HLA ABDR EPLET MISMATCH ANALYSIS FOR DONOR SELECTION IN RENAL TRANSPLANTATION - A COHORT STUDY

Thesis submitted to the
University of Calicut in partial fulfilment of
the requirement for the award of

DOCTOR OF PHILOSOPHY IN BIOTECHNOLOGY

By
NIDHEESH ROY T. A

DEPARTMENT OF BIOTECHNOLOGY
UNIVERSITY OF CALICUT
KERALA, INDIA
JUNE 2022

Dr. K. K. Elyas
Professor
Department of Biotechnology
University of Calicut

CERTIFICATE

This is to certify that the thesis entitled "HLA ABDR eplet mismatch analysis for donor selection in renal transplantation - A cohort study" submitted to the University of Calicut, as a part of fulfillment of Ph.D. program for the award of the degree of Doctor of Philosophy in Biotechnology by Mr. Nidheesh Roy T. A., embodies the results of bonafide research work carried out by him under my supervision and guidance in the Department of Biotechnology, and the thesis has not previously formed the basis for the award of any degrees, diploma, associateship or other similar title or recognition.

University of Calicut

Prof. Dr. K. K. Elyas
Research Supervisor

Dr. K. K. Elyas
Professor
Department of Biotechnology
University of Calicut

CERTIFICATE

This is to certify that all the suggestions and corrections from the adjudicators have been incorporated in the thesis entitled "HLA ABDR eplet mismatch analysis for donor selection in renal transplantation - A cohort study" submitted by Mr. Nidheesh Roy T. A.

University of Calicut

Prof. Dr. K. K. Elyas
Research Supervisor

DECLARATION

I hereby declare that the work presented in this thesis entitled "HLA ABDR eplet mismatch analysis for donor selection in renal transplantation - A cohort study" submitted to the University of Calicut, as partial fulfillment of Ph.D. program for the award of degree of Doctor of Philosophy in Biotechnology is original and carried out by me under the supervision of Dr. K. K. Elyas, Professor, Department of Biotechnology, University of Calicut. This has not been submitted earlier either in part or in full for any degree or diploma of any university.

University of Calicut

Nidheesh Roy T. A

ACKNOWLEDGEMENTS

I am indebted to numerous persons from the beginning of this work and without all that timely help I sincerely believe that I could not have completed this work.

I accord my profound gratitude to my research supervisor Prof. (Dr.) K. K. Elyas., for giving me the chance that I deserved, for the positive arguments and the criticisms, for always telling me to read, for introducing me to a new world of transplantation immunology, for being a good friend during our one-of a kind half-way trip around the world and for the assiduous efforts to bring out the work to this present form.

I am very happy to thank Dr. Feroz Aziz, M. D., MIMS Hospital, Calicut, for his support, kindness, friendliness and for lending me your hand into the world of clinical studies. I admire the way you take care of your patients. I love the doctor in you who cares deeply for his patients. Without your support the field of transplantation immunology might have been a nightmare for me.

I am deeply indebted to my former research guide, Dr. Sailas Benjamin (late), Professor, Department of Botany, University of Calicut, for advising me that I'm not good in wet-lab research rather I should focus on bioinformatics or docking studies, which hurt my ego very bad, but here I am submitting a whole thesis which completely emphasis bioinformatics and protein docking. I am sorry I judged your intelligence. I hope that you rest in peace dear sir.

I gratefully extend my sincere thanks to Prof. (Dr.) P. R. Manish Kumar (Rtd.), Dr. C. Gopinathan (Associate Prof.) and Dr. Smitha V. B., (Asst. Prof.), and all other staffs of Department of Biotechnology and all teaching staffs of Department of Botany and Prof. (Dr.) Abraham Joseph, Department of Chemistry for providing needful help during the research period.

I am grateful to extent my sincere thanks to the former Heads of Department of Botany, Prof. K. Jayaram and Prof. John E. Thoppil., University of Calicut for their whole-hearted help offered in the department during my research period.

I would like to acknowledge the financial support provided by the University Grants Commission, Government of India for granting Rajiv Gandhi National Fellowship for conducting my research work.

I would like to acknowledge Malabar Institute of Medical Sciences, Calicut, India and IQRAA International Hospital & Research Center, Calicut, India for supporting my research work through institutional collaboration.

I would like to acknowledge, Central Sophisticated Instrument Facility (CSIF), University of Calicut for providing the computational facility for conducting my research work.

I am very much thankful to Prof. (Dr.) Mohankumar Chinnamma, for helping me find and inspire the student in me, and for being the best teacher I know, Dr. Salini Bhasker, Scientist, for her immense support and appreciation during the last decade.

I would like to acknowledge Dr. Ramesh (Rtd.) Statistician, Rubber Board, Kottayam and Mr. Praveen., Department of Statistics, University of Calicut for the assistance provided in statistical studies.

I express my sincere gratitude to all my lab-mates and other research scholars of Department of Biotechnology, University of Calicut, for being friendly and suggestive. I am very much thankful to Dr. Anusha T. S., for being there for me and my family.

I convey my heart-felt appreciation to the M. Sc students, '18 - '20 batch, of Department of Biotechnology, University of Calicut, especially Ms. Nivedhya Venas and Ms. C. Sri Charani for completing a good project together as well as for finding a good friend in me.

I convey my genuine thankfulness to my former lab-mates of Enzyme Technology Laboratory, Department of Botany, University of Calicut and all the research scholars of the department for being a good friend to me.

I express my heartfelt gratitude to all my friends in the University, especially Dr. Hareesh E. S., for accepting me the way I am and Dr. Abdul Faisal., for supporting me when I was in need.

I sincerely thank Dr. Resmi S., who's involvement triggered a series of events which eventually lead to me getting invited as the Speaker for 9th World Congress on Immunology and for her sincere support and assistance during the final correction of my thesis.

I express my sincere appreciation to my dear friend, Mr. Bins K. C., who gave me sincere moral support during my post-graduation period as well as all those other times I was in need.

I am grateful to extent my sincere thanks to Ms. Drisya Pedangal., Mr. Ginil Benny and Dr. Vipin Viswanath, TIMD Laboratory, MIMS Hospital, Calicut for sharing their knowledge, expertise, and support during the entire course of my study.

I take this opportunity to thank Mr. Arjun Murali, Mr. Sanal Iqbal and Mr. Vysakh M. S., for their great support during my research period. I would like to specially mention the data analytical assistance provided by Mr. Arjun Murali, during the final period of the study.

The last few years were not easy, thank you Mr. Mohammed Niyas T. T., for talking the stress out of me. Mr. Mohammed Nishan T. T., thank you walking and laughing with me through this tough period. I'm happy that we are who we are, and I hope that it stays the same.

I would like to acknowledge Mr. Akhil (Kannan), my childhood friend, for all his support during these years.

Words cannot adequately express my deep sense gratitude to my family which literately started to fall apart the time I joined for Ph. D. I would like to express my deepest sentiments to my father, Mr. Trikaroyoor Asokan who passed away in an accident on 14th Feb 2015. You will always be remembered because of all the lessons you taught me. To my mother, Mrs. Rita Rugmini, who gave me the hardest time ever, because I was passionate in scientific research and not LDC.

I would like to express my gratitude towards my parents in law and their family for their timely advices and support.

I wish not to formally thank my wife Julia Garvasis and our daughter Layla Ayden, because they haven't finished what they have started; finding the best in me.

I cannot find words to express my love and affection towards my dear dearest, Bailey, who stood for me, aside me and in front of me during the most stressful 27 months in my entire life. I could have never passed that period if it wasn't for you. You taught me what unconditional love is. You taught me when to be patient. You even showed me whom to trust other than myself. Every moment that we had together from the day that I got you, I will consider those not less than anything happened in my life until my last breath. I will and could never forget how bad it hurt you, both physically and mentally, in the last moments of your demise. I strongly believe that you are the best choice I took in my life besides marrying my love. You will stay remembered until my death my good boy, always! When Layla gets to an age where she starts asking questions, you will be the one she misses the most.

Above all these, I owe to the God residing within my human body for making me highly passionate and imaginative, for aiding me in the highest level with which I was able to decode the clue and discover the relation between quantum entanglement and cosmic consciousness with human mind; for making me a good researcher, for enabling me to take the right decisions, for providing enough strength and health while dealing with the tragic situations that I've faced during the pre- and post-lockdown periods occurred as a result of COVID-19 pandemic, for teaching me what patience actually is, for making me understand that the true form of love exists in animals but not in humans, and for all the resources that I needed for successfully completing this research work.

And, I consider this as my worthy chance to express my utmost respect to,
'the matter' that sustains and 'the energy' that balances
the existence of everything in this universe,
for giving me all the second chances.

- NIDHEESH ROY TRIKARIYOOR ASOKAN

Dedicated to

Me; **existing in the parallel universe among the billion other universes, for showing me everything that already happened; Déjà vu.**

Me; **existing in the future, who will not regret this as it is.**

Me; **existed in the past, for surviving everything.**

CONTENTS

ANNEXURES

Annexure I	Table 38
Annexure II	Table 39
Annexure III	Figures 26 - 33
Annexure IV	Tables 40 - 42
Annexure V	Figures 34 a-h
Annexure VI	Tables 43 - 58
Annexure VII	Tables 59 - 73
Annexure VIII	Table 74
Annexure IX	Figures 35 - 51

LIST OF TABLES

Annexure VI

Annexure VII

Table 63: HLA DRB-1sje complex (having highest ΔG values within the 10 complexes) with TCR 2xna.

Table 64: HLA DRB-1aqd complex (having highest ΔG values within the 10 complexes) with TCR 3of6.

Table 65: HLA DRB-1dlh complex (having highest ΔG values within the 10 complexes) with TCR 3of6.

Table 66: HLA DRB-1kg0 complex (having highest ΔG values within the 10 complexes) with TCR 3of6.

Table 67: HLA DRB-1h15 complex (having highest ΔG values within the 10 complexes) with TCR 3of6.

Table 68: HLA DRB-1sje complex (having highest ΔG values within the 10 complexes) with TCR 3of6.

Table 69: HLA DRB-1aqd complex (having highest ΔG values within the 10 complexes) with TCR 4udu.

Table 70: HLA DRB-1dlh complex (having highest ΔG values within the 10 complexes) with TCR 4udu.

Table 71: HLA DRB-1kg0 complex (having highest ΔG values within the 10 complexes) with TCR 4udu.

Table 72: HLA DRB-1h15 complex (having highest ΔG values within the 10 complexes) with TCR 4udu.

Table 73: HLA DRB-1sje complex (having highest ΔG values within the 10 complexes) with TCR 4udu.

Annexure VIII

Table 74: Patient and donor HLA ABDR allele pair which faced graft rejection

LIST OF FIGURES

Annexure V

Figure 34: Ramachandran plot obtained for 8 modelled class II HLA DRB structures using SWISS MODEL.

