XXII[ND] World Congress of Psychiatric Genetics

October 12-16, 2014

Copenhagen, Denmark

Pathways to Therapy and Prevention

To all Participants of the World Congress of Psychiatric Genetics (WCPG XXII):

We welcome you to the beautiful Scandinavian city of Copenhagen, Denmark. The WCPG has chosen the Scandinavian host at a time when psychiatric genetics is poised to understand the pathway from genotype to phenotype and the environmental agents that trigger illness in individuals at risk for mental disorders. The multi-disciplinary field of psychiatric genetics is on the brink of a journey to translate the catalogue of genomic findings for a broad range of disorders to define the disease biology. The Scandinavian venue reminds us of the plethora of information available in the rich resources of homogeneous samples, biobanks and registers that through integrative approaches will prove to be a valuable piece in translating the role of functional risk variants in disease development and progression. Now more than ever, it has become obvious that via collaboration between neuroscience, neurobiology and genetics we will advance towards the identification of promising novel treatment targets for mental disorders.

The mental health research field is now reaping the benefits of recent advances in genomic technology as we have witnessed a surge in the identification of genetic risk factors for mental disorders. These findings have empowered us to now re-evaluate diagnostic boundaries and criteria and seek new ways to integrate the underlying biology with clinical diagnosis. Advances into new areas of discovery and innovation, including the functional characterization of risk variants and the integration of genetics and environmental risk factors into neuroscience, stem cell biology, and even clinical practice have inspired our leading theme of the 2014 WCPG, "Pathways to Therapy and Prevention".

Efforts to revise the DSM and ICD have reignited debates about the boundaries among mental disorders and have fueled calls for an etiology-based classification that would incorporate insights from genetic research. Progress in the field of oncology genetics suggests that the role of integrative genomics in psychiatric biomedical research will have the potential to transform investigations of disease etiology, diagnosis and treatment. In accordance with the Congress theme, we will hear updates on genomics, epigenomics, functional genomics, GxE interactions, pathway-based analyses and novel omics insights into mental disorders. Integrative research requires the employment of novel biostatistic and bioinformatic approaches to facilitate the identification of shared genetic and environmental influences across major mental disorders. In addition to these topics, our program also addresses the specific scientific challenges downstream of gene discovery that, after careful consideration, will place us in a position to prioritize appropriate therapeutic and preventative strategies.

This year's Congress will address all of these issues and more, showcasing the best science from the international community. The meeting will offer a variety of formats and world-renowned speakers to create the most engaging forum for learning, scientific exchange and discussion. Highlights include:

- ***Education Program,*** this year with two concurrent "tracks" of presentations: a Basic Science Track, covering the latest in genomic methods and technologies; and a Clinical Track, including updates on the genetics of mental disorders and clinical applications.
- ***A Keynote Address*** will open the Congress and frame the challenges and new frontiers facing our field.
- ***An innovative Plenary Panel session*** featuring presentations and discussions with leading experts on some of the most exciting and controversial topics in psychiatric genetics. This session will emphasize opportunities for audience participation and debate.

We particularly thank our Program Committee for their tireless efforts in evaluating proposals for symposia,oral, and poster presentations.

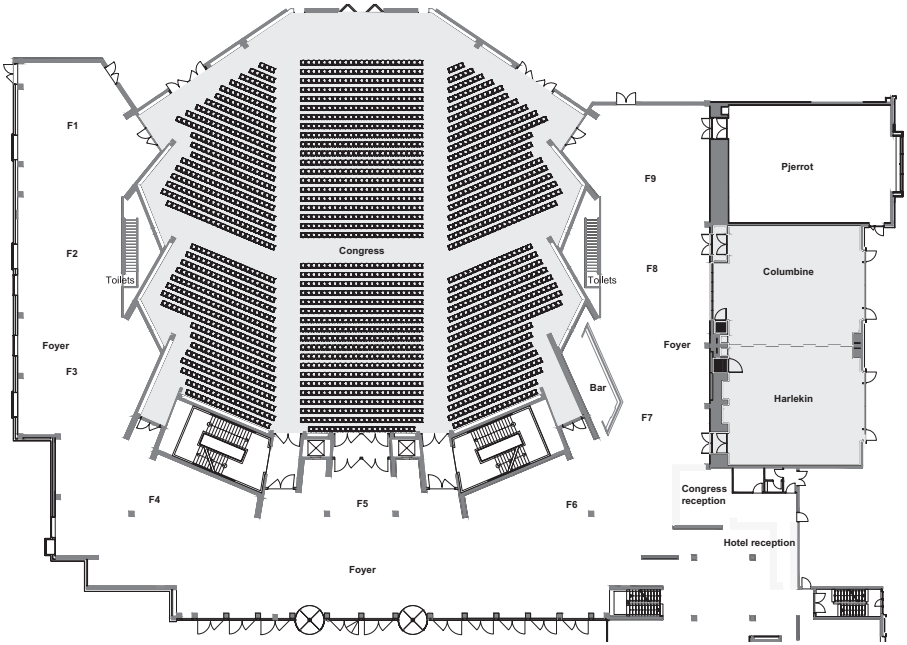
We hope that the great variety of presentations and formats will provide new insights, spark new collaborations, and advance the science of neuropsychiatric genetics. We welcome you to enjoy these four days of intense scientific sessions, as well as the beautiful Copenhagen venue!

Best Regards,
Ole Mors, Ph.D.
Thomas G. Schulze, M.D.
Thomas M. Werge, Ph.D.
2014 WCPG Chairpersons

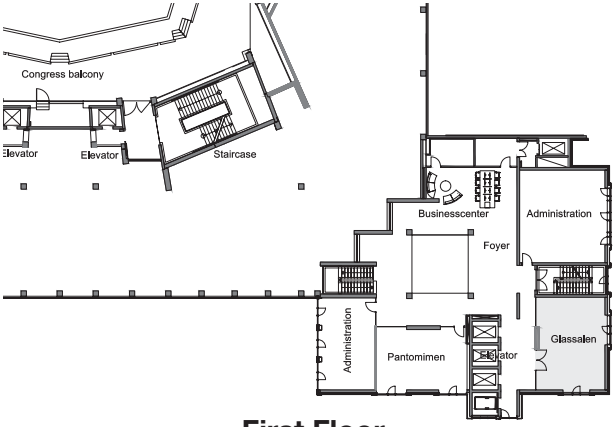
TABLE OF CONTENTS

FLOOR PLANS

Tivoli Congress Center



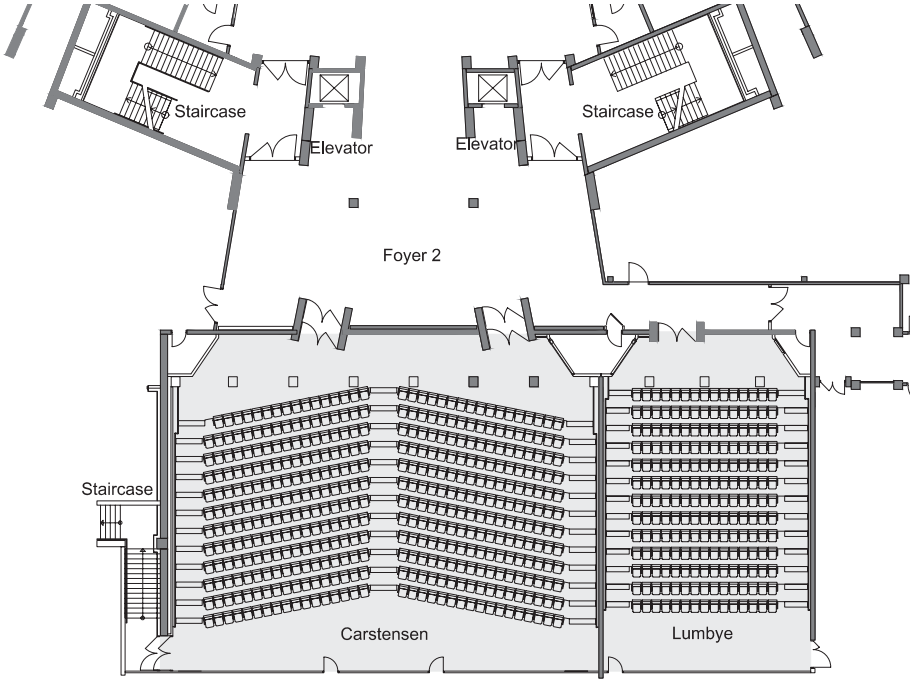
Ground Floor



First Floor

FLOOR PLANS

Tivoli Congress Center



Basement

NOTES

MEETING ANNOUNCEMENTS

REGISTRATION:

Registration for the World Congress is located in the Tivoli Congress Center Ground Foyer.

Date	Time
Saturday, October 11th	10:00 a.m. – 6:00 p.m.
Sunday, October 12th	7:30 a.m. – 6:00 p.m.
Monday, October 13th	7:30 a.m. – 6:30 p.m.
Tuesday, October 14th	7:30 a.m. – 7:30 p.m.
Wednesday, October 15th	7:30 a.m. – 7:30 p.m.
Thursday, October 16th	7:30 a.m. – 12:00 p.m.

Registration Types:
Participant: Scientific Attendee
Student: Full-time graduate student, medical student or in the first two years of a post-doctoral fellowship program at a university in a relevant field.

Registration to the 2014 World Congress includes membership to the International Society of Psychiatric Genetics from the date of the conference through October 31, 2016.

SPEAKER READY ROOM:

The speaker ready room is located in the Glassalen room.

Date	Time
Saturday, October 11th	10:00 a.m. – 5:00 p.m.
Sunday, October 12th	6:30 a.m. – 6:00 p.m.
Monday, October 13th	7:00 a.m. – 6:30 p.m.
Tuesday, October 14th	7:00 a.m. – 6:30 p.m.
Wednesday, October 15th	7:00 a.m. – 7:30 p.m.
Thursday, October 16th	7:30 a.m. – 11:00 a.m.

MEETING ANNOUNCEMENTS

CME:

This activity has been planned and implemented in accordance with the Essential Areas and policies of the European Accreditation Council for Continuing Medical Education. The EACCME designates this live activity for a maximum of **39** *European CME credits (ECMEC).* Physicians should claim only the credit commensurate with the extent of their participation in the activity.

Attendees who want EACCME credit must complete the congress evaluation at the conclusion of the event and attest to the sessions they attended. **There will be a $50.00 USD charge for scientific registrants to obtain EACCME credits.**

UNIVERSITY OF COPENHAGEN COURSE CREDIT:

The educational lectures have been approved by the Graduate School of Health and Medical Sciences, University of Copenhagen as a Ph.D. course.

LEARNING OBJECTIVES:

As a result of participating in this activity, participants should be able to:

- Analyze research consensus about how psychiatric disorders are inherited.
- Correlate morbid risk and the development of specific psychiatric disease when other family members have the illness.
- Assess latest gene findings that have been replicated.
- Utilize genetic testing on patients.
- Illustrate language used in psychiatric genetic studies.

CONFERENCE EVALUATION:

All conference attendees are urged to complete an evaluation of the meeting. Attendees who request CME (EACCME) credit for the meeting are required to complete the evaluation. This form is available on the WCPG 2014 website only. All evaluations must be completed by November 18, 2014.

MEETING ANNOUNCEMENTS

POSTERS:

This year all poster presentations will not be up for the entire congress. There will be three formal poster presentation sessions. Poster presenters are encouraged to be at their poster during the scheduled presentations. All authors are encouraged to upload their poster to the e-poster viewing site. Attendees will be able to view these e-posters online during and after the meeting.

Poster Session I: **Monday, October 13, 12:30 p.m. – 2:30 p.m.**
Poster Session II: **Tuesday, October 14, 11:00 a.m. – 1:00 p.m.**
Poster Session III: **Wednesday, October 15, 4:45 p.m. – 6:45 p.m.**

ABSTRACTS:

Conference abstracts are also available as a PDF document online at www.WCPG2014.org.

DISCLOSURES:

Disclosures for 2014 speakers, plenary, educational session, symposia, oral presentations and poster presenters may be found online at www.WCPG2014.org.

EXHIBITS:

Exhibits are located in the Tivoli Congress Center Ground Foyer.

INSURANCE:

Neither the Local Organizing Committee nor the Congress Secretariat and organizers accept any liability for damages and/or losses of any kind which may be incurred to the Congress participants or by any persons accompanying them, both during the official activities and excursions. Participation in all tours and events is at one's own risk. Participants are advised to obtain insurance against loss, accidents, or damage that could be incurred during the Congress. Congress participants are encouraged to insure valuables.

MEETING ANNOUNCEMENTS

VIDEOTAPING/PHOTOGRAPHY:

Attendees may not photograph, videotape or audiotape presentations at the conference without prior permission from the session chair and presenter.

CORPORATE SUPPORTERS:

Educational Grants:

The International Society of Psychiatric Genetics wishes to express appreciation to the following companies for their support of this educational activity by providing unrestricted educational grants:

Otsuka America Pharmaceutical, Inc. and Lundbeck

Satellite Sessions:

Illumina Symposium
Tuesday, October 14, 11:00 a.m. – 1:00 p.m.
**Please note the Illumina Symposium is not an (EACCME) accredited session.*

The Research Council of Norway Symposium
Sunday, October 11th 1:00 p.m. – 3:45 p.m.
"*Leveraging Population Registries and Biobanks for Neuropsychiatric Research: Experiences from the Nordic Countries and Opportunities for the HORIZON 2020 Initiative of the European Union*"

GOVERNMENT SUPPORTERS:

NIAAA: 5R13AA017055-04, Nurnberger, John I., Conference Support for World Congress on Psychiatric Genetics

TRAVEL AWARD PROGRAM SUPPORT:

The International Society of Psychiatric Genetics expresses appreciation to **The Lundbeck Foundation** for their support by providing funds for the ISPG travel award program.

EXHIBITORS

DNA Genotek

ILLUMINA

Exhibits will be open during the hours listed below. Attendees are encouraged to stop by and visit.

Date	Time
Sunday, October 12	7:30 a.m. – 5:00 p.m.
Monday, October 13	7:30 a.m. – 5:00 p.m.
Tuesday, October 14	7:30 a.m. – 5:00 p.m.
Wednesday, October 15	7:30 a.m. – 5:00 p.m.
Thursday, October 16	7:30 a.m. – 12:00 p.m.

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AWARDS

The Prize Committee and Board of Directors of the International Society of Psychiatric Genetics are pleased to announce the 2014 Honorific Award Winners:

THE MING TSUANG LIFETIME ACHIEVEMENT AWARD:

The Lifetime Achievement Award is awarded each year by the ISPG to a scientist who made a major contribution to the advancement of the field of Psychiatric Genetics.

Dr. Margaret Pericak-Vance, Ph.D., is a genetic epidemiologist and board-certified Ph.D. medical geneticist who is a leader in the integration of genomic and statistical technologies and their application to diseases of public health importance. Dr. Pericak-Vance pioneered the use of novel disease gene mapping methods leading to the first association of a common genetic variant, the apolipoprotein E4 allele (APOE), to late-onset Alzheimer disease. This paper remains one of the most cited papers in biomedical research. Her approach and findings opened the door for countless other discoveries in many human diseases, with the goal of translation of these findings into the discovery of better treatments for afflicting human conditions.

She received a B.A. in biology from Wells College in 1973 and earned her Ph.D. in medical genetics from Indiana University in 1978, training with Dr. P. Michael Conneally. This was followed by postdoctoral training in biostatistics in 1983 with Dr. Robert Elston at the University of North Carolina at Chapel Hill. She is currently the Dr. John T. Macdonald Foundation Professor of Human Genomics and Director of the John P. Hussman Institute for Human Genomics at the University of Miami, Miller School of Medicine. She also holds a faculty appointment in the Department of Neurology and is an Adjunct Professor of Medicine at the Duke University Medical Center.

Dr. Pericak-Vance has a long track record and continuing potential for both innovation and creativity in dissecting the difficult problem of finding genetic variation that underlies disease. Her publication record (more than 595 peer-reviewed papers with an h index of 98) demonstrates outstanding productivity and establishes important milestones in well over 30 human diseases, including those for neurological, psychiatric and ophthalmological diseases. She has played a significant role in five of the six most referenced papers published on

AWARDS

Alzheimer's disease. Her research has been cited approximately 30,000 times in scientific literature, and a vast number of current genetic studies are based, at least in part, on the approaches that she developed. She continues to play key roles in a multitude of national and international collaborative efforts to uncover the genetic landscape of many of these common complex diseases.

Dr. Pericak-Vance is a founding fellow of the American College of Medical Genetics who has received significant and widespread recognition for her research. In 1997, *Newsweek* magazine named Dr. Pericak-Vance to its Century Club: 100 People to Watch as We Move to the Next Millennium. She received the international "Louis D" Scientific Prize from the Institut de France's Academie des Sciences for her Alzheimer disease research in 2001. In 2004, she was elected to the Institute of Medicine and honored as the Hauptman-Woodward Pioneer of Science for her innovative work in Alzheimer's disease genetics. In 2010, she was awarded the Claude Pepper Innovative Research Award, the Hope for Vision Humanitarian of the Year Award, and became an invited member of the European Research Council Executive Agency's advanced grants evaluation panel; she is the only member from the United States on the panel. In 2011, Dr. Pericak-Vance received the Alzheimer's Association Bengt Winblad Lifetime Achievement Award for her lifelong contribution to Alzheimer's disease research, and she was named a fellow of the American Association for the Advancement of Science, for her distinguished contributions to the field of genetics in 2012.

AWARDS

THEODORE REICH YOUNG INVESTIGATOR AWARD:

Theodore (Ted) Reich (1938 – 2003) was the first President of ISPG and was both an outstanding researcher and mentor to young scientists. The award is made for published work on psychiatric genetics that is of exceptional merit to candidates who are 40 years or younger in the year of their nomination.

Benjamin Neale, Ph.D., is an Assistant Professor in the Analytic and Translational Genetics Unit at Massachusetts General Hospital (MGH), instructor in medicine at Harvard Medical School (HMS), and an associated researcher at the Broad Institute. Neale is strongly committed to gaining insights into the genetics of common, complex human diseases. Neale and Mark Daly, both of whom are associated with the Broad Institute and MGH, lead the ADHD Initiative, a collaborative effort that focuses on genomic studies of attention deficit hyperactivity disorder (ADHD).

Neale's research and training have focused heavily on statistical methodology. He has analyzed genetic data from large-scale studies of patients with ADHD, autism, age related macular degeneration, type 2 diabetes, and metabolic disorders. Neale also analyzed data from the first ADHD genome-wide association study (GWAS) meta-analysis, which combined the results of four studies to boost statistical power. Neale contributed to the development of software tools such as PLINK, one of the most frequently used packages for GWAS analysis. In addition to his roles at both the Broad Institute and MGH, Neale is the head of the ADHD psychiatric genetics GWAS analysis committee and an active member of the broader Psychiatric GWAS Consortium analysis committee, which is charged with analyzing all psychiatric data from these largescale genome-wide association studies. Neale also led the design of the exome chip, a genotyping array that captures rare coding variation in a cost-effective manner. To date, over 1.5 million exome chips have been sold.

Neale studied at the University of Chicago and Virginia Commonwealth University, earning a B.Sc. in genetics. He went on to earn his Ph.D. in human genetics from King's College in London, UK. Neale completed his postdoctoral training in Daly's laboratory at Massachusetts General Hospital. In addition to many local research collaborations, he also serves as advisor and analyst to international genetic research consortia on psychiatric diseases.

AWARDS

RICHARD TODD AWARD:

Richard Todd (1952 – 2008) was an internationally known expert on the influences of genetics and environment on psychiatric illness in children. The award is given by the Awards Committee for oral presentation in the category of Childhood Psychiatric Disorders.

Originally from Montreal, Canada, **Nadine Provençal,** completed her B.Sc. in Biology at Laval University in Quebec City, where she studied genetic polymorphisms associated with bipolar disorder with Dr. Nicholas Barden during a research internship. In 2005, she moved back to Montreal to work with Dr. Moshe Szyf and Dr. Richard Tremblay where she received an accelerated transition to doctoral studies in Epigenetics at McGill University in collaboration with the Research Group on Psychosocial Maladjustment in Children (GRIP) and obtained her Ph.D. degree in 2013. For her thesis, she examined the influence of early life adversity on the epigenome of rhesus macaques in collaboration with Dr. Stephen Suomi from the National Institute of Child Health & Human Development (NICHD), as well as the epigenetic marks associated with the development of physical aggression in men. Thereafter, she continued her training through post-doctoral research with Dr. Tremblay and Dr. Sylvana Côté at the University of Montreal and the GRIP where she investigated women and children genomes for epigenetic marks associated with physical aggression. In 2013, she moved to Munich, Germany, to continue her post-doctoral training with Dr. Elisabeth Binder in psychiatric epigenetics at Max-Planck Institute of Psychiatry where she is currently using comprehensive genomic approaches to study the epigenetic mechanisms underlying long-lasting effect of childhood adversity such as child abuse and neglect.

AWARDS

ELLIOT GERSHON PAPER OF THE YEAR AWARD:

In honor of Dr. Elliot Gershon, the International Society of Psychiatric Genetics presents the Gershon Paper of the Year Award to a recipient who has been published in the past year (June, 2013 to present) in the psychiatric genetics field.

Dr. Thomas W. Mühleisen is a Postdoctoral Scientist at the Institute of Neuroscience and Medicine (INM-1; Director: Prof. Katrin Amunts) at Research Center Jülich, Germany, within the research group "Genomic Imaging" (Head: Prof. Sven Cichon). He is also affiliated to the Institute of Human Genetics (Director: Prof. Markus Nöthen) at the University of Bonn, Germany.

His scientific career began in 2002 at the Max-Planck-Institute for Brain Research in Frankfurt, Germany, where he conducted his Ph.D. thesis on a developmental neurobiology project. Between 2005 and 2012, Thomas Mühleisen worked at the Institute of Human Genetics, Department of Genomics at the Life & Brain Center in Bonn, where he developed a strong interest in the genetic analysis of complex diseases, in particular schizophrenia and bipolar disorder (BD). He was a co-PI in MooDS (coordinator: Markus Nöthen), a research network funded by the German Federal Ministry of Education and Research (BMBF). In 2013, he moved to his current position at Research Center Jülich where he works with Sven Cichon on the identification of genetic factors influencing structure and function of the human brain.

So far, Thomas Mühleisen's work has resulted in 90 publications in peer-reviewed journals. He serves as an adhoc reviewer for several journals and is a member of four scientific societies including the International Society of Psychiatric Genetics. At the WCPG in 2010, he received an ECIP Award for an outstanding presentation of the genome-wide association study that identified genetic variation in neurocan (NCAN) as a susceptibility factor for bipolar disorder. This year's Gershon Award is given to Dr. Mühleisen for his major contribution to a paper that reports the identification of the two novel risk loci for BD (Nat Commun. 2014 Mar 11; 5: 3339. doi: 10.1038/ncomms4339). Together with Dr. Markus Leber and Prof. Thomas G. Schulze, Dr. Mühleisen is a first-author on that paper and accepts the award on behalf of all 63 authors. The awarded paper is a result of the collaborative effort of the MooDS consortium.

ECIP TRAVEL AWARDS

The Early Career Investigator Program is sponsored by grants from the NIAAA, the Lundbeck Foundation and the International Society of Psychiatric Genetics. The Society is grateful for their support that makes the travel awards possible.
★ Notates these awardees through the program book.

Congratulations to the 2014 ECIP Travel Awardees:

Alexandrina Al-Djassem
Bulgaria

Mohamed Ali
United Kingdom

Seth Ament
USA

Ana Ching-Lopez
Spain

Toni Clarke
United Kingdom

Lucia Colodro Conde
Australia

Shareefa Dalvie
South Africa

Esben Eickhardt
Denmark

Ibene Ekpor
Nigeria

Vanessa Gonçalves
Canada

Amy Hart
USA

Dmitriy Ivashchenko
Russia

Janos Kalman
Hungary

Chakravarthi Kanduri
Finland

Kounseok Lee
South Korea

Ya-Chin Lee
Taiwan

Dominique Maciejewski
Netherlands

Brady Maher
USA

Mirko Manchia
Italy

Veera Manikandan
Italy

Jacquelyn Meyers
USA

Giselle Monzón
Cuba

Niamh Mullins
United Kingdom

Loes Olde Loohuis
USA

Hansi Pathak
Germany

Jennie Pouget
Canada

Miguel Prieto
Chile

Sahoo Saddichha
India

Jessica Salvatore
USA

Marcos Santoro
Brazil

Nis Suppli
Denmark

Reshma Taj M.J.
India

Martin Tesli
Norway

Michael Way
United Kingdom

Qingqing Xu
China

Anthony Zannas
Germany

ECIP TRAVEL AWARDS

ORAL AND POSTER PRESENTATION AWARDS

The Program Committee selected oral and poster presentation finalists from the ECIP Travel Awardees. The authors will compete for one of three Oral Presentation Awards or Poster Presentation Awards. Oral and poster presentation award finalists are notated throughout the program with an **ECIP** symbol.

ORAL AND POSTER PRESENTATION AWARD FINALISTS:

Seth Ament
USA

T. Bernard Bigdeli
USA

Samuel Chawner
United Kingdom

Shing Wan Choi
Hong Kong

Lucia Colodro Conde
Australia

Donna Cosgrove
Ireland

Esben Eickhardt
Denmark

Jack Euesden
United Kingdom

Vanessa Gonçalves
Canada

Lynsey Hall
United Kingdom

Emma Knowles
USA

Brady Maher
USA

Stefanie Malan-Müller
South Africa

Joanna Martin-United
Kingdom

Semanti Mukherjee
USA

Loes Olde Loohuis
USA

Anil Ori
USA

Antonio Pardiñas
United Kingdom

Jennie Pouget
Canada

Robert Power
United Kingdom

Miguel Prieto
Chile

Nadine Provençal
Germany

Siri Ranlund
United Kingdom

Margarita Rivera
United Kingdom

Douglas Ruderfer
USA

Jie Song
Sweden

Helen Spiers
United Kingdom

Emma Sprooten
USA

Beata Tick
United Kingdom

Gianluca Ursini
USA

Chloe Chung Yi Wong
United Kingdom

Anthony Zannas
Germany

KEYNOTE AND PLENARY SPEAKERS

Keynote Speaker: Karl Deisseroth
Optical Deconstruction of Fully-assembled Biological Systems
October 12, 2014, 4:00 p.m. – 5:00 p.m.
Location: Tivoli Congress Hall

Karl Deisseroth is the D.H. Chen Professor of Bioengineering and of Psychiatry and Behavioral Sciences at Stanford University. A native of Boston, he received his bachelor's degree from Harvard in 1992, his Ph.D. from Stanford in 1998, and his M.D. from Stanford in 2000; he also completed postdoctoral training, medical internship, and adult psychiatry residency at Stanford, and he was board-certified by the American Board of Psychiatry and Neurology in 2006. He continues as a practicing psychiatrist at Stanford with specialization in affective disorders and autism-spectrum disease, employing medications along with neural stimulation. In the engineering school, he serves as Director of Undergraduate Education in Bioengineering and teaches core medical physiology and optics courses. National-scale service has included the NIH BRAIN Initiative Working Group, the Defense Sciences Research Council, and nonprofit disease foundations including NARSAD and the Michael J. Fox Foundation for Parkinson's Research. He was elected to the Institute of Medicine in 2010 and to the National Academy of Sciences in 2012, and selected as a Howard Hughes Medical Institute Investigator in 2013. For developing and applying optogenetics and CLARITY, Deisseroth has received the NIH Director's Pioneer Award (2005), the Zuelch Prize (2012), the BRAIN prize (2013), the Pasarow Prize (2013), and the Perl Prize (2012), and among other awards, was the sole recipient of the 2010 Koetser Prize, the 2010 Nakasone Prize, the 2011 Alden Spencer Prize, the 2013 Richard Lounsbery Prize, and the 2014 Dickson Prize in Science.

KEYNOTE AND PLENARY SPEAKERS

Plenary Session: Richard Weinshilboum
SSRI Pharmacogenomics and Pharmacometabolomics
October 13, 2014, 8:30 a.m. – 9:30 a.m.
Location: Tivoli Congress Hall

Dr. Richard Weinshilboum received B.A. and M.D. degrees from the University of Kansas, followed by residency training in Internal Medicine at the Massachusetts General Hospital, a Harvard teaching hospital, in Boston. He was also a Pharmacology Research Associate at the National Institutes of Health in Bethesda, Maryland, in the laboratory of Nobel Laureate Dr. Julius Axelrod. Dr. Weinshilboum began his affiliation with the Mayo Medical School and Mayo Clinic in Rochester, Minnesota, in 1972 where he is presently Professor of Molecular Pharmacology & Experimental Therapeutics and Internal Medicine as well as Mary Lou and John H. Dasburg Professor in Cancer Genomics Research. He also directs the Pharmacogenomics Program of the Mayo Center for Individualized Medicine and he is Co-Principal Investigator of the US National Institutes of Health (NIH) Pharmacogenomics Research Network Center at the Mayo Clinic. Dr. Weinshilboum's research has focused on pharmacogenetics and pharmacogenomics, and he has authored over 375 scientific manuscripts which address these topics. A major area of investigation initially was the pharmacogenetics of drug metabolism, with a focus on methylation and sulfation but, in recent years, his research has increasingly applied genome-wide pharmacogenomic techniques, especially to study the therapy of breast cancer-rather than candidate gene or candidate pathway-based approaches. Dr. Weinshilboum has been the recipient of many awards and honors including an Established Investigatorship of the American Heart Association, a Burroughs Wellcome Scholar Award in Clinical Pharmacology Award, the Oscar B. Hunter Award of the American Society for Clinical Pharmacology and Therapeutics, the Harry Gold Award of the American Society for Pharmacology and Experimental Therapeutics, the Catecholamine Club Julius Axelrod medal, the U.S. Food and Drug Administration William B. Abrams Lectureship Award, the Edvard Poulsson Award from the Norwegian Pharmacology Society and Distinguished Medical Alumnus Award from Kansas University Medical Center. He has served on the Advisory Councils for two US NIH Institutes, the National Institute of General Medical Sciences (NIGMS) and the National Human Genome Research Institute (NHGRI).

KEYNOTE AND PLENARY SPEAKERS

Plenary Session: Christine Klein

Translating Genetic Findings into Clinical Practice: The Parkinson Example

October 13, 2014, 9:45 a.m. – 10:45 a.m.

Location: Tivoli Congress Hall

Dr. Christine Klein is a Professor of Neurology and Neurogenetics. She studied medicine in Hamburg, Heidelberg, Luebeck (1988-1994), and London (with Dr. N.P. Quinn in 1994/1995). She moved to Boston from 1997-1999 for a fellowship in Molecular Neurogenetics under the mentorship of Dr. X.O. Breakefield. Dr. Klein completed her neurology training at Luebeck University with Dr. D. Koempf in 2004, followed by a series of summer sabbaticals in movement disorders with Dr. A.E. Lang in Toronto, Canada in 2004-2013. She was appointed Lichtenberg Professor at the Department of Neurology of Luebeck University in 2005, where her research has focused on the clinical and molecular genetics of movement disorders. In 2009, Dr. Klein has been awarded a Schilling Section of Clinical and Molecular Neurogenetics at the University of Luebeck and has become Director of the newly founded Institute of Neurogenetics in 2013.

Dr. Klein has published over 300 scientific papers and is the 2008 recipient of the Derek Denny-Brown Award of the American Neurological Association. She is an Associate Editor of 'Movement Disorders' and a member of the editorial board of 'Neurology'. She is head of the Neurogenetics Working Group of the German Neurological Society and a member of the Neuroscience Study Section of the German Research Foundation and of the scientific advisory board of the Bachmann-Strauss Dystonia & Parkinson Foundation (USA) and is the chair-elect of the Congress Scientific Program Committee of the 2016/2017 Annual Congresses of the Movement Disorder Society.

The Institute of Neurogenetics at the University of Luebeck has state-of-the-art know-how with neuroepidemiology, clinical, electrophysiological, and multimodal neuroimaging techniques. The Institute's molecular laboratory focuses on the genetics of movement disorders and the biological consequences of mutations and risk variants in human cellular models.

KEYNOTE AND PLENARY SPEAKERS

Plenary Session: Tine Bryan Stensbøl
NEWMEDS – A Public Private Partnership in Psychiatry – Objectives, Outcomes, Obstacles and Opportunities
October 13, 2014, 4:45 p.m. – 5:45 p.m.
Location: Tivoli Congress Hall

Dr. Tine Bryan Stensbøl is a Director at H. Lundbeck A/S. Tine Bryan Stensbøl graduated from The University of Pharmaceutical Sciences in Copenhagen in 1993, where she continued her Ph.D. studies in Medicinal Chemistry and Molecular Pharmacology within the glutamate field. After a post doc period at the University of Pharmaceutical Sciences, she joined Lundbeck in 2001 as a research scientist. Here she became a team member and later the project lead of one of Lundbeck's discovery projects in depression successfully pushing 4 compounds into development one of which has been approved. Tine now directs a biology-driven focus area at Lundbeck, namely Synaptic transmission Research and is a member of the Global Research Leadership Team responsible for the outlining as well as implementing Lundbeck's global research strategy.

