagues at the Broad Institute, Alex is developing and applying high-throughput bisulfite sequencing technologies for DNA methylation analysis. This should ultimately lead to generating reference epigenomes for many cell types and a better understanding of normal and diseased cellular states.

Joseph NADEAU
Case Western Reserve University, USA
He was a postdoctoral fellow with Jan Klein in the Immunogenetics Department, Max Planck Institute for Biology, Tübingen, Germany, and then with Eva Eicher at the Jackson Laboratory. He served as Associate Staff Scientist, Staff Scientist and Senior Staff Scientist at the Jackson Laboratory, and then Professor, Department of Human Genetics, McGill University, and Medical Scientist, Department of Medicine, Montreal General Hospital. He is currently James H. Jewel Professor and Chair of Genetics Department at Case Western Reserve University School of Medicine., with joint appointments in the Department of Electrical Engineering and Computer Science, the Case Comprehensive Cancer Center, and the Center for Proteomics and Bioinformatics where he also serves as Director of the Division of Bioinformatics. He was a founding member of the International Mammalian Genome Society and co-founding editor of Mammalian Genome. He was founder and director of the Mouse Genome Informatics Project, founder of the Mouse Gene Expression Database Project, and co-founding editor of the journal Systems Biology and Medicine. He has served on review panels and advisory groups at the National Institutes of Health, the National Science Foundation and the Human Genome Database. He has consulted for GlaxoSmithKline, Pharmacia, Celera Genomics, Exelixis, NineSigma and CellTech Chiroscience, and is on the Scientific Advisory Board of Genizon. His research interests include development, cancer and metabolic diseases, mouse models of complex traits, genetics, genomics, bioinformatics and systems biology.

Antoine PETERS
Friedrich Miescher Institute (FMI) for Biomedical Research, Switzerland
Dr. Antoine Peters is a Group Leader at the Friedrich Miescher Institute (FMI) for Biomedical Research in Basel, Switzerland. He received his Ph.D. in 1997 from the Wageningen University in the Netherlands. From 1997 to 2004, he performed his postdoctoral research in the laboratories of Prof. Robert E. Braun at the Washington University in Seattle, USA, and of Prof.
Thomas Jenuwein at the Research Institute of Molecular Pathology (IMP) in Vienna, Austria. Antoine Peters is a recipient of the EMBO Young Investigator Award (2008).

Bing REN
University of California, USA
Dr. Ren is currently head of Laboratory of Gene Regulation at the Ludwig Institute for Cancer Research (LICR) and Professor of Cellular and Molecular Medicine at the University of California, San Diego School of Medicine. He obtained his Ph.D. from Harvard University in 1998, where he studied mechanisms of transcriptional repression under the guidance of Dr. Tom Maniatis. From 1998 to 2001, he continued to research mechanisms of gene regulation and genomics as a postdoctoral fellow in Dr. Richard Young’s laboratory at Whitehead Institute. During this period he invented the ChIP-chip analysis method. When Dr. Ren began his faculty appointment, he combined the ChIP-chip method with genome tiling arrays to investigate the mechanisms of gene regulation in human cells. His group is among the first to demonstrate the use of high-resolution genome tiling arrays for mapping cis-regulatory elements. His recent works include generation of genome-wide maps of promoters, enhancers and insulators in human cells, and the discovery of distinct chromatin modification signatures for promoters and enhancers. He currently leads the San Diego Epigenome Center.

Among the awards that Dr. Ren received are the Young Investigator of Chinese Biological Investigators Society (2007), Sidney Kimmel Scholar award (2002) and Helen Hay Whitney Foundation fellowship (1999).

