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Abstract Session: MHC Evolution, Population Genetics (O9 - O16)

Thursday, April 27th - 10:30-12:00

Auditorium 450

O9/ID 5422

From global population genetic profiles to detailed individual molecular variation in humans and chimpanzees: a new turn in our understanding of MHC diversity and evolution

Alicia Sanchez-Mazas

O10/ID 3097

Creating fully representative MHC reference haplotypes

Nicholas R. Pollock

O11/ID 8033

MICA Copy Number Variations are the Result of Numerous Independent Non-Allelic Homologous Recombination Events

Anja Klussmeier

O12/ID 1551

Telomeres and ageing and their relation with HLA – results from the project “Immunogenetics of Ageing” within 18th IHIWS

Katarzyna Bogunia-Kubik

O13/ID 1600

Classical HLA alleles and long-range haplotypes are under rapid selection among admixed populations

Yang Luo

O14/ID 9773

Human Leukocyte Antigens (HLA) evolutionary divergence (HED) calculator

Bruno Lima

O15/ID 3186

A high-throughput approach to the MHC assembly challenge in disease association

Kristen J. Wade

O16/ID 6913

High Frequency of MICA Gene Deletion Haplotypes in Several Non-European Populations

Anja Klussmeier



New technologies & New Approaches in Immunogenetics (O17 - O24)

Thursday, April 27th - 10:30-12:00

Room 200

O17/ID 6210

The beneficial impact of HLA-E mismatching for patients receiving a less than 10/10 HLA matched hematopoietic cell transplant

Jonathan A.M. Lucas

O18/ID 4650

Clinical relevance of cell-free DNA quantification and qualification during the first month after lung transplantation

Pascal Pedini

O19/ID 685

Full-gene sequence characterization of HLA-DMA, -DMB, -DOA, and -DOB in a panel of International HLA and Immunogenetics Workshop cell lines

Matilda C. Tierney

O20/ID 5097

A randomized trial to assess the clinical utility of renal allograft monitoring by urine CXCL10 chemokine

Stefan Schaub

O21/ID 8439

Characterization of chimpanzee KIR haplotype organizations using Cas9 enrichment and Oxford Nanopore sequencing

Corrine Heijmans

O22/ID 757

TXMatching – a novel software for kidney paired donations

Matěj Röder

O23/ID 4379

HLA loss detection by NGS using STR markers within the MHC region on chromosome 6

Loes van de Pasch

O24/ID 4986

Assessment of a Universal Blood Donor Genotyping Platform

Colin Brown

Abstract Session: NK Cells & KIR (O25-O32)

Thursday, April 27th - 14:30-16:00

Auditorium 450

O25/ID 3713

Chromosomal rearrangements in the KIR gene cluster as evolutionary strategy to protect against evading pathogens

Jesse Bruijnesteijn

O26/ID 7004

Variegated expression of KIR regulated by conserved and diverged promoter regions in humans and macaques

Marit van der Wiel

O27/ID 5716

Polymorphism of HLA and KIR affects severity of COVID-19 by shaping innate and adaptive immunity to SARS-CoV-2

Ticiana Dj Farias

O28/ID 9468

The role of natural killer cells in recurrent pregnancy loss: evaluation of natural killer cell education

Amber Lombardi

O29/ID 1207

KIR2DL2/C1: a potential predictive immunogenetic marker to COVID-19 severity in Spanish patients

Jairo Eduardo Niño Ramirez

O30/ID 9298

Nanopores may replace SMRT reads for dual redundant reference sequencing (DR2S):

Characterization of more than 600 novel KIR alleles

Kathrin Putke

O31/ID 9873

Natural killer cell receptor variation is associated with more aggressive subtypes of breast cancer

Danillo Augusto

O32/ID 4161

HLA class I epitope and KIR diversities in multiple myeloma

Nicky Beelen



Abstract Session: Immunogenetics in Organ Transplantation (O33-O40)

Thursday, April 27th - 14:30-16:00

Room 200

O33/ID 1424

Immunogenomic exploration in a large kidney transplantation genetic cohort reveals a kidney graft failure association with HLA-B*40:01 and KIRD2L2/HLA-C2 combination

