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Advancing Immunopeptidomics Validation of the Method, Improved Epitope Prediction, Peptide-based HLA Typing and Discrimination of Healthy and Malignant Tissue Human T Cell Epitopes and HLA Class II Restriction Elements of Chlamydia Trachomatis Major Outer Membrane Protein The HLA FactsBook Elsevier **The HLA FactsBook presents up-to-date and comprehensive information on the HLA genes in a manner that is accessible to both beginner and expert alike. The focus of the book is on the polymorphic HLA genes (HLA-A, B, C, DP, DQ, and DR) that are typed for in clinical HLA laboratories. Each gene has a dedicated section in which individual entries describe the structure, functions, and population distribution of groups of related allotypes. Fourteen introductory chapters provide a beginner's guide to the basic structure, function, and genetics of the HLA genes, as well as to the nomenclature and methods used for HLA typing. This book will be an invaluable reference for researchers studying the human immune response, for clinicians and laboratory personnel involved in clinical and forensic HLA typing, and for human geneticists, population biologists, and evolutionary biologists interested in HLA genes as markers of human diversity. Introductory chapters provide good general overview of HLA field for novice immunologists and geneticists Up-to-date, complete listing of HLA alleles Invaluable reference resource for immunologists, geneticists, and cell biologists Combines both structural and functional information, which has never been compiled in a single reference book previously Serological specificity of allotypes Identity of material sequenced including ethnic origin Database accession numbers Population distribution Peptide binding specificities T cell epitopes Amino acid sequences of allotypes Key references Antibody Repertoire and Graft Outcome Following Solid Organ Transplantation** Frontiers Media SA **The first real major breakthrough that laid the**

basis of HLA antibody detection in the field of solid organ transplantation, came with the introduction of the complement dependent cytotoxicity (CDC) test in 1964 by Terasaki and McClelland. Since then, methods for antibody detection have evolved remarkably from conventional cell-based assays to the current advanced solid phase systems on the Luminex platform, with increasing degree of sensitivity and specificity. The latter have been indispensable for more accurate identification of donor specific HLA antibodies in broadly reactive allo antisera, and to guide donor selection and kidney paired exchange programs through virtual crossmatching, in addition to serving as excellent tools for initiating pre-transplant desensitization and post- transplant antibody monitoring. Consensus is evolving on the optimal routine employment of these methods in donor selection strategies along with an understanding of the clinical relevance of antibodies detected by each of them. The immunoassays based on the Luminex platform and flow cytometric beads are however unable to discriminate complement fixing from non-complement fixing HLA antibodies. This is important because the former are considered clinically more pertinent in the peri-transplant period. The C1q assay which is a modification of the solid phase assay based on Luminex single antigen beads, which can be used effectively to monitor high dose IVIG desensitization is essentially a surrogate complement fixing assay, retaining the exquisite sensitivity and specificity of the Luminex platform. Currently, information obtained from these assays is preliminary and much needs to be done to standardize technologies and set a consensus ‘MFI cut off’ for antibody positivity. Besides the overriding influence of anti-HLA antibodies on overall solid organ graft survival, immune response to non-HLA antigens has become a topic of substantial interest in recent years. An ever expanding list of non-HLA antigens has been implicated in graft rejection for various organs, of which the most noted are the Major Histocompatibility Complex class I chain-related molecule A (MICA), Vimentin, Myosin, Angiotensin II type 1 receptor (AT1R), Tubulin and Collagen. MICA is one of the most polymorphic and extensively studied non-HLA antigenic targets especially in renal transplantation. Although there are clear indications of MICA antibodies being associated with adverse graft outcome, to date a definitive consensus on this relationship has not been agreed. Because MICA molecules are not expressed constitutively on immunocompetent cells such as T and B lymphocytes, it is of utmost importance to address the impact of MICA donor specific antibodies (DSA) as compared to those that are non- donor specific (NDSA) on graft outcome. The soluble isoform of MICA molecule (sMICA) that is derived from the proteolytic shedding of membrane bound molecules has the potential to engage the NK-cell activating receptor NKG2D and down-regulate its expression. Consequent to the interaction of NKG2D by sMICA, the receptor ligand complex is endocytosed and degraded and thus suppresses NKG2D mediated lysis of the target by NK cells. Thus interaction between NKG2D and sMICA leads to expansion of immunosuppressive/anergic T cells thereby resulting in suppression of NKG2D