Further to this, she is the coordinator of a public private partnership under the Innovative Medicines Initiatives (IMI) umbrella called NEWMEDS, focusing on addressing the major need for improved treatments for depression and schizophrenia and involves 23 partners comprising pharmaceutical companies, SMEs and leading academic institutions in Europe.

KEYNOTE AND PLENARY SPEAKERS

Plenary Session: Oluf Borbye Pedersen
The Gut Microbiota and the Impact on Human Health
October 14, 2014, 8:30 a.m. – 9:30 a.m.
Location: Tivoli Congress Hall

Dr. Oluf Pedersen is since 2007 Founder and Director of Lundbeck Foundation Centre for Applied Medical Genomics in Personalised Disease Prediction, Prevention and Care, Copenhagen (www.lucamp.org) and since 2010 scientific director at Novo Nordisk Foundation Centre for Basic Metabolic Research, Section of Metabolic Genetics, Faculty of Health and Medical Sciences, University of Copenhagen (www.metabol.ku.dk); he is Professor of Molecular Metabolism and Metabolic Genetics, Faculty of Health and Medical Sciences, University of Copenhagen. From 1989 to 2010, he was Chief Physician and Research Director at Steno Diabetes Centre and Hagedorn Research Institute, Copenhagen, a leading European and WHO-collaborative diabetes centre. Dr. Pedersen is a Danish Health Board-authorised Specialist of Internal Medicine (1987) and Specialist of Endocrinology (1987). He has published > 600 scientific papers (h-index 74) with major scientific innovation in multifactorial and cost-effective diabetes care (Steno-2 study), and genetics and gut metagenomics in common metabolic disorders. He has received recognition as evidenced by 14 international and national personal awards and a knighthood; president and chair of the Danish Diabetes Association (1995-2000) – a NGO with about 70,000 members and a professional staff of 35; services as chairman or member on boards of scientific societies, biomedical councils, grant bodies and scientific journals.

KEYNOTE AND PLENARY SPEAKERS

Plenary Session: Preben Bo Mortensen
Epidemiology in Psychiatric Genetics: Putting the E into GxE
October 14, 2014, 1:00 p.m. – 2:00 p.m.
Location: Tivoli Congress Hall

Preben Bo Mortensen is the founding director of the National Centre for Register-based Research (NCRR) at Aarhus University, Denmark and Scientific Director of the Lundbeck Foundation Initiative for Integrative Psychiatric Research, iPSYCH. He is an MD and DrMedSc. He has worked with register-based psychiatric epidemiology for more than two decades. He is an Adjunct Professor at Johns Hopkins University School of Public Health, Department of Mental Health. In 2002, he was awarded the Kurt Schneider Scientific Award for schizophrenia research, in 2004 the Danish August Krogh Award; in 2005 the Thompson Scientific Award as the most cited Danish researcher in psychiatry and psychology; 2010 Knight of the Order of the Dannebrog; and 2012 The Danish SEB/CODAN Honorary Award. PBM is the author of app. 425 scientific papers, primarily in the area of epidemiological studies of schizophrenia and other severe mental disorders, and suicide.

KEYNOTE AND PLENARY SPEAKERS

Plenary Session: Kári Stefánsson

The Use of Genetics to Study Functions and Dysfunctions of the Brain

October 14, 2014, 6:00 p.m. – 7:00 p.m.

Location: Tivoli Congress Hall

Kári Stefánsson, M.D., Dr. Med., has served as President, Chief Executive Officer and a Director since he founded deCODE genetics in August 1996. Dr. Stefánsson was appointed the Chairman of the Board of Directors of deCODE genetics in December 1999. From 1993 until April 1997, Dr. Stefánsson was a professor of Neurology, Neuropathology and Neuroscience at Harvard University. From 1983 to 1993, he held faculty positions in Neurology, Neuropathology and Neurosciences at the University of Chicago. Dr. Stefánsson received his M.D. and Dr. Med. from the University of Iceland and is board-certified in neurology and neuropathology in the United States. He has published numerous articles on the genetics of common/complex diseases and has been among the leaders of the world in the discovery of variants in the sequence of the human genome that associate with the risk of common/complex traits. Dr. Stefánsson was chosen by *Time* magazine as one of the 100 most influential men of the year for 2007 and by *Newsweek* as one of the 10 most important biologists of the 21 century. He was the recipient of the Jakobus Award 2007, The World Glaucoma Association Award for present scientific impact 2007, The European Society of Human Genetics Award 2009, and The Andre Jahre Award 2009.

KEYNOTE AND PLENARY SPEAKERS

Plenary Session: Michael Meaney
Parental Effects on the Epigenome
October 15, 2014, 8:30 a.m. – 9:30 a.m.
Location: Tivoli Congress Hall

Michael J. Meaney is a James McGill Professor of Medicine at Douglas Mental health University Institute of McGill University. He is the Director of the Maternal Adversity, Vulnerability and Neurodevelopment Project and of the Developmental Neuroendocrinology Laboratory of McGill University. Meaney also joined the Singapore Institute for Clinical Sciences in 2008 as a Senior Investigator and leads the Integrative Neuroscience Program. Meaney was educated at Loyola College of Montreal and received his Ph.D. from Concordia University (Montreal) with post-doctoral training in Cell and Molecular Neurobiology at The Rockefeller University. Meaney's primary research interest is that of the stable effects of early experience on gene expression and development, focusing on the influence of variations in maternal care. These studies have led to the discovery of novel epigenetic mechanisms for the influence of early experience. Meaney's research is multidisciplinary and includes studies of behaviour and physiology, to molecular biology and genetics. He has authored over 350 journal articles and has been the recipient of a Scientist Award from the Canadian Institutes for Health Research (CIHR) and a Distinguished Scientist Award from the National Alliance for Research in Schizophrenia and Affective Disorders. He was awarded Lougheed Prize (Alberta Heritage foundation for Medical Research), The Klerman Award (Cornell University), The Patricia Barchas Award (Research in Socio-physiology), The Heinz Lehman Award (Canadian College of Neuropsychopharmacology) and is the Bank of Montreal Fellow for the Canadian Institutes for Advanced Research. In 2012, Meaney was awarded the Order of Canada, the nation's highest citizen honour and the Distinguished Scientist award from the American Psychological Association. He currently holds a CIHR Senior Scientist Award. The Meaney lab was designated as a "Mostly Highly Cited Researcher" in Neuroscience by the Institute for Scientific Information. Graduates from Meaney's lab hold faculty appointments across North America, Asia and Europe, including Columbia University, Queen's University, University of California at Berkley, University of British Columbia, University of Michigan, University of Pennsylvania, the University of Toronto, INSERM (France) and the RIKEN Institute of Japan.

KEYNOTE AND PLENARY SPEAKERS

Plenary Panel Session
Pathways to Therapy and Prevention
October 15, 2014, 9:45 a.m. – 11:45 a.m.
Location: Tivoli Congress Hall

Raimund Buller, M.D., received his M.D. degree from the Johannes Gutenberg University in Mainz, Germany. He is a board-certified psychiatrist in Germany and has worked at the University of Mainz from 1980 to 1991. Since 1998 he has held various clinical research positions in the pharmaceutical industry (Hoffmann-La Roche, Basel, Switzerland; Quintiles Freiburg, Germany and Paris, France). Since 2003, he works with Lundbeck and is based in Paris.

Dr. Buller's research has focused on mood and anxiety disorders, schizophrenia, clinical trial methodology and drug development.

Steven E. Hyman, M.D., is Harvard University Distinguished Service Professor, Director of the Stanley Center for Psychiatric Research at the Broad Institute of MIT and Harvard, and Professor of Stem Cell and Regenerative Biology at Harvard University. The mission of the Stanley Center is to decrease the burden of psychiatric disorders through research. The work of the Center is grounded in (1) unbiased large-scale genetic analysis of schizophrenia, bipolar disorder, and autism; (2) development of new model systems based in stem cell technologies for investigation of disease-associated genes and pathways; and (3) application of emerging molecular information to the discovery of therapeutics.

From 2001 to 2011, Hyman served as Provost of Harvard University, the University's chief academic officer. As Provost, he had a special focus on developing collaborative scientific initiatives that span multiple disciplines and institutions. In that role he helped shape the Broad Institute of MIT and Harvard and Harvard's Wyss Institute for Biologically Inspired Engineering. From 1996 to 2001, he served as Director of the U.S. National Institute of Mental Health (NIMH), where he emphasized investment in neuroscience, emerging genetic technologies, and the establishment of DNA collections to facilitate genetic

Plenary Panel Session
Pathways to Therapy and Prevention
Continued

studies at large scale. He also initiated a series of large clinical trials with the goal of informing practice.

Hyman is President-elect of the Society for Neuroscience, Editor of the Annual Review of Neuroscience, and was founding President of the International Neuroethics Society. He is a member of the Institute of Medicine of the U.S. National Academies where he serves on the governing Council, the Board of Health Science Policy, and chairs the Forum on Neuroscience and Nervous System Disorders which brings together industry, government, academia, and voluntary organizations. He is a fellow of the American Academy of Arts and Sciences, a fellow of the American Association for the Advancement of Science, a fellow of the American College of Neuropsychopharmacology, and a Distinguished Life Fellow of the American Psychiatric Association.

Hyman received his B.A. summa cum laude from Yale College, a B.A. and M.A. from the University of Cambridge, which he attended as a Mellon fellow, and an M.D. cum laude from Harvard Medical School.

Kári Stefánsson
See previous biography on page 27.

Richard Weinshilboum
See previous biography on page 22.

KEYNOTE AND PLENARY SPEAKERS

Plenary Panel Session
Pathways to Therapy and Prevention
Continued

Peter Falkai has been working in the field of psychiatry for 25 years. He obtained his doctor of Medical Science in 1987, specialized in psychiatry in 1992 and completed his postdoctoral thesis (habilitation) in psychiatry in 1995. In 1996, he was appointed Professor of Medical Psychology and vice-chairman of the Department of Psychiatry, University of Bonn, Germany, where he functioned as senior medical director from 1997 to 2002. From 2002 to 2006, Prof. Falkai was appointed full professor and chairman of the Department of Psychiatry and Psychotherapy at the University of Saarland, Germany. From 2006 to 2012, he functioned as full professor and chairman of the Department of Psychiatry and Psychotherapy at the University of Göttingen, Germany. He is currently full professor and chairman of the Psychiatric Department of the Ludwig-Maximilians-University München, Germany.

Prof. Falkai's main research interest is focused on the neurobiology of psychotic disorders, namely schizophrenia, allowing the use of techniques ranging from functional imaging to gene expression in human post-mortem-tissue. He has managed to obtain state funding for numerous of his research projects and leads the Clinical Research Group 241 (KFO241).

In addition to authoring many scientific publication (Hirsch-Index: 43), Prof. Falkai acts as Chief-Editor of The European Archives of Psychiatry and Clinical Neuroscience (EAPCN) and holds positions on the editorial boards of other national and international psychiatric journals. He has been involved in creating treatment guidelines for schizophrenia for the World Federation of Biological Psychiatry (WFSBP) as well as for the German Society of Psychiatry, Psychotherapy and Nervous Diseases (DGPPN), where he was chairman from 2011 to 2012.

He is currently leads the Council of National Societies (NPA) of the European Psychiatric Association (EPA). He was chairman of the German Society of Psychiatry, Psychotherapy and Nervous Diseases (DGPPN) from 2011 to 2012 and Chairman of the Deutsche Gesellschaft für Biologische Psychiatrie (DGBP) from 2007 to 2010. He is a member/on the board of many national and international scientific societies.

KEYNOTE AND PLENARY SPEAKERS

Plenary Session: Daniel Geschwind
Integrative Genomics and the Neurobiology of Autism Spectrum Disorders
October 16, 2014, 10:45 a.m. – 11:45 a.m.
Location: Tivoli Congress Hall

Dr. Daniel Geschwind is the Gordon and Virginia MacDonald Distinguished Professor of neurology, psychiatry and human genetics at the UCLA School of Medicine. He is director of the Neurogenetics Program and the Center for Autism Research and Treatment (CART) and co-director of the Center for Neurobehavioral Genetics in the Semel Institute at UCLA.

Dr. Geschwind obtained an A.B. in psychology and chemistry at Dartmouth College and his M.D./Ph.D. at Yale School of Medicine prior to completing his internship, residency (Neurology), and postdoctoral fellowship at UCLA. He joined the UCLA faculty in 1997, founding the neurogenetics program. His laboratory aims to develop a mechanistic understanding of neuropsychiatric diseases, such as autism and neurodegenerative diseases, and their relationship to the range of normal human higher cognitive function and behavior. The lab's approach relies heavily on computational and bioinformatic methods in addition to wet laboratory experimentation. The ultimate goal is to use these integrative approaches to help develop effective therapeutics for neurologic and psychiatric disorders.

Dr. Geschwind has also put considerable effort into fostering large-scale collaborative patient resources for genetic research and data sharing. He is a strong advocate for data and biomaterial sharing, having provided scientific oversight for the Autism Genetic Resource Exchange (AGRE). He has served on numerous scientific advisory boards, including the Faculty of 1000 Medicine, the Executive Committee of the American Neurological Association, the NIMH Advisory Council and the NIH Council of Councils. He has published over 300 papers and serves on the editorial boards of several journals including Biological Psychiatry, Human Molecular Genetics, Neurobiology of Disease, Neuron and Science. He received the Derek Denny-Brown Neurological Scholar Award from the American Neurological Association in 2004, the Scientific Service Award from Autism Speaks in 2007, the Ruane Prize for Child and Adolescent Psychiatric Research from the Brain and Behavior foundation in 2012, the Taking on Tomorrow Innovation Award (Research/Scientific Breakthrough in Autism) -Boston Children's Hospital in 2013 and is an elected member of the Institute of Medicine of the National Academies.

SCHEDULE AT A GLANCE

SATURDAY, OCTOBER 11, 2014

12:00 p.m. – 12:50 p.m. **Education Sessions**

Basic Science Track: ***Systems Biology*** Lumbye	**Clinical Track:** ***Psychopathology: Current and Future Diagnostic Systems*** Carstensen

1:00 p.m. – 1:50 p.m. **Education Sessions**

Basic Science Track: ***Visualizing Big Data*** Lumbye	**Clinical Track:** ***Systematic Phenotyping Adults*** Carstensen

1:50 p.m. – 2:10 p.m. **Coffee Break**

2:10 p.m. – 3:00 p.m. **Overall Education Session: *The Epidemiology of Psychiatric Disorders***
Carstensen

3:10 p.m. – 4:00 p.m. **Education Sessions**

Basic Science Track: ***DNA Regulation: Transcriptomics*** Lumbye	**Clinical Track:** ***Systematic Phenotyping in Children*** Carstensen

4:10 p.m. – 4:30 p.m. **Coffee Break**

4:30 p.m. – 5:20 p.m. **Education Sessions**

Basic Science Track: ***DNA Regulation: Epigenetics*** Lumbye	**Clinical Track:** ***Neuro-immunogenetics and Inflammation*** Carstensen

NOTES

FULL SCHEDULE

SATURDAY, OCTOBER 11, 2014

Education Sessions

12:00 p.m. – 12:50 p.m.

Basic Science Track: *Systems Biology*
Kasper Lage, Ph.D., Massachusetts General Hospital
Lumbye

Clinical Track: *Psychopathology: Current and Future Diagnostic Systems*
Ray DePaulo, M.D., Johns Hopkins University School of Medicine
Carstensen

1:00 p.m. – 1:50 p.m.

Basic Science Track: *Visualizing Big Data*
Heiko Horn, Ph.D., Massachusetts General Hospital, Harvard Medical School
Lumbye

Clinical Track: *Systematic Phenotyping Adults*
Katherine Burdick, Ph.D., Mount Sinai School of Medicine
Carstensen

1:50 p.m. – 2:10 p.m. **Coffee Break**

2:10 p.m. – 3:00 p.m.

Overall Education Session: *The Epidemiology of Psychiatric Disorders*
Peter Zandi, Ph.D., John Hopkins University
Carstensen

3:10 p.m. – 4:00 p.m.

Basic Science Track: *DNA Regulation: Transcriptomics*
James Knowles, M.D., Ph.D., University of Southern California
Lumbye

Clinical Track: *Systematic Phenotyping in Children*
Kerstin von Plessen, M.D., Ph.D., Child and Adolescent Mental Health Centre Capital Region, University of Copenhagen
Carstensen

FULL SCHEDULE

SATURDAY, OCTOBER 11, 2014

4:10 p.m. – 4:30 p.m. **Coffee Break**

4:30 p.m. – 5:20 p.m. **Basic Science Track: *DNA Regulation: Epigenetics***
Ola Hermanson, Ph.D., Karolinska Institutet
Lumbye

Clinical Track: *Neuro-immunogenetics and Inflammation*
Bob Yolken, M.D., Johns Hopkins University School of Medicine
Carstensen

SCHEDULE AT A GLANCE

SUNDAY, OCTOBER 12, 2014

8:00 a.m. – 8:50 a.m. **Education Sessions**

Basic Science Track: ***Genomics: Arrays and Sequencing Technology*** Lumbye	**Clinical Track:** ***Pharmacokinetics*** Carstensen

9:00 a.m. – 9:50 a.m. **Education Sessions**

Basic Science Track: ***Genetic Epidemiology*** Lumbye	**Clinical Track:** ***Pharmacodynamics*** Carstensen

9:50 a.m. – 10:10 a.m. **Coffee Break**

10:10 a.m. – 11:00 a.m. **Education Sessions**

Basic Science Track: ***Genetic Statistics*** Lumbye	**Clinical Track:** ***Recruitment & Informed Consent (US & EU Perspective)*** Carstensen

11:10 a.m. – 12:00 p.m. **Education Sessions**

Basic Science Track: ***Genetic Risk Prediction*** Lumbye	**Clinical Track:** ***Genetic Testing & Counseling*** Carstensen

12:00 p.m. – 1:00 p.m. **Lunch (on your own)**

1:00 p.m. – 3:45 p.m. **Satellite Symposium:** ***Leveraging Population Registries and Biobanks for Neuropsychiatric Research: Experiences from the Nordic Countries and Opportunities for the HORIZON 2020 Initiative of the European Union***
Carstensen

SCHEDULE AT A GLANCE

SUNDAY, OCTOBER 12, 2014

3:45 p.m. – 4:00 p.m.	**Coffee Break**
4:00 p.m. – 5:00 p.m.	**Official Congress Opening: *Optical Deconstruction of Fully-assembled Biological Systems*** Tivoli Congress Hall
5:00 p.m. – 7:00 p.m.	**Congress Opening Mixer** Tivoli Hotel Foyer North
7:00 p.m. – 8:00 p.m.	**2015 Program Committee Meeting (invitation only)** Harlekin

FULL SCHEDULE

SUNDAY, OCTOBER 12, 2014

Education Sessions

8:00 a.m. – 8:50 a.m.

Basic Science Track: *Genomics: Arrays and Sequencing Technology*
Sven Cichon, Ph.D., University of Basel &
Per Hoffman, Ph.D., University of Bonn
Lumbye

Clinical Track: *Pharmacokinetics*
Michael Steffens, M.D., Federal Institute for Drugs and Medical Devices (BfArM)
Carstensen

9:00 a.m. – 9:50 a.m.

Basic Science Track: *Genetic Epidemiology*
Naomi Wray, Ph.D., The University of Queensland, Queensland Brain Institute
Lumbye

Clinical Track: *Pharmacodynamics*
Freja Herborg Hansen, Københavns Universitet
Carstensen

9:50 a.m. – 10:10 a.m.

Coffee Break

10:10 a.m. – 11:00 a.m.

Basic Science Track: *Genetic Statistics*
Naomi Wray, Ph.D., The University of Queensland, Queensland Brain Institute
Lumbye

Clinical Track: *Recruitment & Informed Consent (US & EU Perspective)*
Layla Kassem, Ph.D., National Institute of Mental Health & Marcella Rietschel, M.D., Central Institute of Mental Health
Carstensen

FULL SCHEDULE

SUNDAY, OCTOBER 12, 2014

11:10 a.m. – 12:00 p.m.	**Basic Science Track:** ***Genetic Risk Prediction*** Naomi Wray, Ph.D., The University of Queensland, Queensland Brain Institute & Hong Lee, Ph.D., The University of Queensland, Queensland Brain Institute ***Lumbye***
	Clinical Track: ***Genetic Testing & Counseling*** Karen Brøndum Nielsen, M.D., Rigshospitalet, Copenhagen University ***Carstensen***
12:00 p.m. – 1:00 p.m.	**Lunch (on your own)**
1:00 p.m. – 3:45 p.m.	**Satellite Symposium:** ***Leveraging Population Registries and Biobanks for Neuropsychiatric Research: Experiences from the Nordic Countries and Opportunities for the HORIZON 2020 Initiative of the European Union*** ****Open to all attendees*** ***Carstensen***
3:45 p.m. – 4:00 p.m.	**Coffee Break**
4:00 p.m. – 5:00 p.m.	**Official Congress Opening:** ***Optical Deconstruction of Fully-assembled Biological Systems*** ***Tivoli Congress Hall***

Chair: Thomas G. Schulze, M.D., Institute for Psychiatric Phenomics and Genomics (IPPG) Ludwig-Maximilians-University Munich
Co-chair: Francis McMahon, M.D., NIH/NIMH
Plenary Speaker: Karl Deisseroth, M.D., Ph.D., Stanford University

This talk will address optical tools for precise, high-resolution investigation of intact biological systems, and application of these tools to study the neural circuit underpinnings of adaptive and maladaptive behavior. Over the past decade, our laboratory has created and developed both optogenetics (a technology for precisely controlling millisecond-scale activity patterns in specific cell types using microbial opsin genes and fiberoptic-based neural interfaces) and CLARITY (a

SUNDAY, OCTOBER 12, 2014

technology to optically resolve high-resolution structural and molecular detail within intact tissues without disassembly). Most recently in optogenetics, our team has developed strategies for targeting microbial opsins and light to meet the challenging constraints of the freely-behaving mammal, engineered a panel of microbial opsin genes spanning a range of optical and kinetic properties, built high-speed behavioral and neural activity-readout tools compatible with real-time optogenetic control, disseminated the tools to thousands of investigators, and applied these optogenetic tools to develop circuit-based insight into anxiety, depression, and motivated behaviors. Distinct from optogenetics, our CLARITY technology can be used to transform intact biological tissue into a hybrid form in which components are removed and replaced with exogenous elements, resulting in a transparent tissue-hydrogel that both preserves, and makes accessible, structural and molecular information for visualization and analysis. With CLARITY, whole mouse brains have now been labeled and imaged, and molecular markers have been used to identify individual structures and projections in banked human brain tissue, thereby unlocking rich sources of information for probing disease mechanisms as well as the native structure and complexity of the nervous system, in a manner complementary to optogenetic approaches.

5:00 p.m. – 7:00 p.m. **Opening Mixer**
Tivoli Hotel Foyer North

7:00 p.m. – 8:00 p.m. **2015 Program Committee Meeting (invitation only)**
Harlekin

NOTES

SCHEDULE AT A GLANCE

MONDAY, OCTOBER 13, 2014

8:30 a.m. – 9:30 a.m. **Plenary Session: *SSRI Pharmacogenomics and Pharmacometabolomics***
Tivoli Congress Hall

9:30 a.m. – 9:45 a.m. **Coffee Break**

9:45 a.m. – 10:45 a.m. **Plenary Session: *Translating Genetic Findings into Clinical Practice: The Parkinson Example***
Tivoli Congress Hall

10:45 a.m. – 11:00 a.m. **Coffee Break**

11:00 a.m. – 12:30 p.m. **Concurrent Oral Presentation Sessions**

Epigenetic Approaches	***The Genomics of Affective Disorders & ADHD***	***Novel "omics" Insights into Schizophrenia and Bipolar Disorder***	***Genomic Approaches in Schizophrenia, Substance Abuse, and PTSD***
Lumbye	Harlekin	Carstensen	Columbine

12:30 p.m. – 2:30 p.m. **Poster Session**
Tivoli Congress Hall Foyer - Ground Floor

2:30 p.m. – 4:30 p.m. **Concurrent Symposia Sessions**

Induced Pluripotent Stem Cell Modelling in Affective Disorders and Psychosis	***New Data about the Genetics of Attention Deficit Hyperactivity Disorder***	***Beyond Bonferroni: Large Scale Inference for Complex Disorders***	***Telomeres and Telomerase in Mood Disorder: Markers for Risk and Treatment?***
Lumbye	Harlekin	Carstensen	Columbine

4:30 p.m. – 4:45 p.m. **Coffee Break**

SCHEDULE AT A GLANCE

MONDAY, OCTOBER 13, 2014

4:45 p.m. – 5:45 p.m. **Plenary Session: *NEWMEDS – A Public Private Partnership in Psychiatry – Objectives, Outcomes, Obstacles and Opportunities***
Tivoli Congress Hall

6:00 p.m. – 8:00 p.m. **Concurrent Symposia Sessions**

New Findings from the Enhancing Neuro Imaging Genetics through Meta-analysis (ENIGMA) Consortium	***Shared Genetics between Depression and Comorbid Physical Conditions***	***Following a Strong Lead: Functional Investigation of GWAS Signals for Schizophrenia***	***A Small Window to Psychiatric Genetics in China***
Lumbye	Harlekin	Carstensen	Columbine

6:00 p.m. – 9:00 p.m. **ISPG Board of Directors Meeting (invitation only)**
Paafuglen/Tulipanen

FULL SCHEDULE

MONDAY, OCTOBER 13, 2014

8:30 a.m. – 9:30 a.m. **Plenary Session: *SSRI Pharmacogenomics and Pharmacometabolomics***
Tivoli Congress Hall

Chair: Ole Mors, Ph.D., Aarhus University Hospital, Risskov
Co-chair: James Kennedy, M.D., CAMH
Plenary Speaker: Richard Weinshilboum, M.D., Mayo Clinic

Major Depressive Disorder (MDD) is a common life-threatening illness that causes significant disability and mortality worldwide. Selective serotonin reuptake inhibitors (SSRIs) are the current standard of care for the drug therapy of MDD, but over half of patients treated with SSRIs fail to achieve remission. It would represent a major advance in the treatment of MDD if we were able to more highly individualize drug therapy for this disease. The development of genome-wide genomic techniques such as genome-wide association studies (GWAS) offered the promise of greater understanding of the pathophysiology(s) and variation in response to the treatment for MDD. We have applied GWAS to study a large single institution trial of citalopram.-escitalopram. therapy for 800 MDD patients at the Mayo Clinic, with the identification of SNP/gene signals related to SSRI drug response phenotypes. However, SSRI genome-wide pharmacogenomic studies have proven, as elsewhere in psychiatry, less informative than they have when applied in other medical disciplines. That may result, in part, from heterogeneity in the underlying pathophysiology of MDD. Therefore, we have added to our study, as an objective, measurable endophenotype, plasma metabolomic assays using samples from these same 800 patients, initially using an LC-electrochemical array (LCECA) platform particularly suited for the quantitative assay of monoamine neurotransmitters and their metabolites to use pharmacometabolomics to "inform" subsequent GWA studies. The purpose was to increase our understanding of molecular factors involved in variation in SSRI clinical response phenotypes. For example, of the 37 metabolites assayed by LCECA in our initial set of studies, baseline plasma serotonin and change in plasma serotonin concentrations during therapy were highly correlated with clinical SSRI response phenotypes. Subsequent GWAS for baseline plasma serotonin identified a genome-wide significant SNP signal near the TSPAN5 gene, and knockdown of that gene in neuroblastoma cell lines resulted in decreased expression of a series of genes encoding enzymes involved in serotonin biosynthesis. Similar informative results for different SNP/gene signals were found when a "pharmacometabolomics-informed pharmacogenomics" research strategy was applied to study plasma kyneurinine concentrations in these same patients. Application of this type of multiple "omics" research strategy may help make it possible to address heterogeneity in molecular mechanisms that contribute to the pathophysiology of MDD and, ultimately, might help us to move toward more highly individualized SSRI therapy of MDD.

9:30 a.m. – 9:45 a.m. **Coffee Break**

FULL SCHEDULE

MONDAY, OCTOBER 13, 2014

9:45 a.m. – 10:45 a.m. **Plenary Session: *Translating Genetic Findings into Clinical Practice: The Parkinson Example***
Tivoli Congress Hall

Chair: Thomas Werge, Ph.D., Institute of Biological Psychiatry
Co-chair: Lynn DeLisi, M.D., VA Boston Healthcare System, Harvard Medical School
Plenary Speaker: Christine Klein, Ph.D., University of Lübeck

Several genes are well validated as causes of a Parkinson's disease (PD) phenotype and a total of 20 genes and gene loci have been assigned a 'PARK' designation. According to a recently revised system of the genetic nomenclature of PD, there are ten confirmed monogenic forms of PD, all of which can be tested for using commercial diagnostic genetic testing. Three of the confirmed forms of hereditary PD follow an autosomal dominant mode of inheritance and seven are recessively inherited. The most common forms are late-onset autosomal dominant parkinsonism with mutations in the *LRRK2* gene and early-onset parkinsonism caused by mutations in the *Parkin* gene. The three dominant forms and three of the seven recessive forms of parkinsonism (Parkin, PINK1, DJ-1) are associated with a clinical picture closely resembling that of idiopathic PD with its cardinal motor features of bradykinesia, resting tremor, rigidity, and postural instability. The remaining four recessive forms (ATP13A2, FBOX07, DNAJC6, and SYNJ1) usually have a juvenile onset and present with atypical, multisystem features including early dementia, eye movement abnormalities, pyramidal signs etc.
Genome-wide association studies (GWAS) have been a major advance in genetic research, enabling the assessment of genetic risk factors associated with PD and other disorders via large-scale, population-based studies. Several GWAS for PD have been reported and three meta-analyses have been performed. All GWAS indicate a strong association to the *SNCA* gene and most studies (depending on the ethnicity of individuals) also confirm association with the *MAPT* gene.
Both the monogenic and the idiopathic forms of PD share common pathophysiological mechanisms converging on oxidative modification, impaired protein degradation, and mitochondrial dysfunction. Therefore, monogenic forms of PD can serve as human model diseases for the idiopathic form. In addition, clinico-genetic studies have been used to improve genotype-phenotype correlations and to reveal the earliest disease signs. Furthermore, there has been significant progress in the development of new disease models, particularly through the use of induced pluripotent stem (iPS) cell-derived neurons.