Paul ROBSON
Genome Institute of Singapore, Singapore
My long-term goal is to gain a full molecular understanding of the developmental and evolutionary origins of the mammalian blastocyst. In the mouse, the implanting blastocyst consists of three cell types that develop over the 4.5 days following fertilization. This involves the reprogramming of the highly differentiated oocyte and sperm genomes into the pluripotent cells of the epiblast (EP; the source of all cell types of the embryo proper and of the embryonic stem (ES) cell), the trophectoderm (TE; the cells contributing to the embryonic components of the placenta), and the primitive endoderm (PE; the extraembryonic endoderm precursors). Our approach is to focus both on identifying the precise temporal and spatial patterns of gene expression through preimplantation development and to identify the transcription factor-DNA interactions occurring. The former is done through global and focused gene expression arrays down to the single cell level with wild-type and genetically manipulated mouse embryos. The TFDNA interactions, performed both globally and locally with respect to the genome, are primarily carried out on cell lines derived from the mammalian blastocyst. From this data we are building a comprehensive understanding of the genetic regulatory network that underlies blastocyst biology. A second aspect of our research is to use comparative genomics strategies to identify the molecular changes that have lead to this uniquely mammalian stage of development. Our primary models of study are mouse preimplantation embryos (and cell lines derived from them) and human ES cells, which provide access to the earliest stages of human development. We hope that knowledge gained from a clear understanding of the molecular development and evolutionary history of the mammalian blastocyst will be directly applicable to potential and real clinical applications in the fields of stem cell therapy and assisted reproduction.

Jonathon SEDGWICK
Jonathon Sedgwick, Ph.D. is the Managing Director and Chief Scientific Officer of the Lilly-Singapore Centre for Drug Discovery (LSCDD). LSCDD is delivering medicines into Eli Lilly’s pipeline in the areas of cancer and metabolic disease, as well as Integrated Informatics tools, and cancer and diabetes Biomarker solutions, to enable Lilly’s goals for personalized medicines. A focus area for the site is to develop capabilities in the area of epigenetics, including drug and biomarker development. Dr. Sedgwick’s research has focused on the role of inflammation
pathways in diseases including autoimmunity as well as cancer, through an understanding of cytokine and cell-survival signaling pathways as well macrophage/microglial roles in these diseases. From October 2004 to May 2008 Dr Sedgwick was based in Indianapolis at Eli Lilly and Company’s Corporate Headquarters as Chief Scientific Officer, Cancer Inflammation Research, overseeing small molecule and biologic drug discovery from target identification and validation into clinical testing. From 1998 to 2004, Dr Sedgwick was a member of the DNAX Research Institute in Palo Alto, California – a biotechnology research centre for Schering Plough Corporation. There he and collaborators discovered a number of key immune regulatory pathways, including the role of the interleukin-23 cytokine in autoimmune inflammation, as well as defining and naming a new T cell subset, Th17. These findings have stimulated new research directions and drug development activities globally. Prior to this, Dr Sedgwick held a number of academic roles over a period of 15 years in the UK, Germany and Australia with significant contributions to the literature on the role of TNF/lymphotoxin as well as T lymphocyte and macrophage biology, to inflammatory diseases and lymphoid development. Dr. Sedgwick has authored or co-authored 120 peer-reviewed, review articles and book chapters.

Rho-Hyun SEONG
Seoul National University, Korea
Dr. Seong received his BS and MS degrees from Seoul National University, and his Ph.D. degree from Stanford University. Following his postdoctoral research at Stanford University Medical Center, he joined the faculty of Seoul National University in 1993, where he is now a full professor. He founded and directed the Research Center for Functional Cellulomics at Seoul National University. Dr. Seong’s work is mainly focused on the differentiation of lymphocytes in mouse. Dr. Seong studies the SWI/SNF chromatin remodeling complex in the development of mouse embryo and immune system. His lab is also working on T-cell differentiation, especially the CD4/CD8 lineage differentiation in the thymus.

Supriya SHIVAKUMAR
Sigma-Aldrich Corporation, USA
Dr. Supriya Shivakumar currently holds the position of Manager for the Functional Genomics Initiative, leading commercialization and new product development efforts for the RNAi and Targeted Genome Editing (TGE) groups.

She completed her PhD at the University of California, San Francisco conducting research in wnt signaling in mouse and C. elegans in the laboratories of Nobel Laureate Dr. Harold Varmus and Dr. Cynthia Kenyon. Her postdoctoral work, studying human papilloma viral E7 signaling in cervical cancer, took her closer to clinical applications of cancer research at the Mount Zion Center for Translational Medicine in Northern California. In business, she has been a key member of startups BioProtocol, a life science protocol portal and BioStreet, a spin-off of Burrill and Company in developing pharmaceutical mergers and alliances.