mediated host innate immunity. These concept support the possible involvement of an immunosuppressive role for sMICA during allotransplantation as shown recently for heart transplantation. This research topic focusses on the clinical utility of investigating the complete antibody repertoire in solid organ transplantation. The HLA System A New Approach Springer Science & Business Media **This volume documents our growing understanding of the human major histocompatibility complex. The application of this information is ever more important as the limits of transplantation continue to be reduced, including the recent success of bone marrow transplantation between unrelated but closely matched individuals. In addition, the need to transfuse platelets in the face of immunologic barriers continues to challenge transfusion services. Thus, the serologic information summarized in this volume is essential for optimal patient care. At the same time, recombinant DNA technology has led to a revolution in our understanding of many aspects of basic biology. Among the advances has been the initial characterization of the structure of some HLA loci. While this will ultimately improve clinical services, constant reference to serologic data is essential so that the powerful new techniques can be applied in the most effective ways. The timing of the First Red Cross International Histocompatibility Workshop is fortunate as it brings together experts from around the world to address the state of the art. We are all grateful to Dr. John Lee and his colleagues for organizing the workshop, and for bringing together in this volume the material to be presented in Beijing during October 17-23, 1990. Leon W. Hoyer, M.D. In Silico Discovery of Novel Cytotoxic T-lymphocyte Epitopes in the HIV-1 Pol Region in Response to Antiretroviral Resistance Mutations The Acquired Immunodeciency Syndrome pandemic continues to have a large social impact. Many advances in the treatment of infection by the causative agent, Human Immunode ciency Virus, have been made in the last three decades. However, this treatment often means a life-long rigorous adherence to treatment and acquisition of resistance mutations to antiretrovirals. Thus far, the e cacy of promising vaccines has been disappointing. In the last decade, interest has grown concerning the interaction between mutations conferring resistance to antiretrovirals and the e ect this has on epitopes recognized by cytotoxic-T-lymphocytes (CTL). Investigating this is a di cult task, owing to both the extreme polymorphism of HIV and the polymorphism of the Human Leukocyte Antigen (HLA) molecules that present peptides to the CTLs. A large amount of HLA-associated CTL escape mutations have been discovered. Together with this, computational approaches in CTL epitope discovery is becoming increasingly accurate. Here, a method of imputing HLA type from patients together with predicting the in uence of anitretroviral mutations was used to discover potential epitopes for the HLA B*15 and B*48 types in the HIV-1 Subtype B pol region. HLA and Disease, An Issue of the Clinics in Laboratory Medicine** Elsevier Health Sciences **This issue of Clinics in Laboratory Medicine, edited by Drs. Julio Delgado and Eszter Lazar-Molnar, will focus on HLA and Disease. Topics include, but are not limited to, The potential**

impact of NGS in HLA and disease association studies, HLA typing by NGS, HLA Antibody Testing: Evolution and Challenges, Diversity of killer cell immunoglobulin-like receptors and disease, Technical Aspects of Crossmatching in Transplantation, HLA Markers in Celiac Disease, HLA Associations in Drug Hypersensitivity Reactions, HLA in BMT, Post-transplant monitoring, HLA epitope matching in transplantation, and Molecular Testing in Post-Transplant Monitoring. HLA and Associated Important Diseases BoD – Books on Demand **This year marks the 60th anniversary of HLA discovery by the French Nobel laureate physician Jean Dausset, as well as the 55th anniversary of the identification and naming of the first HLA. Under such circumstances, both basic HLA research and its clinical applications need a new book that comprehensively reflects the latest achievements in the field. Thus, Professor Xi as Editor has contributed to organize international experts in the areas of HLA-related basic research and clinical applications, to unite their knowledge in chapters covering various related topics, and finally to finish the book "HLA and Associated Important Diseases". The book consists of three sections which mainly include basic theoretical and technological developments, several important HLA-associated autoimmune diseases and HLA-associated infectious diseases. Umbilical Cord Blood Banking for Clinical Application and Regenerative Medicine** BoD – Books on Demand **Umbilical cord blood (UCB) and, more recently, umbilical cord tissue (UCT) have been stored cryopreserved in private and public cord blood and tissue banks worldwide, since the umbilical cord blood was used for the first time in a child with Fanconi anemia with his HLA-identical sibling, following strict guidelines that imply high-quality standards and total rastreability of these units. The hematopoietic stem cells (HSCs) are clinically used in hematopoietic treatments for blood disorders and hemato-oncological diseases. Also, the mesenchymal stem cells (MSCs) isolated from the UCT and UCB, nowadays, can be used as coadjuvants of hematopoietic transplants. In the near future, these stem cells will have a crucial role in regenerative medicine. For this reason, these cells have been tested in several clinical trials and compassive treatments in children and adults, concerning a wide range of pathologies and diseases, for instance, for the treatment of cerebral paralysis. Considering the worldwide availability of UCB and UCT units and the absence of ethical concerns will probably become the best sources for cell-based therapies for hematological and nonhematological pathologies. The UCB will also have a crucial role in neonatology-predictive analysis in the near future. HLA in Health and Disease** Academic Press **This comprehensive and definitive work succeeds and expands on the highly successful HLA and Disease published in 1994. This new edition has been updated, redesigned and reorganised into three sections making it an invaluable reference. The introductory section summarises current knowledge on the structure, function, genetics and evolution of the HLA system. It clarifies its complex and ever changing nomenclature and discusses the mechanisms underlying disease associations with HLA alleles. The second section deals with the**