FULL SCHEDULE

MONDAY, OCTOBER 13, 2014

10:45 a.m. – 11:00 a.m. **Coffee Break**

Concurrent Oral Presentation Sessions

11:00 a.m. – 12:30 p.m. **The Genomics of Affective Disorders & ADHD**
Harlekin

Chair: Barbara Franke, Departments of Human Genetics and Psychiatry, Donders Institute for Brain, Cognition and Behaviour, Radboud University Medical Center
Co-chair: Magnus Haraldsson, University of Iceland

11:00 a.m. - 11:15 a.m. **The Relationship between Common and Rare Genetic Variants in Attention Deficit Hyperactivity Disorder**
Joanna Martin, MRC Centre for Neuropsychiatric Genetics and Genomics, Cardiff University

11:15 a.m. - 11:30 a.m. **ADHD Polygenic Risk Scores Predict ADHD and Aggression in Childhood and Adolescence, but not Anxiety and Depression**
Christel M. Middeldorp, VU University Amsterdam, Biological Psychology

11:30 a.m. - 11:45 a.m. **Shared Genetic Influences between Attention-Deficit Hyperactivity Disorder Traits in the General Population and Clinical Diagnosis in an Independent Sample**
Evie Stergiakouli, MRC Integrative Epidemiology Unit at the University of Bristol

11:45 a.m. - 12:00 p.m. **Of Sequencing and Complex Traits: Gene Discoveries for Depression in a Large Family**
Najaf Amin, Erasmus University Medical Center

FULL SCHEDULE

MONDAY, OCTOBER 13, 2014

12:00 p.m. - 12:15 p.m. **Pathway-based Enrichment Analysis (INRICH) in 9,474 Patients with Bipolar Disorder and 14,278 Controls Suggests an Involvement of NCA.M. Signaling in Disease Etiology**
Sven Cichon, Division of Medical Genetics, Department of Biomedicine, University of Basel

12:15 p.m. - 12:30 p.m. **The Negative Phenotypic Correlation between Depression and Educational Attainment is not Explained by Pleiotropic Genetic Effects: Results in ~25,000 Subjects**
Wouter J. Peyrot, Department of Psychiatry, VU University Medical Center & GGZ

11:00 a.m. – 12:30 p.m. **Epigenetic Approaches**
Lumbye

Chair: Derek Morris, National University of Ireland Galway
Co-chair: David Porteous, University of Edinburgh

11:00 a.m. - 11:15 a.m. **Allele-specific DNA Methylation across Brain and Blood - Identification of Tissue-specific Differentially Methylated Regions**
Sarah Marzi, Institute of Psychiatry, King's College London

11:15 a.m. - 11:30 a.m. **An Epigenome-wide Scan for Autism Susceptibility Loci across Multiple Brain Regions**
ECIP Chloe Chung Yi Wong, Institute of Psychiatry, King's College London

11:30 a.m. - 11:45 a.m. **Exposure to Glucocorticoids during Hippocampal Neurogenesis and Childhood Maltreatment: Mechanisms of System Wide Epigenetic Effects**
ECIP Nadine Provençal, Max Planck Institute for Psychiatry

ECIP – ECIP Finalist

FULL SCHEDULE

MONDAY, OCTOBER 13, 2014

11:45 a.m. - 12:00 p.m. **Cross-tissue Methylomic Profiling Strongly Implicates a Role for Cortex-specific Deregulation of ANK1 in Alzheimer's Disease Neuropathology**
Jonathan Mill, University of Exeter

12:00 p.m. - 12:15 p.m. **Dynamic and Sex-specific Changes in DNA Methylation during Human Fetal Brain Development**
ECIP Helen Spiers, King's College London

12:15 p.m. - 12:30 p.m. **A Large-scale DNA Methylation Analysis of SLC6A4 Using Peripheral Blood Samples of Patients with Bipolar Disorder**
Tempei Ikegame, The University of Tokyo

11:00 a.m. – 12:30 p.m. **Novel "omics" Insights into Schizophrenia and Bipolar Disorder**
Carstensen

Chair: Lena Backlund, Karolinska Institutet
Co-chair: John Rice, Washington University School of Medicine at St. Louis

11:00 a.m. - 11:15 a.m. **Large-scale RNA-sequencing of Schizophrenia Brains by the Commonmind Consortium**
Pamela Sklar, Icahn School of Medicine at Mount Sinai

11:15 a.m. - 11:30 a.m. **Genic Copy Number Variants in an Exome-sequencing Study of 4,978 Schizophrenia Cases and 6,256 Controls**
ECIP Douglas Ruderfer, MSSM

11:30 a.m. - 11:45 a.m. **Rare, Protein-altering Variation in a Swedish Schizophrenia Case-control Cohort of More than 11,000 Individuals**
Giulio Genovese, Broad Institute

ECIP – ECIP Finalist

FULL SCHEDULE

MONDAY, OCTOBER 13, 2014

11:45 a.m. - 12:00 p.m. **Polygenic Risk Scores for Schizophrenia and Bipolar Disorder Predict Creativity**
ECIP Robert Power, Institute of Psychiatry, London

12:00 p.m. - 12:15 p.m. **Polygenic Profile Risk Scores, Psychiatric Family History and the Risk of Schizophrenia**
Esben Agerbo, CIRRAU - Centre for Integrated Register-based Research, National Centre for Register-based Research, Aarhus University

12:15 p.m. - 12:30 p.m. **Biological Insights from 108 Schizophrenia-associated Genetic Loci**
Stephan Ripke, Massachusetts General Hospital

11:00 a.m. – 12:30 p.m. **Genomic Approaches in Schizophrenia, Substance Abuse, and PTSD**
Columbine

Chair: Marcella Rietschel, Central Institute of Mental Health
Co-chair: Gary Donohoe, National University of Ireland, Galway

11:00 a.m. - 11:15 a.m. **GWAS of Posttraumatic Stress Disorder: First Report of the Psychiatric Genomics Consortium - PTSD Group**
Laramie Duncan, Broad Institute of MIT and Harvard

11:15 a.m. - 11:30 a.m. **The Influence of Polygenic Risk Scores on the Association between Infections and Schizophrenia – A Nationwide Danish Study**
Michael Benros, Mental Health Centre Copenhagen, Copenhagen University

11:30 a.m. - 11:45 a.m. **Translating Human Genetics into Novel Target Hypotheses for Schizophrenia**
Sara Paciga, Pfizer

ECIP – ECIP Finalist

FULL SCHEDULE

MONDAY, OCTOBER 13, 2014

11:45 a.m. - 12:00 p.m. **A Bioinformatics Pipeline for Functional Annotation of Common Variants Identified in Schizophrenia GWAS Meta-analysis**
Younes Mokrab, Eli Lilly

12:00 p.m. - 12:15 p.m. **Genome-wide Meta-analyses of FTND Score and the Time to Smoke First Cigarette in the Morning**
Xiangning Chen, Virginia Commonwealth University

12:15 p.m. - 12:30 p.m. **The Genetic Landscape of Cannabis Use: A Meta-analysis including 27,000 Subjects Shows Enrichment of Nominally Significant Associations**
Eske Derks, Academic Medical Center

12:30 p.m. – 2:30 p.m. **Poster Session**
Tivoli Congress Hall Foyer - Ground Floor
*See pages 101-121 for full listing of posters.

Concurrent Symposia Sessions

2:30 p.m. - 4:30 p.m. **New Data about the Genetics of Attention Deficit Hyperactivity Disorder**
Harlekin

Chair: Stephen Faraone, SUNY Upstate Medical University
Moderator: Anita Thapar, Cardiff University School of Medicine

2:30 p.m. – 2:35 p.m. **Introduction**
Stephen Faraone, SUNY Upstate Medical University

2:35 p.m. - 3:00 p.m. **Genome-wide Association Study of a Danish Birth-cohort of ADHD Cases and Controls**
Anders Børglum, Aarhus University

3:00 p.m. - 3:25 p.m. **Genome-wide Association Meta-analysis of ADHD**
Benjamin Neale, Massachusetts General Hospital

MONDAY, OCTOBER 13, 2014

3:25 p.m. - 3:50 p.m. **Utilizing Genetic Architecture to Model Pathway Level Effects in Attention Deficit Hyperactivity Disorder**
Beth Wilmot, OHSU

3:50 p.m. - 4:15 p.m. **Functional Studies of ADHD Candidate Genes**
Jan Haavik, University of Bergen

4:15 p.m. - 4:30 p.m. **Discussion**
Barbara Franke, Departments of Human Genetics and Psychiatry, Donders Institute for Brain, Cognition and Behaviour, Radboud University Medical Center

2:30 p.m. - 4:30 p.m. **Telomeres and Telomerase in Mood Disorder: Markers for Risk and Treatment?**
Columbine

Chair: Catharina Lavebratt, Karolinska Institutet
Moderator: Iiris Hovatta, University of Helsinki

2:30 p.m. – 2:35 p.m. **Introduction**
Catharina Lavebratt, Karolinska Institutet

2:35 p.m. - 3:00 p.m. **Telomeres and Psychiatric Disorders: An Overview**
Catharina Lavebratt, Karolinska Institutet

3:00 p.m. - 3:25 p.m. **Telomere Length and Depressive and Anxiety Disorders**
Brenda Penninx, VU University Medical Center

3:25 p.m. - 3:50 p.m. **Depression and Short Telomeres: Association to Alteration in Shelterin and Telomerase**
Yabin Wei, Karolinska Hospital

3:50 p.m. - 4:15 p.m. **Variable Telomere Length Across Post-mortem Human Brain Regions and Specific Reduction in the Hippocampus of Major Depression**
Adolfo Sequeira, University of California Irvine

4:15 p.m. - 4:30 p.m. **Discussion**
Martin Schalling, Karolinska Institutet

FULL SCHEDULE

MONDAY, OCTOBER 13, 2014

2:30 p.m. - 4:30 p.m.	**Beyond Bonferroni: Large Scale Inference for Complex Disorders** ***Carstensen***

Chair: Peter Visscher, The University of Queensland
Moderator: Wesley Thompson, UC-San Diego

2:30 p.m. – 2:35 p.m.	**Introduction** Peter Visscher, The University of Queensland
2:35 p.m. - 3:00 p.m.	**Mixture Models and Replication Effect Sizes** Andrew Schork, UC San Diego
3:00 p.m. - 3:25 p.m.	**Leveraging Pleiotropy to Improve Gene Discovery and Effect Size Estimation** Ole Andreassen, University of Oslo
3:25 p.m. - 3:50 p.m.	**Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia** Sang Hong Lee, The University of Queensland
3:50 p.m. - 4:15 p.m.	**Leveraging Genomic Information to Inform Genetic Analysis** Mark Reimers, Virginia Institute for Psychiatric & Behavioral Genetics
4:15 p.m. - 4:30 p.m.	**Discussant** Peter Visscher, The University of Queensland

FULL SCHEDULE

MONDAY, OCTOBER 13, 2014

2:30 p.m. - 4:30 p.m.	**Induced Pluripotent Stem Cell Modelling in Affective Disorders and Psychosis** ***Lumbye***

Chair: Melvin McInnis, University of Michigan
Moderator: John Kelsoe, University of California San Diego

2:30 p.m. – 2:35 p.m.	**Introduction** Melvin McInnis, University of Michigan
2:35 p.m. - 3:00 p.m.	**Label-free Optical Imaging of Reprogrammed Bipolar Disorder Patient-derived Cells to Investigate Lithium Responsiveness** Roy Perlis, Massachusetts General Hospital
3:00 p.m. - 3:25 p.m.	**Regulation of Neuronal Development by Risk Genes for Mental Disorders** Guo-Li Ming, Johns Hopkins University
3:25 p.m. - 3:50 p.m.	**High Throughput Small Molecule Screens on iPSC-derived Cells** Sevilla Detera-Wadleigh, National Institute of Mental Health, NIH
3:50 p.m. - 4:15 p.m.	**Interneuron Dysfunction in iPSC Models of Bipolar Disorder** Melvin McInnis, University of Michigan
4:15 p.m. - 4:30 p.m.	**Discussion** Hongjun Song, Johns Hopkins University School of Medicine
4:30 p.m. – 4:45 p.m.	**Coffee Break**

MONDAY, OCTOBER 13, 2014

4:45 p.m. – 5:45 p.m. **Plenary Session: NEWMEDS – A Public Private Partnership in Psychiatry – Objectives, Outcomes, Obstacles and Opportunities**
Tivoli Congress Hall

Chair: Patrick Sullivan, M.D., University of North Carolina at Chapel Hill
Co-chair: Christina Hultman, Ph.D., Karolinska Institutet
Plenary Speaker: Tine Bryan Stensbøl, Ph.D., Lundbeck

Despite remarkable advances in molecular and imaging technologies and nearly 15,000 articles on schizophrenia and depression (S&D) every year, there have been few truly innovative new chemical entities (NCEs) which have made it to the clinic. Three major bottlenecks are holding the field back: i) a lack of pathophysiologically-accurate and relevant animal models guiding the drug discovery of novel chemical entities; ii) a lack of tools and tests in healthy volunteers that can provide early indication of efficacy; and iii) the reliance of clinical trials on symptom-based DSM-categories which inevitably lead to biologically heterogeneous groups of patients. To overcome these limitations, we brought together a consortium consisting of six leading European and an Israeli academic institution, three SMEs, and ten EFPIA partners in the NEWMEDS consortium, under the Innovative Medicines Initiative (IMI), which ties academic expertise in animal models, genetics, functional MRI and PET imaging, clinical settings and analysis methods together with expertise and incentive in drug discovery and development.
To specifically target the challenges in psychiatry the NEWMEDS consortium has: a) developed standardized animal models that focus on reliable cross-species endophenotypes (e.g. cognitive function) and used cross-species methods (MRI, EEG) to bring animal models closer to clinical endpoints; b) developed fMRI and PET based paradigms which may serve as early or surrogate markers to provide guidance for drug development; c) gathered a database of more than 30,000 schizophrenia patients that have been enrolled in clinical trials to learn how we do clinical trials in a more efficient way d) tried to identify pharmacogenetic biomarkers that can be used to stratify patients within an umbrella DSM-diagnosis e) examined a set of genetic abnormalities (CNV) closely linked with Schizophrenia by studying them in human populations and animal models to achieve one-to-one cross-species correlation of the impact of these mutations on cognition, behavior and brain physiology and function.

MONDAY, OCTOBER 13, 2014

It was the ambition of NEWMEDS to pioneer the study of the human and translational biology of rare CNVs associated with Schizophrenia and other disorders. We have managed to undertake a detailed cognitive, psychological and MRI study of the world's largest collection of volunteers with CNVs associated with psychiatric disorders. The results validate our approach of using CNVs to explore disease related mechanisms and to complement this human data we have three different CNV mouse lines of interest to schizophrenia research – the 1q21, 15q13 and 22q11 models. These mouse lines are being shared with partners who are examining their underlying circuit dysfunction using the newly developed measures of hippocampal-prefrontal connectivity and cognitive measures and structural and functional MRI– thus providing the most systematic and detailed mechanistic and behavioral profiling of these CNVs.
The presentation will give an overview of the scientific achievements of the NEWMEDS consortium, discuss the outcome as well as discuss the obstacles and opportunities working in a private public partnership.

Concurrent Symposia Sessions

6:00 p.m. - 8:00 p.m.	**Shared Genetics between Depression and Comorbid Physical Conditions** ***Harlekin***

Chair: Margarita Rivera, Institute of Psychiatry, King's College London
Moderator: Brenda Penninx, VU University Medical Center

6:00 p.m. – 6:05 p.m.	**Introduction** Margarita Rivera, Institute of Psychiatry, King's College London
6:05 p.m. - 6:30 p.m.	**Estimation of the Genetic Correlation between Major Depressive Disorder and Body Mass Index Using Common Genetic Variants** Margarita Rivera, Institute of Psychiatry, King's College London

FULL SCHEDULE

MONDAY, OCTOBER 13, 2014

6:30 p.m. - 6:55 p.m.	**Phenotypic Heterogeneity of MDD: Distinct Genetic Liability for MDD Subtypes?** Yuri Milaneschi, VU University Medical Center/GGZ in Geest
6:55 p.m. - 7:20 p.m.	**Investigating the Role of Pain in Depression with Genetic Data** Lannie Ligthart, VU University
7:20 p.m. - 7:45 p.m.	**Unraveling the Comorbidity between Major Depressive Disorder and the Autoimmune Disorders – Shared Risk Alleles?** Jack Euesden, King's College London
7:45 p.m. - 8:00 p.m.	**Discussion** Aarno Palotie, University of Helsinki

6:00 p.m. - 8:00 p.m.	**A Small Window to Psychiatric Genetics in China** ***Columbine***

Chair: Chunyu Liu, University of Illinois at Chicago
Moderator: Margit Burmeister, University of Michigan

6:00 p.m. - 6:05 p.m.	**Introduction** Chunyu Liu, University of Illinois at Chicago
6:05 p.m. - 6:30 p.m.	**GABRB2 in Schizophrenia and Beyond** Hannah Hong Xue, Hong Kong University of Science and Technology
6:30 p.m. - 6:55 p.m.	**Whole Brain Connectivity Study in Schizophrenia Patients and their Healthy Siblings** Yin Yao, National Institutes of Health
6:55 p.m. - 7:20 p.m.	**Integration of miRNA-mRNA Networks to Elucidate the Complex of Psychiatric Disorders** Chao Chen, Central South University

FULL SCHEDULE

MONDAY, OCTOBER 13, 2014

7:20 p.m. - 7:45 p.m.	**Gene- and Pathway-based Association Analyses of Shared Psychiatric Genomics Consortium Data** Miaoxin Li, The University of Hong Kong
7:45 p.m. - 8:00 p.m.	**Discussion** Pak Sham, The University of Hong Kong
6:00 p.m. - 8:00 p.m.	**Following a Strong Lead: Functional Investigation of GWAS Signals for Schizophrenia** ***Carstensen***

Chair: Gary Donohoe, National University of Ireland Galway
Moderator: Derek Morris, National University of Ireland Galway

6:05 p.m. - 6:30 p.m.	**Proximal Genetic Risk Mechanisms for Schizophrenia: Effects of Genome-wide Significant Risk Variants on Gene Expression in the Human Brain** Nick Bray, Institute of Psychiatry, King's College London
6:30 p.m. - 6:55 p.m.	**Functional Annotation and Cellular Phenotyping of Disease-implicated Variants** Colm O'Dushlaine, Broad Institute
6:55 p.m. - 7:20 p.m.	**Neural Mechanisms Underlying Genome Wide Significant Associations with Schizophrenia** Andreas Meyer-Lindenberg, Central Institute of Mental Health
7:20 p.m. - 7:45 p.m.	**Polygenic Risk of Major Psychiatric Disorder, Cognition and Cognitive Aging** Andrew McIntosh, University of Edinburgh
7:45 p.m. - 8:00 p.m.	**Discussion** Susanne Erk, Department of Psychiatry and Psychotherapy, Division of Mind and Brain Research

FULL SCHEDULE

MONDAY, OCTOBER 13, 2014

6:00 p.m. - 8:00 p.m.	**New Findings from the Enhancing Neuro Imaging Genetics through Meta-analysis (ENIGMA) Consortium** ***Lumbye***

Chair: Sarah Medland, Queensland Institute of Medical Research
Moderator: Barbara Franke, Departments of Human Genetics and Psychiatry, Donders Institute for Brain, Cognition and Behaviour, Radboud University Medical Center

6:00 p.m. – 6:10 p.m.	**Introduction** Sarah Medland, Queensland Institute of Medical Research
6:10 p.m. - 6:40 p.m.	**Common Genetic Variants Influence Human Subcortical Brain Structures in 29,000 People** Derrek Hibar, UCLA
6:40 p.m. - 7:10 p.m.	**ENIGMA Bipolar Disorder and Schizophrenia: Clear Patterns of Brain Structure Abnormalities** Ole Andreassen, University of Oslo
7:10 p.m. - 7:40 p.m.	**Multi-site Genetic Analysis of Diffusion Weighted Magnetic Resonance Scans from the ENIGMA–DTI Working Group** Neda Jahanshad, Imaging Genetics Center, Institute of Neuroimaging and Informatics, Keck School of Medicine of USC
7:40 p.m. - 8:00 p.m.	**Discussion** Nick Martin, Queensland Institute of Medical Research
6:00 p.m. – 9:00 p.m.	**ISPG Board of Directors Meeting (invitation only)** Paafuglen/Tulipanen

NOTES

SCHEDULE AT A GLANCE

TUESDAY, OCTOBER 14, 2014

8:30 a.m. – 9:30 a.m. **Plenary Session: *The Gut Microbiota and the Impact on Human Health***
Tivoli Congress Hall

9:30 a.m. – 9:45 a.m. **Coffee Break**

9:45 a.m. – 11:00 a.m. **ISPG Award Presentations with Talks**
Tivoli Congress Hall

11:00 a.m. – 1:00 p.m. **Poster Session**
Tivoli Congress Hall Foyer - Ground Floor

1:00 p.m. – 2:00 p.m. **Plenary Session: *Epidemiology in Psychiatric Genetics: Putting the E into GxE***
Tivoli Congress Hall

2:00 p.m. – 2:15 p.m. **Coffee Break**

2:15 p.m. – 4:15 p.m. **Concurrent Symposia Sessions**

Endophenotypes for Gene Discovery in Major Mental Disorder	***The Application of Isolated Populations in the Identification of Rare Risk Variants for Psychiatric Disorders***	***Family Genome Sequencing in Bipolar Disorder***	***Eating Disorders: Breakthroughs and New Directions in Genomics and Epigenomics***	***Report of the ISPG Genetic Testing Taskforce***
Lumbye	Harlekin	Carstensen	Columbine	Tivoli Congress Hall

4:15 p.m. – 4:30 p.m. **Coffee Break**

SCHEDULE AT A GLANCE

TUESDAY, OCTOBER 14, 2014

4:30 p.m. – 6:00 p.m. **Concurrent Oral Presentation Sessions**

Schizophrenia: Genomics & More	***Novel Approaches and Tools for Bench and Bedside***	***Affective Disorders: Genomics & More***	***Functional Genomics & Endophenotypes***
Lumbye	Harlekin	Carstensen	Columbine

6:00 p.m. – 7:00 p.m. **Plenary Session: *The Use of Genetics to Study Functions and Dysfunctions of the Brain***
Tivoli Congress Hall

8:00 p.m. – 10:00 p.m. **Networking Reception**
Copenhagen Town Hall (off property)

FULL SCHEDULE

TUESDAY, OCTOBER 14, 2014

8:30 a.m. – 9:30 a.m. **Plenary Session: The Gut Microbiota and the Impact on Human Health**
Tivoli Congress Hall

Chair: Thomas Werge, Ph.D., Institute of Biological Psychiatry
Co-chair: Jordan Smoller, M.D., Massachusetts General Hospital, Harvard Medical School
Plenary Speaker: Oluf Borbye Pedersen, M.D., University of Copenhagen

The study of microbes has intrigued scientists for centuries. With the introduction of cultivation-independent methods, the focus has expanded from investigations of pathogenic organisms to a deeper interest in the symbiotic, non-pathogenic, i.e. commensal microbes, and their interaction with their human host. By far, the largest concentration of microbes is located in the human distal gut, where the vast majority is of bacterial origin. The gut microbiota, which is the collective microbial community in the intestine, exhibits profound effects on human health. In fact the gut microbiota can be regarded as a microbial organ within the human body, and while the host provides for an appropriate environment, the gut microbes execute pertinent functions that the host is unable to perform by itself. These functions include production of short chain fatty acids by fermentation of otherwise indigestible polysaccharides from the diet, and synthesis and absorption of vita.m.ins such as B- and K-vita.m.ins. Importantly, the gut microbiota also plays a significant role in the maturation and adaptation of the immune system and in the defense against pathogens, in regulation of intestinal hormone secretion and in gastrointestinal nerve activity.
The gut microbiota can be described in terms of its composition (which bacteria are present?) and in terms of its functional capability (what functions do the bacteria exert?). To describe the composition of the gut microbiota, microbial DNA is usually extracted from fecal sa.m.ples, as these generally are considered to be representative of the distal colon microbiota, and sequenced either in a targeted or untargeted manner. Describing the functional capability of the gut microbiota is typically done by applying whole-genome shot-gun sequencing which allows characterization of the collective genome of the gut microbiota – the microbiome. The human gut microbiota is estimated to consist of approximately 1,000 prevalent bacterial species, and each individual harbors at least 160 such species. In totol the human intestine harbor about 100 trillion bacteria. It has been suggested that a core microbiome exists as gut bacterial species seem to be

shared among individuals. Yet, based on current evidence this "core microbiome" probably represent a core of common functions necessary for correct functioning of the gut, rather than a core of common organisms.
In this lecture, Pedersen will discuss present knowledge about regulators of the human gut microbiota and give examples of how altered gut microbiota composition and function associate with common diseases. Finally, Pedersen will address the question whether gut microbiota dysbiosis is directly involved in the pathogenesis of common clinical disorders.

9:30 a.m. – 9:45 a.m.	**Coffee Break**
9:45 a.m. – 11:00 a.m.	**ISPG Award Presentations with Talks** Tivoli Congress Hall

Remembering the Future: Alzheimer's Disease as a Model for Neuropsychiatric Disease
Margaret Pericak-Vance, University of Miami, Miller School of Medicine

Late-onset Alzheimer's disease (LOAD), defined by the onset of symptoms after age 60, evolves slowly from mildly impaired memory to severe cognitive loss. It is a progressive neurodegenerative disorder that cannot, as yet, be prevented, and is basically untreatable. An estimated 5.5 million Americans are affected with Alzheimer disease, 90% of whom have LOAD. It is estimated that ~30-40% of the US population over the age of 85 years will have LOAD. The costs related to LOAD are estimated at over $200 billion per year. As the U.S. population ages, it is expected that the number of LOAD cases will increase: by the year 2050, 1 in 45 Americans will be affected, with estimated costs of over 1.2 trillion in US dollars. Similar statistics can be seen worldwide. A critical barrier to lessening the impact of this disease is the limited development of drugs to prevent or treat LOAD, which is mostly attributable to an incomplete understanding of the basic pathologic mechanisms underlying Alzheimer disease. Determining which genes and gene networks contribute to LOAD risk will reveal basic pathogenic mechanisms, highlighting key proteins and pathways for drug development ("druggable targets"). These findings will also contribute to the development of methods for identifying those at greatest risk for LOAD when preventive measures become available, enabling potential prevention before the disease takes its toll. The

identification between 1992 and 1995 of the rare causative variants in Alzheimer disease in *APP*, *PSEN1*, and *PSEN2* were the basis for therapies in clinical trials that have unfortunately had limited success. More recently, *APOE*, the most significant common variant risk factor, has become the focus of clinical trials. Thus, while more effective targets need to be discovered, drug development to date clearly suggests that gene discovery approaches have the potential to identify specific proteins and pathways as therapeutic targets. Since its nascent beginnings in the early 90's, Alzheimer disease genetics has made major strides in our understanding into the pathophysiology of this disease. Within the last five years, over 20 additional common genetic risk factors have been identified. International researchers have come together in order to help stop this potential epidemic. Recently, at the mandate of President Obama, the National Alzheimer's Project Act (NAPA) was established. NAPA contributed to the establishment of the Alzheimer's Disease Sequencing Project (ADSP), with its goal of understanding the genetic contributions to Alzheimer disease in order to define new drug targets for therapeutic intervention. These united efforts represent one of the largest and best-funded projects to date of any human complex disease, and provide a powerful and promising approach to conquer other vexing disorders.

How Can Genetics Inform on Psyciatric Disease?
Benjamin Neale, Massachusetts General Hospital

Human genetics has the potential to inform on a range of different questions relevant to psychiatric illness. From epidemiological insights into the relevance of risk factors through to generating novel biological hypotheses for pathogenic mechanisms, genetics is a platform for gaining traction on these complex and debilitating diseases. In this talk, Neale will review how the success of genetic discovery for psychiatric illness is the first step towards unravelling the nature and causes of these diseases and thus potentially enabling a redefinition of the nosology of psychiatric illness along with powering research for novel therapeutics.

11:00 a.m. – 1:00 p.m. **Poster Session**
Tivoli Congress Hall Foyer - Ground Floor
*See pages 122-141 for a complete list of posters.

FULL SCHEDULE

TUESDAY, OCTOBER 14, 2014

1:00 p.m. – 2:00 p.m. **Plenary Session: Epidemiology in Psychiatric Genetics: Putting the E into GxE**
Tivoli Congress Hall

Chair: Ole Mors, Ph.D., Aarhus University Hospital, Risskov
Co-chair: Naomi Wray, Ph.D., The University of Queensland
Plenary Speaker: Preben Bo Mortensen, M.D., University of Aarhus

Severe mental disorders as schizophrenia, bipolar affective disorder, depression, autism spectrum disorders and ADHD, include some of the most disabling and costly disorders affecting mankind. Their causes are likely to include both important genetic and environmental risk factors. It has become increasingly clear that aetiologies overlap across disorders and that interaction between genetic and environmental factors is key to the pathogenesis.
However, although early 19th century population-based psychiatric genetic studies are among the earliest examples of chronic disease epidemiology, studies of genetic and environmental causes of mental illnesses, respectively, have for many years led relatively separate lives.
In this talk, Mortensen will present a Danish total national birth cohort study, iPSYCH, that integrates longitudinal information on individual and familial exposures, and molecular genetic data. With early results from this study, he will illustrate how environmental data, as well as the traditional epidemiological focus on sources of bias and confounding in observational studies, might inform and assist the current rapid progress in psychiatric genetics.

2:00 p.m. – 2:15 p.m. **Coffee Break**

FULL SCHEDULE

TUESDAY, OCTOBER 14, 2014

Concurrent Symposia Sessions

2:15 p.m. - 4:15 p.m. **The Application of Isolated Populations in the Identification of Rare Risk Variants for Psychiatric Disorders**
Harlekin

Chair: Anders Børglum, Aarhus University
Moderator: Ole Mors, Aarhus University Hospital

2:15 p.m. – 2:20 p.m. **Introduction**
Anders Børglum, Aarhus University

2:20 p.m. – 2:45 p.m. **Psychiatric Disorders and Isolated Populations**
Hreinn Stefansson, deCODE genetics

2:45 p.m. – 3:10 p.m. **The Finnish Population Isolate as an Example in Psychiatric Genetics**
Aarno Palotie, University of Helsinki

3:10 p.m. – 3:35 p.m. **Identification of Rare Variants in an Ashkenazi Jewish Case-control Schizophrenia Cohort**
Todd Lencz, Zucker Hillside Hospital

3:35 p.m. – 4:00 p.m. **Combination of Whole-genome and Whole-exome Sequencing, to Identify Rare and de-novo Variation in Cases of Schizophrenia and Bipolar Disorder from the Faroe Islands**
Francesco Lescai, Aarhus University

4:00 p.m. – 4:15 p.m. **Discussion**
Thomas Als, Aarhus University

FULL SCHEDULE

TUESDAY, OCTOBER 14, 2014

2:15 p.m. - 4:15 p.m. **Eating Disorders: Breakthroughs and New Directions in Genomics and Epigenomics**
Columbine

Chair: Cynthia Bulik, University of California at Chapel Hill
Moderator: Gerome Breen, Institute of Psychiatry, King's College London

2:15 p.m. – 2:20 p.m. **Introduction**
Cynthia Bulik, University of California at Chapel Hill

2:20 p.m. - 2:45 p.m. **A Mega-analysis of Genome Wide Association in Anorexia Nervosa**
Cynthia Bulik, University of California at Chapel Hill

2:45 p.m. - 3:10 p.m. **Gene Environment Interactions and Adolescent Eating Disorder Behaviors: A Population-based Study**
Nadia Micali, UCL Institute of Child Health

3:10 p.m. - 3:35 p.m. **Machine Learning Based Disease Risk Prediction for Anorexia Nervosa**
Yiran Guo, Children's Hospital of Philadelphia

3:35 p.m. - 4:00 p.m. **Eating Disorders and the Epigenome - How (Mal-) Nutrition Changes the Chromatine Code**
Helge Frieling, University of Erlangen-Nurenberg

4:00 p.m. - 4:15 p.m. **Discussion**
Gerome Breen, Institute of Psychiatry, King's College London

FULL SCHEDULE

TUESDAY, OCTOBER 14, 2014

2:15 p.m. - 4:15 p.m. **Report of the ISPG Genetic Testing Taskforce**
Tivoli Congress Hall

Chair: Francis McMahon, NIH/NIMH
Moderator: Philip Mitchell, University of New South Wales

2:15 p.m. – 2:20 p.m. **Introduction**
Francis McMahon, NIH/NIMH

2:20 p.m. - 2:45 p.m. **Copy Number Variations — Role in Counseling**
Elliot Gershon, University of Chicago

2:45 p.m. - 3:10 p.m. **Genetic Tests to Guide Optimal Treatment**
Daniel Müeller, University of Toronto

3:10 p.m. - 3:35 p.m. **Reporting of Incidental or Secondary Findings**
Marcella Rietschel, Central Institute of Mental Health

3:35 p.m. - 4:00 p.m. **Psychological, Ethical and Clinical Implications in Genetic Testing**
Jehannine Austin, University of British Columbia

4:00 p.m. - 4:15 p.m. **Discussion**
Philip Mitchell, University of New South Wales

FULL SCHEDULE

TUESDAY, OCTOBER 14, 2014

2:15 p.m. - 4:15 p.m. **Family Genome Sequencing in Bipolar Disorder**
Carstensen

Chair: John Kelsoe, University of California San Diego
Moderator: James Potash, The University of Iowa Carver College of Medicine

2:15 p.m. – 2:20 p.m. **Introduction**
John Kelsoe, University of California San Diego

2:20 p.m. - 2:45 p.m. **Rare, Non-coding Variants in Calcium Signaling Genes Influence Risk for Bipolar Disorder**
ECIP ★ Seth Ament, Institute for Systems Biology

2:45 p.m. - 3:10 p.m. **Whole Genome Sequencing in a Genetic Isolate**
Maja Bucan, University of Pennsylvania

3:10 p.m. - 3:35 p.m. **WGS of Multiplex Pedigrees**
William Byerly, University of California at Irvine

3:35 p.m. - 4:00 p.m. **Exome Analysis in Trio Families of Bipolar Disorder**
Tadafumi Kato, RIKEN Brain Science Institute

4:00 p.m. - 4:15 p.m. **Discussion**
Peter Zandi, John Hopkins University

★ – Travel Awardee ECIP – ECIP Finalist

FULL SCHEDULE

TUESDAY, OCTOBER 14, 2014

2:15 p.m. - 4:15 p.m.	**Endophenotypes for Gene Discovery in Major Mental Disorder** ***Lumbye***

Chair: Andrew McIntosh, University of Edinburgh
Moderator: Laura Almasy, Texas Biomedical Research Institute

2:15 p.m. – 2:20 p.m.	**Introduction** Andrew McIntosh, University of Edinburgh
2:20 p.m. - 2:45 p.m.	**Endophenotypes for Depression and Heir Value in Gene Discovery** Andrew McIntosh, University of Edinburgh
2:45 p.m. - 3:10 p.m.	**Discovering Schizophrenia Endophenotypes in Randomly Ascertained Pedigrees** David Glahn, Yale, Olin Neuropsychiatry Research Center in the Institute of Living
3:10 p.m. - 3:35 p.m.	**Epistasis Increases Variation Explained in Endophenotypes above the Contribution of the Polygenic Score** Kristin Nicodemus, The University of Edinburgh
3:35 p.m. - 4:00 p.m.	**Adolescent Neurodevelopmental Phenotypes of Bipolar Disorder in a Genetically Isolated Population** Carrie Bearden, UCLA
4:00 p.m. - 4:15 p.m.	**Discussion** David Porteous, University of Edinburgh
4:15 p.m. – 4:30 p.m.	**Coffee Break**

