



12TH ICHG
MONTREAL
11-15 OCTOBER 2011 - MONTREAL CONVENTION CENTRE
WWW.ICHG2011.ORG

PROGRAM AT-A-GLANCE

Registration and Program Pick-up Hours:

Tuesday: 10:00am-7:00pm

Wednesday: 7:00am-6:30pm

Thursday: 7:15am-5:00pm

Friday: 7:30am-5:00pm

Saturday: 7:30am-12:00pm

BOOKMARK
the mobile Web site

view schedule of events, search
for an abstract, and much more.

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PRESENTATIONS AVAILABLE AFTER THE CONGRESS:

**Invited Sessions, Award Presentations, and the
Plenary Sessions will be recorded for posting on the
Congress Web site after the meeting.** These recordings
are free to meeting registrants. Visit the ASHG and
Congress Web site in early November to view these
presentations

Schedule of All Scientific Sessions and Events

All meeting rooms are located in the Convention Center

TUESDAY, OCTOBER 11

4:00pm-5:00pm	1. Opening Performance by Cirque Éloize and Welcoming Remarks	Room 210, Level 2
5:00pm-6:30pm	2. Panel Discussion: Whole Genome Sequencing: To Do It or Not to Do It?	Room 210, Level 2

WEDNESDAY, OCTOBER 12




8:00am-10:00am	3. Plenary Session on Epigenetics	Room 210, Level 2
10:00am-7:00pm	Posters Open (Display of Wednesday Posters Only) <i>Authors are reminded to put posters up and take them down on the same day of presentation.</i>	Exhibit Hall, Level 2
10:00am-4:30pm	Exhibits Open	Exhibit Hall, Level 2
10:00am-4:30pm	Career Resources	Exhibit Hall, Level 2
10:30am-12:30pm	Concurrent <u>Invited</u> Sessions I (4-9)	See page 4 for rooms
12:30pm-2:00pm	Lunch Break, Open Viewing for Wednesday Posters	Exhibit Hall, Level 2
2:00pm-4:00pm	Poster Session I (Wednesday Posters Only) 2:00-3:00pm-odd poster board numbers; authors must be present 3:00-4:00pm-even poster board numbers; authors must be present	Exhibit Hall, Level 2
4:15pm-6:15pm	Concurrent <u>Platform</u> Sessions A (10-19)	See page 9 for rooms
6:15pm-6:40pm	20. ASHG Presidential Address: From Classroom to Courtroom to Clinic: Closing the Education Gaps in Human Genetics	Room 210, Level 2
6:40pm-6:50pm	21. ASHG Award for Excellence in Human Genetics Education Presentation	Room 210, Level 2
6:50pm-7:00pm	22. ASHG Victor A. McKusick Leadership Award Presentation	Room 210, Level 2
7:00pm-7:30pm	23. ASHG Meeting/Announcement of the ASHG Trainee Award and C.W. Cotterman Award Winners	Room 210, Level 2

THURSDAY, OCTOBER 13

7:00am-4:30pm	Posters Open (Display of Thursday Posters Only) <i>Authors are reminded to put posters up and take them down on the same day of presentation.</i>	Exhibit Hall, Level 2
8:00am-10:00am	Concurrent <u>Invited</u> Sessions II (24-29)	See page 4 for rooms
10:00am-4:30pm	Exhibits Open	Exhibit Hall, Level 2
10:00am-4:30pm	Career Resources	Exhibit Hall, Level 2
10:15am-12:15pm	Concurrent <u>Platform</u> Sessions B (30-39)	See page 10 for rooms
12:30pm-2:00pm	Lunch Break, Open Viewing for Thursday Posters	Exhibit Hall, Level 2
12:30pm-12:45pm	40. ASHG Curt Stern Award Presentation	Room 210, Level 2
12:45pm-1:15pm	41. ASHG William Allan Award Presentation	Room 210, Level 2
1:15pm-2:00pm	42. Gruber Genetics Prize Award Presentation	Room 210, Level 2