importance of HLA in the context of different clinical specialities. Individual chapters describe the association between HLA polymorphism and each disease. The final section features chapters on current laboratory practice in histocompatibility and tissue typing. HLA in Health and Disease is essential reading for basic and clinical researchers working in immunology and immunogenetics, transplantation medicine and autoimmunity. It will also be of interest to anyone in the fields of rheumatology, diabetology, nephrology, allergy, dermatology, neurology, endocrinology, cancer biology, respiratory medicine, haematology, molecular biology and biochemistry. Key Features Structure, function and genetics of HLA HLA nomenclature Evolution of HLA polymorphisms HLA associations in arthritis and rheumatology, renal disease, neurology, diabetes and endocrinology, gastroenterology, respiratory disease, ophthalmology, infections, dermatology and psychiatry HLA and organ transplantation Serological and PCR-based methods in HLA typing Cellular techniques in testing histocompatibility Edited and written by an international panel of experts in the field HLA Typing Methods and Protocols Humana Press **This volume explores the rapidly evolving field of HLA typing and its use in both the laboratory setting and in silico methods. The chapters in this book discuss high-throughput methods for HLA typing; wet lab protocols; microarray data and its uses; in silico tools for the identification of HLA alleles from DNA and RNA next-generation-sequencing data, as well as HLA haplotype frequency estimation. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Cutting-edge and practical, HLA Typing: Methods and Protocols is a valuable resource for any researcher interested in learning more about this developing field. Identification and Characterization of HBV Core CTL Epitopes in Indonesian Samples Hepatitis B virus (HBV) is a non-cytopathic virus that causes liver disease with variable duration and severity. During infection, host immune response is responsible for both liver damage and viral clearance. The adaptive immune response, particularly virus-specific cytotoxic T lymphocyte (CTL) response, has been shown to play a major role in HBV infection immunopathogenesis by destroying the infected hepatocytes or eliminating HBV in a non-cytolytic manner. From virus-host interaction perspective, HBV core antigen (HBcAg) has been of interest because it is a major immunological target of CTL. Many human leucocyte antigen (HLA)-restricted HBcAg T cell epitopes have been reported which might be different due to the diverse distribution ethnic-specific HLA in distinct geographical regions. Therefore, it is important to identify and characterize HBcAg CTL epitopes in area with high HBV endemic and high population diversity like Indonesia. To support HBcAg as a promising protein to develop CTL epitope-based vaccine, HBcAg sequences of samples from individuals in Indonesia were analyzed. It was found that the sequences were conserved, and amino acid substitutions observed did not reflect**

the influence of human leucocyte antigen (HLA) types on the HBcAg variability. To develop such a vaccine, the first thing to do is to determine the peptide(s) that must be immunogenic and can interact with HLA class I proteins of Indonesian populations. Using immunoinformatic approaches, 20 HBcAg CTL epitopes (14 nonamers and 6 decamers) against HLA alleles in Javanese, Sundanese-Javanese, and T ernatean populations were identified. These 20 CTL epitopes were also characterized for sequence variation and conservation in 125 HBcAg of Indonesian isolates. Variations of HBcAg CTL epitope were detected, but one variant was found to be predominant in each epitope. By immunoinformatic analysis, different binding affinity was observed for each variant. The difference was found to depend on the location and type of amino acid in related epitope that affect its interaction with HLA binding grooves. The present study describes the use of immunoinformatic approaches as a pilot study to identify HBcAg-CTL epitopes of Indonesian isolates and analyze their conservation and variability. Of 20 CTL epitopes, HBcAg 18-27 was found the best CTL epitope for the Indonesian populations represented by the Javanese, Sundanese-Javanese, and Ternatean. Among the discovered epitope variants, residue FLPSDFFPSI was identified as the best candidate to develop peptide-based vaccine due to its predominance among all isolates studied. This study will be beneficial for developing an approach for successful viral control in hepatitis B patients. Immunobiology of HLA Volume II: Immunogenetics and Histocompatibility Springer **This set reports the results of the 10th International