FULL SCHEDULE

TUESDAY, OCTOBER 14, 2014

Concurrent Oral Presentation Sessions

4:30 p.m. – 6:00 p.m. **Schizophrenia: Genomics & More**
Lumbye

Chair: Manuel Mattheisen, Aarhus University
Co-Chair: Iiris Hovatta, University of Helsinki

4:30 p.m. - 4:45 p.m. **The Impact of CNVs on CNS Function in Schizophrenia**
Andrew Pocklington, Cardiff University

4:45 p.m. - 5:00 p.m. **Functional Analysis of the Schizophrenia and Autism-associated gene, Transcription Factor 4 (TCF4), during Cortical Development**
ECIP ★ Brady Maher, Lieber Institute for Brain Development

5:00 p.m. - 5:15 p.m. **Advanced Paternal Age, De Novo Mutations, Genetic Liability and the Risk of Psychiatric Illness**
Peter Visscher, The University Of Queensland

5:15 p.m. - 5:30 p.m. **Chromatin Immunoprecipitation and Next-generation Sequencing Analysis Implicates Transcription Factor 4 (TCF4) in the Regulation of Neuronal Development and Cell Adhesion Pathways**
Joseph McClay, Virginia Commonwealth University

5:30 p.m. - 5:45 p.m. **SHANK3 Variants Confer Risk for Schizophrenia and Indicate a Genetic Overlap with Autism Spectrum Disorders**
Simone Berkel, Institute of Human Genetics Heidelberg

5:45 p.m. - 6:00 p.m. **Methylomic Profiling of Human Brain Tissue Supports a Neurodevelopmental Origin for Schizophrenia**
Jonathan Mill, University of Exeter

★ – Travel Awardee ECIP – ECIP Finalist

FULL SCHEDULE

TUESDAY, OCTOBER 14, 2014

4:30 p.m. – 6:00 p.m. **Novel Approaches and Tools for Bench and Bedside**
Harlekin

Chair: Engilbert Sigurdsson, University of Iceland-Landspitali
Co-chair: Katharina Domschke, University of Wuerzburg

4:30 p.m. - 4:45 p.m. **Development of a New Technology for Single-cell mRNA-Seq Analysis, on the Scale Required to Analyze the Cellular Complexity of the Brain**
Steven McCarroll, Stanley Center for Psychiatric Research, Broad Institute of MIT and Harvard

4:45 p.m. - 5:00 p.m. **International Breakpoint Mapping Consortium - Identifying Neurodevelopmental and Neuropsychiatric Genes by Saturation of the Human Genome with Chromosomal Breakpoints**
Christina Halgren, Wilhelm Johannsen Center for Functional Genome Research, University of Copenhagen

5:00 p.m. - 5:15 p.m. **PsychChip: Design, Quality Control and Performance**
Stephan Ripke, Massachusetts General Hospital

5:15 p.m. - 5:30 p.m. **Genome-wide Analysis Identifies Common Variants Associated with Neonatal Brain Volumes**
Rebecca Knickmeyer, UNC Chapel Hill

5:30 p.m. - 5:45 p.m. **Linkage of Schizophrenia-related Grey Matter Component to 12q24**
ECIP Emma Sprooten, School of Medicine, Yale University

5:45 p.m. - 6:00 p.m. **Combinatorial Pharmacogenomics for Treatment-resistant Depression: Clinical Validity, Clinical Utility, and Health Economics**
Bryan Dechairo, AssureRx Health

ECIP – ECIP Finalist

FULL SCHEDULE

TUESDAY, OCTOBER 14, 2014

4:30 p.m. – 6:00 p.m. **Affective Disorders: Genomics & More**
Carstensen

Chair: Martin Schalling, Karolinska Institutet
Co-Chair: Elliot Gershon, University of Chicago

4:30 p.m. - 4:45 p.m. **Bipolar Disorder and its Relation to Major Psychiatric Disorders: A Family-based Study in the Swedish Population**
ECIP Jie Song, Karolinska Institutet

4:45 p.m. - 5:00 p.m. **Psychiatric Genomics Consortium (PGC) Bipolar Disorder GWAS of 50,000 Samples**
Eli Stahl, Icahn School of Medicine at Mount Sinai

5:00 p.m. - 5:15 p.m. **Interaction between Genetic Variants and Environmental Adversity in the Etiology of Major Depressive Disorder**
★ Niamh Mullins, King's College London

5:15 p.m. - 5:30 p.m. **Shared Genetic Effects Contributing to Risk of Major Depressive Disorder across European and Han Chinese Populations**
ECIP T. Bernard Bigdeli, VIPBG

5:30 p.m. - 5:45 p.m. **The Effect of the FTO Gene on Body-mass Index is increased by the Presence of Depressive Disorder: A Meta-analysis of 13,701 Individuals**
ECIP Margarita Rivera, Institute of Psychiatry, King's College London

5:45 p.m. - 6:00 p.m. **Familiarity and SNP Heritability of Age at Onset and Episodicity in Major Depressive Disorder**
Panagiotis Ferentinos, University of Athens

★ – Travel Awardee ECIP – ECIP Finalist

FULL SCHEDULE

TUESDAY, OCTOBER 14, 2014

4:30 p.m. – 6:00 p.m. **Functional Genomics & Endophenotypes**
Columbine

Chair: Vidar Steen, University of Bergen
Co-chair: Tadafumi Kato, RIKEN Brain Science Institute

4:30 p.m. - 4:45 p.m. **The Antipsychotic Olanzapine Interacts with the Gut Microbiome to Cause Weight Gain in Mouse**
James Crowley, University of North Carolina at Chapel Hill

4:45 p.m. - 5:00 p.m. **Carriers of a Genome-wide Significant Bipolar Disorder Risk Allele Show Decreased TRANK1 Expression in Neural Progenitor Cells that Is Rescued by Sodium Valproate**
Xueying Jiang, National Institute of Mental Health

5:00 p.m. - 5:15 p.m. **Molecular Mechanisms of D-cycloserine in Fear Extinction: Insights from RNA and MicroRNA Sequencing**
ECIP Stefanie Malan-Müller, Stellenbosch University

5:15 p.m. - 5:30 p.m. **Behavioral and Transcriptomic Alterations in 15q13.3 Homozygous Knockout Mice**
Annika Forsingdal, H. Lundbeck A/S

5:30 p.m. - 5:45 p.m. **Pharmacogenomic Endophenotypes: What Can the Subjective Response to D-amphetamine tell us about Risk for Psychiatric Disorders?**
Abraham Palmer, University of Chicago

5:45 p.m. - 6:00 p.m. **Identifying Endophenotypes for Depression – A Composite Trait Analysis**
ECIP Lynsey Hall, University of Edinburgh

ECIP – ECIP Finalist

FULL SCHEDULE

TUESDAY, OCTOBER 14, 2014

6:00 p.m. – 7:00 p.m. **Plenary Session: The Use of Genetics to Study Functions and Dysfunctions of the Brain**
Tivoli Congress Hall

Chair: Thomas Werge, Ph.D., Institute of Biological Psychiatry
Co-chair: Sarah Bergen, Ph.D., Karolinska Institute
Plenary Speaker: Kári Stefánsson, M.D., deCODE genetics

The primary function of the brain is to be the organ of consciousness. Consciousness has two principal components, alertness and content of consciousness; the content consists of thoughts and emotions. We do not know how the brain generates thoughts and emotions which creates a problem for those of us who are trying to develop an understanding of the pathogenic mechanisms of diseases that primarily affect throughts and emotions such as schizophrenia and bipolar disease. We have been using two genetic approaches to search for biological/biochemical mechansisms brought to bear in the generation /containment of thoughts. One is to submit a large number of Icelanders to several tests of cognitive function and search for variants in the sequence of the germline genome that place people on a normal distribution curve of various aspects of cognition. The second is to take variants in the germline genome that affect the risk of diseases such as schizophrenia and bipolar and determine how they affect cognition in healthy carriers. The session will present results that show how variants that confer large risk of schizophrenia affect cognition in “normal” carriers and even the structure of their brains. Furthermore, we have taken common variants in the genome that associate with schizophrenia and bipolar disorder and constructed a polygenic risk score for these diseases and shown that the score is much higher in members of the creative profession than in several kinds of controls. For the purpose of this study we used membership in artistic societies of painters, writers and dancers as defining the creative professions. The session will also discuss in some detail how the interplay between nature and nurture determines the education an individual eventually gets, his verbal IQ, and his risk of various psychiatric and cardio-vascular diseases. The session will conclude by discussion how the rate of cognitive decline of the elderly is dictated by genetics.

8:00 p.m. – 10:00 p.m. **Networking Reception**
Copenhagen Town Hall (off property)

SCHEDULE AT A GLANCE

WEDNESDAY, OCTOBER 15, 2014

8:30 a.m. – 9:30 a.m. **Plenary Session: *Parental Effects on the Epigenome***
Tivoli Congress Hall

9:30 a.m. – 9:45 a.m. **Coffee Break**

9:45 a.m. – 11:45 a.m. **Plenary Panel Session: *Pathways to Therapy and Prevention***
Tivoli Congress Hall

11:45 a.m. – 12:45 p.m. **ISPG Business Meeting (with lunch)**
Carstensen

12:45 p.m. – 1:00 p.m. **Coffee Break**

1:00 p.m. – 2:30 p.m. **Concurrent Oral Presentation Sessions**

Autism: Genomics & More	***Transdiagnostic Approaches, OCD, and Eating Disorders***	***Schizophrenia: Genomics & More***	***Novel Biostatistics and Bioinformatics***
Lumbye	Harlekin	Carstensen	Columbine

2:30 p.m. – 2:45 p.m. **Coffee Break**

2:45 p.m. – 4:45 p.m. **Concurrent Symposia Sessions**

The Effect of Psychosis Risk Genes across the Phenotypic Spectrum	***Copy Number Variations in Adults with Neurodevelop-mental Disorders***	***Systems Biology Approaches in Psychiatric Disorders***	***Immunomics: Exploring New Territory in Schizophrenia***
Lumbye	Harlekin	Carstensen	Columbine

SCHEDULE AT A GLANCE

WEDNESDAY, OCTOBER 15, 2014

4:45 p.m. – 6:45 p.m. **Poster Session**
Tivoli Congress Hall Foyer - Ground Floor

7:00 p.m. – 9:00 p.m. **Concurrent Symposia Sessions**

Towards Translational Psychiatry: From Genomic Discoveries to Prediction of Treatment Response	***The Interplay between Genetics and Early Trauma in Severe Mental Disorders***	***Genetics and Aggression: The Aggressotype Project***	***Neuro-psychiatric Genetic Research in Latin America***
Lumbye	Harlekin	Carstensen	Columbine

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

8:30 a.m. – 9:30 a.m. **Plenary Session: Parental Effects on the Epigenome**
Tivoli Congress Hall

Chair: Anders Børglum, M.D., Ph.D., Aarhus University
Co-chair: John McGrath, M.D., University of Queensland
Plenary Speaker: Michael Meaney, Ph.D., McGill University

Maternal care directly alters the development of stress responses as well as multiple forms of learning and memory, including fear-related learning. These effects involve stable and tissue-specific changes in transcription. Thus, in the adult hippocampus there are prominent 'maternal' effects on glucocorticoid receptor gene (NR3C1) expression in brain regions in the rat that regulate stress responses, as well as in the expression of genes that encode for sub-units of various glutamate receptors involved in synaptic plasticity and learning. The stable effects of variations in maternal care associate with epigenetic modifications at the level of DNA methylation and post-translational modifications to histones. Recent findings suggest significant effects on levels of 5-hydroxymethylation, as well as histone methylation in the promoter for the GR gene as well as that for Grm1, which encodes for a metabotropic glutamate receptor (mGluR1). Differences in the hippocampal expression of GR and mGluR1 are directly linked to maternal effects of stress responses and hippocampal neuronal function.

Translational studies show comparable effects of parent – offspring interactions in humans, including effects child maltreatment on the epigenetic state of multiple GR gene promoters. Genome-wide analyses of the epigenome with human samples show effects of parental care, as well as of intervention programs that associate with specific endophenotypes. Importantly the effects of these and other environmental conditions on epigenetic states appear to be moderated by genotype, such that variations in DNA methylation can be best predicted by gene x environment models. Proofs of principal studies reveal the influence of the Val66Met bdnf polymorphism in mediating maternal influences on the human epigenome.

Finally, studies in rodent models suggest an epigenetic basis for individual differences in maternal behavior as well as for the transgenerational transmission of such variations. These results of these studies are consistent with those of intervention programs that directly or indirectly target the quality of parent – offspring interactions with effects on the mental health of the offspring. Studies in partnership with intervention programs reveal preliminary evidence for lasting effects on the human epigenome.

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

9:30 a.m. – 9:45 a.m. **Coffee Break**

9:45 a.m. – 11:45 a.m. **Plenary Panel Session: Pathways to Therapy and Prevention**
Tivoli Congress Hall

Chair: James Potash, The University of Iowa Carver College of Medicine
Co-chair: Kerstin Plessen, University of Copenhagen
Participants: Raimund Buller, Lundbeck
Steve Hyman, Broad Institute
Peter Falkai, University of Goettingen
Kári Stefánsson, deCODE genetics
Richard Weinshilboum, Mayo Clinic

11:45 a.m. – 12:45 p.m. **ISPG Business Meeting (with lunch)**
Carstensen

12:45 p.m. – 1:00 p.m. **Coffee Break**

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

Concurrent Oral Presentation Sessions

1:00 p.m. – 2:30 p.m. **Autism: Genomics & More**
Lumbye

Chair: Marian Hamshere, Cardiff University
Co-chair: Ketil Oedegaard, University of Bergen

1:00 p.m. - 1:15 p.m. **Integrative Functional Genomic Studies Identify Differential Activating and Repressive Functions of CHD8 in Neurodevelopmental Pathways Associated with Autism in Neural Precursor Cells**
Michael Talkowski, Massachusetts General Hospital

1:15 p.m. - 1:30 p.m. **What can Genetic Research tell us about Current Psychiatric Nosology? Lessons from Autism**
Susan Santangelo, Maine Medical Center

1:30 p.m. - 1:45 p.m. **Exome Sequencing of Autism Patients Reveals a Mix of Genes with Large and Modest Effects on Liability**
Kaitlin Samocha, Massachusetts General Hospital

1:45 p.m. - 2:00 p.m. **Using Genome-wide GxE Analysis to Search for Potential Modifiers of the Risk Effect of Maternal Smoking on the Expression of Autistic Traits**
Beate St. Pourcain, University of Bristol

2:00 p.m. - 2:15 p.m. **A Functional Genomics Approach to Understand Genetic Variation in (non)neuronal Cell Types Underlying Autism Spectrum Disorders**
Danielle Posthuma, VU University

2:15 p.m. - 2:30 p.m. **Increased Female Burden of Autosomal CNVs in Control Populations**
Lauren Weiss, University of California San Francisco

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

1:00 p.m. – 2:30 p.m. **Transdiagnostic Approaches, OCD, and Eating Disorders**
Harlekin

Chair: Carlos Lopez-Jaramillo, University of Antioquia
Co-chair: August Gabriel Wang, Copenhagen University Hospital

1:00 p.m. - 1:15 p.m. **Differential Genic Burden of Coding and Regulatory Variants in Human Obsessive-Compulsive Disorder: Guided by Natural Canine Model and Induced Mouse Model**
Hyun Ji Noh, Broad Institute of MIT and Harvard

1:15 p.m. - 1:30 p.m. **Core-exome Chip Study of Low-frequency Variants Identifies Genome-wide Significant Hits Associated with Anorexia Nervosa**
Laura Huckins, Wellcome Trust Sanger Institute

1:30 p.m. - 1:45 p.m. **Mega-analysis of Age at Onset of Bipolar Disorder, Major Depressive Disorder and Schizophrenia in the Psychiatric Genomics Consortium**
ECIP T. Bernard Bigdeli, VIPBG

1:45 p.m. - 2:00 p.m. **Genome-wide Search Implicates a Potassium Channel Gene in Cognitive Performance in the Elderly**
Thomas W. Mühleisen, Genomic Imaging Group

2:00 p.m. - 2:15 p.m. **Genes Involved in Left/Right Structural Asymmetry Are Associated with Handedness and Appear to Contribute Neurodevelopmental Disorders**
Silvia Paracchini, University of St. Andrews

2:15 p.m. - 2:30 p.m. **A Genome-wide Association Study of Quantitative Obsessive-compulsive Traits in a Community-based Sample of Children and Adolescents**
Christie Burton, Hospital for Sick Children

ECIP – ECIP Finalist

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

1:00 p.m. – 2:30 p.m. **Schizophrenia: Genomics & More**
Carstensen

Chair: Hreinn Stefánsson, deCODE genetics
Co-chair: Srdjan Djurvic, Oslo University Hospital, University of Bergen

1:00 p.m. - 1:15 p.m. **Emerging Patterns of Schizophrenia Risk Conferred by De Novo Mutation**
Daniel Howrigan, Massachusetts General Hospital

1:15 p.m. - 1:30 p.m. **The Genomics of Treatment Resistant Schizophrenia**
James Walters, Cardiff University

1:30 p.m. - 1:45 p.m. **A Hypothesis-driven Analysis of Genome-wide Association Summary Results from the Psychiatric Genomics Consortium Identifies Novel Nuclear-encoded Mitochondria Susceptibility Loci for Schizophrenia**
★ ECIP
Vanessa Gonçalves, Centre for Addiction and Mental Health

1:45 p.m. - 2:00 p.m. **Parsing Genetic Associations in the MHC in Schizophrenia**
ECIP
Semanti Mukherjee, The Feinstein Institute for Medical Research

2:00 p.m. - 2:15 p.m. **The Genetic and Epidemiological Relationship between Rheumatoid Arthritis and Schizophrenia**
ECIP
Jack Euesden, King's College London

2:15 p.m. - 2:30 p.m. **Methylome-wide Investigation of CpGs that are Created or Destroyed by SNPs Implicates Sites Associated with Schizophrenia in both Blood and Brain**
Karolina Aberg, Center for Biomarker Research and Personalized Medicine, Virginia Commonwealth University

★ – Travel Awardee ECIP – ECIP Finalist

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

1:00 p.m. – 2:30 p.m. **Novel Biostatistics and Bioinformatics**
Columbine

Chair: Stephanie Le Hellard, University of Bergen
Co-chair: Henrik Rasmussen, Mental Health Centre Set Hans

1:00 p.m. - 1:15 p.m. **Genetic Predisposition to Schizophrenia Associated with Increased Use of Cannabis**
Robert Power, Institute of Psychiatry, London

1:15 p.m. - 1:30 p.m. **Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores for Schizophrenia and other Diseases**
Bjarni Vilhjalmsson, Harvard School of Public Health

1:30 p.m. - 1:45 p.m. **Discovery of an Inverse Axis of Risk for Polygenic and Rare Variant Burdens Reveals a Shared Risk Architecture among Psychiatric Traits**
Lea Davis, The University of Chicago

1:45 p.m. - 2:00 p.m. **Developmental Regulation of Human Cortex Transcription at Base-bair Resolution**
Andrew Jaffe, Lieber Institute for Brain Development

2:00 p.m. - 2:15 p.m. **Gene-based Pleiotropy across Five Major Psychiatric Disorders**
Dale Nyholt, Queensland Institute of Medical Research

2:15 p.m. - 2:30 p.m. **Comparison of Model-based Estimators of Population Structure in a GWAS Framework**
ECIP Antonio Pardiñas, Cardiff University

2:30 p.m. – 2:45 p.m. **Coffee Break**

ECIP – ECIP Finalist

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

Concurrent Symposia Sessions

2:45 p.m. - 4:45 p.m. **Copy Number Variations in Adults with Neurodevelopmental Disorders**
Harlekin

Chair: Annick Vogels, University Hospitals Leuven, Department of Human Genetics, KU Leuven
Moderator: Nicholas Bass, Division of Psychiatry, University College London

2:45 p.m. – 2:50 p.m. **Introduction**
Annick Vogels, University Hospitals Leuven, Department of Human Genetics, KU Leuven

2:50 p.m. - 3:15 p.m. **Copy Number Variations in a Large Cohort of Adults with a Dual Diagnosis of Intellectual Disability and Neuropsychiatric Disorders**
Griet Van Buggenhout, University Hospital Leuven

3:15 p.m. - 3:40 p.m. **Cognitive, Psychiatric and Dysmorphic Phenotype in Three Families with Deletion of NRXN1 Gene**
Ramon Novell, Institut Assistencia Sanitaria

3:40 p.m. - 4:05 p.m. **Cognitive and Behavioral Effects of Copy Number Variation at the 16p11.2 BP4-5 Locus**
Sébastien Jacquemont, CHUV, University of Lausanne

4:05 p.m. - 4:30 p.m. **Diagnosing 22q11 Deletion Syndrome in Adults with Neurodevelopmental Disorders**
Annick Vogels, University Hospitals Leuven, Department of Human Genetics, KU Leuven, Belgium

4:30 p.m. - 4:45 p.m. **Discussion**
Andrew McQuillin, UCL

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

2:45 p.m. - 4:45 p.m.	**Immunomics: Exploring New Territory in Schizophrenia** ***Columbine***

Chair: Jennie Pouget, Centre for Addiction and Mental Health
Moderator: James L. Kennedy, Centre for Addiction and Mental Health

2:45 p.m. – 2:50 p.m.	**Introduction** Jennie Pouget, Centre for Addiction and Mental Health
2:50 p.m. - 3:15 p.m. ★ ECIP	**Hypothesis-driven Genome-wide Association Study Highlights the Role of Immune Genes in the Extended Major Histocompatibility Complex in Schizophrenia** Jennie Pouget, Centre for Addiction and Mental Health
3:15 p.m. - 3:40 p.m.	**New Data to Investigate an Old Epidemiological Puzzle: The Negative Association between Schizophrenia and Rheumatoid Arthritis** Naomi Wray, The University of Queensland
3:40 p.m. - 4:05 p.m.	**An Extreme Form of Structural Variation in the Human HLA Locus** Steven McCarroll, Stanley Center for Psychiatric Research, Broad Institute of MIT and Harvard
4:05 p.m. - 4:30 p.m.	**The Microbiome: The Missing Link in the Pathogenesis of Schizophrenia** Robert Yolken, Johns Hopkins
4:30 p.m. - 4:45 p.m.	**Discussion** Paul de Bakker, University Medical Center Utrecht

★ – Travel Awardee ECIP – ECIP Finalist

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

2:45 p.m. - 4:45 p.m. **Systems Biology Approaches in Psychiatric Disorders**
Carstensen

Chair: Kasper Lage, Harvard Medical School, Massachusetts General Hospital, Broad Institute
Moderator: Steven Hyman, Broad Institute

2:45 p.m. – 2:50 p.m. **Introduction**
Kasper Lage, Harvard Medical School, Massachusetts General Hospital, Broad Institute

2:50 p.m. - 3:15 p.m. **Functional Interpretation of Genomes Using Biological Networks**
Kasper Lage, Harvard Medical School, Massachusetts General Hospital, Broad Institute

3:15 p.m. - 3:40 p.m. **Network-based Association Models for Exome-sequencing Data**
Shaun Purcell, Icahn School of Medicine at Mount Sinai

3:40 p.m. - 4:05 p.m. **Data Integration for the Understanding of Comorbidities between Psychiatric Disorders and Other Diseases**
Søren Brunak, Technical University of Denmark

4:05 p.m. - 4:30 p.m. **A Cross-species Neurogenomics Approach to Genetic Basis of Anxiety Disorders**
Iiris Hovatta, University of Helsinki

4:30 p.m. - 4:45 p.m. **Discussion**
Steven Hyman, Broad Institute

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

2:45 p.m. - 4:45 p.m. **The Effect of Psychosis Risk Genes across the Phenotypic Spectrum**
Lumbye

Chair: Anil Malhotra, The Zucker Hillside Hospital
Moderator: Katherine Burdick, Mount Sinai School of Medicine

2:45 p.m. – 2:50 p.m. **Introduction**
Anil Malhotra, The Zucker Hillside Hospital

2:50 p.m. - 3:15 p.m. **Genetic Risk, Neurodevelopment, and the Molecular Pathology of Schizophrenia**
Thomas Hyde, Lieber Institute for Brain Development

3:15 p.m. - 3:40 p.m. **Relationship between Schizophrenia Genes and Neuroimaging Phenotypes in Severe Mental Disorders**
Ole Andreassen, University of Oslo

3:40 p.m. - 4:05 p.m. **GWAS of General Cognitive Ability and Overlap with Schizophrenia**
Anil Malhotra, The Zucker Hillside Hospital

4:05 p.m. - 4:30 p.m. **Additive Genetic Risk Modelling Predicts Phenotypic Heterogeneity in Brain Structure and Cognitive Performance in People with Schizophrenia**
Aristotle Voineskos, University of Toronto

4:30 p.m. - 4:45 p.m. **Discussion**
Michael O'Donovan, Cardiff University

4:45 p.m. – 6:45 p.m. **Poster Session**
Tivoli Congress Hall Foyer - Ground Floor
*See pages 142-162 for poster listing.

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

Concurrent Symposia Sessions

7:00 p.m. - 9:00 p.m. **The Interplay between Genetics and Early Trauma in Severe Mental Disorders**
Harlekin

Chair: Ingrid Melle, Division of Mental Health and Addiction, Institute of Clinical Medicine, University of Oslo
Moderator: Vidar Steen, University of Bergen

7:00 p.m. – 7:05 p.m. **Introduction**
Ingrid Melle, Division of Mental Health and Addiction, Institute of Clinical Medicine, University of Oslo

7:05 p.m. - 7:30 p.m. **Early Life Stress and Long-term Psychopathology: The Role of Epigenetics**
Marco Riva, Dept. Pharmacological & Biomolecular Sciences, University of Milan

7:30 p.m. - 7:55 p.m. **Blood Transcriptomics as Tool to Identify the Long Lasting effects of Childhood Trauma on Psychopathologies Development**
Annamaria Cattaneo, King's College London, Institute of Psychiatry; IRCCS Fatebenefratelli Brescia

7:55 p.m. - 8:20 p.m. **Childhood Trauma and Bipolar Disorders: Severe Clinical Expression and Moderation by Genetic Factors**
Bruno Etain, INSERM U955

8:20 p.m. - 8:45 p.m. **Additive Association between Childhood Trauma and BDNF val66met on Volume of Hippocampal Subfields – Exploring the Role of BDNF RNA**
Monica Aas, Norment, KG Jebsen Centre for Psychosis Research, Oslo University Hospital and Institute of Clinical Medicine, University of Oslo

8:45 p.m. - 9:00 p.m. **Discussion**
Stephanie Le Hellard, University of Bergen

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

7:00 p.m. - 9:00 p.m.	**Neuro-psychiatric Genetic Research in Latin America** ***Columbine***

Chair: Carlos Lopez, University of Antioquia
Moderator: Thomas G. Schulze, Institute for Psychiatric Phenomics and Genomics (IPPG) Ludwig-Maximilians-University Munich

7:00 p.m. – 7:05 p.m.	**Introduction** Carlos Lopez, University of Antioquia
7:05 p.m. - 7:30 p.m.	**Neuro-psychiatric Genetic Research in Costa Rica** Henriette Raventós, Universidad de Costa Rica
7:30 p.m. - 7:55 p.m.	**An Overview of Psychiatric Genetic Studies in Brazil** Homero Vallada, University of Sao Paulo Medical School
7:55 p.m. - 8:20 p.m.	**Immunogenetic Screening in Bipolar Patients from Mexico City** Humberto Nicolini, National Institute of Genomic Medicine INMEGEN
8:20 p.m. - 8:45 p.m.	**Multisystem Phenotypes in Patients with Bipolar Disorder** Carlos Lopez, University of Antioquia
8:45 p.m. - 9:00 p.m.	**Discussion** Thomas G. Schulze, Institute for Psychiatric Phenomics and Genomics (IPPG) Ludwig-Maximilians-University Munich

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

7:00 p.m. - 9:00 p.m.	**Genetics and Aggression: The Aggressotype Project** ***Carstensen***

Chair: Bru Cormand, University of Barcelona
Moderator: Stephen Faraone, SUNY Upstate Medical University

7:00 p.m. – 7:05 p.m.	**Introduction** Bru Cormand, University of Barcelona
7:05 p.m. - 7:30 p.m.	**Aggression in ADHD and Conduct Disorder: Impulsive and Instrumental Subtypes** Barbara Franke, Departments of Human Genetics and Psychiatry, Donder's Institute for Brain, Cognition and Behaviour, Radboud University Medical Center
7:30 p.m. - 7:55 p.m.	**Screening for Novel Aggression Therapeutics in Zebrafish** William Norton, University of Leicester
7:55 p.m. - 8:20 p.m.	**Structural and Functional MRI Changes in Animal Models of Aggression are associated with Alterations in Frontostriatal microRNA Expression** Jeffrey Glennon, Radboud University Medical Center
8:20 p.m. - 8:45 p.m.	**Epigenetics in Mental Disorders: Maternal and Parent of Origin Effects** Tetyana Zayats, Bergen University
8:45 p.m. - 9:00 p.m.	**Discussion** Andreas Reif, University Hospital Würzburg

FULL SCHEDULE

WEDNESDAY, OCTOBER 15, 2014

7:00 p.m. - 9:00 p.m.	**Towards Translational Psychiatry: From Genomic Discoveries to Prediction of Treatment Response** ***Lumbye***

Chair: Po-Hsiu Kuo, Institute of Epidemiology and Preventive Medicine, NTU
Moderator: Chia-Hsiang Chen, Chang Gung Memorial Hospital at Linkou

7:00 p.m. – 7:05 p.m.	**Introduction** Po-Hsiu Kuo, Institute of Epidemiology and Preventive Medicine, NTU
7:05 p.m. - 7:30 p.m.	**Inversely Regulated MicroRNAs in Mouse Hippocampus after Methamphetamine and Electroconvulsive Shock** Yu-Lin Chao, Tzu Chi General Hospital
7:30 p.m. - 7:55 p.m.	**Blood-based Microrna Expression Aberration in Schizophrenia: Trend from Acute Admission to Partial Remission and Relations to Cortical Gray Matters Structures** Wei J. Chen, College of Public Health, National Taiwan University
7:55 p.m. - 8:20 p.m. ★	**Identification of Novel Biomarkers for Manic Episode Using Whole-genome Transcriptome Analysis** Ya-Chin Lee, Institute of Epidemiology and Preventive Medicine, College of Public Health, National Taiwan University
8:20 p.m. - 8:45 p.m.	**A Neural Network Model for Predicting Treatment Response of Antidepressants in Patients with Major Depressive Disorder** Po-See Chen, National Cheng Kung University Medical College
8:45 p.m. - 9:00 p.m.	**Discussion** Chunyu Liu, University of Illinois at Chicago

★ – Travel Awardee

SCHEDULE AT A GLANCE

THURSDAY, OCTOBER 16, 2014

8:30 a.m. – 10:30 a.m. **Concurrent Symposia Sessions**

Utilizing Family-based Information in Genetic Research	***Exploring the Evidence that Postpartum Depression is a more Homogeneous Biological Subtype of Major Depression (MDD)***	***(Epi)genetics and (Epi) genomics of Psychological Treatment Response***	***Genetics of Lithium Response in Bipolar Disorder***
Lumbye	Harlekin	Carstensen	Columbine

10:30 a.m. – 10:45 a.m. **Coffee Break**

10:45 a.m. – 11:45 a.m. **Plenary Session:** ***Integrative Genomics and the Neurobiology of Autism Spectrum Disorders***
Tivoli Congress Hall

11:45 a.m. – 12:00 p.m. Closing Remarks/Congress Adjourns

NOTES

FULL SCHEDULE

THURSDAY, OCTOBER 16, 2014

Concurrent Symposia Sessions

8:30 a.m. - 10:30 a.m.	**Exploring the Evidence that Postpartum Depression is a more Homogeneous Biological Subtype of Major Depression (MDD)** ***Harlekin***

Chair: Naomi Wray, The University of Queensland
Moderator: Trine Munk-Olsen, National Center for Register-Based Research

8:30 a.m. – 8:35 a.m.	**Introduction** Naomi Wray, The University of Queensland
8:35 a.m. - 9:00 a.m.	**Heritability of Perinatal Depression and Genetic Overlap with Major Depressive Disorder** Alexander Viktorin, Karolinska Institutet
9:00 a.m. - 9:25 a.m.	**Application of Latent Class Analysis to Understand the Heterogeneity of Postpartum Depression in an International Perinatal Psychiatry Consortium** Samantha Meltzer-Brody, University of North Carolina at Chapel Hill
9:25 a.m. - 9:50 a.m.	**Evidence for a Genetic Overlap between Postpartum Depression and Bipolar Disorder** Naomi Wray, The University of Queensland
9:50 a.m. - 10:15 a.m.	**The Search for Robust and Reproducible Biomarkers for Postpartum Depression: New Insights and Strategies** Divya Mehta, University of Queensland
10:15 a.m. - 10:30 a.m.	**Discussion** Patrick Sullivan, University of North Carolina

FULL SCHEDULE

THURSDAY, OCTOBER 16, 2014

8:30 a.m. - 10:30 a.m. **Genetics of Lithium Response in Bipolar Disorder**
Columbine

Chair: John Kelsoe, University of California San Diego
Moderator: Thomas G. Schulze, Institute for Psychiatric Phenomics and Genomics (IPPG) Ludwig-Maximilians-University Munich