2:00pm-4:00pm	Poster Session II (Thursday Posters Only) 2:00-3:00pm-odd poster board numbers; authors must be present 3:00-4:00pm-even poster board numbers; authors must be present	Exhibit Hall, Level 2
4:15pm-6:15pm	43. Plenary Debate Session: Current and Emerging Sequencing Technologies	Room 210, Level 2
<u>FRIDAY, OCTOBER 14</u>		
7:00am-4:30pm	Posters Open (Display of Friday Posters Only) <i>Authors are reminded to put posters up and take them down on the same day of presentation.</i>	Exhibit Hall, Level 2
8:00am-10:00am	44. Plenary Debate Session: Owning the Genome	Room 210, Level 2
10:00am-4:30pm	Exhibits Open	Exhibit Hall, Level 2
10:00am-4:30pm	Career Resources	Exhibit Hall, Level 2
10:30am-12:30pm	Concurrent <u>Invited</u> Sessions III (45-50)	See page 6 for rooms
12:30pm-2:00pm	Lunch Break, Open Viewing for Friday Posters	Exhibit Hall, Level 2
2:00pm-4:00pm	Poster Session III (Friday Posters Only) 2:00-3:00pm-odd poster board numbers; authors must be present 3:00-4:00pm-even poster board numbers; authors must be present	Exhibit Hall, Level 2
4:15pm-6:15pm	Concurrent <u>Platform</u> Sessions C (51-60)	See page 12 for rooms
<u>SATURDAY, OCTOBER 15</u>		
8:00am-10:00am	Concurrent <u>Invited</u> Sessions IV (61-66)	See page 6 for rooms
10:30am-12:30pm	67. Plenary Session: Diseases, Populations and Evolution: From the Cellular to the Continental	Room 210, Level 2
12:30pm-1:30pm	Lunch Break	
1:30pm-3:30pm	Concurrent <u>Platform</u> Sessions D (68-77)	See page 14 for rooms
3:45pm-4:30pm	78. Closing Plenary Session: The Grandest Challenge: Bringing Life Sciences from Lab to Village	Room 210, Level 2
4:30pm-5:15pm	79. Closing Remarks	Room 210, Level 2

Please check the printed program and the Congress Web site for the following session tracks:

-  Indicates Education-related events
-  Indicates Trainee-related events
-  Indicates Clinical-related events

Wednesday, October 12: Concurrent Invited Session I (4-9)