Histocompatibility Workshop, in which 362 laboratories collaborated over a three year period in research projects on the classification of HLA genes and their products. Volume 1 describes the experimental design of the workshop studies and their results. Volume 2 is a collection of papers on the latest developments in the molecular biology of HLA systems. Immunobiology of HLA is a valuable reference for tissue typing laboratories, blood banks, and general research programs on HLA and related diseases because it identifies common sources of HLA genes and gene products to be used as reference reagents, and because it is the only complete compilation of the latest research and results in the field. MHC Ligands and Peptide Motifs** Springer Science & Business Media **This book is centered on a comprehensive list of MHC peptide motifs and ligands as known to date, together with selected T cell epitopes, arranged in an easy-to-read fashion. This information is put into context by chapters on MHC gene organization, MHC structure, T cell epitope prediction, antigen processing and T cell responses. In addition, the book provides a great deal of complementary information: amino acid sequences of MHC class I alpha1 and alpha2 domains and of class II alpha1 and beta1 domains, the established or predicted composition and specificity of MHC pockets, notes on MHC nomenclature including old assignments and reference to useful internet addresses. A handy reference manual that should be helpful for all those dealing with MHC-associated peptides. Immunohematology: Principles and Practice** Jones & Bartlett Publishers **Immunohematology: Principles and**

Practice, Third Edition an ideal text for anyone who wants to master the theory and practices of today's blood banking. Histocompatibility Testing World Scientific **This invaluable book provides comprehensive coverage of contemporary serological, cellular and molecular methodologies in histocompatibility testing, and their application to human organ transplantation and transfusion. The contributors are internationally respected authorities in histocompatibility and immunogenetics, and are closely involved in the development or application of state-of-the-art technologies. The first three sections of the book are primarily intended for use as a bench manual for histocompatibility testers, immunologists and immunogeneticists; the fourth and fifth sections, on selection of donors and statistical methods, will further assist medical practitioners involved in clinical transplantation and its outcome. The final section of the book reviews the genetics and clinical relevance of minor histocompatibility antigens. Contents: Foreword:HLA Polymorphism: Origin and Maintenance (W F Bodmer)Introduction:Immune Recognition and the MHC (P Travers)Antibody-Based Histocompatibility Testing:HLA Typing by Alloantibodies and Monoclonal Antibodies (G M Th Schreuder)Screening for HLA-Specific Antibodies (C Brown & C Navarrete)Detection of Soluble HLA (V Rebmann & H Grosse-Wilde)Crossmatching by Lymphocytotoxicity and Flow Cytometry (S Martin & A Harmer)DNA-Based Histocompatibility Testing:PCR-SSP Typing (M Bunce)PCR-SSOP Typing (D Middleton)Sequencing-Based Typing (J Ross)DNA Conformational Analysis (J R Argüello & J A Madrigal)Microsatellite Typing (A Cambon-Thomsen et al.)On-Line HLA Sequence Alignments (G J Laundy & J L Bidwell)Cell-Based Histocompatibility Testing:Cell-Based Histocompatibility Testing (E Kaminski)Donor Selection:Allocation of Solid Organs for Transplantation (P A Dyer & S Sheldon)Selection of Haemopoietic Stem Cell Donors for Transplantation (A Green)Selection of Platelet Donors and Provision of HLA-Matched Platelets (J Harrison & C Navarrete)Statistical Methods:Population Genetics of the Human Major Histocompatibility Complex (R F Schipper et al.)Survival Analysis in Solid Organ Transplantation (P A Dyer)Survival Analysis in Bone Marrow Transplantation (S Richards)HLA and Disease Association: Statistical Considerations(J H Barrett et al.)Minor Histocompatibility Antigens:Minor Histocompatibility Antigens (E Simpson) Readership: Researchers in immunology, histopathology, cell biology and genetics, surgeons and workers in blood transfusion. Keywords:Immunology;Genetics;Immunogenetics;Transplantation;Histocompatibility;Tissue Typing;Human Leucocyte Antigens, HLA;Major Histocompatibility Complex, MHC;Laboratory Methods Core Concepts in Renal Transplantation** Springer Science & Business Media **Though kidney transplantation is considered a routine procedure, there are still significant challenges in post-transplant management. Core Concepts in Renal Transplantation is a clinically focused authoritative guide to the management of kidney transplantation. This comprehensive, state-of-the-art reference summarizes the recent changes in the field of transplantation, offering the complete range of up-to-date information**