Nicolas Vince

O34/ID 3470

In the era of precision medicine: lncRNAs as probable biomarkers to predict allograft rejection

Uma Kanga

O35/ID 1948

Gene expression profiles in 3-month biopsies associate with progression to kidney transplant rejection before detection of histological changes

Mathijs Groeneweg

O36/ID 2989

Precision medicine in liver transplant recipients: donor cell-free DNA as an early marker of post-transplant hepatic injury

Monica Sorbini

O37/ID 9184

Acute and chronic rejection monitoring of pediatric heart transplant recipients through a ddPCR assay based on HLA-DRB1 polymorphism

Monica Sorbini

O38/ID 6616

A genome-wide survival study identifies a novel association between donor genotype and antibody-mediated kidney graft rejection

Vincent Mauduit

O39/ID 4579

The number of donor HLA-derived T-cell epitopes available for indirect antigen presentation determines the risk for vascular rejection after kidney transplantation

Emma Peereboom

O40/ID 9981

Impact of HLA diversity on humoral response to SARS-Cov-2 and HBV vaccines in liver transplant recipients

Jean-Luc Taupin



Abstract Session: Bioinformatics, data analysis in Immunogenetics (O41-O48)

Friday, April 28th - 10:30-12:00

Auditorium 450

O41/ID 848

Unexposed individuals are fully equipped at the genetic level in terms of peptide coverage and T-cell repertoire against SARS-CoV-2: analysis in a cohort of healthy donors and alloHSCT recipients

Stephane Buhler

O42/ID 1862

A new hla-mapper algorithm for alignment optimization of HLA sequences from RNA-seq

Erick Castelli

O43/ID 8886

HLA-3Diff: redefining donor-recipient HLA matching based on three dimensional structure prediction

Léo Boussamet

O44/ID 4733

Human Leucocyte Antigen variation is associated with Cytomegalovirus seropositivity

Juliano Boquett

O45/ID 4099

A large, improved and ancestry-diverse reference panel to impute HLA classical and non-classical class I alleles

Nayane S. B. Silva

O46/ID 8088

Possible Biological Mechanisms Underlying the Association between COVID-19 Severity and HLA-C*04:01

Frieda Jordan

O47/ID 9168

The expanded role of microRNAs in controlling the HLA class I phenotype: Relationship between the 3' UTR and post-transcriptional Gene Regulation

Panagiotis Mallis

O48/ID 3787

Analysis of "Big Data" reveals a new MHC Class I sequence, HLA-OLI, and the location of HLA-Y

Lindley Blair



Abstract Session: Immunotherapy, Gene Therapy, Cellular Therapy (O49-O56)

Friday, April 28th - 10:30-12:00

Room 200

O49/ID 3892

Polymorphic KIR3DL3 expression modulates tissue-resident and innate-like T cells

Paul Norman

O50/ID 7750

Memory CD4+ T cells efficiently recognize divergent HLA-DP immunopeptidomes relevant in allogeneic hematopoietic cell transplantation

Kulvara Kittissares

O51/ID 2944

Discovery of the human cytomegalovirus-specific peptide repertoire naturally processed and presented by infected human antigen presenting cells

Maria Michela Santamarena

O52/ID 4032

Exploring the cryptic HLA-DP immunopeptidome for new targets of T cell immunotherapy in acute myeloid leukemia

Pietro Crivello

O53/ID 5389

Generation and Characterization of third party donor derived AdV, CMV and EBV multivirus specific T cells for therapeutic intervention in patients undergoing Hematopoietic Stem Cell Transplantation

Meenakshi Singh

O54/ID 8869

Optimal population coverage for cellular therapies

Yoram Louzoun

O55/ID 5677

THE STIMULATION OF MEMORY B CELLS FOR THE IDENTIFICATION OF UNACCEPTABLE ANTIGENS IN SOLID ORGAN TRANSPLANTATION

Linh Truong

O56/ID 8779

New regulatory dimensions for transplantation, genetics and stem cell research in the French bioethics law. Consequences for European collaborations

Anne Cambon-Thomsen



Abstract Session: Hematopoietic Stem Cell Transplantation (O57-O64)