10:30 AM–12:30 PM

Room 517BC, Level 5	Room 511, Level 5	Room 210, Level 2	Room 520, Level 5	Room 517A, Level 5	Room 517D, Level 5
<p>SESSION 04 – Deciphering Transgenerational Effects: From Molecular to Statistical Approaches Co-Moderators: Janet S. Sinsheimer, David Geffen Sch. of Med. at UCLA, USA; and Amanda E. Toland, The Ohio State Univ., USA</p>	<p>SESSION 05 – New Insights from Human Pain Genetic Studies Moderator: Inna Belfer, Univ. of Pittsburgh, USA</p>	<p>SESSION 06 – Beyond Genome-Wide Association Study: Integrating Transcriptome, Proteome, and Pathway Data in the Genetic Dissection of Complex Traits Co-Moderators: Marylyn D. Ritchie, Vanderbilt Univ., USA; and Nancy J. Cox, Univ. of Chicago, USA</p>	<p>SESSION 07 – Recent Genetic Advances in Motor Neuron Diseases: Promises and Hurdles to Clinical Interventions Co-Moderators: Lisa L. Baumbach-Reardon, Miller Sch. of Med., Univ of Miami Sch. of Med., USA; and Vincent Timmerman, Univ. of Antwerp, Belgium</p>	<p>SESSION 08 – Molecular Basis and Mechanisms of Recessively Inherited Forms of Osteogenesis Imperfecta (OI) Co-Moderators: Peter H. Byers, Univ. of Washington, USA; and Deborah Krakow, UCLA, USA</p>	<p>SESSION 09 – Genetic Instability in Development, Aging and Cancer Moderator: M. Stephen Meyn, Hosp. for Sick Children, Toronto, Canada</p>
10:30 am Introduction. A. E. Toland.	10:30 am Introduction. I. Belfer.	10:30 am Introduction. N. J. Cox.	10:30 am Introduction. L. L. Baumbach-Reardon.	10:30 am Introduction. P. H. Byers.	10:30 am Introduction. M. S. Meyn.
10:35 am The function of genome-wide meiosis-specific epigenetic marks in recombination. R. D. Camerini-Otero.	10:35 am Novel findings from genetic studies of pain: From rodent models to human clinical pain. M. Costigan.	10:35 am Function-based GWAS to enhance discovery. N. J. Cox.	10:35 am Genetics, pathophysiology and therapeutic developments in SMA. A. Burghes.	10:40 am Molecular basis of OI that results from mutations in CRTAP, LEPRE1, and PPIB. G. Pals.	10:45 am The role of DNA repair in neurologic development and disease. P. McKinnon.
10:55 am Epigenetic consequences of chromosomal translocations. A. K. Naumova.	10:55 am Comparative genomics approach using global functional analysis in Drosophila to identify new candidate genes for human pain genetic research. G. G. Neely.	10:55 am Leveraging comprehensive annotations and pathway information in large scale genomic studies. N. J. Schork.	11:00 am Clinical and genetic update of spinal muscular atrophies. L. L. Baumbach-Reardon.	11:00 am Inactivating mutation in SERPINH1, which encodes the collagen chaperone HSP47, result in severe OI. P. H. Byers.	11:11 am The DNA damage theory of aging — Evidence from nucleotide excision repair mutants. J. Hoeijmakers.
11:15 am Epidemiological overview. J. S. Sinsheimer.	11:15 am Genetic risks in development of chronic pain in humans. L. Diatchenko.	11:15 am Network-based diagnosis and personalized medicine. T. Ideker.	11:25 am Update in CMT, distal SMA and overlapping phenotypes. V. Timmerman.	11:20 am The broad phenotype spectrum of mutations in FKBP10—mild OI, scoliosis, contractures. D. Krakow.	11:37 am Telomere instability and human disease. P. Lansdorp.
11:20 am Intergenerational effects as risk factors for schizophrenia: The case of maternal-fetal genotype incompatibility. C. G. Palmer.	11:40 am Identification of the pain gene CACNG2 using an integrated whole genome-based approach. J. Nissenbaum.	11:35 am Meta-dimensional analysis of phenotypes. M. D. Ritchie.	11:50 am Update in genetics and pathophysiology of amyotrophic lateral sclerosis: New genes and new insights. M. Strong.	11:40 am Implications of mutations that result in recessive forms of OI for treatment of all forms of OI. F. Glorieux.	12:03 pm The role of rare DNA repair gene variants in human cancer. S. Tavtigian.
11:40 am Detecting complex genetic and environmental effects with case-control mother-child pair data. J. Chen.	12:05 pm COMT as a gold standard candidate gene for human pain research. I. Belfer.	11:55 am Integrating interaction and pathway association analysis in genome-wide association studies. T. Becker.		12:00 pm Animal models of OI: Substrates for the measure and development of therapies and mechanisms of disease. B. Lee.	
12:00 pm Investigation of maternal effects, maternal-fetal interactions and parent-of-origin effects (imprinting), using mothers and their offspring. H. Cordell.	12:25 pm Questions and answers. I. Belfer.	12:15 pm Questions and answers. M. D. Ritchie.		12:20 pm Questions and answers. D. Krakow.	
12:20 pm Discussion. A. E. Toland.					