on all the various aspects of basic immunobiology and the medical care of the transplant recipient. Written by a team of renowned authorities in renal transplantation, this concise resource is intended for both the nephrologist and the non-specialist with an interest in kidney transplantation. The Immunogenetics of Natural Killer Cell Alloreactivity [Truncated abstract] Natural killer (NK) cell alloreactivity can be exploited in haploidentical haematopoietic stem cell transplantation (HSCT) to improve graft survival, reduce graft versus host disease and decrease leukaemic relapse. NK cells lyse cells that have reduced expression of class I HLA molecules. In an allogeneic setting, donor NK cells may be activated by the absence of donor (self) class I HLA molecules on recipient cells; the absence of self-epitopes being detected by inhibitory KIR receptors on donor NK cells. The way in which genetic polymorphism of the receptors and ligands affects NK allorecognition of missing self, has not been fully elucidated. HLA-C molecules are divided into two groups, C1 and C2, with KIR2DL1 recognising cells expressing C2 and KIR2DL2 and KIR2DL3 recognising cells expressing C1. Donor NK cells expressing KIR2DL2 or KIR2DL3 can be alloreactive towards a recipient if they lack the C1 epitope and donor NK cells expressing KIR2DL1 can be alloreactive towards a recipient if they lack the C2 epitope. KIR3DL1 recognises the Bw4 epitope present on one-third of HLA-B alleles and certain HLA-A alleles. NK cells from donors expressing KIR3DL1 can be alloreactive towards recipients whose cells lack Bw4. Mismatches of KIR related HLA epitopes does not always results in NK alloreactivity. Therefore it is not possible to reliably predict NK alloreactivity based solely on the donor's HLA type and KIR repertoire and the recipient's HLA type. ... All Bw4-positive HLA-B alleles, with the exception of HLA-B*1301 and B*1302, protected targets from lysis. HLA-A*2402 and HLA-A*3201 unequivocally protected target cells from lysis whereas HLA-A*2501 and HLA-A*2301 provided only weak protection from lysis. KIR3DL1-dependent alloreactive NK clones were identified in donors whose only Bw4 positive allele was HLA-A*2402 but not in donors whose only Bw4 positive HLA allele was HLA-B*1301 or B*1302. Finally this thesis demonstrated that an activating KIR can control NK cell alloreactivity. Donors who are C2 negative and KIR2DS1 positive had NK cells that expressed the activating receptor KIR2DS1 and were capable of lysing cells expressing the C2 epitope. More so, KIR2DS1 dependent NK clones were shown to override inhibitory signals generated by NKG2A interacting with its ligand, HLA-E. The identification of these NK clones has important implications for haploidentical HSCT in that recipient expressing all three NK epitopes, C1, C2 and Bw4 were previously thought to be resistant to alloreactive NK cells controlled by inhibitory receptors. Such patients may be amenable to haploidentical HSCT from C2 negative, KIR2DS1 positive donors. These results will improve the ability to predict NK cell alloreactivity based on a donor's HLA type and KIR repertoire and the recipient s HLA type. HLA Class II Antigens A Comprehensive Review of Structure and Function Springer Science & Business Media **This volume deals with the structure and function of molecules that have, during the**

last decade, turned out to have a central role in immune responses. Trans plantation antigens were discovered and characterized by Gorer about 50 years ago, and the biological basis for the unequalled complexity of their variability between individuals within a species, in spite of extreme conservation between species, was the subject of intense research and discussion for many years. During the days of belief in "immune surveillance" against spontaneously developing tumors, it was suggested that histoincompatibility between members of one species would prevent cancer from being a contagious disease and thus a threat to the species. Immunologists involved in human transplantation had to learn and care about the complexity, especially after 1967, when it was found that HLA antigens were the products of the human MHC. Rejection of HLA-identical sib kidney grafts was so rare, even in those days, that cases of rejection were described in scientific papers. Advancing Immunopeptidomics: Validation of the Method, Improved Epitope Prediction, Peptide-based HLA Typing and Discrimination of Healthy and Malignant Tissue Weiterentwicklung Der Immunpeptidomik: Validierung Der Methode, Verbesserung Der Epitopvorhersage, Peptidbasierte HLA-Typisierung und Unterscheidung Von Gesundem und Bösartigem Gewebe The HLA Complex in Biology and Medicine A Resource Book Boydell & Brewer Ltd **A comprehensive guide to the HLA (Human Leukocyte Antigen) system for immunologists and clinicians, this book contains up-to-date information on the MHC (Major Histocompatibility Complex) and its role in the immune response and in various diseases. The book explores the biological significance and role of the HLA system in organ and haematopoietic stem cell transplantation management. This volume is an invaluable guide to the full spectrum of HLA-related science while also serving as a conceptual and technical resource for those involved in HLA-related research and in clinical or surgical practice. In addition, it will be a primary point of contact for individuals working in other areas who suddenly find that their research is drawing them into the complexities of HLA genetics. Immunogenetics: Advances and Education The First Congress of the Slovak Foundation** Springer Science & Business Media **M. BENcovA Slovak Foundation Education in Immunogenetics Kopanice 25, 821 04 Bratislava Slovak Republic Short History of Slovakia After the end of the 5th century, the major part of Central Europe was dominated by Slavs (Slovaks). They had already in the 7th century settle ments in the vicinity of towns Bratislava, Devin, Nitra to create the Slovak's state formation with the name "The Empire of Sam", territory of which corresponded to that of Slovakia of present. The Empire of Sam was also the first state formation in the Central Europe (as present states Czech Republic, Poland, Hungary, Slovakia etc.) Very important town of this state was Nitra, with the biggest Castle in the Central Europe with his Duke Pribina. The first Church of the Central Europe was built here in the year 830, and it is now considered to be the "Slovak Bethlehem". In the year 880, Nitra also became the first Office of Bishops. Later, the Slovak Duke Pribina and Moravian Duke Mojmir (Moravia corresponded to eastern part of the present Czech Republic)**