Annexure IX

Figure 35: 3D structure complexes between HLA DRB1*01 with a) 1a6a CLIP and b) 4x5w CLIP

Figure 36: 3D structure complexes between HLA DRB1*04 with a) 1a6a CLIP and b) 4x5w CLIP

Figure 37: 3D structure complexes between HLA DRB1*07 with a) 1a6a CLIP and b) 4x5w CLIP

Figure 38: 3D structure complexes between HLA DRB1*08 with a) 1a6a CLIP and b) 4x5w CLIP

Figure 39: 3D structure complexes between HLA DRB1*09 with a) 1a6a CLIP and b) 4x5w CLIP

Figure 40: 3D structure complexes between HLA DRB1*12 with a) 1a6a CLIP and b) 4x5w CLIP

Figure 41: 3D structure complexes between HLA DRB1*14 with a) 1a6a CLIP and b) 4x5w CLIP

Figure 42: 3D structure complexes between HLA DRB1*16 with a) 1a6a CLIP and b) 4x5w CLIP

Figure 43: 3D structure complex, between HLA DRB1*01 with 5 antigen peptides

Figure 44: 3D structure complex, between HLA DRB1*04 with 5 antigen peptides

Figure 45: 3D structure complex, between HLA DRB1*07 with 5 antigen peptides

Figure 46: 3D structure complex, between HLA DRB1*08 with 5 antigen peptides

Figure 47: 3D structure complex, between HLA DRB1*09 with 5 antigen peptides

Figure 48: 3D structure complex, between HLA DRB1*12 with 5 antigen peptides

Figure 49: 3D structure complex, between HLA DRB1*14 with 5 antigen peptides

Figure 50: 3D structure complex, between HLA DRB1*16 with 5 antigen peptides

Figure 51: 3D structure complex, between HLA-Ag with TCR

ABBREVIATIONS

ΔG	-	Gibbs free energy
Å	-	Angstrom
AHG	-	anti-human globulin
ALS	-	anti-lymphocytic serum
AMR	-	antibody-mediated rejection
APC	-	antigen presenting cell
ATG	-	anti-thymocyte globulin
B2M	-	beta 2 microglobulin
CBD	-	chronic beryllium disease
CD	-	cluster of differentiation
CDC	-	complement dependent cell cytotoxicity
CLIP	-	class II-associated invariant chain peptide
CMV	-	Cytomegalo virus
CTL	-	cytotoxic T lymphocytes
CXM	-	crossmatching
DCD	-	donation after circulatory death
DGGE	-	denaturing gradient gel electrophoresis
dNTPs	-	dideoxy nucleotide tri phosphates
DSA	-	donor-specific antigen
DSAb	-	donor-specific antibodies
EMBL	-	European Molecular Biology Laboratory
EMMA	-	Epitope MisMatch Algorithm
ER	-	endoplasmic reticulum
ERAP	-	ER aminopeptidase

FCXM	-	flow cytometry crossmatch
GODT	-	Global Database on Donation and Transplantation
GVHD	-	graft vs host disease
HDA	-	hetero-duplex analysis
HLA	-	Human Leuocyte Antigen
ICs	-	Interatomic or interfacial contacts
IEDB	-	Immune Epitope Database
IgA	-	immunoglobulin A
IgG	-	immunoglobulin G
IgM	-	immunoglobulin M
IMGT	-	international IMmunoGeneTics information
K_d	-	Dissociation constant
kDa	-	kilodalton
MHC	-	Major Histocompatibility Complex
MICA	-	Major histocompatibility complex class I Chain-related gene A antigen
MLC	-	mixed lymphocyte culture
NCBI	-	National Center for Bioinformatic Information
NCFHS	-	Nomenclature Committee for Factors of the HLA System
NGS	-	Next Generation Sequencing
NIH	-	National Institute of Health
NIS	-	non-interacting surface
NLM	-	National Library of Medicine
PCR	-	polymerase chain reaction
PDB	-	Protein Data Bank
PLC	-	peptide-loading complex

PRODIGY	-	PROtein binDIng enerGY
RCSB	-	Research Collaboratory for Structural Bioinformatics
SBT	-	sequence-based typing
SNP	-	single nucleotide polymorphism
SOT	-	solid organ transplantation
SSCP	-	single strand conformational polymorphisms
SSOP	-	sequence-specific oligonucleotide probes
SSP	-	sequence specific primer
T regs	-	T regulatory cells
TAP	-	trypsinogen activation peptide
TCR	-	T-cell receptor
TG	-	Transplant glomerulopathy
TGGE	-	temperature-gradient gel electrophoresis
Th	-	T helper cells
WHO	-	World Health Organization
WHONC	-	World Health Organization Nomenclature Committee
WMDA	-	World Marrow Donation Association
wwPDB	-	Worldwide Protein Data Bank

Preface

Transplantation immuno-biology being very complex, involves antigens, antibodies, antigen presenting cells, helper and cytotoxic T cells, signalling molecules and mechanisms, cytokines, complements, etc. The possibility of not having a graft rejection by exclusively avoiding this trail of immune processes has been elusive. Developments such as anti-lymphocytic serum (ALS), antibody screening, HLA typing, and organ preservation have led to the further improvement in the success of transplantation. This in fact implies the importance of HLA in transplantation immunology. The major histocompatibility complex (MHC) or human leukocyte antigen (HLA) genes were formerly understood as molecules that induce antigenic response in a host tissue against the donor after transplantation. Being highly polymorphic in nature HLA has been known for its complexity as well as its identity in becoming a protein fingerprint of an individual. The HLA contains more than 200 genes and spans 4 megabases situated on chromosome number 6. Among the genes within the HLA are more than 20 loci encoding proteins involved in binding and presentation of the peptide degradation products of proteins to the T cell receptor (TCR). All tissues that express proteins on their surface can initiate an immune response. For successfully performing a transplantation procedure these transplantation antigens should be compatible. Transplantation antigens determine the possibility of rejection when grafted between two genetically different individuals. HLA complex is one such complex gene set which plays a strong role in transplantation. HLA itself being an antigen poses the major risk in transplantation. In recent reports, backing up to a decade, the concept of epitope matching has been further studied and resulted in the identification of eplets - a set of spatially arranged so-called triplet of amino acids which exists when HLA is viewed as a string of amino acid. Eplets represent the key elements of an epitope that elicit specific antibodies.

The present study entitled 'HLA ABDR eplet mismatch analysis for donor selection in renal transplantation - A cohort study' has been focused to ascertain an ideal strategy for selecting unrelated individuals as potential donors for renal

transplantation by analyzing the number of eplet mismatches and structural variations, that everyone possesses, thus eliminating the possibility of an undesired immune reaction observed in our population.

The thesis begins with 1. Introduction, which emphasis on the history and fundamentals of solid organ transplantation. It describes the discovery of HLA and the downstream hurdles faced by clinicians in successfully performing human renal transplantation. The section also gives a brief idea on the discovery of epitope-based matching and the concept of HLA eplets. 2. Review of literature covers, in detail, the structure, classification of HLA, polymorphism in HLA and the role of HLA in antigen presentation. The section also deals with the experimental milestones accomplished for better understanding on donor selection for renal transplantation. The unexplored role of computational biology in transplantation immunology has been detailed towards the end of the review. The 3rd section of the thesis, Materials and methods, lists out the clinical as well as immunoinformatical investigations adapted in the study. The study was conducted from a cohort of 1144 transplant patients and donors (n = 572 pair). Data collection, which includes CDC-cxm between patients and donor and HLA ID of both patients-donor, has been carried out from the Transplantation Immunology and Molecular Diagnostic Laboratory, Department of Nephrology, MIMS Hospital, Calicut, India. The data collection was initiated after receiving approval (IEC Reg. No. ECR/01/inst/KL/2013) for data collection from the institute. Section 4. Results and, 5. Discussions, displays the outcomes and the analysis of the outcomes respectively. 6. Summary & conclusions embodies the essence of the study. The thesis ends with 7. Recommendation for future studies, which can explore the fascinating world of transplantation immunology through the perspective of human T cell receptor, using the aid of immunoinformatical simulations.

1. INTRODUCTION

Until late 30s most of the medical practitioners presided over lethal diseases by the application of 'rear guard strategy'. The treatment for a failed organ such as kidney, liver or heart was diet, medicines, or illogically designed surgeries. These were the only ideal approaches for treating such chronic disease conditions. The early experimental success in transplantation has thus given hope in addressing problems with such life-threatening diseases (Starzl, 1988). Transplantation or grafting is a medical procedure of transfer of living cells, tissue or organ from the body of a donor into the body of the recipient for the purpose of replacing or repairing damaged or non-functional tissues or organs. The kidney is the first organ to be transplanted successfully in humans (Levin et al., 2008). Alongside with the importance and use of antibiotics and immunosuppressants, organ transplantation gained its credit within a short period of time. The advancements in the field of transplantation immunology have immensely grown within the next two decades. Organ transplantation has been considered a miracle since then. The idea of transplantation became possible after the development of the concept of vascular anastomosis and suture techniques by Alexis Carrel, Mathieu Jaboulay, and Julius Dorfler (Black et al., 2018, Watson & Dark, 2012). Using this concept Alexis Carrel described the first kidney auto transplants in dogs and xenograft transplantation from dogs to goat (Ullman, 1914). Jaboulay later in 1906 performed first renal xeno-transplants in humans using pig and goat as donors. The first systematic study of transplantation was reported by Alexis Carrel in 1908, where he interchanged both kidneys in a series of cats and measured the urinary output (Merrill et al., 1956).

Transplantation immuno-biology being very complex, involving antigens, antibodies, antigen presenting cells, helper, and cytotoxic T cells, signaling molecules and mechanisms, cytokines, complements, etc., and so avoiding rejection has been elusive. Developments such as anti-lymphocytic serum (ALS), antibody screening, HLA typing, and organ preservation led to further improvement in the success of transplantation (Black et al., 2018).

The major histocompatibility complex (MHC) or human leukocyte antigen (HLA) genes were formerly understood as molecules that induce antigenic response in a host tissue against the donor after transplantation, also called as transplantation antigens. Being highly polymorphic in nature HLA has been known for its complexity as well as its identity in becoming a protein fingerprint of an individual. The HLA contains more than 200 genes and spans 4 megabases situated on chromosome number 6. Among the genes within the HLA are more than 20 loci encoding proteins involved in binding and presentation of the peptide, the degradation products of proteins, to the T cell receptor (TCR) (Williams, 2001). This in fact implies the importance of HLA in transplantation immunology. The response towards an allograft has always been genetically controlled (Morris et al., 1987). The antigen's involvement in transplantation immunology has been an interesting as well as a debatable topic for over five decades. HLA-encoded proteins can be categorized into three classes, I, II and III (Hood et al., 1983). The mechanism of allorecognition by the adaptive immune system via the recruitment of allo-specific T cells which causes allo-response is as the result of class I and class II HLA; and HLA class III codes for complement proteins (Afzali et al., 2008).

All tissues that express proteins on their surface are capable of initiating an immune response. For successfully performing a transplantation procedure these transplantation antigens should be compatible. Transplantation antigens determine the possibility of rejection when grafted between two genetically different individuals. HLA complex is one such complex gene set which plays a strong role in transplantation. It has been demonstrated that the influence of transplantation antigens in determining the survival of renal graft is stronger for HLA DR matching (Morris et al., 1987).

An important aspect of donor selection for a successful renal transplantation relies on the percentage level of HLA match between the donor and the recipient. Other parameters such as age, blood group, pre-transplant blood transfusions, percentage of reaction in complement-dependent cytotoxicity crossmatching (CDC-cxm) and sensitization of the patient also influence overall success of the graft to a variable degree. The process of donor selection follows two major aspects in transplantation

immunology, CDC-cxm and molecular HLA typing. CDC-cxm identifies the presence of preformed antibody and HLA typing identifies the individual alleles of both patient and donor for allelic matching. Until the twentieth century there was no detailed report on the idea that grafts might fail (Barker and Markmann, 2013). Patients with preformed or donor-specific antibody (DSAb) showed a high degree of allograft failure (Worthington et al., 2013). The presence of such pre-formed antibodies will lead to hyper-acute reaction in the recipient's body. The presence of preformed antibody is found out via CDC-cxm which gives visual confirmation on cell lysis by complements in the presence of antibodies. HLA typing is usually done via two molecular methods, SSP- (sequence specific primer) and SSOP- (sequence specific oligonucleotide probes) PCR. The method allows us to identify the HLA allele specific to each individual via primers designed specifically to amplify class I, HLA ABC and class II, HLA DPDQDR.

It was in the late 50s that a series of scientific discoveries identified and resolved the fact that antibody-mediated immunity (AMR) is the cornerstone of human immunity. AMR or humoral immunity solely depends on the epitopes to which the antibody has been produced against. Epitope or antigenic determinants are portions of a foreign antigen which interacts with the antigen-specific area of an antibody (Delves & Roitt, 1998). An antigen will contain multiple epitopes and an antibody is produced against epitopes rather that the whole antigen or a protein. Epitopes, which are usually used interchangeably with antigenic determinants or antigenic sites, can be classified as B cell epitopes and T cell epitopes based on the types of cellular responses they elicit (Baumgart et al., 1998).

HLA itself being an antigen poses the major risk in transplantation. In recent reports, backing up to a decade, the concept of epitope matching has been further studied and resulted in the identification of eplets - a set of spatially arranged so-called triplet of amino acids which exists when HLA is viewed as a string of amino acid. Eplets represent the key elements of an epitope that elicit specific antibodies (Duquesnoy, 2008). This discovery has changed the way of understanding donor specific antibody reactions. The decade long thought that donor specific antibodies are formed against epitopes changed with the identification of eplets present in HLA. More recently the term 'eplet load' has also been introduced through research articles. Eplets determines

the immunogenicity of an antigen (Duquesnoy, 2002). Within the past few years the concept of eplet matching became a trend in transplantation immunology. The debate still exists whether eplet matching should replace antigen matching (Tambur, 2018). The identification of the presence of eplets of HLA has tremendously changed the way how clinicians viewed organ transplantation. Eplets, being a spatial arrangement of amino acids, exists in the same pattern in all the HLA classes with minor individual differences (eplet mismatches) (Duquesnoy & Marrari, 2020). This minor difference in the pattern of existence of eplets is what which poses the major risk in determining the donor-specific antigen binding (allo-immune) recognition and immune response (Philogene et al., 2020). The identification of eplets has further led to the better understanding of its relation in determining the survival of a transplanted graft (Duquesnoy, 2011). There are reports which states the fact that minimization of mismatches between the eplets present in HLA ABC (class I) and HLA DPDQDR (class II) is better than choosing an unrelated patient-donor allelic pair (Duquesnoy, 2008; Duquesnoy & Marrari, 2020; Hanf et al., 2014; Sapir-Pichhadze et al., 2015; Tambur, 2018).