Thursday, October 13: Concurrent Invited Session II (24-29)

8:00 AM–10:00 AM

Room 511, Level 5	Room 517D, Level 5	Room 517A, Level 5	Room 210, Level 2	Room 520, Level 5	Room 517BC, Level 5
<p>SESSION 24 – Emerging Ethical Issues in Large-Scale International Genomics Research Collaborations Co-Moderators: Jean E. McEwen, NHGRI/NIH, USA; and Pilar N. Ossorio, Univ. of Wisconsin-Madison, USA</p>	<p>SESSION 25 – Neurogenetic Pathways Underlying Speech and Language Disorders Co-Moderators: Dennis Drayna, NIDCD/NIH, USA; and Simon E. Fisher, Max Planck Inst. for Psycholinguistics, Nijmegen, Netherlands</p>	<p>SESSION 26 – The Nucleus, a Transcription Factory Co-Moderators: Alexandre Reymond, Univ. of Lausanne, Switzerland; and Bernice E. Morrow, Albert Einstein Col. of Med., USA</p>	<p>SESSION 27 – Cancer Genomics Co-Moderators: Paul T. Spellman, Oregon Hlth. & Sci. Univ., Benicia, CA, USA; and Thomas J. Hudson, Ontario Inst. for Cancer Res., Canada</p>	<p>SESSION 28 – Translational Approaches to Mitochondrial Research Moderator: Fernando Scaglia, Baylor Col. of Med., USA</p>	<p>SESSION 29 – Changing Trends in Prenatal Diagnosis Co-Moderators: Louanne Hudgins, Stanford Univ., USA; and Diana Bianchi, Tufts Med. Ctr., USA</p>
08:00 am Introduction. J. E. McEwen.	08:00 am Finding genetic variants that underlie stuttering. D. Drayna.	08:00 am Transcription and the nuclear periphery: Edge of darkness? W. Bickmore.	08:00 am Introduction. T. J. Hudson.	08:00 am Introduction. F. Scaglia.	08:00 am The big picture: Changing trends in prenatal diagnosis. M. Evans.
08:05 am Ethical issues in international genomics research collaborations: Perspectives from Canada. B. M. Knoppers.	08:24 am Neurogenetic pathways regulated by FOXP2, a gene mutated in speech and language disorder. S. E. Fisher.	08:30 am Transcription factories and nuclear organization of the genome. P. Fraser.	08:10 am The Cancer Genome Atlas. S. Gabriel.	08:05 am The biogenesis and role of complex I in human disease. J. A. M. Smeitink.	08:30 am It's all detectable in a first trimester sonogram (or not!). R. D. Wilson.
08:25 am Ethical issues in international genomics research collaborations: Perspectives from Sub-Saharan Africa. C. Rotimi.	08:48 am The role of ATP2C2 and C-MIP in specific language impairment. D. Newbury.	09:00 am DNase I hypersensitive sites comprehensively define regulatory DNA and encode epigenetic memory of developmental fate. J. A. Stamatoyannopoulos.	08:35 am The oral cancer genome. P. P. Majumder.	08:30 am Characterization of new genes implicated in mitochondrial translation. E. A. Shoubridge.	09:00 am Array CGH in the prenatal setting: Indications and limitations. J. Vermeesch.
08:45 am Ethical issues in international genomics research collaborations: Perspectives from the U.K. J. Kaye.	09:12 am Functional analysis of dosage sensitive genes at 7q11.23 involved in syndromes of speech and language impairment. L. Osborne.	09:30 am Population genetics and genomics of cellular phenotypes. E. T. Dermitzakis.	09:00 am The Stomach Cancer Genome Project. H. Yang.	09:00 am The role of mitochondrial dynamics in human disease. D. C. Chan.	09:30 am Sequencing maternal plasma DNA for non-invasive prenatal diagnosis. R. Chiu.
09:05 am Ethical issues in international genomics research collaborations: Perspectives from Japan. E. Suda.	09:36 am Gene function analysis of FoxP2 in songbirds. C. Scharff.		09:25 am The pancreatic cancer genome. J. McPherson.	09:30 am Choosing between glycolysis and oxidative phosphorylation: A tumor's dilemma? R. Rossignol.	
09:25 am Ethical issues in international genomics research collaborations: A global perspective. A. Chakravarti.			09:50 am Questions and answers. P. T. Spellman.		