joined their formations to common state "Greate Moravian Empire". The strongest King of the Great Moravian Empire was Svatopluk (864 A. D.), who spread his empire over Czech Republic, Hungary and part of Poland, Ukraine and eastern Germany of present, which at that time still did not exist as state formations. A Novel HLA–DRB1*10:01–Restricted T Cell Epitope From Citrullinated Type II Collagen Relevant to Rheumatoid Arthritis Histocompatibility Testing 1984 Report on the Ninth International Histocompatibility Workshop and Conference Held in Munich, West Germany, May 6–11, 1984 and in Vienna, Austria, May 13–15, 1984 Springer Science & Business Media **Epitope Discovery and Synthetic Vaccine Design** Frontiers Media SA **Immune Regulation** Springer Science & Business Media **Leukocyte culture conferences have a long pedigree. This volume records some of the scientific highlights of the 16th such annual con ference, and is a witness to the continuing evolution and popularity of leukocyte culture and of immunology. There is strong evidence of the widening horizons of immunology, both technically, with the obviously major impact of molecular biology into our understanding of cellular processes, and also conceptually. Traditionally, the 'proceedings' of these conferences have been published. But have the books produced really recorded the major part of the conference, the informal, friendly, but intense and some times heated exchanges that take place between workers in tackling very similar problems and systems and which are at the heart of every successful conference? Unfortunately this essence cannot be incorpo rated by soliciting manuscripts. For this reason, we have changed the format of publication, retaining published versions of the symposium papers, but requesting the workshop chairmen to produce a summary of the major new observations and areas of controversy highlighted in their sessions, as a vehicle for defining current areas of interest and debate. Not an easy task, as the workshop topics were culled from the abstracts submitted by the participants, rather than being on predefined topics. The unseasonal warmth in Cambridge was reflected in the atmos phere of the conference, the organization of which benefited from the administrative skills of Jean Bacon, Philippa Wells, Mr. Peter Irving, and Mrs. HIV Molecular Immunology Mlc-typing in man-hl Blood Banking and Transfusion Medicine Basic Principles & Practice** Elsevier Health Sciences **Ever since the discovery of blood types early in the last century, transfusion medicine has evolved at a breakneck pace. This second edition of Blood Banking and Transfusion Medicine is exactly what you need to keep up. It combines scientific foundations with today's most practical approaches to the specialty. From blood collection and storage to testing and transfusing blood components, and finally cellular engineering, you'll find coverage here that's second to none. New advances in molecular genetics and the scientific mechanisms underlying the field are also covered, with an emphasis on the clinical implications for treatment. Whether you're new to the field or an old pro, this book belongs in your reference library. Integrates scientific foundations with clinical relevance to more clearly explain the science and its application to clinical practice.**

Highlights advances in the use of blood products and new methods of disease treatment while providing the most up-to-date information on these fast-moving topics Discusses current clinical controversies, providing an arena for the discussion of sensitive topics. Covers the constantly changing approaches to stem cell transplantation and brings you the latest information on this controversial topic. HLA and Disease Associations Springer Science & Business Media **The human leukocyte antigen (HLA) or tissue types are the products of a rapidly developing field of knowledge within the last 20 years. In the early stages of the research many investigators suspected the existence of a complex series of transplantation antigens, but it was widely believed that these antigens would not be well-defined even in this century. Yet in the last two decades as many as 124 different HLA antigens determined by at least 7 very closely linked genes located on the short arm of chromosome 6 have been identified and subsequently agreed upon by an international nomenclature committee. 