The use of computational biological techniques in research is not new information, but the transformation of clinical practices based on computational studies has been finding its pace in the last two decades. And recently the use of computer algorithms has become a pivotal tool in the betterment of understanding diseases (McGuire et al., 2011). The role of computational statistics methodologies in developing superior data analysis tools has improved the quality of 'evidence-based computational statistics' (Boulesteix et al., 2017). The same has been mostly used in this study, which enables us to get a better understanding about HLA epitopes as well as HLA eplets. HLA Matchmaker is a structurally based algorithm which considers HLA as a string of antigenic determinants represented by eplets. In every polymorphic HLA there exists a set of spatially arranged triplet of amino acids which determines the immunogenicity of that protein or antigen. HLA matchmaker algorithm determines histocompatibility at the epitope rather than antigen level allo-immune responses. The algorithm provides an assessment of patient-donor HLA compatibility at the structural level. Eplets can be classified into two, antibody verified, and non-antibody verified eplets. The former

is those which are known to elicit an immune response by reacting with an antibody, the latter are those which does not cause any immune reaction (Duquesnoy, 2006). The HLA Matchmaker algorithm is different from conventional methods of counting the numbers of mismatched HLA alleles, rather helps in identifying the presence of shared amino acid eplet patterns among dissimilar alleles (Duquesnoy, 2002). This can be used to identify possible allelic matches through eplet matching. In 2007, Duquesnoy and Askar demonstrated that the eplet version of HLA Matchmaker has provided itself to be clinically useful and in 2019, Duquesnoy and team added that the database of the Matchmaker and eplet registry needed much updating as it provides an incomplete description of the structural HLA epitope repertoire.

Epitopes are those immunogenic regions of an antigen that are composed of polymorphic sequence of amino acid residues, which has been recently termed eplets. The evolution of HLA molecular typing methods has progressively enabled a much more accurate determination of the three-dimensional structure that forms the antibody accessible regions of an antigen. About 3 decades ago, Terasaki's group reported the influence of HLA epitope mismatching on kidney transplant survival (Duquesnoy, 2017). The possibility of epitope matching to be superior to broad antigen HLA matching still exists, since the allocation of donor kidneys to patients with a more favorable epitope compatibility profile might lead to better allograft outcomes rather than a broad HLA analysis (Kamoun et al., 2017; Larkins et al., 2019).

Several reports have highlighted the association between greater numbers of eplet mismatches and adverse allograft outcomes. The approaches using eplet mismatch rather than broad antigen HLA mismatches has been successfully implemented in organ transplantation since the last two decades (Larkins et al., 2019). After the introduction of HLA Matchmaker algorithms more investigations at transplant centers worldwide have suggested that HLA epitope matching is associated with better transplant outcome. The application of computational biological techniques has provided solid evidence that HLA class I and class II mismatches with low eplet loads are less likely to induce antibody responses (Duquesnoy, 2017). Molecular docking being the strongest bioinformatics method in the run, use of molecular interaction study is the next better way in understanding the intermolecular interactions. Here,

the use of HLA Matchmaker, molecular modeling and protein docking has been efficiently utilized to understand HLA sequence and the antigen structure to its amino acid level. The fact that variation lies within the binding area of the protein structure has been efficiently proved using protein docking study.

The present study entitled 'HLA ABDR eplet mismatch analysis for donor selection in renal transplantation - A cohort study' has been focused to ascertain an ideal strategy for selecting unrelated individuals as potential donors for renal transplantation by analyzing the number of eplet mismatches and structural variations, that each individual possesses, thus eliminating the possibility of an undesired immune reaction observed in our population. This reduces the implementation of strong combinatorial immunosuppression and thereby, the selection of unrelated individuals having matching eplets. The investigation progressed through different steps including clinical data collection, eplet mismatch analysis, molecular modeling, protein docking and biostatistical analysis. The major objective of the whole study was to identify an appreciable correlation between the acquired clinical data, eplet mismatch analysis and HLA structural information in comparison with the corresponding molecular models. The study is proposed as a new approach, which combines transplantation immunology and immunoinformatics.

The following objectives were investigated to achieve the present results.

i. Identification of percentage of pre-formed antibody in patient using CDC-crossmatching

ii. Identification of HLA ABDR alleles of patient and donor via molecular typing

iii. HLA ABDR eplet mismatch analysis using HLA Matchmaker

iv. Analysis of structural similarity of selected HLA alleles with matching eplets using protein structure modeling

v. Protein docking and comparative analysis of binding affinity between HLA-Ag-TCR tri-molecular complex for the identification of compatible HLA DRB structures

vi. Biostatistical analysis on HLA ABDR eplet mismatches in relation with renal graft survival

2. REVIEW OF LITERATURE

Understanding immunology is challenging and human immune system is one of the most amazingly complex as well as the most magnificent wonders molded by co-existing with the micro-organisms over the course of evolution. The immune system functions to protect the body from overwhelming infection. The immune system contains multi-level pathogen scanning methods which includes common physical barriers. The entry of a common pathogen triggers the immune system to act in two ways. One responds quickly in a non-specific manner, which is composed of cellular (phagocytes) and chemical components (cytokines) - the innate immunity and the other occurs more slowly, specific to the infection, having cells (T and B) that express more receptors against the pathogen - the adaptive immunity.

A strong and healthy immune system always portrays its remarkable and precise ability to distinguish between 'self' and 'non-self' within the body. The failure of this mechanism leads to autoimmune condition (Ayala Garcia et al., 2012; Miyadera et al., 2015; Tsai & Santamaria, 2013). The control of immune responses towards non-self-entities within the body is where the story of major histocompatibility complex (MHC) commence - a group of complex genes that controls multiple aspects of the immune response. MHC or the human leukocyte antigen (HLA) is those genes that code for self-markers on all cell surfaces. This complex gene group was identified during the studies aimed at understanding the molecules responsible for rejection occurring during solid organ transplantation. Until the identification of MHC in 1967, almost every effort to transplant an organ or tissue from one human to another had been unsuccessful for many decades. The World Health Organization Nomenclature Committee (WHONC), in 1968 designated that the MHC in human can be named as HLA (human leukocyte antigen) (Chinen & Buckley, 2010).

Since the historical discovery of HLA in 1967 is confirmed by the fact that, according to the Global Database on Donation and Transplantation (GODT) gathering data from 194 countries in 6 World Health Organization (WHO) regions: Africa (AFR), The Americas (AMR), Eastern Mediterranean (EMR), Europe (EUR), South-East Asia

(SEAR) and Western Pacific (WPR), in 2019 around 150,000 solid organ transplantations were performed per year worldwide (figure 1). An increase over 4.8% was reported from 2018-2019.

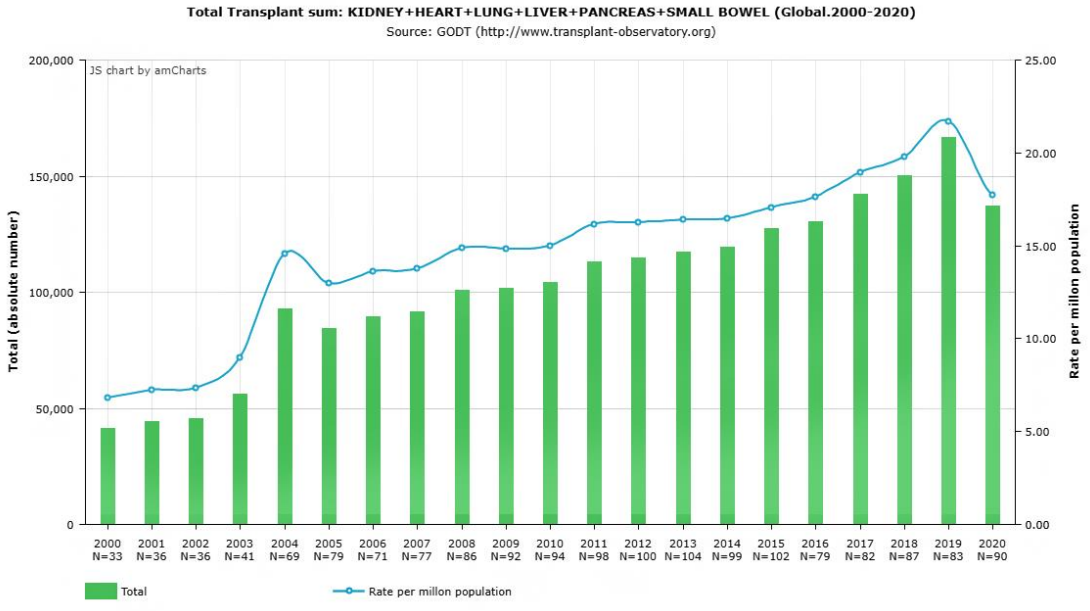


Figure 1: Total number of solid organ transplantation carried out between the years 2000-2020 (http://www.transplant-observatory.org)

An approximate number of 140,000 transplantations have been performed in 2018 globally, of which 65% were kidney transplants with 36.2% living donor (figure 2). In 2019, the number of deceased donors was calculated to be almost 40,000 making a total of 17.5 transplants per hour. Of the total number of transplants in 2019, 37% are kidney transplants with 22% actual donation after circulatory death (DCD). According to World Marrow Donation Association (WMDA) an approximate number of 39 million matching donors in 247 organizations from 55 different countries have been listed in the database since 1994 (https://wmda.info). Multiple research have coined the fact that for bone marrow transplantation a donor must match a minimum of 6 HLA markers and for renal transplantation a minimum match of 4 HLA markers are needed.

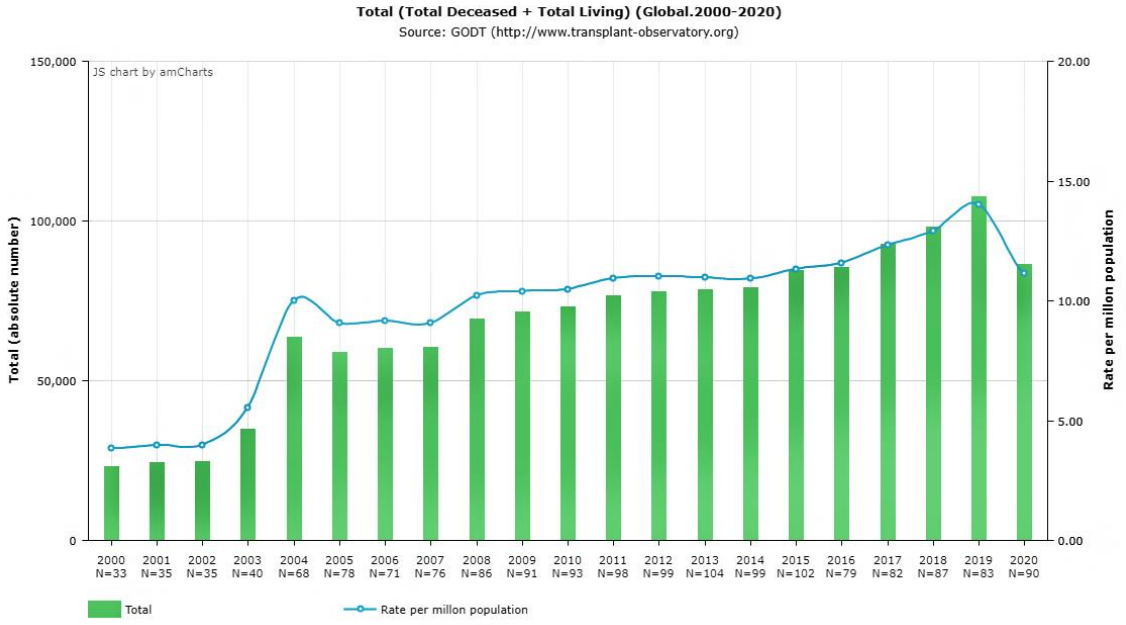


Figure 2: Total number of kidney transplantation carried out between the years 2000-2020 (http://www.transplant-observatory.org)

Transplantation is the optimal choice for all the cases of end stage organ failures which affects kidneys, liver, etc. Progresses in transplantation immunology, especially in solid organ transplantation, have allowed the exponential growth of organ and tissue transplantation in medicine over the last 2 decades. The advanced techniques involved in the field of SOT have delivered revolutionary attempts in patient survival.