Friday, October 14: Concurrent Invited Session III (45-50)

10:30 AM–12:30 PM

Room 517BC, Level 5	Room 517A, Level 5	Room 517D, Level 5	Room 210, Level 2	Room 520, Level 5	Room 511, Level 5
SESSION 45 – Functional Noncoding RNAs in Mammalian Systems and Disease Co-Moderators: Ahmad M. Khalil, Case Western Reserve Univ. Sch. of Med., USA; and Leonard Lipovich, Wayne State Univ. Sch. of Med., USA	SESSION 46 – Mechanisms of Embryonic Development and Organogenesis: Insights into Human Birth Defects Moderator: Anthony Wynshaw-Boris, Univ. of California, San Francisco Sch. of Med., USA	SESSION 47 – One and the Same? Twins, Epigenetics and the Elucidation of Complex Genetic Traits and Diseases Moderator: Eric Vilain, Univ. of California, Los Angeles, USA	SESSION 48 – Individual Resequencing for Complex Trait Genetics Co-Moderators: Benjamin M. Neale, Massachusetts Gen. Hosp., USA; and Mark J. Daly, Broad Inst., Cambridge, MA, USA	SESSION 49 – International Policies Regarding the Retention and Use of Residual Dried Blood Spot Specimens after Newborn Screening Moderator: Michele Lloyd-Puryear, HHS, Rockville, MD, USA	SESSION 50 – Exploring International Approaches to the Evaluation of Genetics Education Co-Moderators: Kate Reed, NCHPEG, Lutherville, MD, USA; and Victor B. Penchaszadeh, Ctr. for Genet. and Publ. Hlth., Buenos Aires, Argentina
10:30 am Introduction. A. M. Khalil.	10:30 am Introduction. A. Wynshaw-Boris.	10:30 am Introduction. E. Vilain.	10:30 am Introduction. B. M. Neale.	10:30 am Introduction. M. Lloyd-Puryear.	10:30 am Introduction. K. Reed.
10:40 am Nuclear-retained noncoding RNAs. D. L. Spector.	10:40 am Left-right asymmetry and its inborn errors. H. Hamada.	10:35 am Contributions of twin studies towards elucidating disease etiology. N. Martin.	10:35 am Next-generation sequencing in seven common diseases. P. Donnelly.	10:35 am Recommendations from the Secretary's Advisory Committee on Heritable Disorders in Newborns and Children. R. R. Howell.	10:35 am Educating a country: Genetics education for health professionals in the United Kingdom. P. Farndon.
11:05 am Antisense noncoding RNAs in human neurological disorders. C. Wahlestedt.	11:05 am Primary cilia and Hedgehog signaling. K. Anderson.	11:05 am Large scale methylation in discordant twins. T. Spector.	10:58 am Large-scale sequencing of schizophrenia and bipolar disorder. S. M. Purcell.	10:55 am Treasure trove or baby DNA database? S. Terry.	10:55 am Evaluating genetic education in Latin America. V. B. Penchaszadeh.
11:30 am Endogenous siRNAs and noncoding RNA-derived small RNAs are expressed in adult mouse hippocampus and are upregulated in olfactory discrimination training. N. R. Smalheiser.	11:30 am Formation of the vertebral column: From clocks to scoliosis. O. Pourquie.	11:35 am Epigenetic differences in twins: Clues for complex disorders. A. Petronis.	11:21 am Next-generation sequencing to resolve complex genetic architectures. J. Barrett.	11:15 am Australian national policy for the use and storage of biologic samples. J. M. Fletcher.	11:15 am Genetics education and program evaluation in Australia. S. Metcalfe.
11:55 am Modulating gene expression by targeting noncoding RNAs. D. Corey.	11:55 pm X-linked lethal mutations: Mouse models of human congenital syndromes. J. Rossant.	12:05 pm Twins, sexual orientation and age. E. Vilain.	11:44 am Next-generation sequencing of multiple sclerosis. C. Cotsapas.	11:35 am Policy for the storage and use of residual dried blood spot specimens after newborn screening: The view from Canada. F. A. Miller.	11:35 am Developing and evaluating genetics education in developing countries. H. Hamamy.
12:20 pm Summary. L. Lipovich.	12:20 pm Question and answers. A. Wynshaw-Boris.		12:07 pm Sequencing analysis of quantitative traits. G. Abecasis.	11:55 am Secondary uses of dried blood spots collected for newborn screening: Public benefits and public understanding. C. Dezateux.	11:55 am Development of a novel evaluation approach for genetics education in the United States. E. Edelman.
				12:15 pm Questions and answers. M. Lloyd-Puryear.	12:15 pm Questions and answers. V. B. Penchaszadeh.