Erwei SONG
Sun-Yat-Sen University, China
Dr. Song earned his MD and Ph.D at Sun-Yat-Sen University of Medical Science in 2000. Thereafter, Dr. Song received his postdoctoral training at Essen University Hospital in Germany from 1999-2001, and at Harvard Medical School from 2002-2004. He became instructor of Harvard Medical School in Jan 2004, and went back to Sun-Yat-Sen University in Sep 2004 to set up his own lab. Dr. Song is now professor of breast surgery, National Changjiang Scholar, and vise president of the No.2 Affiliated Hospital of Sun-Yat-Sen University.

For the past few years, Dr. Song focused his research work on the studies of RNA interference as a therapeutic approach. His publication “RNA interference targeting Fas protects mice from fulminant hepatitis” in “Nature Medicine” was the first report that siRNAs could be used therapeutically in whole animal disease model, and the results were chosen as representative data in the “Top 10 Scientific Breakthrough of 2003” by Science. To further harness RNAi to
treat diseases, he explores different strategies to deliver siRNA into specific cell populations in vivo, and validates suitable disease targets for RNAi therapy. He is first author of the manuscript published in the June issue of “Nature Biotechnology”, entitled “Antibody-mediated in vivo delivery of short interfering RNAs via cell surface receptors”, which demonstrated the value of single-chain antibody to deliver siRNA into specific cell types. The paper was selected as cover story by the journal. Recently at Sun-Yat-Sen University, he led a research team studying the contribution of microRNAs in the stemness of breast cancer initiating cells, and published his findings in “Cell” as corresponding author.

Toshikazu USHIJIMA
National Cancer Centre Research Institute, Japan
Dr. Toshikazu Ushijima, Chief of Carcinogenesis Division, National Cancer Center Research Institute (NCCRI), Tokyo, graduated from University of Tokyo School of Medicine in 1986. He started his research career at NCCRI in 1989, and took his current position in 1999. He developed one of the first genome-wide screening techniques for changes in DNA methylation, MS-RDA, in 1997. MS-RDA was used to identify a novel tumor-suppressor gene in gastric cancers and to isolate many genes aberrantly methylated in breast cancers, pancreatic cancers, and melanomas. In neuroblastomas, the CpG island methylator phenotype was shown to be a good prognostic marker that is more powerful than MYCN amplification. His most well-known work is demonstration that H. pylori infection induces aberrant DNA methylation in gastric mucosae, and that the accumulation produces an epigenetic field for cancerization. Now, his research interest is moving forward to clarification of target genes and molecular mechanisms for methylation induction.

Bas VAN STEENSEL
Netherlands Cancer Institute, The Netherlands
Bas van Steensel is principal investigator at the Netherlands Cancer Institute in Amsterdam, the Netherlands. He received his Ph.D. in 1995 from the University of Amsterdam, where he studied the role of nuclear organization in gene regulation by steroid receptors. He worked as a postdoctoral fellow in the laboratory of Dr. Titia de Lange at the Rockefeller University (New York, NY, USA), where he elucidated some of the functions of the human telomere-binding proteins TRF1 and TRF2. In 1998 he joined the laboratory of Dr. Steven Henikoff at the Fred Hutchinson Cancer Research Center (Seattle, WA, USA), where he developed a new technique for whole-genome mapping of in vivo protein-DNA interactions. In 2000 he received a fellowship from the Netherlands Academy of Sciences and started a research group at the University of Amsterdam. In 2002 he joined the Netherlands Cancer Institute, where his laboratory continues to develop and apply new genomics methodologies to analyze the structure and regulatory functions of chromatin. He is recipient of a European Young Investigator Award (2005) and he is EMBO Member (since 2008).