8:30 a.m. – 8:35 a.m. **Introduction**
John Kelsoe, University of California San Diego

8:35 a.m. - 9:00 a.m. **An Update from the Consortium on Lithium Genetics (ConLiGen): Phenomic and Genomic Studies**
Urs Heilbronner, University Medical Center Göttingen

9:00 a.m. - 9:25 a.m. **Investigating Responders to Lithium as a Distinct Subgroup of Bipolar Disorder**
Martin Alda, Dalhousie University

9:25 a.m. - 9:50 a.m. **Genome-wide Association Study of Lithium Response in a Swedish Population**
Sarah Bergen, Karolinska Institute

9:50 a.m. - 10:15 a.m. **Distinct Cellular Phenotypes Associated with Good and Poor Response to Lithium in Bipolar Disorder**
John Kelsoe, University of California San Diego

10:15 a.m. - 10:30 a.m. **Discussion**
Roy Perlis, Massachusetts General Hospital

FULL SCHEDULE

THURSDAY, OCTOBER 16, 2014

8:30 a.m. - 10:30 a.m.	**(Epi)genetics and (Epi)genomics of Psychological Treatment Response** ***Carstensen***

Chair: Thalia Eley, Institute of Psychiatry, Kings College London
Moderator: Gerome Breen, Institute of Psychiatry, King's College London

8:30 a.m. – 8:35 a.m.	**Introduction** Thalia Eley, Institute of Psychiatry, Kings College London
8:35 a.m. - 9:00 a.m.	**A Genomewide Association Study of Response to Cognitive Behavioral Therapy in a Globally-ascertained Cohort of Children with Anxiety Disorders** Jonathan Coleman, Institute of Psychiatry, King's College London
9:00 a.m. - 9:25 a.m.	**Epigenetic Factors and Response to Psychological Therapy** Susanna Roberts, King's College London
9:25 a.m. - 9:50 a.m.	**Changes in GR and FKBP5 Methylation in Response to PTSD Treatment** Rachel Yehuda, Mount Sinai School of Medicine/ JJ Peters VAMC
9:50 a.m. - 10:15 a.m.	**Genomic and Epigenomic Predictors of Differential Response to Cognitive Behavioral Therapy vs. Antidepressant Drug Treatment in Major Depression** Elisabeth Binder, Max-Planck Institute of Psychiatry, Dept. of Translational Research in Psychiatry
10:15 a.m. - 10:30 a.m.	**Discussion** Thalia Eley, Institute of Psychiatry, Kings College London

FULL SCHEDULE

THURSDAY, OCTOBER 16, 2014

8:30 a.m. - 10:30 a.m.	**Utilizing Family-based Information in Genetic Research** ***Lumbye***

Chair: Pippa Thomson, Institute of Genetics and Molecular Medicine
Moderator: William Hennah, Institute for Molecular Medicine Finland (FIMM)

8:30 a.m. – 8:35 a.m.	**Introduction** Pippa Thomson, Institute of Genetics and Molecular Medicine
8:35 a.m. - 9:00 a.m.	**Advantages of Using Family Cohorts to Study Neuropsychiatric Disorders** Guy Rouleau, Monteal Neruological Institute and Hospital
9:00 a.m. - 9:25 a.m.	**Linkage and Sequencing in a Brazilian Bipolar Family with 111 Moods Disorder Cases** Simone de Jong, King's College London
9:25 a.m. - 9:50 a.m.	**Utilization of Large Randomly Ascertained Human Pedigrees to Identify Rare Functional Variants Influencing Risk of Psychiatric Disorders** John Blangero, Texas Biomedical Research Institute
9:50 a.m. - 10:15 a.m.	**Identifying Genetic Influences in Familial Recurrent Major Depression by Exome Sequencing** Pippa Thomson, Institute of Genetics and Molecular Medicine
10:15 a.m. - 10:30 a.m.	**Discussion** Andrew McIntosh, University of Edinburgh
10:30 a.m. – 10:45 a.m.	**Coffee Break**

FULL SCHEDULE

THURSDAY, OCTOBER 16, 2014

10:45 a.m. – 11:45 a.m. **Plenary Session: *Integrative Genomics and the Neurobiology of Autism Spectrum Disorders***
Tivoli Congress Hall

Chair: Vidar Steen, M.D., University of Bergen
Co-chair: Camilla Stoltenberg, M.D., Norwegian Institute of Public Health
Plenary Speaker: Daniel Geschwind, M.D., Ph.D., UCLA

Autism Spectrum Disorders (ASD) have significant genetic contributions from both common and rare genetic variants. The burgeoning identification of rare variants that increase risk for ASDs coupled with the estimation of the contribution from many common variants of low effect size have led to new appreciation of its genetic heterogeneity. This question of "many genes, common pathways?" has spawned many laboratories to search for the presence of convergent biological processes, or pathways in the disorder. We have reasoned that mapping risk genes onto transcriptomic networks derived from normal brain development, or from direct comparisons of ASD post mortem brain to controls would provide a framework for these questions. We have previously shown using microarrays, that there is a shared transcriptomic pattern in post mortem ASD cortex in about ⅔ of cases. Here, we present data from RNAseq in a larger cohort, about ½ of which overlap with our previous study. These data strongly support and extend the previously identified transcriptomic alterations observed in ASD brain, showing shared transcriptional changes in more than ½ of the cases. Furthermore, these changes are of higher magnitude in cerebral cortex than in cerebellum, few reaching significance in cerebellum. In addition to mRNA and splicing changes in ASD, we identify non-coding RNA changes that include several lncRNAs dysregulated in ASD brain that appear to be primate specific.
In parallel, work we have mapped ASD risk genes onto transcriptomic networks representing normal human brain development and identified convergent co-expression patterns. Newly identified recurrent variants not used for the original analysis are also enriched in the developmental co-expression modules that we previously identified as containing ASD-related genetic variation, validating our network approach for prioritizing and understanding genetic variation in the context of neural development and circuit function. These data suggest a primary genetic deficit affecting glutamatergic neurons, especially those in superficial cortical laminae in a subset of ASD, consistent with the model of developmental dysconnection. The specificity of the observed molecular pathological changes in ASD brain still needs to be explored relative to other neurodevelopmental and neuropsychiatric disorders.

11:45 a.m. – 12:00 p.m. **Closing Remarks / Congress Adjourns**

NOTES

POSTERS

MONDAY, OCTOBER 13, 2014

EARLY CAREER INVESTIGATOR'S POSTER AWARD FINALISTS

1 **Neurocognitive Deficits in the General Population and Composite** ECIP **Genetic Risk Score for Attention Deficit Hyperactivity Disorder**
Joanna Martin, Marian L. Hamshere, Evangelia Stergiakouli, Michael C. O'Donovan, Anita Thapar

2 ★ **Examining the Specificity of Neuroticism as an Endophenotype for** ECIP **Depression using a Polygenic Risk Score Approach**
Lucia Colodro Conde, Karin Verweij, Enda Byrne, Robert Power, Nick Martin, Sarah Medland

3 **Common Genetic Variants Associated with Bipolar Disorder and** ECIP **Co-existing Medical Conditions**
Miguel Prieto, Euijung Ryu, Jyotishman Pathak, Gregory Jenkins, Anthony Batzler, Alfredo Cuellar- Barboza, Mark Frye, Joanna Biernacka

4 **Exploring the Genetic and Environmental Relationships between** ECIP **Dimensional Trait Measures and Categorical Constructs of Autism**
Beata Tick, Emma Colvert, Fiona McEwen, Sarah Curran, Emma Woodhouse, Victoria Hallett, Stephanie Lietz, Angelica Ronald, Robert Plomin, Fruhling Rijsdijk, Francesca Happe, Patrick Bolton

5 ★ **Enrichment Analysis of Genomic Features, to Identify Genome-** ECIP **wide Patterns of Insertions/Deletions in Cases of Psychiatric Disorders from the Faroe Islands**
Esben Eickhardt, Thomas D. Als, Manuel Mattheisen, Mette Nyegaard, Ditte Demontis, Jakob Grove, Gudrid Andorsdottir, Marjun Biskopstø, August G. Wang, Ole Mors, Lars Bolund, Jun Wang, Anders Børglum, Francesco Lescai

6 **Pleiotropic Gene PDE5A Identified for Emotion Recognition and** ECIP **Amygdala Volume using Linkage and Association Analysis**
Emma Knowles, David Reese McKay, Jack Kent, Emma Sprooten, Melanie Carless, Joanne Curran, Marcio de Almeida, Thomas Dyer, Harald Goring, Rene Olvera, Peter Fox, Laura Almasy, John Blangero, David Glahn

★ – Travel Awardee ECIP – ECIP Finalist

POSTERS

7 ★ **Epigenetic Regulation of the FKBP5 Gene by Age and Major**
ECIP **Depression: Implications for Age-related Disease**
Anthony Zannas, Torsten Klengel, Charles Nemeroff, Tania Carrillo-Roa, Christine Heim, Bekh Bradley, Kerry Ressler, Elisabeth Binder

8 **The Development of Cognition and Psychotic Experiences in**
ECIP **Children at High Risk of Schizophrenia: A Longitudinal Study of 22q11.2 Deletion Syndrome**
Samuel Chawner, Maria Niarchou, Michael Owen, Marianne van den Bree

9 **Whole Transcriptomic Analysis on Immediate Effect of Maternal**
ECIP **Immune Activation on Fetal Brain Development**
Shing Wan Choi, Johnny Sheung Him Kwan, Qi Li, Chok King Tomy Hui, Hiu Man Vicki Ling, Yu On Jana Leung, Pak-Chung Sham

10 **Polygenic Scores from the MiR137 Pathway Explain Variability in**
ECIP **Cognitive Performance Patients with Schizophrenia and Controls**
Donna Cosgrove, Derek Morris, Ric Anney, April Hargreaves, Psychiatric Genomics Consortium, Michael Gill, Aiden Corvin, Gary Donohoe

11 ★ **Genome-wide Burden of Deleterious Coding Variants Increased in**
ECIP **Schizophrenia**
Loes Olde Loohuis, Jacob Vorstman, Anil Ori, Kim Staats, Tina Wang, Joseph DeYoung, Group Consortium, Rita Cantor, Roel Ophoff

12 **Schizophrenia EWAS Highlights Regions Previously Associated**
ECIP **through GWAS**
Anil Ori, Jennifer Listgarten, James Zou, Loes Olde Loohuis, Marco Boks, René Kahn, Jason Ernst, Roel Ophoff

13 **A Polygenic Risk Score Analysis of Psychosis**
ECIP **Endophenotypes**
Siri Ranlund, Kuang Lin, Steven Bakker, David Collier, Benedicto Crespo-Facorro , Assen Jablensky, Rene Kahn, Luba Kalaydjieva, Andrew McIntosh, Dan Rujescu, Jim Van Os, Wellcome Trust WTCCC2, Cathryn Lewis, Robin Murray, John Powell, Elvira Bramon

★ – Travel Awardee **ECIP** – ECIP Finalist

14 **Divergent Transcription of the BDNF Gene in Human and Mouse Brain: Relevance for Schizophrenia** ECIP

Gianluca Ursini, Giovanna Punzi, Joo Heon Shin, Kristen Maynard, Eugenia Radulescu, Bin Xie, Venkata Mattay, Joel Kleinman, Thomas Hyde, Keri Martinowich, Daniel Weinberger

ADHD

15 **Evaluation of the Polygenic Burden of Rare Coding Variants in ADHD Risk Genes through Whole-exome Sequencing**

Ditte Demontis, Søren Østergaard, Barbara Franke, Andreas Reif, Jan Buitelaar, Klaus-Peter Lesch, Francesco Lescai, Jakob Grove, Qibin Li, Jieqin Liang, Hui Jiang, Yingrui Li, Jun Wang, Ole Mors, Simon Glerup, Anders Børglum

16 **Missense Dopamine Transporter Mutations Associate with Adult Parkinsonism and ADHD**

Freja Hansen, Tina Skjørringe, Saiqa Yasmeen , Natascha Arends, Michelle Sahai, Kevin Erreger, Thorvald Andreassen, Ian Law, Lars Pinborg, Harald Sitte, Claus Loland, Harel Weinstein, Aurelio Galli, Lena Hjermind, Lisbeth Møller, Ulrik Gether

17 **The G Protein-coupled Receptor Kinase Interacting ArfGAP 1 (GIT1) Gene Affects Neuronal Morphology in Drosophila Melanogaster, but is not Associated with ADHD and Related Traits in Humans**

Marieke Klein, Monique van der Voet, Benjamin Harich, Kimm van Hulzen, Marten Onnink, Tulio Guadalupe, Psychiatric Genomics Consortium ADHD Working Group, Johanne Groothuismink, Annette Schenck, Jan Buitelaar, Alejandro Arias-Vasquez, Barbara Franke

18 **Approaching the Possible Role of HESR1/Hey1 and NR4A2/Nurr1 Transcription Factors Genes in ADHD Susceptibility**

Nina R. Mota, Lucas A. de Azeredo, Diego L. Rovaris, Evelise R. Polina, Rafael G. Karam, Carlos A.I. Salgado, Katiane L. Silva, Paulo Belmonte-de-Abreu, Vanessa R. Paixão-Côrtes, Luis A. Rodhe, Eugenio H. Grevet, Claiton H.D. Bau

ECIP – ECIP Finalist

POSTERS

AFFECTIVE DISORDERS

19 **Clinical Characteristics and Polygenic Risk in Bipolar Disorder**
Sofie Aminoff, Martin Tesli, Francesco Bettella, Srdjan Djurovic, Ole Andreassen, Ingrid Melle

20 **Review and Pathway Analysis of Mitochondrial Dysfunction in Bipolar Disorder**
Sarah Bergen, Charlotte Holst, Colm O'Dushlaine, Mikael Landén

21 **Neurotrophic Factors in Depression in Response to Treatment**
Henriette Buttenschon, Leslie Foldager, Betina Elfving, Pia Poulsen, Rudolf Uher, Ole Mors

22 **A Lark or an Owl as a Genetically Determined Trait Predisposing to Mood Disorders**
Monika Dmitrzak-Weglarz, Joanna Pawlak, Piotr Czerski, Monika Wilkosc, Malgorzata Maciukiewicz, Anna Leszczynska-Rodziewicz, Joanna Hauser, Wanda Ciarkowska

23 **Heritability of Major Depressive Disorder (MDD) Explored Through Age of Onset**
Ana Maria Fernandez, Donald J. MacIntyre, Blair H. Smith, Lynne J. Hocking, Sandosh Padmanabahn, David J. Porteous, Ian J. Deary, Pippa A. Thomson, Chris S. Haley, Andrew M. McIntosh

24 **Morbid Risk for Major Psychoses in First Degree Relatives of Bipolar I Probands by Age-of-onset Classes Derived through Admixture Analysis**
Maria Grigoroiu-Serbanescu, Marcella Rietschel, Joanna Hauser, Piotr M. Czerski, Stefan Herms, Xianqing Sun, Priya Wickramaratne, Robert C. Elston

25 **Association Study of Acid Phosphatease 1 Gene Polymorphism Rs300774 with Attempted Suicide in Mood Disorder Patients**
Pawel Kapelski, Joanna Pawlak, Monika Dmitrzak, Maria Skibinska, Dorota Zaremba, Joanna Hauser

26 **Bipolar Affective Disorders in the Arab World: Clinical Manifestations and Genomic Findings**
Ziad Kronfol, Karsten Suhre, Elie Karam, Pankaj Kumar, Ilhem Diboun, Hanif Khalak, Yasmeen Assad, Grace Aranki, Melvin McInnis

POSTERS

27 **The BRIDGES Study: Whole-genome Sequencing for Bipolar Disorder**

Adam Locke, on behalf of the BRIDGES Study

28 **Examining the Impact of Parental Depression on Adolescent Internalizing and Externalizing Problems in a Genetically Informative Design: A Children-of-twins Study**

Tom McAdams, Thalia Eley

29 **Assessment of First Degree Relatives of Bipolar Disorder Probands Shows Enrichment of Polygenic Risk Alleles in both Affected Relatives and Young At-risk Individuals**

Philip Mitchell, Jan Fullerton, Dan Koller, Howard Edenberg, Tatiana Foroud, Hai Liu, Anne Glowinski, Melvin McInnis, Holly Wilcox, Andrew Frankland, Gloria Roberts, Peter Schofield, John Nurnberger

30 ★ **Independent Test Fails to Replicate Blood Biomarkers for Suicidality**

Niamh Mullins, Karen Hodgson, Katherine Tansey, Nader Perroud, Wolfgang Maier, Ole Mors, Marcella Rietschel, Joanna Hauser, Neven Henigsberg, Daniel Souery, Katherine Aitchison, Anne Farmer, Peter McGuffin, Gerome Breen, Rudolf Uher, Cathryn Lewis

31 **An Online Approach to Increase Depression Cases for Genome-wide Analyses in Existing Biobanks in the Netherlands**

Brenda Penninx, Mariska Bot, Christel Middeldorp, Eco de Geus, Johannes Smit, Dorret Boomsma

32 **Multimarker Analysis Demonstrate the Involvement of the BDNF-NTRK2 and Mirna Processing Pathways in Suicidal Behavior in Major Depressive Disorder and Bipolar Affective Disorder**

Attila Pulay, Janos Réthelyi

33 **Exome Sequencing in Families with Highly Penetrant Forms of Bipolar Disorder**

Alexander Shaw, Claudio Toma, Richard Allcock, Eric Moses, Philip Mitchell, Peter Schofield, Janice Fullerton

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34 **HTR2A Variation is Associated with Diurnal Preference in a Korean Young Population**
Hye-Min Song, Hae-In Kim, Heon-Jeong Lee, Chul-Hyun Cho, Joung Ho Moon, Ho-Kyoung Yoon, Seung-Gul Kang, Young-Min Park, Leen Kim

35 **Differences in MicroRNA Expression in Lymphoblasts from Suicide Completers and Non-suicidal Subjects with Bipolar Disorder**
Alessio Squassina, Paola Niola, Juan Pablo Lopez, Donatella Congiu, Cristiana Cruceanu, Valeria Deiana, Caterina Chillotti, Martin Alda, Gustavo Turecki, Maria Del Zompo

36 ★ **No Association of Serotonin-transporter-linked Polymorphic Region (5-HTTLPR) Genotype with Risk of Depression after Diagnosis of Colorectal Cancer**
Nis Suppli, Susanne Oksbjerg Dalton, Christoffer Johansen, Lars Vedel Kessing, Terrie Moffit, Avshalom Caspi, Jens Drachmann Bukh

37 **Sequence Analysis of Drug Target Genes with Suicide Severity in Bipolar Disorder**
Clement Zai, Vanessa Goncalves, Vincenzo de Luca, Arun Tiwari, Jo Knight, John Vincent, James Kennedy

38 **Serotonin Transporter Gene Variants are Associated with Increased Risk of Suicide in an HIV-positive Ugandan Population**
Sian Hemmings, Allan Kalungi, Soraya Seedat, Moses Joloba, Eugene Kinyanda

ANXIETY DISORDER

39 **Whole-exome Sequencing in Obsessive-Compulsive Disorder Identifies Rare Gene Mutations Involved in Immunological Pathways**
Carolina Cappi, Helena Brentani, Leandro Lima, Stephan Sanders, Juliana Diniz, Michael Walker, Viviane Reis, Ana Hounie, Daniel Mariani, Fabio Oki, Renato Puga, Roseli Shavitt, David Pauls, Euripedes Miguel, Thomas Fernandez

40 **Elevated Expression of Alzheimer's Disease-risk Gene SORL1 in Catecholaminergic Neurons Results in Anxiety-related Behavior**
Simon Glerup, Ditte Demontis, Jesper Lundhede, Ole Mors, Anders Børglum, Anders Nykjær, Henriette Buttenschøn, Søren Østergaard

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POSTERS

41 **Essential Oils of Myrtus Communis L. Produce a Non-sedating Anxiolytic Effect in Mice Model of Anxiety**
Eyob Kebede, Ephrem Engidawork, Kaleab Asres

42 **Who is Afraid of Heights? A Genome-wide Screen for Acrophobia Susceptibility Loci in a Finnish Isolate**
Zuzanna Misiewicz, Tero Hiekkalinna, Tiina Paunio, Teppo Varilo, Iiris Hovatta

AUTISM

43 **Genome-wide Significant Common Snps Associated with Schizophrenia Show Significant Direction Effect in Autism Spectrum Disorder**
Richard Anney, Autism Spectrum Disorder Group

44 **Whole Transcriptome Analysis of Neuronal Differentiation Identifies Novel Gene-network Clusters Enriched for Autism Risk Genes**
Denise Haslinger, Silvia Lindlar, Regina Waltes, Simone Fulda, Christine M. Freitag

45 **Towards Novel Biomarkers for Autism using an Integrative Genomic Approach on Discordant Sibling Pair Design**
Tony Kam-Thong, Laurent Essioux, Pierandrea Muglia, Will Spooren, Bertram Mueller-Myhsok, Enrico Domenici, Italian Autism Network

46 **Brain-specific FOXP1 Deletion Impairs Neuronal Development and Causes Autistic-like Behaviour**
Gudrun Rappold, Claire Bacon, Miriam Schneider, Corentin Le Magueresse, Henning Fröhlich, Christian Gluch, Hannah Monyer, Gudrun Rappold

47 **Using eQTLs to Dissect the 16p11.2 Autism Locus**
Kaanan Shah, Kathryn M. Tsang, Lauren A. Weiss, Nancy J. Cox

48 **OPEN BOARD**

49 **Phenotypic Spectrum Associated with PTCHD1 Deletions and Truncating Mutations**

John Vincent, Ayeshah Chaudhry, Abdul Noor, Kate Baker, Frederic Laumonnier, Annick Toutain, Ina Schanze, Constance Schrander-Stumpel, Angela Brady, F. Lucy Raymond, David Chitayat, David Dyment, Servi Stevens, Brian Chung Hon-Yin, Stephen Scherer, Melissa Carter

BIOSTATISTICS / BIOINFORMATICS

50 **Population Structure and Cryptic Relatedness of the Isolated Population of the Faroe Islands**

Thomas Als, Francesco Lescai, Ditte Demontis, Oddbjørg Johansen, Mette Nyegaard, Hans Dahl, Manuel Mattheisen, Marjun Biskopstø, Jakob Grove, Lars Bolund, Gudrid Andorsdottir, August Wang, Ole Mors, Wang Jun, Anders Børglum

51 **Comparing Methods for Genome-wide Gene-environment Interaction Analysis**

Leslie Foldager, Jakob Grove, Thomas Als

52 **In Silico Levels of LPHN1 Differentially Expressed in Bipolar Disorder Cases Discovered using Predixcan**

Hae Kyung Im, Kaanan Shah, Eric Gamazon, Lea Davis, Nancy Cox

53 **Copy Number Variation (CNV) Study of iPSYCH Project**

Shengting Li

54 **A Framework to Evaluate the Quality of Protein Interaction Network**

Hong Sain Ooi, Jakob Grove, Mikkel Heide Schierup, Ole Mors, Anders Børglum, Manuel Mattheisen

55 **Application of Conditional Regression and Multiple-SNP Analyses to PGC GWAS for Schizophrenia Identifies Additional Signals of Association**

Tatiana Polushina, Thomas Espeseth, Srdjan Djurovic, Ole Andreassen, Vidar Steen, Stephanie Le Hellard

POSTERS

56 **Allele-specific Copy-number Discovery from Whole-genome and Whole-exome Sequencing**
Jin Szatkiewicz, Weibo Wang, Wei Wang, Wei Sun

DEMENTIA

57 **Common Alzheimer Risk Alleles and Cognitive Decline**
Jonas Mengel-From, Mikael Thinggaard, Matt McGue, Kaare Christensen, Lene Christensen

ELSI, COUNSELING AND GENETIC TESTING

58 ★ **Predictive Test in Psychiatric Genetics: Attitudes and Intentions among Potential Users and Providers in a Cuban Population Sample**
Giselle Monzón, Beatriz Marcheco Teruel, Lissette Evelyn Fuentes Smith, Ole Mors

59 **Ethical Aspects of Predictive Genetic Testing**
Stephanie Witt, Jana Strohmaier, Christine Schmäl, Bert Heinrichs, Maria Alex, Dirk Lanzerath, Marcella Rietschel

ENDOPHENOTYPES

60 **A Polygenic Risk Score Derived from a GWAS Investigating Schizophrenia is Associated with Memory Performance in Healthy Young Subjects**
Virginie Freytag, Tobias Egli, Annette Milnik, Dominique J.-F. de Quervain, Andreas Papassotiropoulos, Christian Vogler

61 **Genetic Polymorphisms of Histone Deacetylase 5 and Emotional Memory in Healthy Young Adults**
Francina Hartmann, Dominique J.-F. de Quervain, Andreas Papassotiropoulos, Angela Heck

62 **Genetic Modulators of Dyslexia Related MMR**
Bent Müller, Arndt Wilcke, Gesa Schaadt, Johannes Boltze, Holger Kirsten

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POSTERS

63 **Psychotic-like Experiences in Non-clinical Samples and its Association with Several Candiate Genes for Psychosis**
Araceli Rosa, Marta de Castro-Català, Elionora Peña, Paula Cristóbal-Narváez, Thomas R. Kwapil, Neus Barrantes-Vidal, Araceli Rosa

64 **The Influence of Genes on Constructs in the "Positive Valence Systems" Domain of Research Domain Criteria (RDoC): A Systematic Review**
Stephen Glatt, Jonathan Hess, Daniel Kawaguchi, Stephen Faraone

EPIGENETICS

65 **Mother's Attachment Style Leaves Systemic Marks in the DNA Methylation Profiles of Newborn Children**
Antti-Jussi Ammala, Jukka Alasaari, Johanna Liuhanen, Katri Kantojärvi, Juulia Paavonen, Anneli Kylliäinen, Linnea Karlsson, Outi Saarenpää-Heikkilä, Lili Milani, Marjukka Pajulo, Hasse Karlsson, Tiina Paunio

66 **Epigenetic Variation in Twins and Trio's**
Dorret Boomsma, Jenny van Dongen, Gonneke Willemsen, Erik Ehli, Gareth Davies, Eka Suchiman, Rick Jansen, Joyce van Meurs, Bastiaan Heijmans, Eline Slagboom, BIOS BBRMI-NL

67 **Genome-wide Methylomic Sequence Analysis of Monozygotic Twins Discordant for Schizophrenia**
Emma Dempster, Mike Weedon, Joe Burrage, Jaakko Kaprio, Timothea Toulopoulou, Tim Spector, Marc Bohlken, Hilleke Hulshoffpol, Igor Nenadic, Robin Murray, Jonathan Mill

68 **Developmental Methylation QTLs in Human Brain Development: Implications for Neuropsychiatric and Neurodegenerative Disease**
Eilis Hannon, Helen Spiers, Joana Viana, Ruth Pidsley, Katie Lunnon, Chloe Wong, Nicholas Bray, Jonathan Mill

69 **The Epigenome of Fear**
Shane McCarthy, Sandra Ahrens, Nabil Azamy, W. Richard McCombie, Bo Li

70 **Changes in GCH1 Gene Expression and Methylation in the Blood of Patients with First-episode Psychosis**

Vanessa Ota, Cristiano Noto, Ary Gadelha, Marcos Santoro, Eduardo Gouvea, Roberta Stilhano, Leticia Spindola, Bruno Ortiz, Patricia Silva, João Sato, Sang Han, Quirino Cordeiro, Rodrigo Bressan, Sintia Belangero

71 **DNA Methylation Analysis of CACNA1C in Bipolar Disorder**

Anna Szyszka, Anja Pen, Andrew McQuillin, Anne Hedemand, Thomas D. Als, Alessia Niamh, Alexandra Jarram, Nicklas H. Staunstrup, Anders L. Nielsen, Francesco Lescai, Jakob Grove, Ole Mors, Ditte Demontis, Anders D. Børglum, Mette Nyegaard

72 **Lower DNA Methylation of Glucocorticoid Receptor Gene Promoter 1F in Chronic Fatigue Syndrome**

Elise Vangeel, Filip Van Den Eede, Titia Hompes, Benedetta Izzi, Jurgen Del-Favero, Greta Moorkens, Diether Lambrechts, Kathleen Freson, Stephan Claes

FUNCTIONAL GENOMICS & MODEL ORGANISMS

73 **RNA-Seq Translation: Blood and Brain in Mice Model for 22q11 Deletion**

Marcelo Bertalan, Thomas Werge, Jacob Nielsen, Jes Brix Lauridsen, Michael Didriksen, Ib Vestergaard Klewe

74 **Identifying the Protein Interactions of the Epigenetic Modifier Proteins Zeb1 and Zeb2**

Tue Fryland, Jane Hvarregaard Christensen, Anders Lade Nielsen, Niels Gregersen, Johan Palmfeldt, Anders D. Børglum

75 **Genome Engineering of Human Neural Cells at Psychiatric Risk Genes Using CRISPR/Cas9**

Matthew Hill, Meng Li, Mike Owen, Derek Blake

76 **Interaction among Childhood Trauma and Functional Polymorphisms in the Serotonergic Pathway in Depressive Disorders**

Sandra Van der Auwera, Hans-Jörgen Grabe

MISCELLANEOUS OTHER PSYCHIATRIC DISORDERS

77 **Cross Psychiatric Disorder Analysis Reveals Overlapping Gene Expression Patterns and Disorder Specific Signatures**

Simone de Jong, Stephen Newhouse, Declan Murphy, Philip Asherson, Patrick Bolton, Charlotte Tye, Karen Ashwood, Ellie Wilson, Liya Sun, Sanghyuck Lee, Fiona Gaughran, Robin Murray, Peter McGuffin, Sarah Curran, Richard Dobson, Gerome Breen

78 **Core-exome Chip Study of Low-frequency Variants Identifies Genome-wide Significant Hits Associated with Anorexia Nervosa**

Laura Huckins, Konstantinos Hatzikotoulas, Laura Thornton, Lorraine Southam, WTCCC3 Consortium, GCAN Consortium, David Collier, Patrick Sullivan, Cynthia Bulik, Eleftheria Zeggini

79 **Identifying Neurodevelopmental Orthologs in Caenorhabditis Elegans to Unravel Cellular Phenotypes of Neuropsychiatric Disorders**

Olivia Mendivil Ramos, Cristina Aguirre-Chen, Shane E. McCarthy, Pippa Thomson, Melissa Kramer, Kathryn L. Evans, Douglas Blackwood, Michael Gill, Aiden Corvin, David Porteous, Chris Hammell, W. Richard McCombie

80 **Genome-wide Association Study of Violent Offending in Finnish Cohort of Criminal Offenders**

Marja-Riitta Rautiainen, Jari Tiihonen, Tiina Paunio

81 **A Large Study of Probands with Multiple Limb Amputations Provides Evidence that Individual Predisposition Influences the Development and Course of Phantom Pain or Sensations and Residual Limb Pain**

Fabian Streit, Robin Bekrater-Bodmann, Martin Diers, Stefan Wüst, Ze'ev Seltzer, Herta Flor, Marcella Rietschel

82 **The Functional GRM3 Kozak Sequence Variant rs148754219 affects the Risk of Schizophrenia and Alcohol Dependence as well as Bipolar Disorder**

Niamh O'Brien, Michael J. Way, Radhika Kandaswamy, Alessia Fiorentino, Sally I. Sharp, Giorgia Quadri, Alex Jarram, Adebayo Anjorin, Greg Lydall, Allan D. Thomson, Nicholas J. Bass, Marsha Y. Morgan, David Curtis, Andrew McQuillin

POSTERS

NEUROIMAGING

83 **Genetics of Structural Connectivity and Information Processing in the Brain**
Sudheer Giddaluru, Thomas Espeseth, Alireza Salami, Lars T. Westlye, Anders Lundquist, Stephanie Le Hellard, Lars Nyberg

84 **Identification of RGS7BP as a New Candidate for Obsessive-Compulsive Disorder Based on its Association with Dorsolateral Prefrontal Cortex Volume**
Kimm van Hulzen, Geert Poelmans, Marcel Zwiers, Tulio Guadalupe, Jan Buitelaar, Barbara Franke

85 **Brain Connectivity Changes Associated with Disease Expression and Resilience in Bipolar Disorder**
Danai Dima, Gerome Breen, Sophia Frangou

OTHER

86 **Effects of Canine OXTR Alleles and Epialleles on Gene Expression**
Zsofia Banlaki, Melinda Bence, Zsofia Viranyi, Dora Koller, Maria Sasvari-Szekely, Zsolt Ronai

87 **Genome Wide Significant Locus for Research Diagnostic Criteria Schizoaffective Disorder Bipolar Type**
Elaine Green, Liz Forty, Katherine Gordon-Smith, Christine Fraser, Detelina Grozeva, Alex Richards, Marian Hamshere, George Kirov, Michael Owen, Lisa Jones, Michael O'Donovan, Nick Craddock, Ian Jones

88 **NPAS2 Gene Variants are Associated with Chronotype in a Healthy Korean Young Population**
Heon-Jeong Lee, Jin-Sook Jung, Joung-Ho Moon, Chul-Hyun Cho, Ho-Kyoung Yoon, Seung-Gul Kang, Young-Min Park, Leen Kim

89 **Exome Sequencing in an Extended Family with Bipolar Disorder**
John Rice, Tian-Xiao Zhang, David T. Chen, Jen C. Wang, Francis J. McMahon

POSTERS

90 ★ **Case-control & Family Based Association Study of Brain Derived Neurotrophic Factor (BDNF) Gene with Obsessive Compulsive Disorder (OCD) in South Indian Population**
Reshma Taj M.J., Biju Viswanath, Meera Purushottam, Y.C. Janardhan Reddy, Sanjeev Jain

91 **Explaining the Variable Penetrance of CNVs: Parental Intellectual Level Modulates the Expression of Intellectual Impairment Caused by the 22q11.2 Deletion**
Jacob Vorstman, Petra W.J. Klaassen, Sasja N. Duijff, Henriette F.N. Swanenburg de Veye, Frits A. Beemer, Gerben Sinnema, Elemi J. Breetvelt

92 **Low Activity Alleles of Maoa Gene are Associated with Measures of Hostility**
Laura Mandelli, Vladimir Carli, Alessandro Serretti, Marco Sarchiapone

93 **Novel Intellectual Disability Genes Identified by Exome Sequencing**
Xavier Estivill

PHARMACOGENETICS

94 **Genetic Variation of Carboxylesterase 1 in a Population of Healthy Danes – Paving the Way for Individual Treatment of ADHD with Methylphenidate**
Ditte Bjerre, Laura Ferrero, Claus Stage, INDICES Consortium, Henrik Rasmussen

95 **Determination of Biomolecular Networks Involved in Antipsychotic Induced Tremors**
Marco Calabrò, Antonio Drago, Alessandro Serretti, Concetta Crisafulli.