Saturday, October 15: Concurrent Invited Session IV (61-66)

8:00 AM–10:00 AM

Room 517D, Level 5	Room 517BC, Level 5	Room 520, Level 5	Room 511, Level 5	Room 517A, Level 5	Room 210, Level 2
SESSION 61 – Human Molecular Cytogenetics: Functional Nuclear Architecture and Disease Moderator: Thomas Cremer, LMU Biocenter, Germany	SESSION 62 – Quantitative Traits in Neurogenetics: The Future of Phenotyping in Neurological, Psychiatric and Developmental Disorders Co-Moderators: Barbara Franke, Radboud Univ. Nijmegen Med. Ctr., Netherlands; and Tricia A. Thornton-Wells, Vanderbilt Univ., USA	SESSION 63 – Lysosomes and Genetic Diseases Co-Moderators: Andrea Ballabio, Telethon Fndn. Inst. of Genet. and Med., Naples, Italy; and David C. Rubinsztein, Cambridge Inst. for Med. Res., U.K.	SESSION 64 – Nutrigenomics: Genotype by Environment Interaction and Disease Risk Co-Moderators: Jose M. Ordovas, USDA at Tufts Univ., USA; and Chao-Qiang Lai, USDA at Tufts Univ., USA	SESSION 65 – Status and Prospects of Genetic Therapy for Major Mendelian Diseases Co-Moderators: Gert-Jan B. van Ommen, Leiden Univ. Med. Ctr., Netherlands; and Brunhilde Wirth, Univ. Hosp. of Cologne, Germany	SESSION 66 – Intellectual Disability and Autism: Two Sides of the Same Coin Co-Moderators: Charles E. Schwartz, Greenwood Genet. Ctr., Greenwood, SC, USA; and Giovanni Neri, Catholic Univ. of Rome, Italy
08:00 am Chromosome territories and the interchromatin space: Topography of transcription, DNA replication and repair. T. Cremer.	08:00 am Introduction. B. Franke.	08:00 am Introduction. A. Ballabio.	08:00 am Introduction. J. M. Ordovas.	08:00 am Antisense-based exon skipping as a therapy for DMD and other disorders. G-J. B. van Ommen.	08:00 am Introduction. C. E. Schwartz.
08:30 am The genome in three dimensions. J. Dekker.	08:05 am Biomarkers in psychiatry: From genetics to biology to predictive medicine. A. B. Niculescu.	08:05 am Role of the lysosomal sialidase NEU1 as negative regulator of lysosomal exocytosis in pathogenesis. A. d'Azzo.	08:05 am Understanding GxE interaction and cardiovascular disease risk. C-Q. Lai.	08:25 am The use of HDAC inhibitors to upregulate SMN2 in SMA. B. Wirth.	08:05 am Aspects of clinical genetics in autism spectrum disorders: Patient evaluation, diagnostic tests and counseling of families. F. Gurrieri.
09:00 am Nuclear lamina - genome interactions. B. van Steensel.	08:25 am Low CD38 expression in lymphoblastoid cells is associated with autism, correlates with IQ and social skills and is reversed by all-trans retinoic acid. R. Ebstein.	08:25 am The curious case of CLN3. B. L. Davidson.	08:25 am Interaction between whole grain foods and genetic variants on diabetes risk. J. A. Nettleton.	08:50 am From gene to bedside: Translating lessons from Fragile X syndrome. S. Warren.	08:28 am Disruption of synaptic pathways in intellectual disability and autism spectrum disorders. J. D. Buxbaum.
09:30 am Role of lamins in normal and pathological nuclear architecture. S. A. Adam.	08:45 am Intermediate imaging phenotypes and risk mechanisms of psychiatric disorders. P. Kirsch.	08:45 am Autophagy, a guardian against neurodegeneration. D. C. Rubinsztein.	08:45 am Pharmacogenetics: Understanding an individual's response to fenofibrate intervention by genome-wide association study. D. K. Arnett.	09:15 am Recombinant AAV gene therapy of Leber congenital amaurosis. S. G. Jacobson.	08:51 am Copy number variation and variability in neuropsychiatric disease. E. E. Eichler.
	09:05 am Genomic imaging: The identification of genes involved in brain structure and function. J. Blangero.	09:05 am Role of the endo-lysosomal system in neurodegenerative diseases. R. A. Nixon.	09:05 am Epigenomics: Understanding individual differences in response to nutrition and aging? J. C. Mathers.	09:40 am Questions and answers. G-J. B. van Ommen.	09:14 am Functional impact of global rare copy number variation in autism spectrum disorder. S. W. Scherer.
	09:25 am Putting it all together: ENIGMA, enabling neuroimaging genetics through meta-analysis. S. E. Medland.	09:25 am Modulating lysosomal function and cellular clearance. A. Ballabio.	09:25 am Effects of genetic variants and nutritional factors on metabolic disease among Chinese populations. X. Lin.		09:37 am Functional genomic investigations of autism suggests molecular convergence. D. Geschwind.
	09:45 am Questions and answers. T. A. Thornton-Wells.	09:45 am Discussion. A. Ballabio.	09:45 am Questions and answers. J. M. Ordovas.		