2.1 Structure and classification of HLA

The major histocompatibility complex (MHC) or human leukocyte antigen (HLA) genes code for cell surface proteins which play an important role in the immune response. The HLA genes are encoded by a set of 21 protein-coding loci on chromosome 6 at 21st position (6p21) which also codes for other pseudogenes (Sanchez-Mazas, 2020) (Figure 3). HLA is about 0.1% of the total genome in humans to a size of about 3.6 million base pairs (~3.6 Mbp) (Ayala Garcia et al., 2012). There are many loci encoded by HLA such as HLA-A, HLA-B, HLA-C, HLA-DP, HLA-DM, HLA-DO, HLA-DQ and HLA-DR. The HLA genes exhibits high rate of polymorphism and hence the haplotype of HLA is very large. HLA is classified into 3, class I, class II and class III based on the source of antigens presented and its specific function.

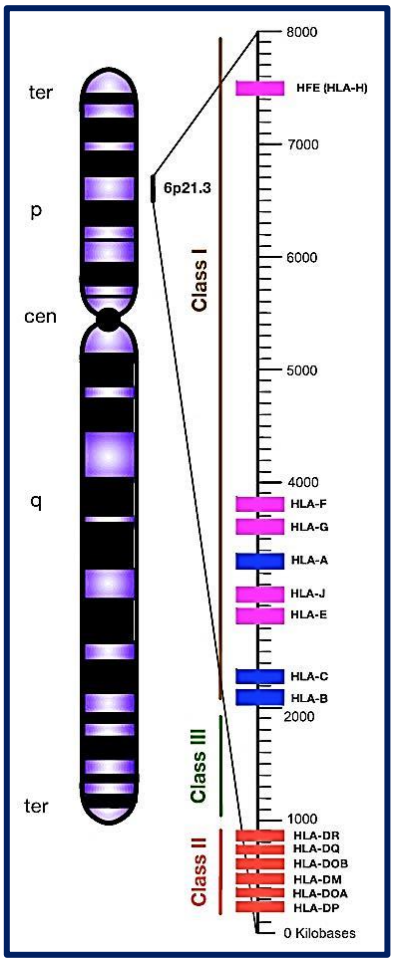


Figure 3: Position and organization of human leukocyte antigen (HLA) genes on human chromosome 6 (Crux & Elahi, 2017)

2.1.1 Types of HLA

HLA class I molecules are ubiquitously expressed on all nucleated cells and have well established immunological functions. The class I HLA present endogenous antigens to T cells and are sub-divided into 2 categories - HLA class I a and the non-classical HLA class I b (Bartl & Weissman, 1994). The class I a HLA is classified into 3 major types, HLA-A, HLA-B and HLA-C which exhibits high rate of polymorphism. The non-classical class I receptor molecules are also expressed on the cell like, HLA-E, HLA-F, HLA-G and MHC class I polypeptide-related sequence A (MICA) has poorly understood cellular or immunological functions (Perreault et al., 1990). The expression of HLA G is known to be mainly restricted to the placental tissue and amniotic fluid and share 86% similarity with the classical HLA class I genes. (Dudek &

Purcell, 2016; Kyurkchiev, 2017). The HLA class I molecules are functionally active cellular receptor proteins which are assembled in the endoplasmic reticulum (ER). They consist of a heavy chain having 3 domains (α1, α2, and α3) and an immunoglobin-like domain called β2 microglobulin (B2M), a protein chain which is coded by B2M gene which is positioned at loci 15q21. The chains of class I HLA, α1 chain and B2M are bound together non-covalently. The primary α1 and α2 domains together make the peptide-binding cleft which binds to an intracellular digested peptide. Binding of peptide to the HLA class I molecule changes the molecule to acquire a stable configuration. Classical HLA class I molecules have a trans-membrane domain on α3 chain which helps in attaching to the cell membrane. The molecular weight of the α chain and B2M protein is approximately 45 kDa, and 12 kDa, respectively.

The HLA class II molecules are hetero-dimers in nature having a α1, α2 chain and a β1, β2 chain. The hetero-dimer chains are bound non-covalently and expressed on the membrane surface. HLA class II molecules present exogenous antigens and are expressed only on antigen-presenting cells (APC). The class II α1 and β1 domains form the peptide-binding cleft that binds to the exogenous peptide originated from foreign bodies such as an infections bacterium. Like HLA class I molecule, class II molecules also acquire stable configuration on binding with the peptide. The molecular weight of α chain and β chain is approximately 34 kDa and 29 kDa respectively (Janeway Jr et al., 2001; Nakamura et al., 2019; Alelign et al., 2018). The 3 major antigens of class II HLA are HLA-DR, HLA-DQ and HLA-DP. The genes included in class II are those codes for α and β chain encoding genes, such as HLA-DRA1, HLA-DRB1, HLA-DQB1, etc. Both class I and class II hetero dimers have a variable extracellular and relatively constant trans-membrane and an intra-cytoplasmic domain (William, 2001).

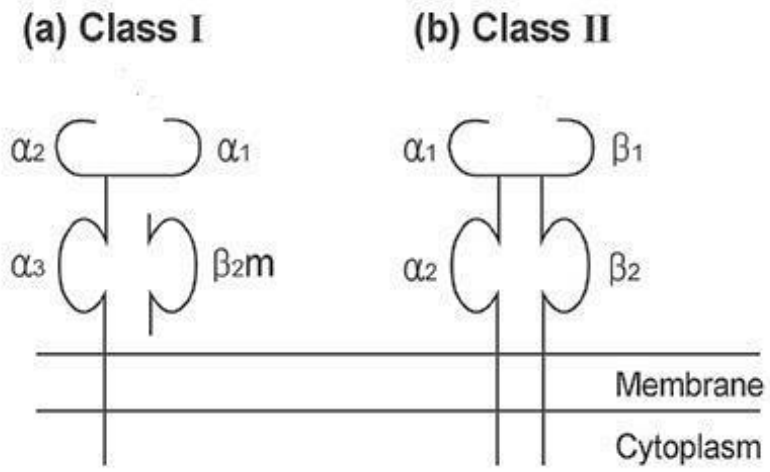


Figure 4: A simplified line diagram of class I and class II HLA showing the α and β chains

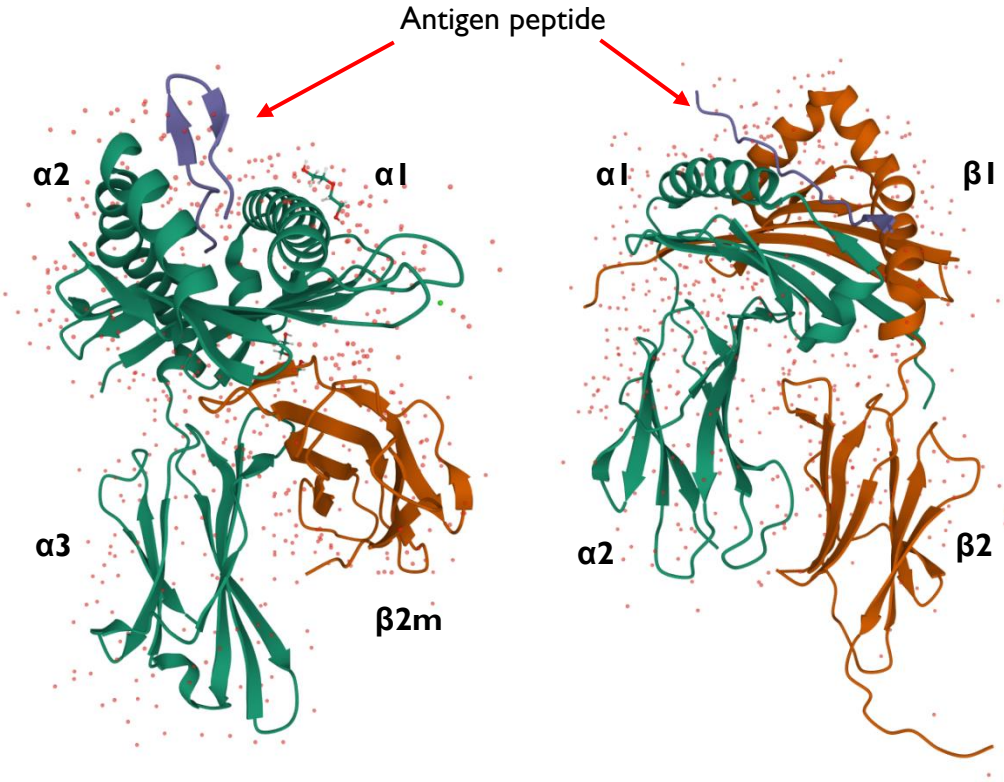


Figure 5: Crystal structures of Class I HLA A with antigen peptide, pdb ID - 4U6X (Hassan et al., 2015) and Class II HLA DR with antigen peptide, pdb ID - 1AQD (Murthy & Stern, 1997)

2.1.2 Nomenclature

After the designation of human MHC to HLA by World Health Organization Nomenclature Committee (WHONC), in 1968, the significant need for the development of a standardized HLA nomenclature for better understanding of HLA system arose. As far as the clinical application of HLA is depended on the level of understanding its sequence, the nomenclature is the most critical development established yet (Hurley, 2021). The Nomenclature Committee for Factors of the HLA System (NCFHS) has overseen the development and usage of nomenclature based on serologic specificities, cellular responses, and DNA sequences. The activities and decisions of this committee have been directed through multiple international workshops carried out since 1964, which continues today. Multiple websites provide a curated database of the HLA sequence of over 23,000 HLA alleles which follows the current nomenclature.

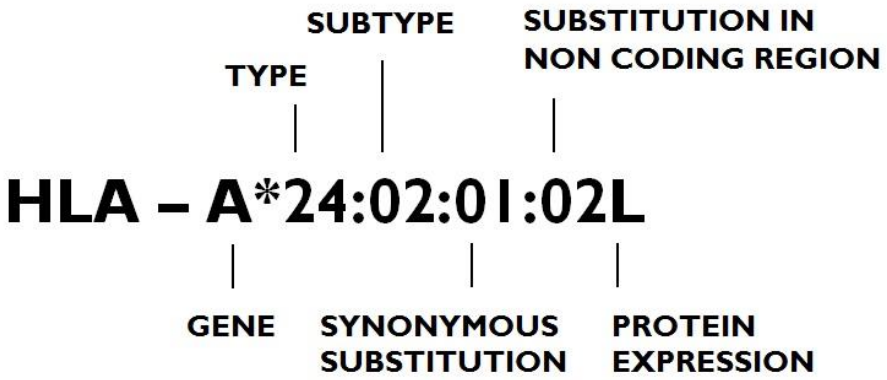


Figure 6: An example of HLA nomenclature
(http://hla.alleles.org/nomenclature/naming.html)

Each HLA allele name has a unique number/ID corresponding to 4 sets of digits (8 digit in total) which are separated by colons. The length of the allele designation depends on the sequence of the allele identified by SSP/SSOP-PCR, which gives low, intermediate and high-resolution HLA typing. The increasing resolution of HLA typing increases from left to right of the designated nomenclature (figure 6). All the alleles receive at least 4 digits as its ID which shows the first 2 sets of digits separated by an

‘ * ’ sign after the gene of class I, II or III. The digits before the first colon describe the HLA type, which often shows the serological antigen carried by an allotype. The next sets of digits are used to list the subtypes, which are addressed in order in which the DNA sequence have been determined. Alleles that differ by synonymous nucleotide substitutions, also called silent or non-coding substitutions, within the coding sequence are marked by third set of digits. Alleles that only differ by sequence polymorphisms in the introns, or in the 5' or 3' untranslated regions that flank the exons and introns are marked using the fourth set of digits.

In addition to the unique allele HLA ID, there are additional suffixes that may be added to an allele to indicate its expression status. Alleles that have no expression status, called the 'Null' alleles, have been given the suffix ‘N’. All the other alleles that have been shown to be alternatively expressed are represented by suffix ‘L’, ‘S’, ‘C’, ‘A’, or ‘Q’. The suffix 'L' represents 'Low' cell surface expression when compared to normal levels. The suffix 'S' is used to denote an allele specifying a protein which is expressed as a soluble or 'Secreted' molecule. The 'C' suffix is assigned to alleles that produce proteins that are expressed in the 'Cytoplasm' but not on the cell surface. An 'A' suffix indicates an 'Aberrant' expression, and a 'Q' suffix is used when the expression of an allele is 'Questionable', when the mutations seen in the allele affect normal expression levels in other alleles.