96 **Genome-wide Association Study of Lymphoblast Cell Viability after Clozapine Exposure**
Sera Anne Jytte de With, T. Wang, S.L. Pulit, W.G. Staal, W.W. van Solinge, P.I.W. de Bakker, R.A. Ophoff

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POSTERS

97 **Pharmacogenetics of Methylphenidate Response in Adult Attention-Deficit/Hyperactivity Disorder**
Tor-Arne Hegvik, Kaya Kvarme Jacobsen, Mats Fredriksen, Stefan Johansson, Tetyana Zayats, Jan Haavik

98 **Pharmacogenetic Markers Associated with Abstinence Length in Alcohol-dependent Subjects Treated with Acamprosate**
Victor Karpyak, Joanna Biernacka, Jennifer Geske, Gregory Jenkins, Julie Cunningham, Michelle Skime, Josef Frank, Markus Nöthen, Marcella Rietschel, Falk Kiefer, Karl Mann, Richard Weinshilboum, Mark Frye, Doo-Sup Choi

99 **The Role of Phosphoinositol, Hypothalamic-Pituitary-Adrenal and Glutamatergic Systems in Lithium Response in Bipolar Patients: Association with GRIK2 and GRIK5 Genes**
Marina Mitjans, Esther Jiménez, Jose Manuel Goikolea, Pilar Alejandra Saiz, Mari Paz García-Portilla, Julio Bobes, Eduard Vieta, Antonio Benabarre, Bárbara Arias

100 **Are HTR1A and HTR2A Polymorphisms Related to Treatment Response? A Pharmacogenetics Study of ECT Patients**
Martinus van de Bilt, Carolina do Prado, Luiz Rigonatti, Sergio Rigonatti, Leda Talib, Wagner Gattaz

101 **Clozapine-induced Agranulocytosis/Granulocytopenia is Associated with Rare HLA-DQB1 and HLA-B Alleles**
L. Fredrik Jarskog, Ingolf Cascorbi, Michael Dettling, Anil K. Malhotra, Jimmi Nielsen, Dan Rujescu, Thomas Werge, Deborah L. Levy, Richard C. Josiassen, James L. Kennedy, Jeffrey A. Lieberman, Mark J. Daly, Patrick F. Sullivan

102 ★ **Systematic Functional Characterization of CYP2D6 Allelic Variants in the Chinese Han Population**
Qingqing Xu, Shengying Qin, Lin He

103 **Further Evidence that the Myelin Receptor DDR1 is Involved in Schizophrenia**
Nerea Abasolo, Cinta Gas, Isaias Mena, Joaquin Valero, Ana Gaviria, Lourdes Martorell, Elisabet Vilella

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POSTERS

SCHIZOPHRENIA

104 **Research into Polygenic Liability to Schizophrenia Holds Promise for New Insights into This illness: A Systematic Literature Review and Assessment of Likely Future Developments**

Olesya Ajnakina, Anirban Dutt, Conrad Iyegbe, Robin M. Murray

105 **Clinical Association of ZNF804a Variants in Patients with Refractory Schizophrenia**

Yi-Ling Chien, Yu-Li Liu, Sheng-Chang Wang, Yao-Sheng Chang

106 **Genome-wide and Gene-based Analysis of Symptomatic-dimensions of Psychotic Illness Based on a New Three-factor Schizophrenia-specific Model of the Operational Criteria Checklist**

Anna Docherty, T. Bernard Bigdeli, Alexis C. Edwards, Michael C. Neale, Silviu Bacanu, Donghyung Lee, Arden Moscati, Brandon S. Wormley, Dermot Walsh, F. Anthony O'Neill, Kenneth S. Kendler, Brien P. Riley, Ayman H. Fanous

107 **Genome Wide Association Study Involves miRNA Gene Sets in Schizophrenia**

Mads Engel Hauberg, Jakob Grove, Anders D. Børglum, Manuel Mattheisen

108 **Analysis of White Matter Related Genes across the Schizophrenia – Autism Continuum**

Mar Fatjó-Vilas, Claudia Prats, Maria José Penzol, Oussama Kebir, Laura Pina, Gilles Martinez, Fayçal Mouffak, Carmen Moreno, Nemat Jaafari, Edith Pomarol-Clotet, Salvador Miret, Ana González-Pinto, Victor Peralta, Mara Parellada, Marie-Odile Krebs, Lourdes Fañanás

109 **Homozygosity Profile and Exome Variants of Two Large Consanguineous Pakistani Pedigrees with Schizophrenia and Bipolar Disorders**

Qin He, Sirui Zhou, Amirthagowri Ambalavanan, Mehtab Christian, Dan Spiegelman, Alexandre Dionne-Laporte, Amelie Johnson, Emmanual Rafail, Mike Denton, Muhammad Qasim Brohi, Ridha Joober, Marie-Pierre Dubé, Lynn DeLisi, Guy A. Rouleau, Lan Xiong

110 **Systematic Association Analysis of Human Micrornas with Schizophrenia**

Andrea Hofmann, Andreas Forstner, Franziska Degenhardt, Gerhardt Schratt, Markus Nöthen

POSTERS

111 **Investigating the Role of Rare Variation in Cognitive Deficits in Schizophrenia**
David Kavanagh, James Walters, Michael O'Donovan, Michael Owen, UK10K Project Consortium

112 **Relationship between LSAMP Gene and Schizophrenia**
Kati Koido, Sven Janno, Tanel Traks, Madis Parksepp, Roman Balõtšev, Triin Eller, Anne Must, Sulev Kõks, Jakov Shlik, Innar Tõru, Eduard Maron, Veiko Vasar, Eero Vasar Vasar

113 **Polygenic Profile of Susceptibility and Modifier Genetic Variants in Schizophrenia Characterized by Early Onset and Attention Deficit**
Jia-Ying Lee, Po-Chang Hsiao, Po-Hsiu Kuo, Yin-Ju Lien, Shi-Heng Wang, Chih-Min Liu, Hai-Gwo Hwu, Chien-Hsiun Chen, Jer-Yuarn Wu, Wei J. Chen

114 **Schizophrenia, Flies and Salience Dysregulation Syndrome: Investigating the Regulation of Calcium Channel Gene CACNA1C in Drosophila Melanogaster**
Lisha Ma, Kevin A. McGhee

115 ★ **Pattern of Gene Expression in Different Stages of Schizophrenia: A Pilot Comparison of Induced Pluripotent Stem Cell-derived Neurons with Post Mortem Cerebral Cortex**
Mirko Manchia, Clement Zai, James Kennedy, Bernardo Carpiniello

116 **Exome Sequencing Analysis in Multiply Affected Families Implicates ITGB4 in Psychosis**
Andrew McQuillin, Niamh O' Brien, Alexandra Jarram, Nicholas Bass, Kate Wolfe, Adebayo Anjorin, Radhika Kandaswamy, Robert Blizard, David Curtis, Andrew McQuillin

117 **Detection of Somatic Retrotransposition at Single Nucleotide Resolution in Patients with Psychiatric Disorders**
Masaki Nishioka, Miki Bundo, Akane Yoshikawa, Fumichika Nishimura, Takao Ishii, Wataru Ukai, Eri Hashimoto, Chihiro Kakiuchi, Kiyoto Kasai, Tadafumi Kato, Kazuya Iwamoto

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118 **Evidence for an Epistatic Effect between Neuritin-1 and Dysbindin-1 Genes on the Risk for Schizophrenia Spectrum Disorders**

Claudia Prats, Salvador Miret, Mª José Muñoz, Mara Parellada, Sílvia Campanera, Luisa Lázaro, María Martín, Ignacio Ibáñez, Generós Ortet, Manuel J. Cuesta, Ana González-Pinto, Lourdes Fañanás, Mar Fatjó-Vilas

119 **Genome-wide Significant Schizophrenia Risk Variation on Chromosome 10q24 is Associated with Altered Cis-regulation of NT5C2 in the Human Brain**

Rodrigo Rafagnin Duarte, Claire Troakes, Matthew Nolan, Robin M. Murray, Nicholas J. Bray

120 **De novo Mutations of LRRC7, KHSRP, ADAMTS9, and Zinc Finger MYND-type Containing Transcriptional Repressor ZMYND11 Identified in Schizophrenia by Exome Sequencing of 16 Case-parent Trios**

János Réthelyi, Júlia Koller, Vivien Hársfalvi, Attila Pulay, Péter Balicza, Szilvia Magyarósi, Attila Horváth, Gábor Zahuczky, Tibor Nagy, István Likó, György Németh, Zoltán Urbányi, Endre Barta, Judit Benkovits, László Nagy, Judit Mária Molnár

121 **Frequency of the CYP2D6 * 6 Allelic Variant in a Sample of Cuban Patients with Schizophrenia**

Hilda Roblejo-Balbuena, Laritza Del Toro Bordado, Salvador González Pal, Beatriz Marcheco Teruel, Giselle Monzón Benítez, Iliana Rosado, Alejandro Esperón Alvarez, Lilia Marín Padrón

122 **Disruption of the miR-137 Primary Transcript Results in Early Embryonic Lethality in Mouse**

Kensuke Sakamoto, James J. Crowley, Ann L. Collins, Rebecca J. Lee, Randal J. Nonneman, Martilias S. Farrell, NaEshia Ancalade, Joshua W. Mugford, Kara L. Agster, Viktoriya D. Nikolova, Sheryl S. Moy, Patrick F. Sullivan

123 **Examining Common Genetic Overlap between Schizophrenia and Cognition**

Katherine Tansey, Leon Hubbard, David Linden, Michael O'Donovan, Michael Owen, James Walters, Stan Zammit

124 ★ **Polygenetic Overlap between Schizophrenia and Parkinson's Disease**

Martin Tesli, Yunpeng Wang, Martin Tesli, Rahul S. Desikan, Wesley K. Thompson, Mathias Toft, Andrew J. Schork, Per Svenningsson, Manu Sharma, Thomas Gasser, Verena Zuber, Aree Witoelar, Erik Jönsson, Srdjan Djurovic, Anders M. Dale, Ole A. Andreassen

125 **Novel Rare Disruptive Variants in Rho GTPase Activating Protein 10 (ARHGAP10) in Schizophrenia and Autism Spectrum Disorder**

Chenyao Wang, Daisuke Tsuboi, Itaru Kushima, Akira Yoshimi, Yukako Nakamura, Hiroki Kimura, Yuto Takasaki, Branko Aleksic, Daisuke Mori, Michio Suzuki, Hiroshi Ujike, Masashi Ikeda, Toshiya Inada, Nakao Iwata, Kozo Kaibuchi, Norio Ozaki

126 **Evaluating Rare Variants of Glycine Cleavage System Genes in Schizophrenia by Metabolomic Profilings**

Akane Yoshikawa, Fumichika Nishimura, Aya Inai, Yosuke Eriguchi, Masaki Nishioka, Mamoru Tochigi, Yoshiya Kawamura, Tadashi Umekage, Kayoko Kato, Tsukasa Sasaki, Yoshiaki Ohashi, Kazuya Iwamoto, Kiyoto Kasai, Chihiro Kakiuchi

127 **Common Polygenic Variation and Risk for Childhood-onset Schizophrenia**

Kwangmi Ahn, Steven An, Judith Rapoport

128 **Schizophrenia Polygenic Risk Scores Associated with Family History of Schizophrenia and Clinical Heterogeneity**

Patrick Sullivan, Christina M. Hultman, Stephanie Williams, Stephan Ripke, Cynthia M. Bulik, Pamela Sklar, Shaun Purcell, Jung-Ying Tzeng, Thomas Werge, Merete Nordentoft, Anders D. Børglum, Ole Mors, Schizophrenia Working Group of the Psychiatric Genomics Consortium, Preben Bo Mortensen, Esben Agerbo

129 **SorCS2 Modulates Synaptic Activity of GluN2B – A Potential Link to Schizophrenia**

Peter Ovesen, Ulrik Bolcho, Mai Marie Holm, Simon Glerup, Anders Nykjær

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POSTERS

SUBSTANCE ABUSE

130 ★ **An Analysis of Protein-altering Mutations in the Acetaldehyde Metabolizing Enzyme ALDH1B1 in a Cohort of British and Irish Dependent Drinkers**
Mohamed Ali, Michael Way, Andrew McQuillan, Marsha Morgan

131 **Candidate Gene Association Study of Heroin and Amphetamine Addiction Reveals Common and Specific Effects**
Radka Kaneva, Gyulnas Dzhebir, Ivan Popov, Olga Bletcheva, Georgi Vasilev, Reni Tzveova, Vanio Mitev, Ivo Kremensky, Alexandre Todorov, Jasmin Vassileva

132 **Variation in P2RX7 is Associated with Alcoholism in Men with Adverse Childhood Environment – Evidence for a Gene-environment Interaction**
Johanna Liuhanen, Outi Mantere, Siddheswar Utge, Pia Soronen, Sami Pirkola, Timo Partonen, Erkki Isometsä, Tiina Paunio

133 **Genetic Influences on DSM-IV Indicators of Alcohol Dependence: Evidence for a Common Genetic Liability**
Rohan Palmer, John McGeary, Andrew Heath, Matthew Keller, Valerie Knopik

134 **Association between Histone Deacetylase 3 Gene and Medication Overuse: A Pilot Study in Medication Overuse Headache Patients**
Claudia Pisanu, Donatella Congiu, Alessio Squassina, Stefano Caproni, Massimiliano Sestu, Paola Sarchielli, Alessandra Cherchi, Maria Del Zompo, Paolo Calabresi

135 ★ **Family Genetics of Alcohol Dependence: Co-aggregation and Co-morbidity among First (FDRs) and Second Degree Relatives (SDRs) of Alcohol Dependent Probands**
Sahoo Saddichha

136 **Smoking Behavior: Investigation of the Interplay between Environmental and Genetic Risk Factors**
Jens Treutlein, Jana Strohmaier, Josef Frank, Thomas Muhleisen, Franziska Degenhardt, Stephanie Witt, Thomas G. Schulze, Sven Cichon, Markus Nothen, Marcella Rietschel

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137 **Sulfur Aminoacid Metabolic Process Pathway may Modulate Bipolar Disorder with Alcohol Dependence Comorbidity**
Antonio Drago, Alessandro Serretti

TECHNOLOGY – SEQUENCING

138 **Use of Ion Torrent for High-throughput Targeted Next Generation Sequencing**
Noa Carrera, Lyudmila Georgieva, David Kavanagh, Adrianne Davis, Kiran Mantripragada, George Kirov, Michael Owen, Michael O'Donovan

139 **Microtargeting Pools to Achieve Efficient and Cost Effective Variant Discovery in Large Samples Sets**
Sara Goodwin, Melissa Kramer, Jenifer Parla, Scott Ethe-Sayers, Panchajanya Deshpande, Richard McCombie

POSTERS

TUESDAY, OCTOBER 14, 2014

ADHD

1 **Genetic Analysis of ADHD Traits in Adults: Results from the "Study of ADHD Trait Genetics in Adults" (SAGA) Consortium**

Alejandro Arias-Vásquez, Harmen Draisma, Dina Vojinovic, Tessel Galesloot, Jouke Jan Houtenga, Brenda Pennix, Marta Ribases, Najaf Amin, Sandra Kooij, Bru Cormand, Antoni Ramos-Quiroga, Ilja Nolte, Catarina Hartman, Cornelia van Duijn, Barbara Franke, Dorret Boomsma

2 **Perinatal Risk Factors Interacting with Candidate Genes in Predicting the Developmental Course of Attention Deficit/ Hyperactivity Symptoms into Late Adolescence**

Djûke Brinksma, P.J. Hoekstra, B. van den Hoofdakker, C.A. Hartman, A. de Bildt , J.K. Buitelaar, A. Dietrich

3 **Targeting Defect of a Single Amino Acid Deletion Mutant of the Glucose Sensor SGLT3 Associated with Attention Deficit Hyperactivity Disorder**

Maximilian Friedrich, Erhard Wischmeyer, Dietmar Geiger, Silke Groß-Lesch, Sina Koller, Hermann Koepsell, Marieke Klein, Barbara Franke, Klaus-Peter Lesch, Frank Döring

4 **Influence of ADHD Polygenic Risk on Neurocognitive Functioning in Young Adults**

Alexandros Hatzimanolis, Nikolaos Smyrnis, Anna Moes, Pallav Bhatnagar, Dan Arking, Nicholas Stefanis, Dimitrios Avramopoulos

5 **Testing Neuropsychological Intermediate Phenotype: A Comparison of the Children with ADHD, their Unaffected Siblings and Typically Developing Children**

Hyo-Won Kim, Kee Jeong Park, Hyun-Jeong Lee

6 **Genetic Influences on Multiple Measures of Fear Processing**

Kate Langley, Stephanie van Goozen, Karen Schepman, Anita Thapar

POSTERS

7 **Functional Glucocorticoid Receptor Gene Variants and Childhood ADHD**

Andrea Schote-Frese, Martina Bonenberger, Haukur Palmason, Christiane Seitz, Jobst Meyer, Christine Freitag

AFFECTIVE DISORDERS

8 **An Investigation into Risk-taking as a Potential Phenotype for Bipolar Disorder**

Heike Anderson-Schmidt, Linda Gebel, Andreas Glöckner, Thomas G. Schulze

9 **Regulated Sortilin Shedding Balances Synaptic Input and is Linked to Bipolar Disorder**

Ulrik Bølcho, Simon Glerup, Ken-Ichi Inoue, Mette Nyegaard, Ditte Demontis, Pippa Thomson, David Porteous, Jesper Lundhede, Søren Ostergaard, Henriette Buttenschon, Jens Nyengaard, Ernst-Martin Fuchtbauer, Ole Mors, Anders Borglum, Kimmo Jensen, Anders Nykjær

10 ★ **Genetic Association Analysis of 85 Candidate Polymorphisms for Major Depression: Preliminary Results from the PISMA-ep Study**

Ana Ching-López, Margarita Rivera, Jorge Cervilla, Esther Molina, Kathryn McKenney, Blanca Gutiérrez

11 **The Quality of Sleep as a Subphenotype in Association Studies of "clock genes" in Mood Disorders**

Piotr Czerski, Monika Dmitrzak-Weglarz, Joanna Pawlak, Monika Wilkosc, Malgorzata Maciukiewicz, Anna Leszczynska-Rodziewicz, Joanna Hauser, Wanda Ciarkowska

12 ★ **Bipolar Disorder: Whole Genome Sequencing in a Large Afrikaner Family**

Shareefa Dalvie, Morne Du Plessis, Gerrit Botha, James Knowles, Raj Ramesar, Dan Stein

13 **Linkage Analysis Implicates a Locus on Chromosome 7q21 with Catatonic Psychosis**

Jose Estrada, Cynthia Camarillo, Javier Ordonez, Albana Dassori, Juan Manuel Peralta, Mercedes Ramirez, Salvador Contreras, Laura Almasy, Henriette Raventos, Michael Escamilla

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POSTERS

14 **Genome-wide Analysis of microRNA Coding Genes in Bipolar Disorder**

Andreas J. Forstner, Andrea Hofmann, Thomas W. Mühleisen, Markus Leber, Thomas G. Schulze, Jana Strohmaier, Franziska Degenhardt, Jens Treutlein, Per Hoffmann, Stephanie H. Witt, Gerhard Schratt, Tim Becker, Marcella Rietschel, Sven Cichon, Markus M. Nöthen

15 **The Risk for Major Depression Conferred by Childhood Maltreatment Is Multiplied by BDNF and SERT Genetic Vulnerability**

Blanca Gutierrez, Juan A. Bellón, Margarita Rivera, Esther Molina, Michael King, Louise Marston, Francisco Torres-González, Berta Moreno-Kustner, Jorge Cervilla

16 **Shared Genetic Risk between Depression and Co-morbid Somatic Disorders**

Gabriella Juhasz, Peter Marx, Bence Bolgar, Gyorgy Bagdy, Peter Antal

17 **Exome Sequencing Identifies de novo Mutations in Bipolar Disorder**

Muneko Kataoka, Nana Matoba, Kumiko Fujii, Tadafumi Kato

18 **Arntl Gene Variant and Seasonal Variations in Mood and Behavior**

Hae-In Kim, Heon-Jeong Lee, Chul-Hyun Cho, Joung-Ho Moon, Ho-Kyoung Yoon, Seung-Gul Kang, Young-Min Park, Leen Kim

19 **OPEN BOARD**

20 **Investigating Genetic and Environmental Associations between Depression Symptoms and Body Mass Index among European and African-American College Students**

Roseann Peterson, Hermine Maes, Vernell Williamson, Dylan Vrana, Kenneth Kendler, Danielle Dick, Bradley Webb

21 **Genetics in Bipolar Disorder - Associations with Cognition and Obesity**

Alexandra Rieger, Nina Lackner, Armin Birner, Elisabeth Weiss, Erwin Petek, Christian Windpassinger, Urs Heilbronner, Hans-Peter Kapfhammer, Martina Platzer, Frederike Fellendorf, Eva Reininghaus, Susanne Bengesser

POSTERS

22 **Influence of Adverse Childhood Experiences on Depression: Possible Mechanism through DNA Methylation of HPA Axis Related Genes**

Jen-Hsiu Shen, Li-Chung Chuang, Yi-Hang Chiu, Ming-Chyi Huang, Po-Hsiu Kuo

23 **CNV Predictions in ADHD, Autism, and Affective Disorders**

Thomas Sparsø, Marcelo Bertalan, Jonas Grauholm, Mads Hollegaard, SSI, BROAD, iPSYCH

24 **VAMP7 is a Gene of Interest in Bipolar Disorder and Catatonia**

Robert Stowe, Christine Tyson, Monica Hrynchak, Trevor Hurwitz, William Honer

25 **Do the Interactions between Perceived Parenting Style and 5 VNTRs, Mediate Depressive Symptoms in Adolescents?**

Evelien Van Assche, Tim Moons, Annelies Janssens, Steven De Laet, Roosmarijn Jansen, Wim Van Den Noortgate, Luc Goossens, Stephan Claes

26 ★ **Association of Tryptophan Hydroxylase 1 A218C Polymorphism in Patients with Mood Disorder in Calabar, Nigeria**

Ibene Ekpor, Mary Kooffreh, Emmanuel Essien, Abdullahi Halilu, Alexandar Audu, Thomas Emedoh, Achor Francisca, Deji Owatti, Bassey Edet, Owoidoho Udofia

27 **Sequencing of VMAT1 (SLC18A1) Identifies Rare Novel Variants that Are Functional in Vitro and Associated with Bipolar Disorder**

Falk Lohoff, Sneha Narasimhan, Rachel Hodge, Glenn Doyle

28 **Bipolar Disorder Genetic Variation in the miR-708 Gene and its Binding Targets**

Andrew McQuillin, Niamh O' Brien, Alexandra Jarram, Adebayo Anjorin, Radhika Kandaswamy, Robert Blizard, David Curtis

ANXIETY DISORDER

29 **Depression, Anxiety and Somatoform Disorder Trajectories across Adolescence in Relation with Later Diagnosis of Major Depressive Disorder: A Longitudinal Twin Study**

Baptiste Couvy-Duchesne, Margie Wright, Ian Hickie, Narelle Hansell, Nick Martin

★ – Travel Awardee

30 **hsa-miR-4717-5p Regulates RGS2 and is Associated with Anxiety-related Traits**
Leif Hommers, Andreas Ströhle, Alexander Gerlach, Tilo Kircher, Volker Arolt, Andrew Gloster

31 **Social Phobia is more Prevalent in Females with Serotonin Transporter Gene Linked Promoter Polymorphism I/I Genotype**
Triin Kurrikoff, Kirsti Akkermann, Evelyn Kiive, Jaanus Harro

32 **The Genetic Biobank in the Faroe Islands and Panic Disorder**
August Gabriel Wang, Noomi Gregersen, Hans Atli Dahl, Marjun Biskopsstø, Oddbjørg Johansen, Birita Clementsen, Tormódur Stórá, Ole Mors, Anders Børglum, Gudrid Andorsdóttir

AUTISM

33 **CNVs on Chromosome 22q11.2 Reveal Different Phenotypes in Autism Patients**
Hsin-I Chen, Hsiao-Mei Liao, Chia-Hsiang Chen, Wei-Hsien Chien, Susan Shur-Fen Gau

34 **Reduced Astrocytic Labelling and Decreased Numbers of Activated Microglia in the Neurexin 1 Alpha Knockout Rats**
Hannah Grayton, Frederic Esclassan, Zeshan Ahmed, Michael J. O'Neill, David A. Collier

35 **CNTNAP2 Gene in High Functioning Autism**
Edna Grünblatt, Anna Werling, Regina Taurines, Elise Bobrowski, Ronnie Gundelfinger, Marcel Romanos, Susanne Walitza

36 **Results of Genome Wide Association Study of Autism in a Population Based Danish Cohort**
Julian Maller, Autism Working Group

37 **Uncovering the Molecular Function of AUTS2- A Protein Involved in Brain Development and Autism**
Marina Risman, Laura Malki-Feldman, Galya Monderer-Rothkoff, Malka Nissim-Rafinia Nissim-Rafinia, Eyal Ben-David, Eran Meshore, Sagiv Shifman

POSTERS

38 **Mutations in Chromatin Related Genes in Autism Spectrum Disorder**

Reut Suliman, Sagiv Shifman

39 **Screening for Mutations in Non-syndromic Autosomal Recessive Intellectual Disability Genes in Non-consanguineous Intellectual Disability and Autism Populations**

John Vincent, Kirti Mittal, Nasim Vasli, Amy McNaughton, Anna Mikhailov, Melissa Hudson, Christian Windpassinger, Laila Al Ayadhi, Wolfgang Kaschnitz, Patrick Magee, James Stavropoulos, Melissa Carter, Muhammad Ayub, Xudong Liu

40 **Common EIF4E Variants Modulate Risk for Autism Spectrum Disorders in the High-functioning Range**

Regina Waltes, Johannes Gfesser, Denise Haslinger, Katja Schneider-Momm, Monica Biscaldi, Anette Voran, Christine M. Freitag, Andreas G. Chiocchetti

BIOSTATISTICS / BIOINFORMATICS

41 **Genetic Risk Variants in Schizophrenia: Identifying Disease Relevant Interactions**

Bathilde Ambroise, James Walters, Jennifer Moran, Steve McCarroll, Michael Owen, Michael O'Donovan, Valentina Escott-Price, Andrew Pocklington

42 **Gene-based Analysis in the PGC Schizophrenia GWAS**

Valentina Escott-Price, Peter Holmans, Psychiatric Genomics Consortium, Schizophrenia Working Group of the PGC, Michael Owen, Michael O'Donovan

43 **Building Better Classifiers: Optimizing Models of Heterogeneous Neuropsychiatric Disorders Derived from High-dimensional Data**

Stephen Glatt, Thomas Quinn, Daniel Tylee

44 **Crosstalk between Heritable and Non-heritable Genome Variations in Psychiatric Diseases: From Genes to Environment and Back Again**

Ivan Iourov, Svetlana Vorsanova, Maria Zelenova, Oxana Kurinnaia, Irina Demidova, Alexey Kolotii, Victor Kravets, Kirill Vasin, Yuri Yurov

45 **ForestSV 2.0: Statistical Learning for Improved Structural Variant Discovery**

Jacob Michaelson, Ethan Bahl, Dheeraj Malhotra, Madhusudan Gujral, Jonathan Sebat

46 **Estimating Causal Variant Allele Frequency and Prioritising Loci for Sequencing**

Paul O'Reilly, Clive Hoggart

47 **Most Pairs of Rare Genetic Variants within the Same Gene are Found on the Same Chromosome**

Elliott Rees, Davy Kavanagh, Menachem Fromer, Douglas Ruderfer, Peter Holmans, Jennifer Moran, Kimberly Chambert, Steve McCarroll, Ed Scolnick, Pamela Sklar, Shaun Purcell, Michael Owen, Michael O'Donovan, Geroge Kirov

48 **A Spatiotemporal Systems Biology Approach to Understanding Autism Spectrum Disorder and Schizophrenia**

Arthur Willsey, Stephan Sanders, James Noonan, Kathryn Roeder, Bernie Devlin, Nenad Sestan, Matthew State

ELSI, COUNSELING AND GENETIC TESTING

49 **Disclosure of Psychiatric Manifestations of 22q11.2 Deletion Syndrome: A Retrospective Chart Review Documenting Clinical Practice of Medical Geneticists**

Jehannine Austin, Serena Talcott Baughman, Emily Morris

50 **Attitudes towards Genetic Research and Predictive Testing in Psychiatric Disorders among Providers and Consumer Groups – A German Pilot Study**

Jana Strohmaier, Christine Schmäl, Stephanie H. Witt, Markus Reitt, Franciska Illes, Dan Rujescu, Thomas G. Schulze, Marcella Rietschel

51 **Genetic Association Studies of Schizophrenia Risk Variants with Cognitive and Neuroimaging Phenotypes: A GENUS Consortium Project Update**

Gabriëlla Blokland, Tracey Petryshen, on behalf of the GENUS Consortium

POSTERS

ENDOPHENOTYPES

52 **Comt Val/Met Polymorphism Predicts the Effect of tDCS on Executive Functioning**

Vanessa Nieratschker, Christoph Kiefer, Kathrin Giel, Rejko Krüger, Christian Plewnia

53 **Personality Traits as an Endophenothype in Genetic Studies on Suicidality in Bipolar Disorder**

Joanna Pawlak, Monika Dmitrzak-Weglarz, Malgorzata Maciukiewicz, Pawel Kapelski, Piotr Czerski, Anna Leszczynska-Rodziewicz, Dorota Zaremba, Joanna Hauser

54 **Polygenic Contribution of Fragile X Mental Retardation Protein Targets on Cognition in Narrow and Broad Psychosis: The Use of Coding SNPs versus Linkage Disequilibrium (LD) Pruning**

Alexandros Rammos, Lara Neira Gonzalez, Eric Kelleher, April Hargreaves, The Wellcome Trust Case-Control Consortium 2, Gary Donohoe, Derek Morris, Aiden Corvin, Michael Gill, Kristin Nicodemus

55 **Is the Life Extension Factor Klotho Related to Human Cognition? A Meta-analysis**

Christian Vogler, Annette Milnik, Virginie Freytag, Dominique de Quervain, Andreas Papassotiropoulos

EPIGENETICS

56 **Orbitofrontal Cortex Mirnas in Post-traumatic Stress Disorder**

Melanie Carless, Jennifer Neary, Hemant Kulkarni, Thomas Hyde, Joel Kleinman, Robert Ursano, David Benedek, Dianne Cruz, Douglas Williamson, Keith Young

57 **Newborn Females Show Higher Stress-independent Methylation of the 5-HTT than Males**

Helene Dukal, Josef Frank, Maren Lang, Jens Treutlein, Maria Gilles, Isabell Wolf, Bertram Krumm, Renaud Massart, Moshe Szyf, Manfred Laucht, Michael Deuschle, Marcella Rietschel, Stephanie Witt

58 **DNA Methylation at the PGCP and KITLG Loci Mediates the Influence of Childhood Trauma on Cortisol Response: A Genome Wide DNA Methylation Study of the Acute Stress Response**

Lotte Houtepen, Christiaan Vinkers, René Kahn, Marian Joëls, Marco Boks

59 **Epigenome-wide Analysis of Methylation in a Family with a Balanced t(1;11) Translocation Co-segregating with Major Mental Illness**

Daniel L. McCartney, Rosie M. Walker, Douglas H. Blackwood, J. Kirsty Millar, Pippa A. Thomson, Andrew M. McIntosh, W. Richard McCombie, David J. Porteous, Kathryn L. Evans