1 Extensive international collaboration fueled by the potential clinical application of these antigens to clinical transplantation has advanced the field rapidly. There were nine inter national histocompatibility workshops held during this period. Although iden tification of HLA antigens was of primary clinical importance in transplantation 2 and of great basic interest in human genetics and anthropology, a rather un expected bonus has been the determination that HLA antigens are associated with disease susceptibility to a greater extent than any other known genetic marker in man. In the past, many genetic polymorphisms have been suspected to be associated with diseases. The most extensively studied markers are blood groups, enzymes, and serum proteins. A comprehensive account of published studies, totalling approximately 1,000, of these markers is available in a book by Mourant et al. HIV Immunology and HIV SIV Vaccine Databases 2003** DIANE Publishing **Henry's Clinical Diagnosis and Management by Laboratory Methods: First South Asia Edition_e-Book** Elsevier India **To interpret the laboratory results. To distinguish the normal from the abnormal and to understand the merits and demerits of the assays under study. The book attempts to train a laboratory medicine student to achieve sound knowledge of analytical methods and quality control practices, to interpret the laboratory results, to distinguish the normal from the abnormal and to understand the merits and demerits of the assays under study. P53 Immune Response in Breast Cancer Patients: Assessment of CTL Recognizing the HLA-A2.1 Restricted, Wild-Type Sequence P53 264-272 Epitope Approximately 30% of breast cancer patients are p53 sero-positive and have detectable anti-p53 T cell proliferative responses. Tumors expressing mutant p53 molecules have an enhanced potential to present wild- type-sequence (wt) p53 epitopes derived from mutant p53 for T-cell recognition. Vaccines targeting these epitopes would be broadly applicable. HLA-A2.l-restricted CTL-recognizing wt P53 264-272 and 149-157 peptides have been generated from PBMC obtained from healthy donors and/or oral cancer patients. A subset of these donors were found to be non-responsive to the P53**

264-272 peptide, and altered peptide ligands of this epitope were identified that induced CTL from PBMC that were non-responsive to the parental peptide. Currently, precursor CTL (pCTL) for the P53 264-272 epitope present in unstimulated PBMC can be identified by 4-color flow cytometry using soluble PE-conjugated HLA-AO2Ol/p53 peptide tetrameric complexes (tetramers). An analysis of anti-p53 pCTL in the peripheral circulation and tumors of breast cancer patients was done with tetramers for the wt P53 264-272 and 149-157 peptides. An analysis of genomic p53 exons 5-8 of the patients' tumors, when available, was also performed. The results of this study provide a basis for further investigation of the anti-p53 responses of breast cancer patients and will facilitate p53-based immunotherapy of breast cancer. Current Issues and Future Direction in Kidney Transplantation BoD – Books on Demand **The here presented book covers different areas of clinical and scientific interest, reaching from donor evaluation to newest methods in immunological diagnostics. But also aspects of daily care of transplant recipients can be found in the carefully selected chapters. Everything driven by the aim to improve the care for all of our transplanted patients. Immunoinformatics** Springer Science & Business Media **In contrast to existing books on immunoinformatics, this volume presents a cross-section of immunoinformatics research. The contributions highlight the interdisciplinary nature of the field and how collaborative efforts among bioinformaticians and bench scientists result in innovative strategies for understanding the immune system. Immunoinformatics is ideal for scientists and students in immunology, bioinformatics, microbiology, and many other disciplines. History of HLA Ten Recollections** UCLA Immunogenetics Center **P53 Immune Responses in Breast Cancer Patients: Assessment of CTL Recognizing the HLA-A2.1 Restricted, Wild-type Sequence P53 (264-272) Epitope; Frequencies of Tetramer+ T Cells Specific for the Wild-Type Sequence P53 (264-272) Peptide in the Circulation of Patients with Head and Neck Cancer; The Ability of Variant Peptides to Reverse the Nonresponsiveness of T Lymphocytes to the Wild-Type Sequence P53 (264-272) Epitope This document contains three papers focusing on the analysis of anti-p53 cellular immune responses of breast, head, neck, and oral cancer patients. The research was undertaken to provide insights into the potential of p53-based vaccines for immunotherapy of these cancers. The first paper, by Albert B. DeLeo, is entitled "p53 Immune Responses in Breast Cancer Patients: Assessment of CTL Recognizing the HLA-A2.1 Restricted, Wild-type Sequence p53 (264-272) Epitope." In this study, methodologies were developed to detect anti-wild-type p53 CD8+ and CD4+ T-cells present in the peripheral circulation and tumor infiltrating lymphocytes (TILs) obtained from cancer patients by flow cytometry analysis using soluble HLA/peptide tetramers. In the second paper, "Frequencies of Tetramer + T Cells Specific for the Wild-Type Sequence p53 (264-272) Peptide in the Circulation of Patients with Head and Neck Cancer," by Thomas K. Hoffmann, et al. (Cancer Research v62 p3521-3529, June 15 2002), frequencies of wild-type p53 (264-272) peptide-specific CD8+ T cells were determined in**