2.1.3 Polymorphism in HLA and its importance

Mutation causes variation and the most common mutation is the single nucleotide polymorphism (SNPs). SNPs usually occurs throughout an individual’s DNA, on an average of 1/1000 nucleotides. SNPs become more unique when it occurs in DNA between genes. This creates a specific change in the gene’s function or receptor characteristics. This may sometimes lead to diseased conditions like auto-immunity, complex heart diseases, diabetes or even cancer. The genotypic variations those occur as a result of SNPs in HLA alleles are represented by its nomenclature. The 2nd set of digits which represent the subtypes are termed as a result of SNPs in the HLA parent allele sequence (figure 6).

HLA is known to be the most polymorphic gene complex in human body, thus making it sequentially unique to every individual. The genetic variations occurring in classical HLA genes is primarily considered as a result of recombination as well as adaptation to microbial infections during the course of evolution. Commonly, in each family, the chance of occurrence of having the same HLA set is always 25%, a 25% chance of having no inheritance (zero sharing) and a 50% chance of inheriting 1 whole gene/haplotype between siblings. Of all the markers that everyone possess half is inherited from each parent. So, each sibling who shares the same parent has a 25% chance of having an allelic match.

In transplantation immunology the need for a perfectly matched donor mostly relies on this inherited percentage of HLA alleles. HLA alleles being known for their high polymorphic nature are also known to be having a high degree of homology. It has been reported that, about 70% of all the patients waiting for a transplant will not be able to acquire a fully matched donor, 4-digit match up to subtype level, from their family. This takes the search for matched unrelated donors for transplant recipients. The identification of HLA type aids the process of finding a near to perfect HLA matched unrelated donor. Greater the number of HLA mismatches, greater the chance of graft rejection. In fact, the studies suggest that the presence of mismatched HLA antigens on the donor graft can lead to the formation of de novo DSAb, which is directly associated with graft rejection (Duquesnoy et al., 2008; Sapir-Pichhadze et al., 2015).

Given the fact that the extensively polymorphic HLA pose as a protein fingerprint among each individual, and at least 10 % of all T cells will act against any foreign particle/HLA resulting in strong immune reaction, the development of transplantation immunology regimen in administration of immunosuppression and successful transplantation is nothing less than remarkable.

2.2 HLA and antigen presentation

Antigen presentation is the action of adaptive immunity, a strictly controlled cellular action, which plays the fundamental role in immune recognition and reaction or simply a prerequisite for activation of adaptive immune mechanism. This is the

process by which the HLA proteins, carrying processed antigen peptides, are expressed on cellular surfaces, specifically antigen presenting cells, to be recognized by T cell carrying T cell receptors. The human immune system is a highly complex mechanism which is equipped with cellular and chemical weapons able to disarm any invading pathogen. HLA class I molecules present the antigens to cytotoxic T-cells (T_c) expressing CD8+ co-receptors through the endogenous or intracellular pathway. HLA class II molecules through exogenous or extracellular pathway present the antigens to helper T-cells (T_H) expressing CD4+ co-receptors (Schmidt et al., 2013). The activation of both CD4+ and CD8+ releases inflammatory cytokines, resulting in amplified immune response in presence of class III HLA - the complement system.

In the field of renal transplantation, HLA class I associated immune reaction is one of the major reasons for hyper acute rejection. Donor-derived or patient-derived APC can initiate the process of graft rejection via necrotic cell death. The mechanism is classified into 3 pathways: direct, indirect and semi-direct pathway of antigen presentation. The direct pathway induces humoral allo-immunity via donor APC through allograft-specific CD8+ cytotoxic T cells, which results in cellular immune response involving class I HLA proteins, thereby damaging the donor tissue/cells leading to the rejection of the transplanted graft (Van Besouw et al., 2005). The pathway by which recipient APC process and present donor antigen to recipient CD4+ T cells is termed as indirect pathway. The non-processed donor HLA is usually identified by recipient APC and presented to self CD4+ T cells. This is the semi-direct pathway. There are scientific reports stating the fact that the activated CD4+ T cells and which carry both donor-derived HLA as well as self-HLA class II has a means of peptide level communication (Benichou & Thomson, 2009; Nakamura et al. 2019). Blocking of the CD28/B7 pathway has also shown to prevent acute and chronic rejection in several animal models (Gladow et al., 2020; Lakkis et al., 1997; Larsen et al., 1996; Vanhove et al., 2019).

2.2.1 Class I peptide loading pathway and rejection

HLA class I molecule assembly is carried out in the ER. Before the assembly, heavy chain is stabilized by the chaperone calnexin. Peptide-loading complex (PLC) which consists of TAP (transporter associated with antigen presentation), tapasin, class I HLA, ERp57 and calreticulin plays an important role in peptide processing. The foreign protein is degraded into smaller peptides ranging from 2-25 amino acids, by cytosolic proteases in the proteasomes (Blum et al., 2013; Calabia-Linares et al., 2011; Leone et al., 2013). Peptides of length 8-10 amino acids are translocated from cytosol to ER by TAP with the help of Tapasin (Reimann & Schirmbeck, 1999). During the process of peptide processing the pre-assembled HLA complex is stabilized by chaperone proteins (calreticulin, Erp57, protein disulphide isomerase (PDI) and tapasin). The PLC loads the peptide onto the pre-assembled HLA class I complex causing the release of the stabilizer chaperone proteins. The ER aminopeptidase (ERAP), also called as the 'molecular ruler', trims the peptides processed in the cytosol in ER, before it binds with the class I HLA. The class I HLA-Ag peptide complexes is transported out of ER and presented on the cell surface. The HLA-peptide complex present on the cell surface is recognized by receptors present on the cytotoxic T-cells (TCR).

The interaction between the CD8+ co-receptor molecule, T-cell receptor and the peptide on the surface of the T cell and the HLA class I molecules triggers the action for apoptosis. This is the first signal, and this interaction is called three-signal activation model. The second and third signals are the interaction between CD28 on T-cells and CD80/86 on the APC, followed by the production of cytokines by APC. CD28 promotes clonal expansion of T cells. This totally activated T-cells induce a strong and specific cytotoxicity to the targeted cells. CTLs migrate to the graft and recognize the graft cells by allogeneic class I HLA molecules. The cytotoxic T cells destroy the graft either via perforin-granzyme pathway or the FasL pathway leading to apoptosis (Han et al., 2004; Li & Raghavan, 2010).

There are several reports that explain the ability of viruses that evade the HLA presentation by targeting the HLA antigen presentation pathway, which helps them

become invisible within the cell and the avoids the cell being target for effector cells. While a few subvert the class I HLA antigen presentation the others target TAP, making sure that no antigen is being presented for CD8+ T cells (Ahn et al., 1996; Hansen & Bouvier, 2009; Lamers et al., 2018; Tomazin et al., 1996; Waithman et al., 2014).

2.2.2 Class II peptide loading pathway and rejection

The α- and β-chains of HLA class II molecules are assembled in the ER where they are stabilized by an invariant chain (Ii). The hetero dimer HLA class II molecule along with invariant chain is transported through golgi complex into the HLA class II compartment. This cellular compartment is acidic in pH and activates cathepsin S and cathepsin L proteases which digest the invariant chain leaving an 9-16 amino acid peptide in the binding cleft of class II HLA commonly known as the CLIP (CLass II associated Invariant chain Peptide) (Cresweell, 1996; Günther et al., 2010; van Lith et al., 2010). This CLIP is then exchanged with antigenic peptide, which usually range between 12-15 amino acid length, that are derived through endosomal pathway with the help of chaperone HLA-DM and HLA-DO in B cells (Busch et al., 2000; Chen & Jensen, 2008; Chou et al., 2008; Chou & Sadegh-Nasseri 2000; Fujii et al., 1998; Ghosh et al., 1995; Karlsson, 2005; Münz, 2012; Roche, 1995). The class II HLA-Ag peptide complex is transported onto the cell surface and presented to CD4+ T cells resulting in the clonal expansion of CD4+ T cells. The encountering of the HLA-Ag peptide complex with TCR thus resulting in activation of complement system and facilitation of cytotoxicity via phagocytosis and opsonization - the non-autophagy pathway (Gregers et al., 2003).

Class II associated graft rejection is usually chronic. The selection of a class II HLA matched donor can greatly aid in avoiding the chance of chronic graft rejection (Hsia et al., 1993; Muczynski et al., 2001). The process of indirect pathway of graft rejection indicates the mechanism of class II HLA associated graft injury leading to chronic graft rejection or dysfunction.

2.2.3 Class III HLA and its role in transplantation

Unlike the other 2 classical HLA molecules, class III HLA is not directly involved with antigen presentation and a few of them acts as signaling molecules. Class III HLA also known as the complement system carries out the 'effector mechanism' or the inflammatory immune response which is augmented by a multiple set of plasma proteins. More than 20 complement proteins are continuously produced in the body by the hepatocytes, in a pro-active from. Of the 5 main classes of antibodies, IgM and IgG activates the pro-active complements to active form via proteolytic cleavage.

Studies have shown that complement activation aids in allograft injury, commonly via antibody-mediated rejection. The fact that modulation of the responses of T and B cells complements towards antigens.

2.2.4 Types of graft rejection

In transplantation immunology, the complex immune responses that results in rejection of the transplanted organ or the graft is always a hurdle to overcome. Antibodies are always involved in rejection in one way or the other. There are three major types of allograft rejection based on immunological characteristics and histopathology. They can be either antibody mediated rejections or cellular rejections mediated by T cells. The types are: hyper acute rejection, acute rejection and chronic rejection (Bingman & Faber, 2004; Hecker et al., 2009; Salvalaggio et al., 2009). The hyper acute rejection occurs within minutes to hours after transplantation. This is because of the presence of anti-donor antibody in the host. The activation of complement system after the recognition of donor antibody induces an influx of neutrophils and stimulates coagulation. The rejection process happens even before vascularization of the graft. This type of rejection is generally unresponsive to any clinical treatment. One of the existing pre-transplant procedures by which this can be detected is CDC-crossmatching. The second type of rejection is the acute rejection, which is usually caused by the mismatch between donor and recipient class I and II HLA alleles (Chalasani et al., 2004; Gwinner, 2004). The recruitment of inflammatory cytokines upon activation of cytotoxic T lymphocytes eventually leads to necrosis of the transplanted graft. Administrations of immunosuppressant cocktails have shown

to prevent that chance of acute renal failures (Abou-Jaoudé et al., 2021; Adebiyi et al., 2021; Choi & Chandraker, 2019; Leighton & Wilson, 2020). For the past 2 decades, a combination of double or triple immunosuppressants have been used in renal transplantation. Although acute graft rejection is treatable, it poses a serious risk factor in affecting the long-term survival (Duni et al., 2021, Mahdi, 2013; Menon, 2017). The third type of rejection is the chronic rejection, which occurs usually within months to years after transplantation. Even though the transplanted organ still is in place the allo-HLA molecules expressed by the graft tissue might gradually result in degradation of the organ. Chronic rejection is a progressive reaction, which ultimately leads to graft injury and is the major cause for long-term graft loss (Kloc & Ghobrial, 2014; Mehta, 2009; Rose & Hutchinson, 2009; Zhang, et al., 2009).

Thus, understanding the complex molecular and cellular activities which aids to rejection of a transplanted organ or graft is essential for the development of novel strategies for the selection of a prefect donor.

2.3 Laboratory investigations involved in transplantation

The survival of a graft in case of solid organ transplantation always relies on the degree of matching between a patient and a donor. The analysis and quantification of HLA allele matching always ensures the possibility of graft survival for at least a short period of time. This degree of matching is always determined by the availability of an HLA allele matched donor. HLA allele matching is still considered as the major genetic determinant for ensuring graft survival.

It is a known fact that the transplantation of foreign tissue induces both antibody-mediated as well as cellular immune reactions in the recipient body. The identification of presence of pre-formed antibody in the recipient body as well as the ID of HLA alleles of both donor and the recipient is the most important pre-transplant procedures in case of renal and bone marrow transplantation. To understand the intensity of such immune reactions there are serological and molecular biological methods. Mixed lymphocyte culture (MLC), CDC crossmatching, flow cytometry crossmatching, etc., are used for the determination of pre-formed antibody in the recipient's body. SSP-PCR, SSOP-PCR, SBT (sequence-based typing)-PCR etc., is used

for identifying the unique HLA allele ID of both patient and donor (Emerson et al., 2014).