60 **Functional Location of Long Term Effects of Early Trauma on DNA Methylation**

Julius Pape, Tania Carrillo-Roa, Nadine Provencal, Anthony S. Zannas, Bekh Bradley, Kerry J. Ressler, Elisabeth B. Binder

61 **Identification of Epigenetic Variants Associated with Neuropsychiatric Disorders in Perinatal and Postmortem Tissue Applying Agnostic and Genome-wide Methodologies**

Nicklas Staunstrup, Anna Szyszka, Anders Nielsen, Stine Bak, Marit Nielsen, Mette Nyegaard, Mads Hollegaard, Jørn Olsen, Carsten Obel, Niels Bilenberg, Maj Vinberg, Karl-Anton Dorph-Petersen, Jens Nyengaard, Anders Børglum, Ole Mors

62 **Epigenetic Modification of NR3C1 and SLC6A4: A Plausible Biological Mechanism for Linking Early Life Adversity and Later Internalizing Disorders**

Lisette van Der Knaap, Floor van Oort, Tineke Oldehinkel, Frank Verhulst, Harriette Riese

63 **The Effects of Smoking on Cognition: An Epigenetic Study**

Vanja Vukojevic, Annette Milnik, Philippe Demougin, Fabian Peter, Attila Stetak, Dominique J.-F. de Quervain, Andreas Papassotiropoulos

POSTERS

FUNCTIONAL GENOMICS & MODEL ORGANISMS

64 **A Neural Network Model for Predicting Treatment Response of Antidepressants in Patients with Major Depressive Disorder**
Po-See Chen, Hui Hua Chang

65 **Neuropsychiatric Phenotypes in Mice Lacking BDNF or its Receptors**
Simon Glerup, Mathias Kaas

66 **Female Brd1+/- Mice Display Reversible Depressive Phenotype, Neurochemistry, Neuronal Morphology and Transcriptome that are Consistent with Major Depressive Disorder**
Anto Praveen Rajkumar Rajamani, Per Qvist, Ross Lazarus, Nicoletta Nava, Gudrun Winther, Nico Liebenberg, Veerle Paternoster, Tue Fryland, Mette Nyegaard, Jens Nyengaard, Gregers Wegener, Ole Mors, Jane Christensen, Anders Børglum

67 **Dopamine-related ADHD Genes Share a Behavioral Signature in Drosophila**
Monique van der Voet, Benjamin Harich, Barbara Franke, Annette Schenck

MISCELLANEOUS OTHER PSYCHIATRIC DISORDERS

68 **Gene X Environment Interactions and Borderline Personality Disorder**
M.J. Arranz, Ana Martin-Blanco, Marc Ferrer, Joaquim Soler, Juliana Salazar, Daniel Vega, Oscar Andión, Cristina Sanchez-Mora, Matilde Elices, Juan-Carlos Pascual

69 **Lessons from the iPSYCH Mega Study; Preparation of DNA Samples from More than 80,000 Danes**
Marie Bækvad-Hansen, Jesper Poulsen, Jonas Grauholm, Marianne Pedersen, iPSYCH PI-group, Sissel Vorstrup, David Hougaard, Mads Hollegaard

70 **The Oxytocin Receptor Gene and Aggressive Antisocial Behavior in Humans**
Daniel Hovey, Måns Lindstedt, Anna Zettergren, Lina Jonsson, Jonas Melke, Nora Kerekes, Henrik Anckarsäter, Paul Lichtenstein, Lars Westberg

POSTERS

71 **Genetic Variants in Neurotrophins and ADHD Dimensions**
Amaia Hervás, Aitana Bigorra, Ayhesa Ruiz, Silvina Guijarro, Bru Cormand, Vanessa Richarte, Cristina Sanchez-Mora, M.J. Arranz

72 **The Role of Genetic Variation in the Thiamine and Folate System in Susceptibility to Wernicke-Korsakoff's Syndrome and the Alcohol Dependence Syndrome**
Giorgia Quadri, Irene Guerrini, Allan Thomson, Michael Way, Iain Smith, Nicholas Bass, Marsha Morgan, Andrew McQuillin

73 ★ **Genome-wide Association Study of Adult Antisocial Behavior Identifies ABCB1**
Jessica Salvatore, Fazil Aliev, Alexis Edwards, Tim Bigdeli, John Kramer, Arpana Agrawal, Victor Hesselbrock, Michie Hesselbrock, Howard Edenberg, Xiaoling Xuei, Samuel Kuperman, Tatiana Foroud, Danielle Dick

74 **OPEN BOARD**

75 **Genome-wide Significant Common Variant Associations in Fragile X Syndrome**
Stephanie Williams, Anna Kähler, Jin Szatkiewicz, Yunjung Kim, Ann Collins, Molly Losh, Annette K. Taylor, Joseph Piven, Deborah Hatton, Mark J. Daly, Patrick F. Sullivan

76 **OPEN BOARD**

NEUROIMAGING

77 **A Schizophrenia-related Multiallelic Gene Score is Associated with Brain Morphometry in Healthy Young Adults**
Leo Gschwind, Virginie Freytag, Klara Spalek, Christian Vogler, Annette Milnik, Dominique de Quervain, Andreas Papassotiropoulos

78 **Polymorphisms within the Serotonin Transporter Promoter and Brain Morphology**
Ardesheer Talati

★ – Travel Awardee

POSTERS

OTHER

79 **Polygenic Scores from Large GWAS Applied to Smaller Samples**
Tobias Egli, Annette Milnik, Virginie Freytag, Christian Vogler, Dominique De Quervain, Andreas Papassotiropoulos

80 **Gene-set Analyses of Episodic Memory Performance and Episodic Memory-related Brain Activation**
Angela Heck, David Coynel, Matthias Fastenrath, Sandra Ackermann, Horst Bickel, Leo Geschwind, Frank Jessen, Hanna Kaduszkiewicz, Wolfgang Maier, Annette Milnik, Christian Vogler, Klara Spalek, Michael Wagner, Dominique de Quervain, Andreas Papassotiropoulos

81 **Genetic Influences on Socioemotional Development in Infants at 8 Months: Preliminary Findings**
Katri Kantojärvi, Johanna Liuhanen, Julia Jaatela, Anneli Kylliäinen, Outi Saarenpää-Heikkilä, Juulia Paavonen, Tiina Paunio

82 **A Comparison of Multivariate Genome-wide Association Study Methods**
Heather Porter, Cathryn Lewis, Paul O'Reilly

83 **Brain Derived Neurotrophic Factor Gene Polymorphisms, Healthy Lifestyle and Cognition in Healthy Subjects from Polish Population**
Agnieszka Szalkowska, Monika Wilkosc, Maria Sibinska, Joanna Hauser, Aleksander Araszkiewicz

84 **Predictors of Pathogenic Copy Number Variation in Adults with Idiopathic Intellectual Disability and Co-morbid Neuropsychiatric Disorders**
Kate Wolfe, Nick Bass, McQuillin Andrew, Andre Strydom

85 **Gene Environment Interactions in Tourette Syndrome: The Tourette International Collaborative Genetics (TIC Genetics) Study**
Mohamed Abdulkadir, Andrea Dietrich, Pieter Hoekstra, Gary Heiman, Jay Tischfield

86 **From Gene to Mean: A Meta-analysis of Genome-wide Association Data on Antisocial Behavior. The Broad Antisocial Behavior Consortium**

Jorim Tielbeek, Ada Johansson, Danielle Posthuma, Sarah Medland, Arne Popma, Tinca Polderman, Steve Faraone

87 **Gene-based Analyses of GWAS Data on Conduct Disorder Symptoms in African and European-Americans**

Irwin Waldman, Devon LoParo, Joshua Weinstock, Alisha Pollastri, Henry Kranzler, Lindsay Farrer, Joel Gelernter

PHARMACOGENETICS

88 **A Microarray Study Identifies Expression Signatures of Positive Response to Lithium Treatment in Bipolar Disorder and Cluster Headache Patients**

Claudia Pisanu, Marta Costa, Donatella Congiu, Paola Niola, Ignazio Piras, Andrea Angius, Raffaella Ardau, Maria Erminia Stochino, Alessandra Cherchi, Arianna Deidda, Giovanni Severino, Antonio Persico, Martin Alda, Maria Del Zompo, Alessio Squassina

89 **Hypothalamic-Pituitary-Adrenal System and Neurotrophic Factors and Clozapine Response: Association with FKBP5 and NTRK2 Genes**

Barbara Arias, M. Mitjans, M. Vázquez, A. González, R. Penadés, A. Pons, G. Massana, J. Munro, M.J. Arranz, R. Catalán

90 **Non-replication of Association of the GADL1 SNP rs17026688 with Lithium Response in Han Chinese**

Margit Burmeister, Sheng Li, Chen Zhang, Zhiguo Wu, Haozhi Li, Lin He, Jun Li, Yiru Fang

91 **Individualized Medicine: Pharmacogenetic Assessment & Clinical Treatment (IMPACT)**

Sheraz Cheema, Nicole Braganza, Deanna Herbert, Anashe Shahmirian, Michelle Murray, Arun Tiwari, Tasha Cate-Carter, Natalie Freeman, David Irwin, Eva Brandl, Umakajan Umakanthan, Gwyneth Zai, Clement Zai, Daniel Mueller, James Kennedy

92 **Pharmacoepigenetics of Depression: A Role of 5-HTT DNA Hypomethylation?**
Katharina Domschke, Nicola Tidow, Kathrin Schwarte, Jürgen Deckert, Klaus-Peter Lesch, Volker Arolt, Peter Zwanzger, Bernhard Baune

93 **Transcriptomics and the Mechanisms of Antidepressant Efficacy**
Karen Hodgson, Katherine Tansey, Giovanni Coppola, Rudolf Uher, Timothy Powell, Gerome Breen, Peter McGuffin, GENDEP Investigators, Richard Dobson

94 **New Insights from Cell Adhesion Molecules in Antidepressant Action: Role of ITGB3 and GAP43 Genes**
Laura Mandelli, Concetta Crisafulli, David Gurwitz, Julia Stingl, Raffaella Calati, Diego Albani, Rosalba Martines, Edoardo Spina, Marco Calabrò, Siegfried Kasper, Joseph Zohar, Daniel Souery, Stuart Montgomery, Juien Mendlewicz, Alessandro Serretti

95 **GWAS in Antipsychotic-induced Weight Gain in Schizophrenia Patients**
Daniel Mueller, Eva J. Brandl, Arun K. Tiwari, Clement C. Zai, Nabilah I. Chowdhury, Tamara Arenovich, Jiangshan J. Shen, James L. Kennedy

96 **ABCB1 Polymorphism as a Clue to Refractoriness in a Sample of Mood Disorders Patients Undergoing ECT**
Carolina Prado, Martinus van de Bilt, Luiz Felipe Rigonatti, Fernanda Lopes, Sergio Rigonatti, Leda Talib, Wagner Gattaz

97 **ECIP** **Intersecting Large-scale Genetic Studies of Schizophrenia with Drug Target Information to Inform Drug Design**
Douglas Ruderfer, Alexander Charney, Ben Readhead, Swedish Schizophrenia, PGC Schizophrenia, Shaun Purcell, Joel Dudley, Pamela Sklar

98 **Exome Array Analysis of Clozapine-associated Neutropenia**
James Walters, Marian Hamshere, Alexander Richards, Anna Leonenko, David Kavanagh, Stephan Ripke, Jennifer Moran, Kimberly Chambert, Giulio Genovese, Benjamin Neale, Steven McCarroll, Jackie Goldstein, Dan Rujescu, Michael O'Donovan, Michael Owen

ECIP – ECIP Finalist

POSTERS

SCHIZOPHRENIA

99 **Is Physical Exercise Associated with Increased BDNF mRNA and Improved Cognition in Patients with Psychoses?**
Monica Aas, Srdjan Djurovic, Ole A. Andreassen, Ingrid Melle

100 **An Investigation into Transcriptomic Correlates of Antipsychotic Medication Usage**
Olesya Ajnakina, Stephen Newhouse, Anita Acharya, John Lally, Daniel J. Leirer, Hamel Patel, Charles Curtis, Gerome Breen, Fiona Gaughran, Marta Di Forti, Richard Dobson, Conrad Iyegbe, Robin M. Murray

101 **Evidence for Association of Pro-inflammatory Cytokine Gene Polymorphisms with Schizophrenia in South Indian Population**
Moinak Banerjee, Lekshmy Srinivas, Neetha N.V., Chandrasekharan Nair, Priya M. Allencherry

102 **Identification of de novo Mutations in Patients with Schizophrenia**
Franziska Degenhardt, Friederike Schroeder, Jana Strohmaier, Per Hoffmann, Stefan Herms, Fabian Streit, Andrea Hofmann, Holger Thiele, Janine Altmüller, Peter Nürnberg, Sven Cichon, Marcella Rietschel, Markus M. Nöthen

103 **Changes in Global Gene Expression during Long-acting Antipsychotic Exposure in Rat: Searching for Genetic and Pharmacogenetic Predictors in Psychotic Disorders**
Inger Duus, Kari Ersland, Silje Skrede, Vidar Steen

104 **Involvement of the Neuritin 1 Gene in Schizophrenia-spectrum and Bipolar Disorders and its Impact on Age at Onset and Cognitive Functioning**
Mar Fatjó-Vilas, Claudia Prats, Edith Pomarol-Clotet, Luisa Lázaro, Carmen Moreno, Sara Lera, Salvador Miret, Ignacio Ibáñez, Maria Giralt, Manuel J. Cuesta, Victor Peralta, Generós Ortet, Mara Parellada, Ana González-Pinto, Peter J. McKenna, Lourdes Fañanás

POSTERS

105 **Dopamine Alterations in a Mouse Model of the 1q21.1 Microdeletion Syndrome**

Kim Fejgin, Jacob Nielsen, Florence Sotty, Jes B. Lauridsen, Vibeke Nielsen, Dorte Clausen, Peter H. Larsen, Claus T. Christoffersen, Trine N. Jørgensen, Ib V. Klewe, Michael Didriksen

106 **Thousands of Blood Spots from an Ocean of Filter Papers: Metadata Analysis from the iPSYCH Project**

Jonas Grauholm, Marie Bækvad-Hansen, Jesper Poulsen, Marianne Pedersen, iPSYCH PI-group, Sissel Vorstrup, David Hougaard, Mads Hollegaard

107 **How Might the Non-coding ZNF804A Variant rs1344706 Increase Risk for Schizophrenia and Bipolar Disorder?**

Jonathan Hess, Stephen Glatt

108 **Molecular Signature in Olfactory Neuronal Epithelium that Is Correlated with Cognitive Impairment in Schizophrenia**

Yasue Horiuchi, Yoichiro Takayanagi, Tiffany Ho, Katsunori Tajinda, Nicola G. Cascella, David Schretlen, Jonathan Pevsner, Akira Sawa

109 **Screening, Identification, and Functional Analysis of Novel Missense Mutations in the NDE1 Gene in Japanese Patients with Schizophrenia**

Hiroki Kimura, Daisuke Tsuboi, Chenyao Wang, Itaru Kushima, Takayoshi Kiode, Masashi Ikeda, Akira Yoshimi, Yuto Takasaki, Aleksic Branko, Hiroshi Kunugi, Tadafumi Kato, Takeo Yoshikawa, Nakao Iwata, Kozo Kaibuchi, Norio Ozaki

110 **SorCS2 in Postnatal Development of GABAergic Interneurons in the Hippocampus**

Simon Mølgaard, Simon Hansen, Jens Nyengaard, Simon Glerup, Anders Nykjær

111 **Interaction between DISC1, FOXP2 and TUBA1A Increases Risk for Psychosis and Influences IQ and Verbal IQ Performance**

Lara Andrea Neira Gonzalez, Alexandros Rammos, Eric Kelleher, April Hargreaves, The Wellcome Trust Case-Control Consortium 2, Gary Donohoe, Derek Morris, Michael Gill, Aiden Corvin, Kristin K. Nicodemus

112 **Expression Profiles as a Predictive Biomarker of Schizophrenia**
Yuko Okahisa, Masashi Ikeda, Manabu Takaki, Shinji Sakamoto, Hiroshi Ujike, Nakao Iwata, Yosuke Uchitomi

113 **Functional Gene Clusters and Pathways in Schizophrenia: Results from the Schizobank Whole Exome Sequencing Study**
Attila Pulay, János Réthelyi, Júlia Koller, Attila Horváth, Péter Balicza, Gábor Zahuczky, Endre Barta, István Likó, György Németh, Róbert Urbányi, Krisztián Nagy, Judit Mária Molnár, László Nagy, Hungarian Schizobank Consortium

114 **Identification and Functional Characterization of Rare SHANK2 Variants in Schizophrenia**
Slavil Peykov, Simone Berkel, Michael chön, Kerstin Eiss, Birgit Weiss, Gerhard Schratt, Markus Noethen, Tobias Boeckers, Marcella Rietschel, Gudrun Rappold

115 **Exome Array Analysis in Schizophrenia**
Alexander Richards, Ganna Leonenko, James Walters, Peter Holmans, Stephan Ripke, Benjamin Neale, Steven McCarroll, Kimberley Chambert, David Kavanagh, Jennifer Moran, Giulio Genovere, Michael Owen, Michael O'Donovan

116 **Psychotic Experiences in Adolescence Show High Genetic Stability and High Genetic Overlap with Traits of Depression**
Angelica Ronald, Helena Zavos, Philip McGuire, Daniel Freeman

117 **Genomic Approaches for the Identification of High-risk Genetic Factors for Schizophrenia and Bipolar Disorder: A Population-based Study**
Cecilia Salvoro, Giovanni Vazza, Cinzia Bertolin, Maria Luisa Mostacciuolo

118 **Aquaporin Genetic Polymorphism and Polydipsia in Schizophrenia**
Takahiro Shinkai, Kenji Yamada, Yukie Tokutsu, Jun Nakamura

119 **Genomic Regions Involved in Human Evolution are Enriched of Associations with Schizophrenia**
Saurabh Srinivasan, Francesco Bettella, Morten Mattingsdal, Aree Witoelar, Rahul Desikan, Andrew J. Schork, Wesley K. Thomson, Verena Zuber, Yunpeng Wang, Anders Dale, Srdjan Djurovic, Ole A. Andreassen

120 **Investigating the Genetics of Cognition within Schizophrenia: A PGC Study**
Katherine Tansey, PGC Schizophrenia Cognition Group

121 **Genome Sequencing in Families with Schizophrenia**
Debby Tsuang, Michael Dorschner, David Hanna, Sulgi Kim, Ellen Wijsman

122 **Significant Enrichment of Disease-specific Polymorphisms Surrounding MicroRNAs Suggests Further Involvement in Schizophrenia and Bipolar Disorder**
Vernell Williamson, Mohammed Mamdani, Gowon McMichael, Silviu Bacanu, Vladimir Vladimirov

123 **Transcriptome Analysis of Lymphoblastoid Cell Line from Schizophrenia and Bipolar Disorder**
Akira Yoshimi, Branko Aleksic, Shohko Kunimoto, Itaru Kushima, Yukako Nakamura, Hiroki Kimura, Yuto Takasaki, Chenyao Wang, Jingrui Xing, Akihiro Hirakawa, Masashi Ikeda, Nakao Iwata, Norio Ozaki

124 **OPEN BOARD**

125 **Parental Age, Birth Order, and Neurodevelopmental Disorders**
Alison Merikangas, Ricardo Segurado, Eric Kelleher, Denise Hogan, Catherine Delaney, Michael Gill, Louise Gallagher, Aiden Corvin, Elizabeth Heron

126 **Hypoxia Response Genes Moderate the Impact of Obstetric Complications on Psychiatric Symptomatology in a Population-based Twin Cohort**
Bart Rutten, Sinan Guloksuz, Marjan Drukker, Rainald Schmidt-Kastner, Gunter Kenis, Wolfgang Viechtbauer, Ehsan Pishva, Marieke Wichers, Nele Jacobs, Evert Thiery, Catherine Derom, Inez Myin-Germeys, Ruud vanWinkel, Jim van Os

127 **Hippocampal Pruning as a New Theory of Schizophrenia Etiopathogenesis**
Antonio Drago, Alessandro Serretti

POSTERS

SUBSTANCE ABUSE

128 **Alcoholism Interacts with Epigenetics to Control Cis-regulation of Opioid Gene in Human Brain: Underlying Cell-type Specific Changes in Methylation Coherence in Promoter CpG Island**
Georgy Bakalkin, Daniil Sarkisyan, Hiroyuki Watanabe, Olga Kononenko, Tatiana Yakovleva, Igor Bazov

129 ★ **Polygenic Risk for Alcohol Addiction and the Association with Cognitive, Mood and Personality Traits in the General Population**
Toni Clarke, Joel Gelernter, Henry Kranzler, Lindsay Farrer, Andrew Smith, Ana-Maria Fernandez- Pujals, Donald MacIntyre, Blair Smith, Lynne Hocking, Sandosh Padmanabhan, Caroline Hayward, David Porteous, Ian Deary, Andrew McIntosh

130 ★ **The Association of Polymorphisms in Dat (40 Bp VNTR, C/T 3'UTR) and DBH (-1021 C/T) Genes with the Severe Complications of Alcohol Withdrawal Syndrome**
Dmitriy Ivashchenko, Sergey Shuvalov, Natalya Chuprova, Alexander Kibitov

131 **Association of Prodynorphin (PDYN) Variants with Heroin Abuse in Bulgarian and Roma Subjects**
Gyulnas Dzhebir, Momchil Nikolov, Olga Beltcheva, Antoaneta Galabova, Antoaneta Ljubenova, Elena Jankova, Dorita Krasteva, Vanio Mitev, Ivan Popov, Ivo Kremensky, Radka Kaneva, Alexandre Todorov

132 ★ **Novel Genetic Variant Implicated in Genome-wide Study of Substance Use in Two Independent Majority African-American Populations**
Jacquelyn Meyers, Lynn Almli, Sandro Galea, Alison Aiello, Monica Uddin, Derek Wildman, Bekh Bradley, Kerry Ressler, Karestan Koenen

133 **Genetic Effects on Comorbid Drug Dependence: Consistent Effects across Measurements**
Rohan Palmer, Leslie Brick, John McGeary, Matthew Keller, Valerie Knopik

134 **OPEN BOARD**

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POSTERS

135 **DRD4 and SLC6A4 are not Associated with Sustained Binge Drinking in Young Adults**

Matthew Sloan, Gisele Contreras, Marie-Pierre Sylvestre, Erika Dugas, Robert Wellman, Jennifer O'Loughlin, Nancy Low

136 ★ **The Ile148Met Mutation in PNPLA3 does not Influence Alcohol Dependence Risk in the British and Irish Population but Significantly Influences the Risk of Developing Alcohol Related Cirrhosis**

Michael Way, Andrew McQuillin, Ian Smith, Raquin Cherian, Audrey Hillman, Karim Dar, Marsha Morgan

137 **Genome-wide Association Study of Alcohol Use Phenotypes in Spit for Science: An Ethnically Diverse, Longitudinally Assessed Population of US College Students**

Bradley Webb, Vernell Williamson, Alexis Edwards, Roseann Peterson, Dylan Vrana, Fazil Aliev, James Clifford, Danielle Dick, Kenneth Kendler

TECHNOLOGY – SEQUENCING

138 **An Efficient Screening Method for Simultaneous Detection of Recurrent Copy Number Variants (CNVs) Associated with Psychiatric Disorders using Quantitative Interspecies Competitive PCR**

Javier Costas, Julio Rodriguez-Lopez, Noa Carrera, Manuel Arrojo, Mario Paramo, Eduardo Paz, Angel Carracedo

139 **Deep Whole-genome Sequencing Based Analysis of Mosaic Mobile Element Insertions in Adult Human Tissue**

Xiaowei Zhu, Anna-Sophie Fiston-Lavier, Dmitri Petrov, Michael Snyder, Douglas Levinson

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POSTERS

WEDNESDAY, OCTOBER 15, 2014

ADHD

1 **A Genome Wide Association Study of a Quantitative ADHD-related Endophenotype in a Community-based Sample of Children and Adolescents**

Christie Burton, Jennifer Crosbie, Lauren Erdman, Annie Dupuis, Andrew Paterson, Paul Arnold, Russell Schachar

2 **A Genome-wide Association Meta-analysis of Continuous Measures of Attention Deficit Hyperactivity Disorder Symptoms in Nine Population-based Pediatric Cohorts**

Maria Groen-Blokhuis, Anke Hammerschlag, Beate St Pourcain, Maciek Trzaskowski, Peter van der Most, Carla Tiesler, Wei Ang, Natalia Vilor Tejedor, Jonas Bacelis, Jane Ebejer, EArly Genetics & Lifecourse Epidemiology (EAGLE) Consortium

3 **Established and New ADHD Candidate Genes and their Association with White Matter Measures of the Brain**

Martine Hoogman, Anais Harneit, Marten Onnink, Jeanette Mostert, Janneke Dammers, Jan Buitelaar, Barbara Franke

4 **The Interaction Effect of the Tryptophan Hydroxylase-2 G-703T Genotype and Stressful Life Events on Inattentive and Hyperactive Behaviour in Adolescents**

Evelyn Kiive, Mariliis Vaht, Toomas Veidebaum, Jaanus Harro

5 **Quantitative Association between Dopamine Transporter Gene (DAT1) and Attention-Deficit/Hyperactive Disorder (ADHD) Related Mood Instability Traits in Healthy Adults**

Yong Sik Kim, Seong Hoon Jeong, Eun-Jeong Joo

POSTERS

AFFECTIVE DISORDERS

6 **Genome-wide Interaction and Pathway Analysis on SSRI Response in Japanese Patient with Major Depression**

Masaki Kato, Chiara Fabbri, Alessandro Serretti, Shinpei Nonen, Yoshiteru Takekita, Junichi Azuma, Toshihiko Kinoshita, International SSRI Pharmacogenomics Consortium

7 ★ **Identification of Novel Biomarkers for Manic Episode Using Whole-genome Transcriptome Analysis**

Ya-Chin Lee, Ming-Chyi Huang, Chung-Feng Kao, Hsi-Chung Chen, Po-Hsiu Kuo

8 **A Direct Test of the Diathesis-stress Hypothesis using Polygenic Risk Scores**

Nick Martin, Sarah Medland, Baptiste Couvy-Duchesne, Miguel Renteria, Lucia Colodro Conde, Byrne Enda, Wray Naomi, Rob Power, Karin Verweij

9 **Childhood Physical Abuse and CNR1 Gene are Involved in the Presence of Depressive Symptomatology in the General Population: a Gene-environment Approach**

Marina Mitjans, Mar Fatjó-Vilas, Silvia Alemany, Helena Villa, Jorge Moya, Manuel Ibáñez, Generós Ortet, Lourdes Fañanás, Bárbara Arias

10 ★ **Association Study of the Triallelic 5-HTTLPR/rs25531 Polymorphism in the Serotonin Transporter Gene and Affective Disorders**

Alexandrina Al-Djassem, Gyulnas Dzhebir, Mina Ivanova, Mladen Penchev, Olga Beltcheva, Vanio Mitev, Vihra Milanova, Radka Kaneva

11 **Bipolar Disorder and ER-Stress**

Susanne Bengesser, Nina Lackner, Eva Reininghaus, Bernd Reininghaus, Armin Birner, Frederike Fellendorf, Martina Platzer, Kristijan Filic, Robert Queissner, Alexandra Rieger, Anna Painold, Erwin Petek, Robert Fuchs, Christian Windpassinger, Hans-Peter Kapfhammer, Sandra Liebmann-Wallner

12 **Self Efficacy as a Novel Phenotype for Psychiatric Genetics**

Monika Budde, Thomas G.Schulze

★ – Travel Awardee

POSTERS

13 ★ **The Relationship between FTO gene, Body Mass Index and Depression: Preliminary Results from a Spanish Population Study**
Ana Ching-López, Margarita Rivera, Jorge Cervilla, Esther Molina, Kathryn McKenney, Blanca Gutiérrez

14 **Unravelling the Comorbidity between Major Depressive Disorder and the Autoimmune Disorders – Shared Risk Alleles?**
Jack Euesden, Andrea Danese, Ian Scott, Cathryn Lewis

15 **Age-of-Onset Variation in Bipolar I Disorder and Replication in the Romanian Population of Top Associated SNPs Discovered by Recent Genome-wide Studies of Major Psychoses**
Maria Grigoroiu-Serbanescu, Stephanie Heilman, Tim Becker, Carmen C. Diaconu, Markus M. Noethen, Franziska Degenhardt

16 **Rare Mutations and Copy Number Variations Identified in Patients with Bipolar Disorder Affect Inhibitory Synapses**
Stephane Jamain, Sourour Mansour, Lucie Chevallier, Aude Nicolas, Bruno Etain, Bijan Ghaleh, Diana Zelenika, Chantal Henry, Jean-Pierre Kahn, Frank Bellivier, Jean-Christophe Poncer, Marion Leboyer, Sabine Levi

17 **Gene Expression in Major Depressive Disorder**
Rick Jansen, Patrick F. Sullivan, Vered Madar, Andrew I. Brooks, Fei Zou, Wei Sun, Kai Xai, Yuri Milaneschi, Eco J. de Geus, Johannes H. Smit, Gerard van Grootheest, Gonneke Willemsen, Dorret I. Boomsma, Fred A. Wright, Brenda W.J.H. Penninx

18 **Neurocognitive Impairment in Bipolar Patients and Study of Disc 1 Genetic Polymorphisms**
Gyulnas Dzhebir, Vessela Stoyanova, Iglika Vasileva, Theodora Taneva, George Kirov, Radka Kaneva, Vihra Milanova

19 **Phenotypic and Genetic Overlap in Bipolar Disorder and Migraine**
Sarah Knott, Liz Forty, Lisa Jones, Ian Jones, Katherine Gordon-Smith, Nick Craddock

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POSTERS

20 ★ **Association Study of ZNF804A Gene with Bipolar I and II Disorder in the Korean Population**

Kounseok Lee, Iksoo Huh, Seunghyong Ryu, Ji Hyun Baek, Eun-Young Cho, Taesung Park, Kyooseob Ha, Kyung Sue Hong

21 **Trio Based Exome Sequencing Suggests the Role of Calcium Homeostasis-related Rare Variants in Bipolar Disorder**

Nana Matoba, Muneko Kataoka, Kumiko Fujii, Tadafumi Kato

22 **Whole Genome DNA Sequencing and Follow-up Genotyping in Bipolar Disorder**

Niamh O' Brien, Alexandra Jarram, Adebayo Anjorin, Radhika Kandaswamy, Ole Mors, Anders Borglum, Mette Nyegaard, David Curtis, Andrew McQuillin

23 **Polymorphisms in STIP1 Gene Predispose to Major Depressive Disorder in Polish Patients**

Beata Narozna, Aleksandra Szczepankiewicz, Anna Leszczynska-Rodziewicz, Joanna Pawlak, Monika Wilkosc, Aleksandra Rajewska-Rager, Malgorzata Maciukiewicz, Alicja Bejger, Joanna Hauser

24 **Characterizing the Effects of Antidepressants on Human Hippocampal Neural Stem Cells**

Timothy Powell, Tytus Murphy, Sandrine Thuret, Gerome Breen

25 **Medical Internship as a Model to Identify Genes Associated with Depression under Stress**

Srijan Sen, Laura Scott, Margit Burmeister, Yindra Puentes

26 **A Genetic Variant in 12q13, Possible Risk for Bipolar Disorder, Associated with Depressive State Accounting for Stressful Life Events**

Ayu Shimasaki, Kenji Kondo, Takeo Saito, Kosei Ikeda, Nakao Iwata Esaki, Masashi Ikeda, Nakao Iwata

27 **Metabolic Risk Genes Associated with Increased Fasting Glucose in Bipolar Disorder and Bipolar Disorder Per se**

Dzana Sudic Hukic, Lena Backlund, Catharina Lavebratt, Louise Frisén, Ewa Ehrenborg, David Erlinge, Agneta Hilding, Harvest F. Gu, Claes-Göran Östenson, Martin Schalling, Urban Ösby

★ – Travel Awardee

28 **Association between ST8SIA2 Gene Polymorphisms and the Risk of Bipolar Disorder and Schizophrenia in the Korean Population**
Soyung Yang, Ik Soo Huh, Seunghyong Ryu, Ji Hyun Back, Eun-young Cho, Taesung Park, Ji Sun Kim, Kyooseob Ha, Kyung Sue Hong

29 **COX-2 Gene Expression Correlates with Frontal Functions in Depressive Disorders**
Piotr Galecki

ANXIETY DISORDER

30 **Obsessive-Compulsive Symptoms in a Genetic Epidemiological Twin Family Sample: Genome-wide Association and Beyond**
Danielle Cath, Anouk den Braber, Nuno Zilhao-Nogueira, Dirk Smit, Dorret Boomsma

31 **The Genes for Treatment Study: A Multi-site Trial of Clinical and Genetic Predictors of Response to Cognitive Behaviour Therapy in Paediatric Anxiety Disorders**
Jennie Hudson, Robert Keers, Thalia Eley, Susanna Roberts, Jonathan Coleman, Gerome Breen, Kathryn Lester