Marian WALHOUT
University of Massachusetts Medical School, USA
Marian Walhout obtained her B.S. (1992) and Ph.D. (1997) degrees from Utrecht University, The Netherlands. She did her post-doctoral work at Harvard Medical School in the lab of Dr. Marc Vidal. She is currently an Associate Professor at the University of Massachusetts Medical School, in the Program of Gene Function and Expression. Her lab pioneered the use of gene-centered (gene-to-protein) methods for the identification of transcription factor-target gene interactions and gene regulatory networks.

Chia-Lin WEI
Genome Institute of Singapore, Singapore
Dr. Wei’s research interest is to characterize the impacts of epigenetic modifications and chromatin structures on gene expression program in development by applying ultrahigh throughput next generation sequencing platform. She pioneered in using the pair end ditag (PET) sequencing approach to interrogate the stem cell genomes for their functional units,
transcription networks and architectures. The PET technology has been adapted to decipher the epigenome and nuclear organization.

**Guo-Liang Xu**
**Chinese Academy of Sciences, China**
Dr. Guo-Liang Xu (B.S. Biology, Zhejiang University 1985 and M.S. Institute of Genetics, CAS, 1988). He received his Ph.D training in 1993 at the Max-Planck-Institute for Molecular Genetics, Berlin, Germany and pursued post-doctoral studies at Columbia University, Department of Genetics and Development, USA (1995-2001). He then returned to China to become a Principal Investigator at the Institute of Biochemistry and Cell Biology, CAS, Shanghai. His current scientific research investigates genomic DNA methylation in mammalian development. His major focus is de novo DNA methyltransferases Dnmt3a, Dnmt3b and Dnmt3L and their interaction with chromatin. His recent research covers epigenetic regulation of blood glucose level, germ cell maturation and thymus development.

**Qiang Yu**
**Genome Institute of Singapore, Singapore**
Dr. Qiang Yu is a currently a group leader of Cancer Biology and Pharmacology program at Genome institute of Singapore. He obtained his Ph.D. in 1998 from Queen's University at Kingston in Canada and did his postdoctoral training at National Cancer Institute of USA. He joined GIS in 2002 as a Principal Investigator and his research interest include cancer therapeutics, cancer genomics and epigenome analysis and pharmacological modulation of chromatin in cancer.

**Jingde Zhu**
**Shanghai Cancer Institute, China**
The research in Jingde Zhu’s group is supported by both Central and local governments in China and the 6th Frame program from Europe. Dr. Zhu has published over fifty papers in the peer-review journals, including Cell, NAR, CCR, Oncogene, JBC, Cancer Gene Therapy, Cell Research, and etc. He is the inventor of one approved US patent and one filed US PCT. He is also the inventor of four approved and two filed patents in China. He has organized four international conferences and spoken in over forty conferences in life sciences in last three years.
About the Genome Institute of Singapore
www.gis.a-star.edu.sg

The Genome Institute of Singapore (GIS) is a member of the Agency for Science, Technology and Research (A*STAR). It is a national initiative with a global vision that seeks to use genomic sciences to improve public health and public prosperity. Established in 2001 as a centre for genomic discovery, the GIS will pursue the integration of technology, genetics and biology towards the goal of individualized medicine. The key research areas at the GIS include Systems Biology, Stem Cell & Developmental Biology, Cancer Biology & Pharmacology, Human Genetics, Infectious Diseases, Genomic Technologies, and Computational & Mathematical Biology. The genomics infrastructure at the GIS is utilized to train new scientific talent, to function as a bridge for academic and industrial research, and to explore scientific questions of high impact.

About the Agency for Science, Technology and Research (A*STAR)
www.a-star.edu.sg

The Agency for Science, Technology and Research (A*STAR) is the lead agency for fostering world-class scientific research and talent for a vibrant knowledge-based Singapore. A*STAR actively nurtures public sector research and development in Biomedical Sciences, and Physical Sciences and Engineering, and supports Singapore's key economic clusters by providing intellectual, human and industrial capital to our partners in industry and the healthcare sector. It oversees 23 research institutes, consortia and centres located in Biopolis and Fusionopolis, and the area in their vicinity, and supports extramural research in the universities, hospitals, research centres, and with other local and international partners.

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