Following are the pre-transplant procedures involved in the analysis of presence of anti-HLA antibody or other pre-formed antibody in the recipient as well as molecular techniques for the identification of HLA alleles of both patient and donor.

2.3.1 Complement dependent cytotoxicity (CDC) crossmatching

In 1964, Paul Terasaki and his colleagues developed the immunological profiling method called complement-dependent cytotoxicity crossmatching (CDC-cxm). And for the past 5 decades this method has been helping clinicians to understand much about the presence of pre-formed antibody in the donor serum against the recipient lymphocytes. CDC crossmatching is usually performed between known reactive donors who are likely to develop hyper-acute reaction. Such antibodies are produced as a result of any previous exposure to external antigens, like, blood transfusion, pregnancy and earlier transplantation.

The procedure involves the reaction between patient serum and lymphocytes of the donor, which is mixed in a multi-well plate, later called the Terasaki plate. The reaction is amplified by the addition of complements. In the presence of donor-specific antibodies, the complement gets activated through the classical pathway due to binding of the antibodies to the donor lymphocytes. This causes lymphocytolysis. The sensitivity of this technique can be enhanced by the addition of antihuman globulin (AHG). AHG molecules bind to each donor-specific antibody in the antigen-antibody complex. This increases the sensitivity of the reaction so that those DSAbs that is non-reactive will give an ample amount of cellular deterioration. The percentage of the dead cells is observed by visual confirmation through an inverted phase contrast microscope. The strength of the reaction is used as semi-quantitative analysis (Mulley & Kanellis, 2011; Sağıroğlu et al., 2012).

The amount of cell deterioration gives the idea on the presence of pre-formed antibody against the donor cells. The difference in HLA expression between T cells and B cells can influence the level of cell lysis. T cells do not constitutively express

class II HLA, so the positive T cell crossmatch may be due to antibodies to HLA class I only. HLA class I and class II both are expressed on B cells, so the positive crossmatch reflects antibodies against HLA class I and class II or both.

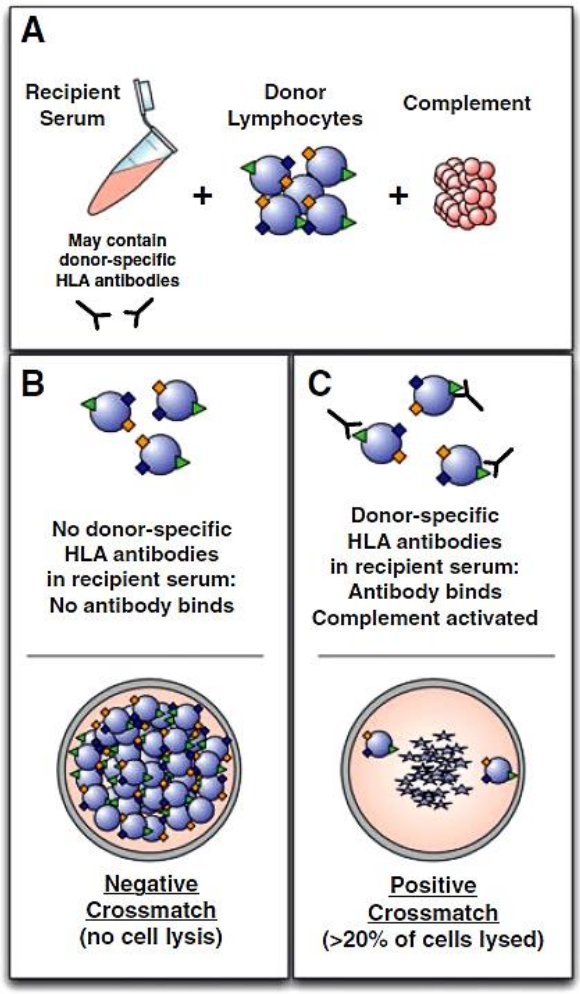


Figure 7: Schematic of CDC crossmatch assay (Mulley & Kanellis, 2011)

2.3.2 Flow cytometry crossmatching (FCXM)

Flow cytometry crossmatching (FCXM) is a highly sensitive method developed in the 1980s for identifying cellular intensity and separation of cells from a mixed cell population. The technique is much more specific and fast which can be used to detect the antibodies that bind to donor lymphocytes through marker assisted cellular separation. Flow cytometry crossmatching is built within a technology that is used to analyze the physical and chemical characteristics of particles in a fluid as it passes

through at least one laser. The technique uses cell components which are fluorescently labeled followed by excitation using laser to emit light at varying wavelengths (Bub et al., 2013; Lindemann et al., 2010; Michalska et al., 2002).

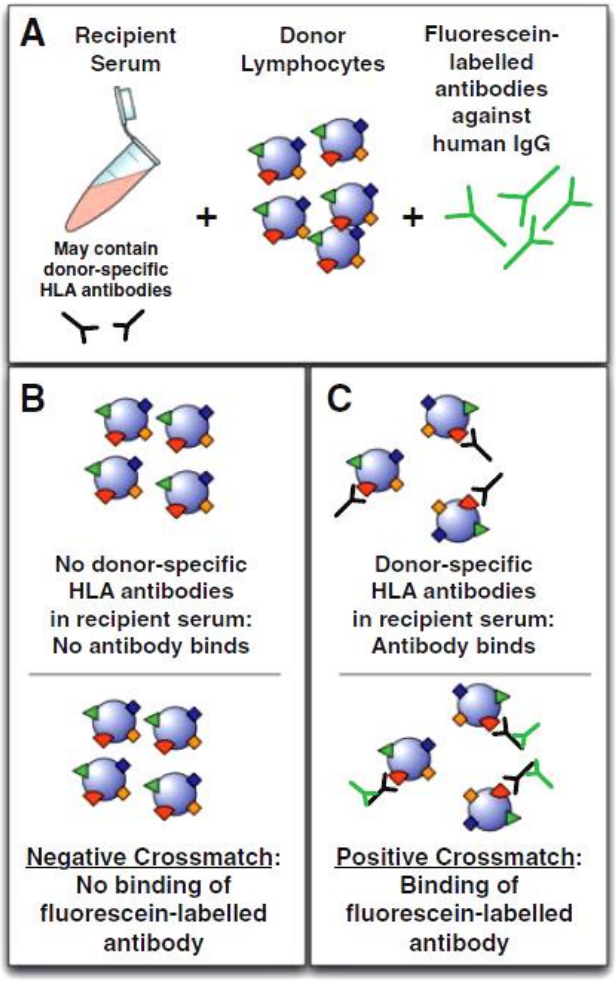


Figure 8: Schematic of Flow crossmatch assay (FCXM) (Mulley & Kanellis, 2011)

Flow crossmatches are more sensitive than standard CDC crossmatch and can be used to detect very low levels of DSAbs. The procedure typically follows the basic CDC-cxm procedure, which uses donor lymphocytes and serum of patients. Flow crossmatch reaction involves the addition of a cocktail of fluorescent tags like FITC, and CD markers like CD3, CD19, etc., for T & B cells which are then mixed with prepared sample and incubated to allow the antibodies to bind to donor lymphocytes. Different fluorescently labeled detection antibodies can be used specifically to detect

different subtype of antibodies like IgG, IgM, IgA (Ayna et al., 2011; Lemaître et al., 2004; Metes et al., 2003).

2.3.3 HLA typing

HLA typing is one of the most beneficial techniques for clinicians which help them to identify the unique HLA class I and II allele of both patient and donor. HLA typing is the process of analyzing the level of compatibility between tissues of patient and donor before transplantation. This is one of the most crucial pre-transplant techniques carried out to ensure that both the patient and donor carry the same HLA allele so that the patients' T lymphocytes do not generate an immune response on recognizing the donor HLA, or simply, to bridge the reaction by mutual recognition of immune cells in unrelated individuals. Other than identical twins, no two individuals carry the same HLA allele, making the HLA complex a 'protein fingerprint' (Liu et al., 2021). Tissue typing helps in identifying and comparing the HLA markers in the patient cell with that of the donors. A single HLA mismatch increases the chance of graft rejection by 13%, which goes up to 64% if all six HLA alleles are mismatched or unmatched. There is also a relative importance criterion between the HLA alleles with HLA DR being the most important, followed by HLA B and HLA DQ. HLA DPB appears to be important during the subsequent transplants when first transplant fails (DeVos et al., 2012; Malhotra, et al., 2000). High level HLA matching hence proves to be essential.

HLA polymorphisms are detected through exons 2 and 3 of HLA class I α genes and exon 2 of class II genes that determine the specificity of antigen binding (Cao et al., 1999). HLA typing methods are PCR based methods which can be categorized into three classes. The first class includes sequence-based typing or sanger-based typing (SBT); a technique based on dideoxy chain termination method (Sanger-based) coupled with capillary electrophoresis, and sequence-specific oligonucleotide probes (SSOP), which are secondary methods to detect PCR products containing polymorphisms internally. The second class includes sequence-specific primer (SSP) amplification in which PCR directly detects the polymorphisms. The third class includes techniques which detects conformational changes in the physical

characteristics of different alleles due to single nucleotide substitution by hetero-duplex analysis (HDA), a biochemical method used to detect point mutation, single-strand conformational polymorphism (SSCP), a simple yet sensitive technique used to detect mutation and genotyping, denaturing gradient gel electrophoresis (DGGE) and temperature-gradient gel electrophoresis (TGGE), which uses either temperature or a chemical gradient to denature the DNA sample as it moves across the acrylamide gel.

The most popular and clinically relevant methods used currently, include sequence-specific oligonucleotide probes (SSOP) and sequence-specific primer (SSP) amplification (Trowsdale, 2011).

2.3.3.1 Sequence-specific primer (SSP) PCR

This method was initially developed by Olerup and Zetterquist, in early 90s for HLA DR genes. Later SSP typing system for the HLA A, B, C, DRB1, DRB3, DRB4, DRB5, and DQB1 alleles were also developed by Bunce & Welsh in 1994. The method is a simple form of semi-automated multiplex polymerase chain reaction carried out by amplifying the DNA isolated from both donor and recipient. Each well of the PCR tube has multiple primers complementary to the specific HLA allele. SSP-PCR is a simple modification to normal PCR analysis that extends the applicability of the technique to those genes for which only partial sequence is available and allows rapid genome walking from known into unknown regions of the chromosome (Lavant et al., 2011; Shyamala & Ames, 1989).

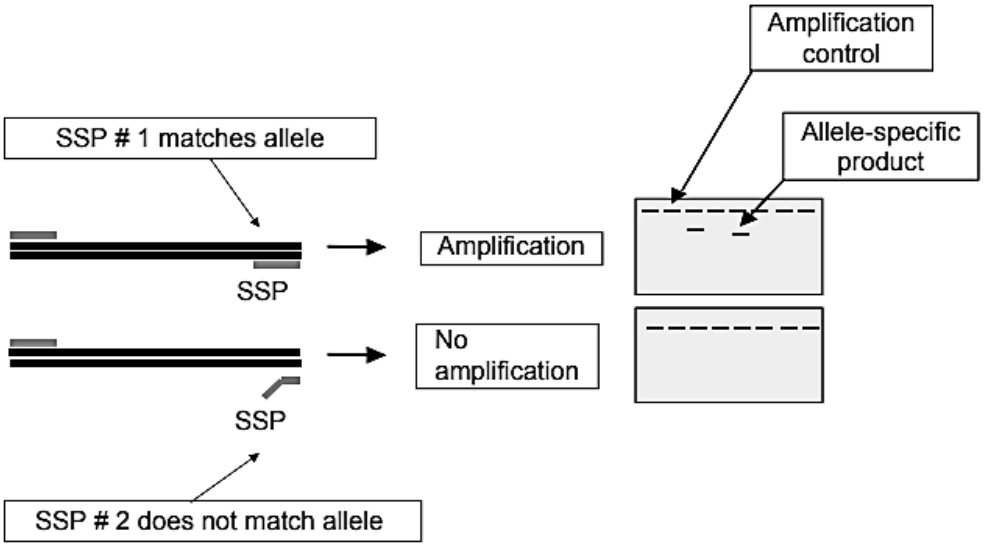


Figure 9: Schematic representation of sequence-Specific Primer (SSP) (O'Gorman & Donnenberg, 2008)

2.3.3.2 Sequence-specific oligonucleotide probes (SSOP) PCR

SSOP typing was one of the first HLA typing methods to be developed for identifying HLA class II genes; class I HLA allele SSOP typing was developed later (Cao et al., 1999). The basic principle of the method is that amplified DNA is mixed with oligonucleotide probes that are complementary to specific segments of DNA of different alleles. Primers amplify all known alleles of the HLA locus in one PCR tube which require genotyping. Exons 2 and 3 are co-amplified as one PCR product for HLA class I and exon 2 is amplified for HLA class II. There are two formats for this method - dot blot format and reverse dot blot format. In dot blot format target DNA is amplified by PCR and then immobilized on a nylon membrane. Nylon membrane being positively charged binds negatively charged DNA strongly. The DNA bound membrane is then placed in a container containing hybridization solution. The hybridization solution contains oligonucleotide probes labeled with non-radioactive reporter such as biotin. Biotin can be detected by streptavidin conjugated enzyme (horse-radish-peroxidase) followed by incubation with a chromogenic substrate. Non-hybridized oligonucleotide probes are removed by stringency washes. Since this format was inconvenient, reverse dot blot format was developed. This format contains

a panel of immobilized probes to which labeled PCR products was added. Advantage of SSOP typing is that it can be used for large number of samples (Alelign et al., 2018).