	Room 210, Level 2	Room 517BC, Level 5	Room 517D, Level 5	Room 517A, Level 5	Room 520, Level 5	Room 511, Level 5	Room 516, Level 5	Room 710A, Level 7	Room 710B, Level 7	Room 510, Level 5	
	SESSION 10 – Population Genetics Co-Moderators: Cornelia M. Van Duijn, Erasmus MC, Netherlands; and Andrew G. Clark, Cornell Univ., USA	SESSION 11 – Genomics I: Structural Variation Co-Moderators: Heather Mefford, Univ. of Washington, USA; and Lars Feuk, Uppsala Univ., Sweden	SESSION 12 – Neurogenetics I: Autism Co-Moderators: Laurie Weiss, Univ. of California, San Francisco, USA; and Jonathan Sebat, Univ. of California, San Diego, USA	SESSION 13 – Clinical Genetics I: Genotype-Phenotype Correlation in Syndromes Co-Moderators: Poh-San Lai, National Univ. of Singapore, Singapore; and Gunnar Houge, Haukeland Univ. Hosp., Bergen, Norway	SESSION 14 – Chromosome Organization and Cancer Cytogenetics Co-Moderators: Mary Shago, Hosp. for Sick Children, Univ. of Toronto, Canada; and Marilyn M. Li, Baylor Col. of Med., USA	SESSION 15 – Genetic Testing and Counseling Co-Moderators: Alain Verloes, Hosp. Robert Debre, France; and Michele Ramsay, NHLS, Johannesburg, South Africa	SESSION 16 – Statistical Genetics I: Functional Consequences of Genetic Variation Co-Moderators: Camilla Day, CIDR/NIH, USA; and Adebowale Adeyemo, Howard Univ., USA	SESSION 17 – Molecular Basis I: Skin and Inflammatory Disorders Co-Moderators: Gail Herman, Nationwide Children's Hosp., USA; and Cisca Wijmenga, Univ. Groningen, Netherlands	SESSION 18 – Biochemical Genetics Co-Moderators: Hans Andersson, Tulane Univ. Med. Ctr., USA ; and Nancy Braverman, McGill Univ., Canada	SESSION 19 – Cardiovascular Genetics I: Complex Traits Co-Moderators: Stuart Macgregor, Queensland Inst. Med. Res., Australia; and Joanne Curran, Texas Biomed. Res. Inst., USA	
4:15	3 The Kaiser Permanente/UCSF Genetic Epidemiology Research Study on Adult Health and Aging: Developing a novel fully-automated system to assay telomere lengths and preliminary results on a cohort of 100,000. K. Lapham et al.	11 An integrated map of genetic variation in over 1000 human genomes. G. McVean.	19 Full exome sequencing of autism cases, families, and controls. B. M. Neale et al.	27 HDAC8 mutations in Cornelia de Lange syndrome. M. A. Deardorff et al.	35 Rapid detection of copy number imbalances and balanced translocations in multiple myeloma by translocation array CGH. S. A. Morton et al.	43 Intragenic copy number changes detected by an exon-targeted array in patients with neurodevelopmental disorders. S. W. Cheung et al.	51 Multivariate linkage analysis points to a shared genetic component between mycobacteria-triggered TNF production and innate resistance to tuberculosis infection. A. Cobat et al.	59 Rare de novo and common variations implicate <i>CARD14</i> as psoriasis susceptibility locus 2. C. T. Jordan et al.	67 <i>NBEAL2</i> is mutated in gray platelet syndrome and is required for biogenesis of platelet alpha-granules. T. Vilboux et al.	75 Multiple novel loci conferring risk to coronary artery disease identified in a study of 63,253 cases and 126,820 controls. S. Kanoni et al.	4:15