the peripheral circulation of patients with squamous cell carcinoma of the head and neck (SCCHN). T cells of 30 HLA-A2.1+ patients and 31 HLA-A2.1+ healthy individuals were evaluated by multicolor flow cytometry analysis using peptide HLA-A2.1 complexes (tetramers). The third study, "The Ability of Variant Peptides to Reverse the Nonresponsiveness of T Lymphocytes to the Wild-Type Sequence p53 (264-272) Epitope," by Thomas K. Hoffmann et al. (Journal of Immunology v168 p1338-1347, 2002), sought to increase the responsive rate to the wild-type p53 (264-272) peptide of peripheral blood mononuclear cells (PBMC) obtained from normal donors and patients by identifying more immunogenic variants of this peptide. Two such variants were generated by amino acid exchanges at positions 6 (6T) and 7 (7W) of the peptide. The 7W variant peptide has potential for immunotherapy of nonresponsive oral cancer patients. Janeway's Immunobiology Garland Science **The Janeway's Immunobiology CD-ROM, Immunobiology Interactive, is included with each book, and can be purchased separately. It contains animations and videos with voiceover narration, as well as the figures from the text for presentation purposes. Immunological Responses to Fungal Epitope Peptides Introduction: Fungi are common aeroallergens responsible for at least 3% - 10% of allergic diseases worldwide, with the proportion hugely variable in different populations. Treatment is complicated by viable nature and disease causing ability of the allergen and is often only palliative. Thus, this study aimed to serve as a pilot investigation to design novel anti-allergy therapeutics to cure allergy at the molecular level. It investigates the effect of wild type fungal peptides and corresponding variant peptides on allergy associated immunological responses - cellular and cytokine based - to use such variant peptides to cause the delicate shift from an allergic to a normal immune response. Further, the study explores the role of bioinformatics in investigating allergy and designing novel therapeutics. Methods: This study used ProPred, a bioinformatics software, to predict wild type peptides from selected allergens of Aspergillus fumigatus and Alternata alternaria for a target population. These were then modified to generate single amino acid variants. Both these peptide sets were tested to compare the cellular and cytokine patterns they generated in sensitised (n = 3) and healthy volunteers (n = 3) to check for anti-allergy responses that may be exerted by certain variants. The recruited population was also subjected to skin prick testing (SPT, n = 46) to check for co-sensitisations patterns and HLA typing (n = 40) to evaluate ProPred accuracy for peptide prediction. This study also attempted an in silico search for unknown Penicillium chrysogenum allergens by comparing known Penicillium and A. fumigatus allergens to identify probable agents of co-sensitization. Results: Of the wild type and variant peptides tested in this study, one variant peptide - peptide 1.1v from Asp f 2 - was successfully identified to change the cellular and cytokine profile to promote an anti-allergic response when compared to its corresponding wild type form (1.1o). This candidate is a good target for further investigation for use in peptide immunotherapy. Further, 8 shared allergens**

between A. fumigatus and P. chrysogenum were identified that may possibly be agents of co-sensitization between these species. SPT results indicated maximum subject co-sensitization between A. fumigatus and Candida albicans and P. chrysogenum. HLA typing results demonstrated the efficiency of ProPred to be 96.29%, thus implying that bioinformatics can effectively be used to study allergy in this novel manner. Conclusion: This study has demonstrated that variant peptides with a single amino acid change can cause the delicate shift from an allergic to a healthy immune response in sensitised subjects. This approach - in combination with other allergy associated factors such as epitope specificity for HLA types and inherent co-sensitization patterns in a population - can effectively be used to design peptide candidates for immunotherapy to target allergy at the molecular level. With promising results obtained in this pilot study, this approach guarantees further investigation in immunotherapy. This study has also demonstrated that bioinformatics can be effectively used to design and execute allergy studies in a targeted and inexpensive manner. Evaluation of Peptide Based Vaccines and Inhibitors to Prevent the Onset of HTLV-1 Associated Diseases Abstract: HTLV-1 is the etiologic agent of ATL, HAM/TSP, as well as other inflammatory disorders. In the absence of a prophylactic vaccine for HTLV-1 or effective treatment for HAM/TSP, three peptide based strategies were evaluated. Prophylactic vaccination was evaluated using two B-cell epitope immunogens derived from the envelope glycoprotein in squirrel monkeys. Protective efficacy of the peptides could not be adequately evaluated because all monkeys spontaneously resolved the challenge with EVO/1540 cells. The stronger the cytolytic response against HTLV-1, the less likely one is to develop HAM/TSP. To increase the cytolytic responses of HTLV-1 infected individuals, computer algorithms were used to identify HLA-A*0201 restricted peptides from Gag, Tax, and Pol proteins. Peptides with optimal anchor residues were synthesized as wild-type epitopes, but peptides with suboptimal anchor residues were synthesized along with epitope enhanced mutants that possessed optimal anchor residues. Enhanced mutants increased cytolytic responses against the wild-type epitope, but were unable to lyse an HLA-A*0201 positive, HTLV-1 infected cell line. These results suggest that the Tax 11-19 epitope may be the only relevant HLA-A*0201 restricted epitope for vaccination. HAM/TSP patients generally have an elevated provirus load, which may contribute to disease. To limit cell-to-cell transmission of virus, peptide fusion inhibitors were evaluated for their ability to inhibit HTLV-1-mediated syncytia. Strategies employed included the use of L-amino acid and retro-inverso peptides form the P400 and P197 regions of Env. This dissertation shows three different peptide based approaches that could be used to combat various aspects of HTLV-1 and associated diseases.