Friday, April 28th - 14:30-16:00

Auditorium 450

O57/ID 6533

HLA-DP permissive mismatch subsets confer reduced aGvHD risks and improved disease control after hematopoietic cell transplantation for acute leukemia and myelodysplastic syndromes

Esteban Arrieta Bolaños

O58/ID 873

T cells can be activated by epitopes presented on HLA-C*04:09N

Carlotta Welters

O59/ID 8963

Longitudinal tracking of T-cell receptor repertoire reconstitution after allogeneic hematopoietic stem cell transplantation

Antonia Schäfer

O60/ID 3205

Associations between HLA Evolutionary Divergence and clinical outcome of matched related or unrelated stem cell transplantation: a study from the EBMT Cellular Therapy and Immunobiology Working Party

Pietro Crivello

O61/ID 736

The role of Recipient Specific Antibodies (RSA) in transplant outcome. Analysis of a group of family donors selected for patients undergoing haploidentical transplantation

Annamaria Pasi

O62/ID 9591

HLA evolutionary divergence (HED) influences the outcome of haploidentical hematopoietic stem cell transplantation in adult patients with hematological malignancies

Debora Jorge Cordeiro

O63/ID 798

Combined imputation of HLA genotype and race leads to better donor-recipient matching

Yoram Louzoun

O64/ID 5359

Genetic variation in HLA genes: impact on transplant compatibility in a Brazilian admixed population

Heloísa S Andrade



Abstract Session: Autoimmunity, Infection, Reproduction & Cancer (O64-O72)

Friday, April 28th - 14:30-16:00

Room 200

O65/ID 7848

A Protective HLA Extended Haplotype Outweighs the Major COVID-19 Risk Factor Inherited from Neanderthals in the Sardinian Population

Stefano Mocci

O66/ID 1174

HLA-A*03:01 significantly predicts strong humoral response at six months after mRNA vaccination: results from the observational prospective cohort study RENAISSANCE

Roberto Crocchiolo

O67/ID 7087

NEGR1 genetic variants and risk for virological failure in the HIV-positive Botswanan population

Martin Morin

O68/ID 2751

Copy number variation of the C4L gene isoform is associated with risk for multiple sclerosis

Jacqueline Williams

O69/ID 8515

HLA-E expression in HPV infected Cervical Carcinoma

Ritu Aggarwal

O70/ID 5590

HLA binding-groove motifs are associated with myocarditis induction after Pfizer-BioNTech BNT162b2 vaccination

Gil Benedek

O71/ID 7952

HLA-Bw4 is Associated with Pediatric Acute-Onset Neuropsychiatric Syndrome (PANS)

Kerry Kizer

O72/ID 7171

Fight against COVID-19: functional and structural study of the T cell response

Stephanie Gras



Best Abstract Session (O1-O9)

Saturday, April 29th - 08:30-10:00

Great Auditorium

O1/ID 4927

Forward or reversed binding of peptides within the HLA-DP peptidome is mainly determined by the HLA-DPB1 allele but with a key role for the HLA-DPA1 chain

Michel Kester

O2/ID 941

Single cell transcriptomics to identify leukemia-intrinsic and -extrinsic bone marrow correlates of immune escape and post-transplantation relapse

Marco Punta

O3/ID 6126

Highly specific Latent Membrane Protein 2A-targeting T-Cell Receptor-engineered T cells with inducible Interleukin-18 expression as promising tool to treat Epstein-Barr Virus-associated malignancies

Philip Mausberg

O4/ID 7583

Proteome analysis of drug susceptible HLA-B*57:01+ cells reveals the pivotal mechanisms of HLA-mediated Carbamazepine hypersensitivity

Funmilola Josephine Haukamp

O5/ID 2276

The evolution of MHC class I loss in a newly emerged transmissible cancer in Tasmanian devils

Kathryn Hussey

O6/ID 1570

Bw4 ligand and direct T-cell receptor binding induced selection on HLA-A and -B alleles

Yoram Louzoun

O7/ID 6775

The 18th International HLA and Immunogenetics Workshop (IHIWS) HLA immunogenic epitope project

Cynthia Kramer

O8/ID 9702

Spatial composition of decidual immune cells in oocyte donation pregnancies in relation to fetal-maternal HLA incompatibility

Xuezi Tian