4:30	4 Natural selection in the cholera endemic Ganges River delta region. E. Karlsson et al.	12 Dysfunction is the normal state: Analysis of gene-disrupting variants in 1,094 human genomes. D. G. MacArthur et al.	20 Exome and targeted sequencing in sporadic autism spectrum disorders identifies severe de novo mutations. B. J. O'Roak et al.	28 Mutations in <i>RAD21</i> as a cause of a new cohesinopathy. F. J. Kaiser et al.	36 Development and validation of a CGH microarray for clinical diagnosis of hematological malignancies. S. A. Yatsenko et al.	44 Genome-wide testing the most frequent genetic diseases optimizes abnormal gene identity and test reliability. R. V. Lebo et al.	52 Major histocompatibility complex association to rheumatoid arthritis is explained by polymorphic amino acids in the binding grooves of HLA-DR, HLA-B, and HLA-DP. P. I. W. de Bakker et al.	60 Clinical transcriptome sequencing and analysis of a patient with spiny follicular hyperkeratoses of unknown etiology. K. V. Fuentes Fajardo et al.	68 A novel human peroxisome biogenesis disorder affecting peroxisome division. H. R. Waterham et al.	76 Twenty-nine common variants associated with blood pressure and cardiovascular disease risk: The International Consortium for Blood Pressure Genome-Wide Association Studies. G. B. Ehret et al.	4:30
4:45	5 Contrasting human X-linked and autosomal variation in population-scale whole genome sequencing. A. Keinan et al.	13 Dual function of DNA sequences: Coding exons function as enhancers of nearby genes. N. Ahituv et al.	21 Whole exome sequencing identifies novel changes in <i>AP4M1</i> , <i>CDKAL1</i> and <i>SYNGAP1</i> in extended multiplex autism families. H. N. Cukier et al.	29 Pitt Hopkins syndrome: Further delineation of the neurological phenotype. Description of 32 novel patients and proposition of a diagnostic criteria score. S. Whalen et al.	37 Identification of a novel palindrome-mediated translocation associated with the t(3;8) of hereditary renal cancer. T. Kato et al.	45 Bringing current research technology to the clinic: The Manton Center for Orphan Disease Research Gene Discovery Core. M. C. Connolly et al.	53 Multiple signals of association at known loci explain additional phenotypic variation and reveal complex patterns of association. A. R. Wood et al.	61 Exome sequencing identifies rare recessive IL1F5 variants in generalised pustular psoriasis. A. Onoufriadis et al.	69 Mutations in <i>ABCD4</i> cause a new inborn error of vitamin B ₁₂ metabolism. J. C. Kim et al.	77 A large-scale genome-wide association study of PR interval identifies 41 loci associated with atrial and atrioventricular conduction. A. Isaacs et al.	4:45
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