The concept of immobilized probes on nylon membrane was further extended to bead based systems such as Luminex technology where probes are immobilized on beads. The Luminex multiplex assays apply color-coded superparamagnetic beads coated with analyte-specific antibodies. The technology is designed to maximize multiplexing capacity and flexibility and maintain specificity. Currently, SSP-, SSOP and qPCR lead in the commercial kit market for intermediate resolution HLA genotyping. Despite the recurrent uncertain outcomes, Sanger SBT has been considered as gold standard for high-resolution HLA typing (Smith et al., 2019).

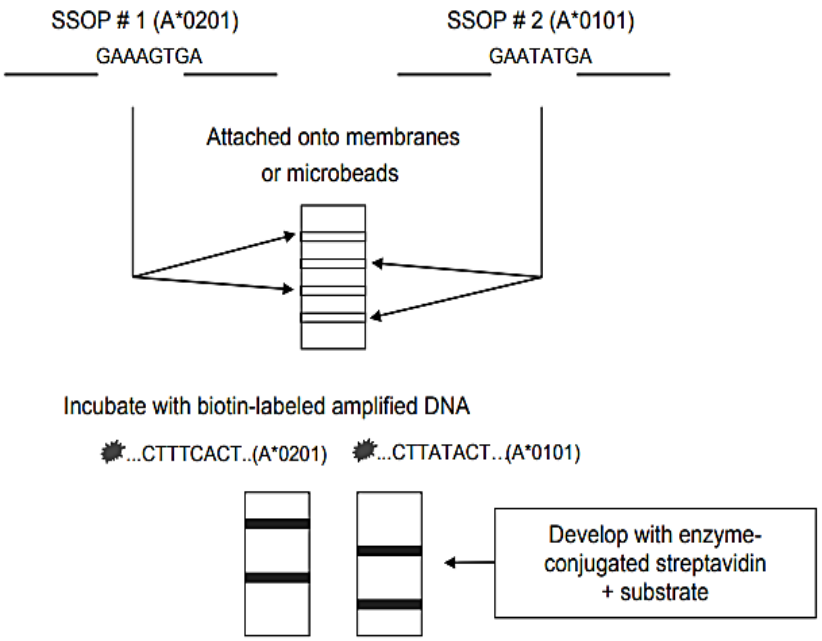


Figure10: Schematic of sequence-specific oligonucleotide probe (SSOP) hybridization method (O'Gorman & Donnenberg, 2008)

2.3.4 Next Generation Sequencing

Next generation sequencing revolutionized the human genome sequencing allowing the whole genome to be sequence within hours. Progress in NGS technology has paved its way into medical genomics with many clinical applications like genetic diagnosis and personal medicine. Next generation sequencing offers the ability to

produce an enormous value of data within a short period of time. The various strategies rely on four aspects - template preparation, sequencing and imaging, genome alignment and assembly. The sequencing results are then analyzed by bioinformatics tools to map the individual reads to reference genome (Emerson et al., 2014; Alelign et al., 2018).

High resolution HLA matching has become a necessity for improving the certainty of graft survival, mostly in renal transplantation. The procedure allows a better understanding of donor-recipient compatibility for SOT (Tambur et al., 2021). HLA genes being complex cannot be comprehensively elucidated with direct sequencing approaches without ambiguity. HLA typing by NGS can generate unambiguous results using a single assay and analysis program. Sequencing of the complex HLA allele genes can also provide critical insights into immune disorders.

2.4 Immunoinformatics and transplantation immunology

The advances in computer science and technology have been breathtakingly enormous. The impact of applications like human genome sequencing as well as HLA allele sequencing has extended both molecular and immunological data in many folds. Immunoinformatics or computational immunology is a field which involves the high-throughput bioinformatics approaches to immunology, a field of science evolved as a bridge between experimental and computational immunology. Understanding the fact that biological interpretations is never a hundred percent accurate, and everything changes with time, the possibilities of using bioinformatics data to interpret, understand and to solve scientific problems through computational biology becomes the finest method of choice. Immunoinformatics make up all the algorithms which lessen the cost and time for immunological analysis. There are multiple applications of immunoinformatics which also includes vaccine development (Dhanda et al., 2017).

Considering the field of transplantation immunology, the allelic information of each patient and donor acquired via HLA typing methods itself is a set of unique immunoinformatical data which can be further used to study about allele related graft rejections. The introduction of HLA typing methods followed by the elucidation of 3D structure of HLA proteins helped in understanding the complex sequence patterns

they exhibit. By acquiring the HLA allele information, it is easy to study the nucleotide and amino acid sequence, as well as its active functional 3-dimensional structure. Other than HLA allele data, analysis of amino acid sequence of B cell and T cell receptor, the structural aspects of CD markers, variations in an antibody structure, amino acid peculiarities in signal peptides, active sites of enzymes, etc., are also immunoinformatical data, which can be analyzed and studied using computational biological tools.

HLA allelic data being one of the pivotal study areas in transplantation immunology, analysis of HLA amino acid sequence of both donor and recipient can provide highly relevant information on the possibilities of chronic immunological reactions. Protein as well as peptide docking studies of HLA-antigen complexes and HLA-antigen-TCR complexes via bioinformatics tools can aid in understating the strength of immune reactions that takes place inside a host system. Protein-peptide docking between an antigen peptide and HLA complex can be preferably used to study antigen presentation of class I and II HLA, and protein-protein docking between an HLA-antigen complex and T cell receptor, can be utilized for analysis of binding and further downstream processes after binding of T cell receptor.

All the protein function is depended on their structure. In case of the highly polymorphic HLA alleles, a single nucleotide polymorphism itself can lead to generation of a new HLA subtype. Therefore, by acquiring the amino acid sequence and effective use of bioinformatics tools HLA proteins can be modeled and studied for understanding their ability in binding and presenting an antigenic peptide. The two major primary biological data repositories are NCBI and PDB through which much of the immunological information can be easily acquired. National Center for Biotechnology Information or the NCBI is a division of National Library of Medicine (NLM) at the National Institute of Health (NIH). NCBI provides online provision of biomedical as well as genetically derived information and bioinformatics analytic tools (Tatusova et al., 2013). There are approximately 150,000 HLA allele nucleotide sequence data in NCBI. This includes both partial coding sequence (cds) as well as complete gene.

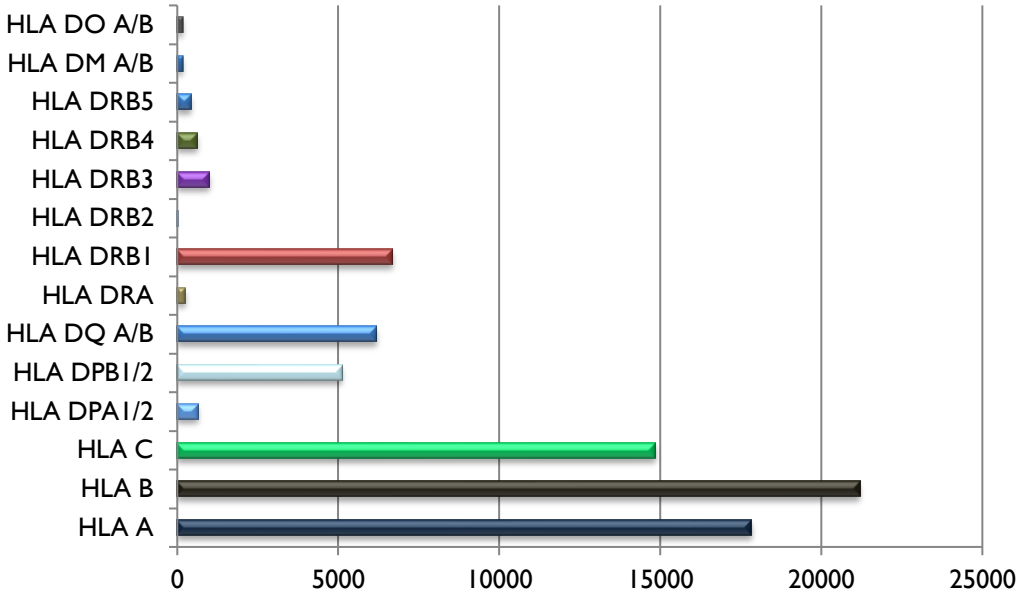


Figure 11: Approximate number of HLA class I and class II nucleotide sequences deposited in NCBI between the years 1993-2022

While NCBI holds most of the nucleotide sequences the structural as well as amino acid sequence data can easily be acquired from the primary structural database, PDB. Established in 1971 and becoming the first open-access digital source in biological sciences, the protein databank or PDB is the single global repository of experimentally determined 3D structures of biological macromolecules and their complexes. There are more than 180,000 entries managed by Worldwide Protein Data Bank organization (wwPDB). Till 2019, more than 690 HLA structures have been deposited in PDB.

There are other discrete and specific databases for immunology even though the data required can easily be acquired through NCBI, DDBJ or EMBL. Major immunoinformatics system includes immunological databases, sequence analysis, structure modeling and immunogenomics. There are more than 30 databases involved with immunology. IMGT (international ImMunoGeneTics information system), is a WHO approved database which provides data on MHC of human and other vertebrates. The database contains more than 15 integrated online tools for sequence, gene and structural analysis. MHCPEP is a database which contains details of MHC-binding peptides; BCIpep is a database of all B cell epitopes and IEDB (Immune Epitope Database) are a few of the immunological databases. NetMHC, is an online tool which

predicts the binding of peptides to several different HLA alleles using artificial neural networks, HLA Eplet Registry which provides details on HLA eplets and HLA allele frequency.

2.4.1 Epitopes and Eplets

Epitopes are those areas of an antigen which make up its antigenic property, or they are the immunologically active portion of an antigen. All though epitope is an operational or working definition, in a 3 dimensionally active antigenic molecule the number and size of the antigenic area determines its relation in evoking an immune response. An antigen can have single or multiple epitopes (Sypek, 2018). The term epitope is often used interchangeably with antigenic sites as well as antigenic determinants.

Typically, a functional epitope covers an area of 15 Å of the antigen (Tambur et al., 2014). Based on the native tertiary folding of a protein, epitopes can become B cell epitopes and T cell epitopes. This can be as a result of sequential or non-sequential amino acids of the protein and those made of non-sequential amino acids are called conformational epitopes. B cell epitopes, being hydrophilic, always tend to be on the surface of the antigen and does not always require an MHC dependent action. B cell epitopes can be protein as well as polysaccharides or lipopolysaccharides and are recognized by B cell receptors or antibodies. Large antigens always have overlapping B cell epitopes. T cell epitope involves a hetero-trimer tertiary complex which usually consists of an HLA, antigen peptide and T cell receptor. T cell epitopes are hydrophobic internal linear peptides usually formed by antigen processing and always involves antigen presenting cells and HLA complexes which usually ends up in humoral response. Unlike B cell epitopes, T cell epitopes are always protein-based components. Because of their dependency towards T cell activation, such protein antigens are called T-dependent antigens and those molecules like polysaccharide or lipopolysaccharide antigens, those contain repeating epitope units, which activate B cells without the need for antigen processing and presentation to T cells are called T-independent antigens. While the epitopes of polysaccharide antigens make up the short burst of immune responses, the epitope regions of T-dependent antigens contribute in the development

of long-term B cell memory. Epitopes, by their structural conformation, has 2 characteristics namely antigenicity, the ability to bind with an antigen and immunogenicity, the ability to evoke an immune response. While antigenicity depends on the structural alignment of the antigen, immunogenicity depends on the structural difference between the immunizer and the responding homologous protein. Such properties of an epitope, both B cell as well as T cell; make them dynamic in nature in around an antigenic protein relative to the sequence of the epitopes to which antibodies or TCR recognize. And such minor structural differences between dynamic epitopes determine its action after reacting with the responsive homologous protein. The investigations and analysis of histocompatibility at epitope level has a high impact in transplantation immunology as it helps in the identification of donor specific immunogenic epitopes as well as the level of immunogenicity (Argani, 2019; Duquesnoy & Marrari, 2009; Tambur & Claas, 2015).