32 **Obsessive Compulsive Disorder – A Risk Factor for Schizophrenia? A Nationwide Study**
Sandra Meier, Liselotte Petersen, Marianne G. Pedersen, Mikkel C.B. Arendt, Philip R. Nielsen, Manuel Mattheisen, Ole Mors, Preben B. Mortensen

33 **Genetics of Symptom Dimensions of Obsessive-Compulsive Disorder and Family History of Hoarding, Trichotillomania, or Body Dysmorphic Disorder**
Gwyneth Zai, David Pauls, Clement Zai, Vanessa Goncalves, Karen Wigg, Margaret (Peggy) Richter, James Kennedy

AUTISM

34 **Homozygous Deleterious Mutation of SHANK1 Gene in a Pakistani Pedigree**
Qin He, Sirui Zhou, Amirthagowri Ambalavanan, Claire S. Leblond, Dan Spiegelman, Sandra Laurent, Christian Sindhi, Zohair Nanjiani, Saima Rasheed, Baudouin Forgeot-d'Arc, Chantal Caron, Laurent Mottron, Lan Xiong

POSTERS

35 **The Clinical and Neurocognitive Phenotypes of the CNS Patterning Gene Variants in Autism Spectrum Disorders**

Yi-Ling Chien, Susan Shur-Fen Gau, Jenny Chang

36 **Screening for Rare Inherited Variation in a Multiplex Family with Autism and Language Disorders**

Lina Jonsson, Carmela Miniscalco, Mats Johnson, Camilla Fardell, Christopher Gillberg, Tommy Martinsson, Jonas Melke

37 **Low Mitochondrial DNA Content in Peripheral Blood Monocytic Cells from Adult Patients who Present Autism Spectrum Disorders and Intellectual Disability**

Lourdes Martorell, Helena Torrell, Alba Valiente, Rafael Martínez-Leal, Ma José Cortés, Yolanda Alonso, Elisabet Vilella

38 **Gene-environment Interactions in Autism: Copy Number Burden and Air Pollution Exposure Combine to Provide Significant Risk**

Scott Selleck, Dokyoon Kim, Santhosh Girirajan, Heather Volk, Sarah Pendergrass, Irva Hertz-Picciotto, Marylyn Ritchie

39 **Duplication of the SHOX Gene at Chromosome Xp22.33 is a Risk Factor for Autism Spectrum Disorders and other Neurodevelopmental Phenotypes**

Maria Tropeano, Deirdre Howley, C. Ellie Wilson, Joo Wook Ahn, Clodagh M. Murphy, Dene Robertson, Richard J.B. Dobson, Mark Pitts, Jessica Bramham, Philip Asherson, Sarah Curran, Caroline Mackie Ogilvie, David A. Collier, Grainne M. McAlonan, Declan G. Murphy

40 **Further Investigations of the Relation between Polymorphisms in Sex Steroid Related Genes and Autistic-like Traits**

Anna Zettergren, Lina Jonsson, Daniel Hovey, Jonas Melke, Henrik Anckarsäter, Paul Lichtenstein, Lars Westberg

BIOSTATISTICS / BIOINFORMATICS

41 **Using Phased Haplotypes to Investigate Recessive Effects in Schizophrenia**

David Curtis

42 **Making Sense of Gene Associations: Efficient Generalized Gene-set Analysis for GWAS Data**
Christiaan de Leeuw, Tom Heskes, Joris Mooij, Danielle Posthuma

43 **Variation in the Promoter of the Gene Encoding Carboxylesterase 1, the Principal Enzyme in the Metabolism of Methylphenidate, Affects Potential Transcription Factor Binding Sites**
Laura Ferrero-Miliani, Ditte Bjerre, Majbritt Busk Madsen, Henrik Berg Rasmussen, Indices Consortium

44 **LandScape: A Simple Method for Aggregating P-Values and Other Stochastic Variables without a Priori Grouping**
Jakob Grove, Jonatan Schaumburg-Müller Pallesen, Leslie Foldager, Carsten Wiuf

45 **Elucidating the Genetic Architecture of Psychiatric Disorders by Genome-wide, Gene-environment Interaction Approaches**
Michel Nivard, Conor Dolan, Abdel Abdellaoui, Gonneke Willemsen, Jouke Jan Hottenga, Iryna Fedko, Christel Middeldorp, Dorret Boomsma

46 **Loss of Power in Trio Design under a Polygenic Model**
Wouter J. Peyrot, Brenda W.J.H. Penninx, Naomi R. Wray

47 **The Design and Application of "SuRFR": An R Package to Prioritize Variants from Genomics Data Based on Functional Annotation**
Niamh Ryan, Stewart W. Morris, Richard W. McCombie, David J. Porteous, Martin S. Taylor, Kathryn L. Evans

48 **Trait Based Association Analyses for Psychiatric Phenotypes**
Fazil Aliev, Jessica Salvatore, Silviu-Alin Bacanu, Danielle Dick

ELSI, COUNSELING AND GENETIC TESTING

49 **Whole Genome Sequencing – New possibilities, New Dilemmas**
Anna Sundby, Merete Watt Boolsen, Mette Ebbesen, Ole Mors

POSTERS

ENDOPHENOTYPES

50 **The Association between the Catechol O-Methyltransferase Val158Met Polymorphism and Alexithymia in Obsessive-Compulsive Disorder**

Minjung Koh, Se Joo Kim, Jee In Kang, Kee Namkoong

51 **A Schizophrenia Polygenic Score Analysis in an Independent Psychosis Sample**

Elvira Bramon, Siri Ranlund, Kuang Lin, Maria Arranz, Steven Bakker, David Collier, Assen Jablensky, René Kahn, Luba Kalaydjieva, Andrew McIntosh, Dan Rujescu, Jim Van Os, WTCCC2 Consortium, Cathryn Lewis, Robin Murray, John Powell

52 **P300 Event-related Potential Endophenotype is Associated with Polygenic Risk for Schizophrenia and Bipolar Disorder**

Mei-Hua Hall, Chia-Yen Chen, Bruce Cohen, Dost Öngür, Jordan Smoller

53 **Characterization of the Rey Visual Design Learning Test as a Suitable Cognitive Task for Quantitative Trait Analysis**

Annette Milnik, Lisa DAstolfo, Francina Hartmann, Tobias Egli, Christian Vogler, Dominique de Quervain, Andreas Papassotiropoulos

54 **Does the BDNF Val66Met Polymorphism Play a Role on Predicting Psychotic-like Experiences by Childhood Trauma?**

Araceli Rosa, Marta de Castro-Català, Martine van Nierop, Neus Barrantes-Vidal, Thomas R. Kwapil, Paula Cristóbal-Narváez, Ruud van Winkel, Araceli Rosa

55 **Association between an Oxytocin Receptor Gene Variant and Face Recognition as well as Related Amygdala Activation**

Lars Westberg, Anna Zettergren, Joakim Svärd, Johanna Lovén, Daniel Hovey, Johanna Milding, Natalie Ebner, Håkan Fischer

POSTERS

EPIGENETICS

56 **Glucocorticoid Receptor Gene Methylation and Borderline Personality Disorder**

M.J. Arranz, Marc Ferrer, Joaquim Soler, Juliana Salazar, Daniel Vega, Oscar Andión, Cristina Sánchez- Mora, Maria Jesús Arranz, Albert Feliu-Soler, Juan Carlos Pascual

57 **Locus-specific Repressive DNA Methylation Counterbalanced by Transcription Factor Binding to the Promoter CpG Island Drives Neuronal Subpopulation-selective Prodynorphin Expression in the Human Brain**

Igor Bazov, Daniil Sarkisyan, Hiroyuki Watanabe, Olga Kononenko, Dineke Verbeek, Mumtaz Malik Taqi, Kanar Alkass, Henrik Druid, Tatiana Yakovleva, Georgy Bakalkin

58 **Genomic Methylation Signatures in Anxious-Depressive Psychopathology: A Comprehensive Approach Based in Informative Mz Twins Pairs**

Aldo Córdova-Palomera, Silvia Alemany, Mar Fatjó-Vilas, Ximena Goldberg, Igor Nenadic, Lourdes Fañanás

59 **Effects of Electroconvulsive Stimulation on p11 Promoter Methylation in Humans and Rats**

Alexandra Kleimann, Wiebke Theilmann, Claudia Brandt, Mathias Rhein, Alexandra Kotsiari, Wolfgang Sperling, Michael Gröschl, Johannes Kornhuber, Wolfgang Löscher, Stefan Bleich, Helge Frieling

60 **Global DNA Hypomethylation and its Correlation with Decreased Betaine Level in Peripheral Blood of Patients with First-episode Schizophrenia**

Yui Murata, Miki Bundo, Masaki Nishioka, Fumiko Sunaga, Harumi Saida, Shinsuke Koike, Kiyoto Kasai, Kazuya Iwamoto

61 **MicroRNA Regulation of Candidate Genes in Tourette Syndrome**

Luca Pagliaroli, Andrea Vereczkei, TamasAranyi, Csaba Barta

62 **Epigenetic Regulation of Neuregulin in a Rat Model for Schizophrenia**

Mathias Rhein, Marcel-René Muschler, Joachim K. Krauss, Stefan Bleich, Helge Frieling, Kerstin Schwabe

63 **Effect of Mood Stabilizers and Quetiapine on DNA Methylation in Human Neuroblastoma Cells**

Hiroko Sugawara, Miki Bundo, Tatsuro Asai, Fumiko Sunaga, Junko Ueda, Jun Ishigooka, Kiyoto Kasai, Tadafumi Kato, Kazuya Iwamoto

64 **Correlation between CpG SNPs in HTR1B and Global Methylation in Suicide Attempters and Non-Attempters**

Vincenzo de Luca, Ali Bani Fatemi, Clement Zai, John Strauss, Ahmed Hassan

FUNCTIONAL GENOMICS & MODEL ORGANISMS

65 **Identification of a Novel Protein/DNA Binding Motif Targeted by BRD1**

Tue Fryland, Annelaura Nielsen, Jane Christensen, Anders Børglum

66 **Dysfunction of the Neuronal Sorting Receptor SorLA Results in Elevated GDNF Activity, Dopaminergic Defects, and ADHD-like Behavior in Mice**

Camilla Gustafsen, Ditte Olsen, Maria Lume, Jens R. Nyengaard, Anders Hay-Schmidt, Dirk Bender, Peder Madsen, Mart Saarma, Anders Nykjaer, Claus Munck Petersen, Simon Glerup

67 **A Functional-linkage Gene Network Designed for the Nervous System**

Julia Steinberg, Frantisek Honti, Cynthia Sandor, Caleb Webber

MISCELLANEOUS OTHER PSYCHIATRIC DISORDERS

68 **Case Only Recurrent Variation in Transmembrane AMPA Receptor Regulators is Associated with BD, SZ and ADS**

Niamh O'Brien, Yi Lin, Alessia Fiorentino, Michael Way, Sally I. Sharp, Giorgia Quadri, Alex Jarram, Irene Guerrini, Iain Smith, Allan D. Thomson, Nicholas Bass, Marsha Y. Morgan, David Curtis, Andrew McQuillin

69 **Exploration of the Association between Bipolar Disorder Risk Genes and MRNA Expression in the Human Brain**
Robert Blizard, Daniah Trabzuni, Manuel Guelfi, John Hardy, Hugh Gurling, Andrew McQuillin

70 **Probing the Shared Polygenic Underpinnings of Anorexia Nervosa and Five Other Major Psychiatric Disorders**
Laura Huckins, Karen Mitchell, Laura Thornton, WTCCC3 Consortium, GCAN, David Collier, Patrick Sullivan, Cynthia Bulik, Eleftheria Zeggini

71 ★ **Shared Genetic and Environmental Influences on Non-suicidal Self Injury and Suicidal Ideation. Different Outcomes, Same Etiology?**
Dominique Maciejewski, Hanneke E. Cremers, Michael T. Lynskey, Pamela A. F. Madden, Andrew C. Heath, Dixie J. Statham, Nicholas G. Martin, Karin J.H. Verweij

72 **Building a High thoughput Pipeline for the iPSYCH Megastudy**
Jesper Poulsen, Marie Bækvad-Hansen, Jonas Grauholm, Marianne Pedersen, iPSYCH PI-group, Sissel Vorstrup, David Hougaard, Mads Hollegaard

73 **Managing Parental Stress with Eye Movement Desensitization and Reprocessing Resource Development Installation**
Zita Shomlea

74 **Neuropeptide Y (NPY) and Suicide**
August Gabriel Wang, Pernille Koefoed, Anne Sophie Jacoby, David Woldbye, Henrik Berg Rasmussen, Sally Timm, Henrik Dam, Klaus Jakobsen, Merete Nordentoft, Gesche Jürgens, Holger Sørensen, Ole Garsdal, Marianne Hvid, Thomas Werge

NEUROIMAGING

75 **The Polymorphism of YWHAE, a Gene Encoding 14-3-3epsilon, and Brain Morphology in Schizophrenia: A Voxel-based Morphometric Study**
Michio Suzuki, Mikio Kido, Yukako Nakamura, Kiyotaka Nemoto, Tsutomu Takahashi, Branko Aleksic, Atsushi Furuichi, Yumiko Nishikawa, Masashi Ikeda, Kozo Kaibuchi, Nakao Iwata, Norio Ozaki

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OTHER

76 **Replication of GWAS Susceptibility Loci for Bipolar Disorder and Schizophrenia Cohorts in Latino Populations**

Suzanne Gonzalez, Erika Villa, Marco Rodriguez, Mercedes Ramirez, Juan Zavala, Regina Armas, Salvador Contreras, Albana Dassori, Javier Contreras, Robin Leach, Deborah Flores, Alvaro Jerez, Henriette Raventós, Alfonso Ontiveros, Humberto Nicolini, Michael Escamilla

77 ★ **Investigation of Psychological and Genetic Factors Influencing Stress Perception in Psoriasis, a Stress-linked Dermatologic Disease**

Janos Kalman, Gergely Drotos, Anna Juhasz, Agnes Feher, Robert Kui, Magdolna Gaal, Rozsa Havancsak, Xenia Gonda, Sandor Rozsa, Lajos Kemeny, Zoltan Rihmer, Zoltan Janka

78 ★ **Transcriptional Modulation of Neurotransmission by Music Listening**

Chakravarthi Kanduri, Pirre Raijas, Minna Ahvenainen, Anju Philips, Liisa Ukkola-Vuoti, Harri Lahdesmaki, Irma Jarvela

79 **Genome-wide Association Study of Pathological Gambling**

Maren Lang, Tagrid Leménager, Fabian Streit, Mira Fauth-Bühler, Franziska Degenhardt, Stephanie H. Witt, Frank Josef, Falk Kiefer, Hans-Jörgen Grabe, Ulrich John, Markus M. Nöthen, Christian Meyer, Hans-Jürgen Rumpf, Friedrich Martin Wurst, Marcella Rietschel, Karl F. Mann

80 **The Right Not to Know and its Implications for Psychiatric Genetics**

Markus Reitt, Alexandra Weber, Franziska Friske, Christian Lenk, Marcella Rietschel, Barbara Zoll, Wolfgang Engel, Gunnar Duttge, Wolfgang Poser

81 **Targeted Re-sequencing of SLITRK1 in Japanese Patients with Tourette Syndrome Using Next-generation Sequencing**

Aya Inai, Hitoshi Kuwabara, Fumichika Nishimura, Kayoko Kato, Yosuke Eriguchi, Takafumi Shimada, Masaomi Furukawa, Tsukasa Sasaki, Mamoru Tochigi, Chihiro Kakiuchi, Kiyoto Kasai, Yukiko Kano

★ – Travel Awardee

82 **Investigation of Anorexia Nervosa Susceptibility Loci in Three Densely Affected Pedigrees**
Zeynep Yilmaz, Stephanie N. Williams, Rachael J. Bloom, Patrick F. Sullivan, Cynthia M. Bulik

PHARMACOGENETICS

83 **PDE7B, NMBR and EPM2A Variants and Schizophrenia: A Case-control and Pharmacogenetics Study**
Soo-Jung Lee, Changsu Han, Ashwin A. Patkar, Chi-Un Pae, Alessandro Serretti

84 **Genetics of Treatment-induced Side Effects in the STEP-BD Study**
Alessandro Serretti, Chiara Fabbri

85 **The Complexity of Genetic Effects in Pharmacogenetics: Focus on Neuroplasticity, Environmental Stress and Response to Antidepressants**
Roberta Emiliani, Diego Albani, Alessandro Serretti

86 **A Molecular Pathway Analysis of the Glutamatergic – Monoaminergic Interplay may Predict the Number of Depressive Records during Citalopram Treatment**
Antonio Drago, Concetta Crisafulli, Alessandro Serretti

87 **Genome-wide Association Study Identifies Common Variants Associated with Metabolism of Psychotropic Drugs**
Lavinia Athanasiu, Lisa Lena Hormazabal Smorr, Martin Tesli, Jan Ivar Røssberg, Ida E. Sønderby, Olav Spigset, Srdjan Djurovic, Ole A. Andreassen

88 **Are Genetic Variants able to Differentially Predict Sexual Dysfunction in Men Following Treatment with Citalopram or Reboxetine? Findings from a Randomised Controlled Trial**
Andrew Crawford, Sarah Lewis, Karen Hodgson, Peter McGuffin, Katherine Aitchison, David Nutt, Tim Peters, Philip Cowen, Michael O'Donovan, Nicola Wiles, Glyn Lewis

89 **Assessing Gene Expression Changes in Mouse Brain with Chronic Haloperidol Treatment**
Paola Giusti-Rodriguez, Yunjung Kim, James Crowley, Randal Nonneman, Allison Ryan, Corey Quackenbush, Wei Sun, Fernando Pardo-Manuel de Villena, Patrick Sullivan

90 **Combining Genetic and Clinical Variables to Optimize Prediction of Antidepressant Treatment Response in the GENDEP Project: A Machine Learning Approach**
Raquel Iniesta, Katherine E Tansey, Wolfgang Maier, Marcella Rietschel, Ole Mors, Joanna Hauser, Neven Henigsberg, Daniel Souery, Jens Wendland, Peter McGuffin, Rudolf Uher

91 ★ **Polymorphisms in HTR3A, CYP1A2, DRD4 and COMT and Response to Clozapine in Treatment-Resistant Schizophrenia: A Gene-gene Interaction Analysis**
Veera R. Manikandan, Anto P. Rajkumar, Lakshmikirupa S., Chithra Chittybabu, Anju Kuruvilla, Alok Srivastava, Poonkuzhali B., Kuruthukulangara S. Jacob, Molly Jacob

92 **Can CYPS Phenotypes Influence Refractoriness Mood Disorders? A Pharmacogenetics Study with Patients Undergoing ECT**
Carolina Prado, Luiz Rigonatti, Sergio Rigonatti, Leda Talib, Wagner Gattaz

93 **The Effect of Clozapine on Gene Expression Using Rnaseq**
Sally Sharp, Jonathan Weymer, Andrew McQuillin

94 **The Role of Rare Coding Variants in Psychopathology and Treatment Response in Chinese Patients with Schizophrenia**
Hei Man Wu, Zhen Xing Yang, MiaoXin Li, Qiang Wang, Pak-Chung Sham, Tao Li

SCHIZOPHRENIA

95 **Associations between Variations in TPH1 and SLC6A4 Genes and Schizophrenia Susceptibility: A Study in the Cuban Population**
Beatriz Marcheco, Teresa Collazo, Manuel Gomez, Enny Morales, Giselle Monzón, Evelyn Fuentes, Antonio Caballero, Danys de las Nieves Milian, Gina Galan, Yasmany Llanes, Jaime Valenti, Rafael Ventura

★ – Travel Awardee

96 **Mechanisms of Schizophrenia Suggested by miRNA Sequencing of Peripheral Blood Mononuclear Cells: Preliminary Results from the North American Prodromal Longitudinal Study (NAPLS)**

Clark Jeffries, Stephen Glatt, Sharon Chandler, Thomas Stark, Eugene Yeo, NAPLS Consortium, Diana Perkins, Ming Tsuang

97 **Downregulation of CNR1, AKT1 and COMT in Patients with Treatment Resistant Schizophrenia**

Patricia Silva, Leticia Spindola, Vanessa Ota, Ary Gadelha, Marcos Santoro, Cristiano Noto, Eduardo Gouvêa, Bruno Ortiz, Rodrigo Bressan, Jair Mari, Sintia Belangero

98 **Exome Sequence Data from Multigenerational Families Implicate AMPA Receptor Trafficking in Neurocognitive Impairment and Schizophrenia Risk**

Mark Kos, Melanie Carless, Juan Peralta, Marcio Almeida, Ruben Gur, Michael Pogue-Geile, David Roalf, Vishwajit Nimgaonkar, Joanne Curran, Ravi Duggirala, David Glahn, John Blangero, Raquel Gur, Laura Almasy

99 **Sex Differences of EEG Coherences in Schizophrenia**

Yu Sang Lee

100 **Whole Exome Sequencing of Schizophrenia Patients with High Level of Autozygosity**

Chiara Magri, Edoardo Giacopuzzi, Paolo Valsecchi, Michele Traversa, Rita Gardella, Giuseppe Borsani, Sergio Barlati, Emilio Sacchetti, Massimo Gennarelli

101 **Investigation of Telomere Length in Different Stages of Schizophrenia**

Daniela Martinez, Lucas Rizzo, Patrícia Silva, Ary Gadelha, Vanessa Ota, Marcos Santoro, Letícia Spíndola, Cristiano Noto, Eduardo Gouvea, Dayvis Rocha, Ricardo Sato, Quirino Cordeiro, Rodrigo Bressan, Elisa Brietzke, Sintia Belangero

102 **Correction for Environmental Stratification Implicates FKBP5 as Genetic Risk Factor for First-episode Psychosis**

Olesya Ajnakina, Marta DiForti, Anna Kolliakou, Anthony S. David, Paola Dazzan, John Powell, Carmine Pariante, Valeria Mondelli, Craig Morgan, Robin M. Murray, Helen L. Fisher, Conrad Iyegbe

103 **Exonic Sequencing and Association Study of the GNB1L on Chromosome 22q11.2 as a Candidate Gene of Schizophrenia**
Min-Chih Cheng, Yun-Jhong Lin, Chia-Hsiang Chen

104 **Pharmacogenomic Biomarkers as Clinical Decision Making Tools for Clozapine Treatment of Schizophrenia**
Evanthia Achilla, David A. Collier, Danai Dima, Sophia Frangou, Christiane Gasse, Ina Giegling, Marinka Helthuis, James H. MacCabe, Jonathan Mill, Marcella Rietschel, Dan Rujescu, Engilbert Sigurdsson, Hreinn Stefánsson, James Walters, CRESTAR Consortium

105 **Meta-analysis of Positive and Negative Symptoms Reveals Schizophrenia Modifier Genes, including Neuregulin 1**
Alexis Edwards, T. Bernard Bigdeli, Anna Docherty, Silviu Bacanu, Teresa DeCandia, Dermot Walsh, F.A. O'Neill, Kenneth Kendler, Brien Riley, Ayman Fanous

106 **Variation in Six Autosomal Short Tandem Repeat Markers and their Inbreeding Effects on Schizophrenia Patients of a Rural South Indian Community**
Suhas Ganesha, Adhikarla Syama, Rakshathi Basavaraju, Meera Puroshottam, C. Naveen Kumar, Jagadisha Thirthalli, K.K. Suresha, U. Arunachala, Sanjeev Jain

107 **Specific Synaptic and Glial Functions Contribute to the Common Risk of Multiple Psychiatric Disorders**
Anke Hammerschlag, Andrea Goudriaan, Mark Verheijen, Tinca Polderman, Matthijs Verhage, Guus Smit, Danielle Posthuma

108 **Genetic and Environmental Predictors of Functional Capacity in Psychotic Disorders**
Carsten Rygaard Hjorthøj

109 **Differential Gene-expression Analysis of First-episode Psychosis**
Conrad Osamede Iyegbe, Conrad Iyegbe, Daniel Leirer, Stephen Newhouse, Marta DiForti, Hamel Patel, Charlie Curtis, Gerome Breen, Robin Murray, Richard Dobson

110 **Heat Shock Alters the Expression of Schizophrenia and Autism Candidate Genes in an Induced Pluripotent Stem Cell Model of the Human Telencephalon**

Herb Lachman, Mingyan Lin, Dejian Zhao, Anastasia Hrabovsky, Erika Pedrosa, Deyou Zheng

111 **Rare Alleles Altering Schizophrenia Risk Occur in Exons and Noncoding Functional Sequences**

Erik K. Loken, Silviu-Alin Bacanu, Dermot Walsh, F. Anthony O'Neill, Kenneth S. Kendler, Brien P. Riley

112 **Investigation of the Somatic Common Deletion in Mitochondrial DNA in Mood Disorders and Schizophrenia**

Firoza Mamdani, Brandi Rollins, Ling Morgan, P. Adolfo Sequeira, Marquis P. Vawter

113 **Analysis of the DISC1 Interactome**

William McCombie, Shaolei Teng, Shane McCarthy, Kathryn L. Evans, Melissa Kramer, J. Kirsty Millar, Andrew McIntosh, Pippa Thomson, Douglas Blackwood, Ian Deary, David Porteous

114 **Exome Sequencing of Monozygotic Twins Discordant for Schizophrenia and Delusional Disorder**

Fumichika Nishimura, Akane Yoshikawa, Kayoko Kato, Tsukasa Sasaki, Kiyoto Kasai, Chihiro Kakiuchi

115 **Contribution of Genetic and Environmental Risk Factors to Schizophrenia-relevant Phenotypes**

Sergi Papiol, Beata Stepniak, Christian Hammer, Sarah Everts, Begemann Martin, Hannelore Ehrenreich

116 **Indications of Early Developmental Loss of Function of Fast-spiking Interneurons in Brd1+/- Mice**

Per Qvist, Tue Fryland, Arne Mørk, Anto P. Rajkumar, Mette Nyegaard, Ole Mors, Michael Didriksen, Anders D. Børglum, Jane H.Christensen

POSTERS

117 **Analysis of Rare Recessive Mutation from Exome Sequencing Data Implicates Voltage-gated Sodium Channel Genes in Schizophrenia**

Elliott Rees, George Kirov, James Walters, Davy Kavanagh, Alexander Richards, Menachem Fromer, Douglas Ruderfer, Peter Holmans, Jennifer Moran, Kimberly Chambert, Steve McCarroll, Ed Scolnick, Pamela Sklar, Shaun Purcell, Michael Owen, Michael O'Donovan

118 **Replication and Cross-phenotype Study Based upon Schizophrenia GWASs Data in the Japanese Population: Support for association of MHC Region with Psychosis**

Takeo Saito, Kenji Kondo, Yoshimi Iwayama, Ayu Shimasaki, Branko Aleksic, Kazuo Yamada, Tomoko Toyota, Eiji Hattori, Hiroshi Ujike, Toshiya Inada, Hiroshi Kunugi, Tadafumi Kato, Takeo Yoshikawa, Norio Ozaki, Masashi Ikeda, Nakao Iwata

119 ★ **Neurodevelopment Genes are Differentially Expressed in Blood of Subjects At-risk Mental State (ARMS) for Psychosis Compared to First Episode of Psychosis (FEP) Patients and Health Controls**

Marcos Santoro, Ary Gadelha, Vanessa K. Ota, Graccielle Cunha, Elson Asevedo, Cristiano Noto, Leticia Spindola, Patricia Silva, Elisa Brietzke, Quirino Cordeiro, Rodrigo Bressan, Sintia Belangero

120 **A Genome-wide Association Study of Neurocognitive Impairments in Schizophrenia: Markers Identified by Polygenic Score Approach**

Yu-Hsuan Shih, Po-Chang Hsiao, Po-Hsiu Kuo, Yin-Ju Lien, Shi-Heng Wang, Chih-Min Liu, Ching-Ing Tseng, Hai-Gwo Hwu, Wei J. Chen

121 **Heritability of Dimension-specific Psychotic Experiences Captured by Common Genetic Variants in a Community Sample of Adolescents**

Dominika Sieradzka, Robert Power, Daniel Freeman, Alastair Cardno, Frank Dudbridge, Angelica Ronald

122 **Mutation Screening in GRIN2A and GRIN2B with Schizophrenia and Autistic Spectrum Disorder in Japanese Population**

Yuto Takasaki, Takayoshi Koide, Chenyao Wang, Hiroki Kimura, Shohko Kunimoto, Akira Yoshimi, Yukako Nakamura, Itaru Kushima, Jingrui Xing, Branko Aleksic, Masashi Ikeda, Nakao Iwata, Norio Ozaki

★ – Travel Awardee

123 **The 22q11.2 Deletion Syndrome in Adults with a Dual Diagnosis of Severe Psychiatric Disorder and Moderate to Severe Intellectual Disability**

Elfi Vergaelen, Annick Vogels, Ann Swillen, Stephan Claes, Eddy Weyts, Richard Caeyenberghs, Griet Van Buggenhout

124 **Association between Polymorphisms of the Human Mu-Opioid Receptor Gene and Schizophrenia**

Junzhe Xu, Eric DeBalski, Sophie Wang Wang, Daniel Li, Steven Dubovsky

125 **Shared Common Variants in Schizophrenia and Lung Cancer**

Verena Zuber, Mariella de Biasi, Aree Witoelar, Yunpeng Wang, Francesco Bettella, Andrew J. Schork, Wesley K. Thompson, PGC SCZ Working Group, Cornelia M. Ulrich, Rayjean J. Hung, Loic Le Marchand, Christopher Amos, Anders M. Dale, Srdjan Djurovic, Ian G. Mills, Ole A. Andreassen

126 **Whole Genome Sequencing Study of Multiply-affected Schizophrenia and Bipolar Disorder Families from the Portuguese Island Population**

Ayman Fanous, Kelly Benke, Brion Maher, Tim Bigdeli, James Knowles, Helena Medeiros, Janet Sobell, Elizabeth Bevilacqua, Jennifer Moran, James Nemesh, Giulio Genevese, Robert Handsaker, Colm O'Dushlaine, Michele Pato, Steven McCarroll, Carlos Pato

SUBSTANCE ABUSE

127 ★ **Which Alcohol Use Disorder Criteria Account for the Association of ADH1B with Alcohol Dependence?**

Amy Hart, Kevin Lynch, Joel Gelernter, Henry Kranzler

128 **Genetic Signature of Heroin Dependence: A Proof-of-Concept Study**

Chia-Hsiang Chen, Shaw-Ji Chen, Tsu-Wang Shen, Ding-Lieh Liao, Hsin Chou Yang, Kuang-Chi Chen

129 **Association of Cognitive Function with a5 Nicotinic Acetylcholine Receptor Genotype**

Elemi Breetvelt, Maartje Aukes, Marco Boks, Kim Cerrone, Rick Grobbee, Rene Kahn

★ – Travel Awardee

POSTERS

130 **Association of Variants in MicroRNA Biogenesis Pathway Genes and Alcohol Dependence Risk**
Huseyin Gedik, Mehmet Emin Erdal, Senay Gorucu Yilmaz, Cem Sengul, Hasan Herken

131 **Genome Wide Association Study of Heroin Dependence in a Han Chinese Sample**
Gursharan Kalsi, David Collier, Steve Newhouse, Richard Dobson, Tao Li, Philip Asherson

132 **Genetic Risk Prediction and Neurobiological Understanding of Alcoholism**
Alexander Niculescu, Daniel Levey, Helen Le-Niculescu, Josef Frank, Mikias Ayalew, Nitika Jain, Brigid Kirlin, Rebecca Learman, Zachary Rodd, Anantha Shekhar, Markus Nothen, Richard Sherva, Andrew Smith, Henry Kranzler, Marcella Rietschel, Joel Gelernter

133 ★ **Functional Investigation of the ALDH2 Promoter: A Regulatory Genetic-epigenetic Interplay**
Hansi Pathak, Mani Haschemi, Mathias Rhein, Helge Frieling

134 **A Genomewide Association Study of Alcohol Dependence in the Irish Affected Sib Pair Study of Alcohol Dependence**
Brien Riley, Laura Hack, Amy Adkins, Tim Bigdeli, Michael Grotewiel, Jill Bettinger, Andrew Davies, Carol Prescott, Danielle Dick, B. Todd Webb, Kenneth Kendler

135 **The Genetic Determinants of Binge Drinking in Humans: A Review of the Literature**
Matthew Sloan, Joshua Ejdelman, Nancy Low

TECHNOLOGY – SEQUENCING

136 **Separation of Oligodendrocyte Nuclei from Human Postmortem Brains**
Miki Bundo, Taeko Miyauch, Takao Ishii, Wataru Ukai, Eri Hashimoto, Kiyoto Kasai, Tadafumi Kato, Kazuya Iwamoto

★ – Travel Awardee

137 **Detection of Somatic Mutations in Exome Sequencing Studies**
Giulio Genovese, Sam Rose, Shaun Purcell, Jennifer Moran, Menachem Fromer, Kimberly Chambert, Patrick Sullivan, Pamela Sklar, Christina Hultman, Steven McCarroll

138 **Next-generation Sequencing of Synaptic Genes in Familial Major Depressive Disorder**
Mehdi Pirooznia, Tao Wang, Fayaz Seifuddin, James B. Potash, Peter P. Zandi, Fernando S. Goes

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX

AUTHOR INDEX