The term 'eplet' was introduced into literature in early 2000 and has found its way into transplantation immunology very recently by becoming a trending topic in organ transplantation. Eplets are linearly distant and spatially adjacent configurations of amino acids triplets within a 3-3.5 Å radius in 3-dimentional conformation of an HLA protein complex. Within the last decade the analysis of eplets, its properties and its relation to graft survival has increased the understanding towards better possibilities in renal transplantation. Eplets, being a spatial arrangement of amino acids, exists in the same pattern in all the HLA classes with minor individual differences termed eplet mismatches (Duquesnoy et al., 2005). Eplets represent the theoretical description of all possible functional HLA epitopes. The nomenclature of eplets follows the amino acid number and single letter code of the associated polymorphic residue. For example, 76ANT represents an eplet containing alanine at 76th position, asparagine at 77th and threonine at 78th position and is present in a number of class I HLA alleles like HLA A*24:04, A*26:02, A*29:01, etc.; 69TNT represents an eplet containing threonine at 69th, asparagine at 70th and threonine at 71st position and is present in a number of class I HLA alleles like HLA B*08:01, B*13:02, B*14:01,B*15:02 etc.; 4R represents an eplet containing arginine at 4th position, and is present in a number of class II HLA alleles like HLA DRB1*01:01, DRB1*03:01, DRB1*08:01, etc., 46VY represents an

eplet containing valine at 46th position and tyrosine at 47th and is present in a number of class II HLA alleles like HLA DQB1*03:03, DQB1*04:03, DQB1*05:03, etc.

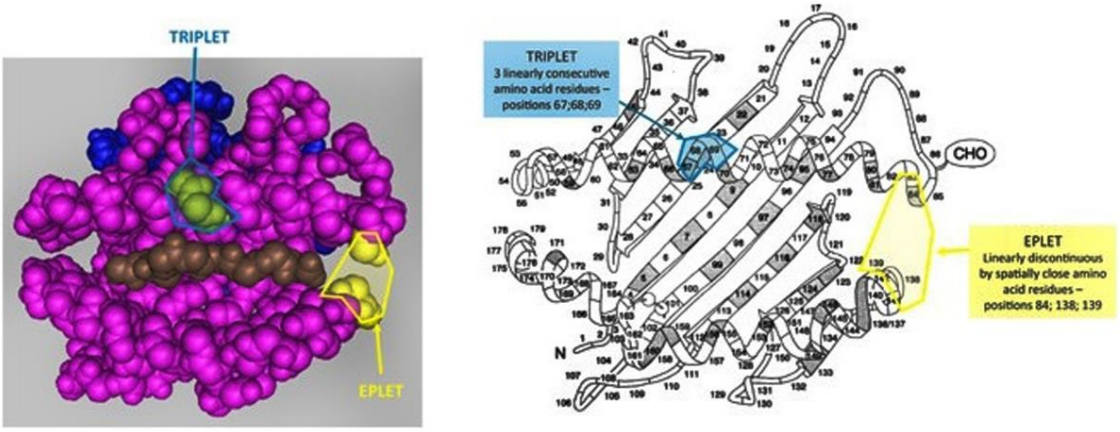


Figure 12: Triplets and eplets represented in space-fill model and plane-ribbon model (http://www.epitopes.net/what.html)

The fact that eplets as well as epitopes share the same area in 3-dimensional space in an antigenic protein complex, the eplets pose an important role in disclosing the immunological mechanisms that takes place during transplantation. This being the idea behind identifying the eplets in the first place, understanding the patterns of such shared amino acid sequences in unrelated individuals can be advantageously utilized to hand-pick potential donors having matched eplets for renal transplantation rather than selecting an HLA allele matched unrelated donor. Many structural epitopes have residue variations, that do not significantly alter their reactivity pattern with allo-antibodies. Antibody specificity is generally directed to those functional eplets with arrangements of dominant amino acid residues. Profiling of epitope and eplet of both patient and donor for understanding the degree of similarity can highly favor in predicting unwanted graft loss in future. The ideal way in which this can be executed is through computational biological approaches and the use of immunological simulation techniques.

2.4.1.1 Association of epitope/eplet mismatches and graft rejection

The concept of HLA epitope and HLA eplet matching carried out as a part of immunological profiling has provided the clinicians with a better hand in predicting

the possibility of chronic graft rejection in case of renal transplantation. Given the fact that, in 3D space, each HLA has multiple epitopes and each epitope has a unique set of eplets, considering the process of epitope and eplet matching between donor and recipient as a pre-transplant procedure seems highly significant. As the term histocompatibility suggests, understanding the structural aspects of each HLA protein complex can be used to identify structural compatibility between unmatched HLA allele rather than analyzing the incompatibility between very distant HLA alleles. Because the degree of structural compatibility is always dependent on the phenotype of HLA of the recipient, it is never to be excluded that the donor HLA allele should be structurally similar in terms of epitope or eplets. There are reports that anti-HLA antibodies have been strongly associated with increased risk of rejection and graft loss. Nonetheless, not all eplet mismatches elicits an immune response, indicative of a difference in immunogenicity of individual eplet mismatches. Multiple research in the past decade have demonstrated the fact that reduction of HLA-DR, HLA-DQ and HLA-DP mismatching at the eplet level can reduces allograft rejection and can improve transplant outcome (Argani, 2019; Lim et al., 2016; Sapir-Pichhadze et al., 2020; William et al., 2016).

2.4.2 HLA Matchmaker: A Tool for Eplet Analysis

In 2001, Prof. Duquesnoy published an article explaining the possibilities of using a specifically designed algorithm for analyzing the sequential mismatches between HLA alleles of patient and donor selected for transplantation, called HLA Matchmaker, a tool that determines HLA compatibility at structural level. Within the next 5 years he published 10 papers explaining both histocompatibility determination and HLA eplet matching as a strategy for renal transplantation as well as specifying its relevance in prediction of chronic graft rejection. The program HLA Matchmaker was originally introduced as a matching tool for HLA antigen rather than amino acids. Now HLA Matchmaker is a standard tool for analyzing HLA allele eplet mismatches as well as in identifying the possibility of acceptable mismatches which is considered for highly sensitized renal transplant patients (Duquesnoy et al., 1990). HLA Matchmaker is the only algorithm based on experimentally defined antibody-verified eplets. In terms of

humoral allo-immune response, HLA Matchmaker determines histocompatibility at eplet level rather than at antigen level.

HLA Matchmaker considers spatial triplet amino acids as motifs for immunogenic epitopes, stating the fact that antibodies are formed against those immunogenic epitopes resulting in antibody mediated rejection. The program itself is a sophisticated database which contains all the reported eplets of class I HLA ABC and class II HLA DPDQDR proteins. The program is designed as eplet mismatch calculators which can be used as a stand-alone excel worksheet. The program contains multiple worksheets; data entry, mismatch calculator, and specific list of all eplets in class I and II HLA. The HLA Matchmaker is provided as downloadable format through the website http://www.epitopes.net/what.html. The site is updated every 6 months and provides the user with 5 different programs. 1) The ABC Antibody Analysis Program which helps in the identification of eplet-associated antibody specificities and determination of eplet-based mismatched allele acceptability. 2) The ABC Eplet Matching Program which helps in determining the eplet loads, eplet listings and frequencies for up to 1000 donor-recipient combinations. 3) The DRDQDP Antibody Analysis Program which helps in the determination of antibody specificities against single locus and interlocus class II eplets and assessment of eplet-based mismatched allele acceptability. 4) The DRDQDP Eplet Matching Program which determines the eplet loads, eplet listings and frequencies for up to 1000 donor-recipient combinations and 5) the MICA Antibody Analysis helps which in the comparative analysis of MICA of patient and donor.

The recent updated versions of the HLA Matchmaker program are based on the data acquired form modeling of crystallized complexes of antibodies with different protein antigens. Now that the term eplet has been strictly related with the triplet polymorphic residues of an HLA protein residing within a 3 Å radius and epitopes being the higher arrangement of eplets residing within 15 Å radius, the interpretation of immunogenicity of an antigen has become clearer. Understanding the position, number and frequency of each eplet in both classes, I and II of donor and recipient can positively favor the process of transplantation, as the strong reason of chronic graft rejection might include the role of immunogenic eplets. Having the idea that minor structural difference in eplet can in turn convert an antigenic epitope to an immuno-

dominant epitope, this can be associated with increased immunogenicity. A major effort should be taken to include the epitope as well as eplet data and turn it into a clinically useful strategy.

Before considering the potential use of epitope or eplet matching in renal transplantation there are several factors to take into consideration as there are scientific gaps in the literature related to epitopes and eplets. To start with, there is very less scientific or clinical establishment of relation between association of immunogenic eplet mismatches and clinical outcome of renal transplantation (Lemieux et al., 2021). This results in a state that whether the use of total eplet mismatches or the number of immunogenic eplets should be considered for immunological risk assessment of the patient. Second, the unavailability of high-resolution HLA typing data could hinder the interpretation of HLA eplets, yet the 4-digit HLA typing has given promising results in minor population. Understanding the expression level of an HLA allele can provide the clinicians with more specific data which can be used to initiate a better strategy for renal transplantation.

2.4.3 EMMA: Epitope MisMatch Algorithm

The progressive development of technologies has paved its way resulting in the success of solid organ transplantation to a greater extent and has now reached a phase where the decision remains whether to consider allelic matching or switch to epitope matching. The fact that structurally based HLA matching can assist in the identification of compatible HLA allele pair and provide a decent allo-graft outcome, the method of 'epitope matching' is now a trending topic in organ transplantation which is supported via several publications (Duquesnoy, 2008; Lim et al., 2018; Tambur, 2018). In 2019, an HLA epitope mismatch algorithm named EMMA was released favoring the possibility of identifying epitope mismatch rather than eplet mismatch for class I and II HLA in renal transplantation. EMMA is a very user-friendly bioinformatic tool used to analyze class I and class II compatibility at amino acid level. The program was developed at the Department of Immunology, LUMC, by Dr. Sebastiaan Heidt, Dr. Dave Roelen and Dr. Frans Claas which is freely accessible through the website https://hla-emma.com/.

HLA-EMMA helps in simultaneous comparison of amino acid sequences of class I and class II HLA of patient with that of donor and determines the polymorphic solvent accessible amino acid mismatches that are likely to be identified by B cell receptors. The identification of such solvent accessible amino acid positions is carried out through publicly available crystal structures and open-source prediction tools with relative solvent accessibility (Kramer et al., 2020). The program works in collaboration with several HLA databases, HLA structure prediction tools and open-source immunological websites like IMGT/HLA, RCSB-PDB, pHLA3D, PORTER PALEALE 4.0 and NETSURF 2.0. The program aims to define the course of immunogenicity of specific HLA amino acid mismatches rather than eplet mismatches on class I and II HLA between a potential donor and recipient.

While Duquesnoy's HLA Matchmaker follows inter-locus comparison of HLA class I, the default setting of HLA-EMMA works as an intra-locus comparison algorithm between each amino acids of individuals. This promotes the precise identification of compatible mismatches rather than considering the triplet amino acid groups which might contain incorrectly classified or theoretical compatible amino acids. The use of EMMA alongside HLA Matchmaker can become a source for investigating the comparison between inter- vs intra-locus HLA class I and II mismatches.

2.4.4 Protein docking in HLA compatibility analysis

The enormous nucleotide data generated as a result of human genome project has paved way for sequence-based analysis of genetic as well as clinical conditions of individuals. For getting more clear idea on the value of such sequential data, much detailed study is needed about its function and its evolutionary significance. The in-depth sequential digging of nucleotide data has now become secondary as much of the developments in biotechnological as well as clinical field has been progressing with specific protein structural alignment, analysis and comparison. While nucleotide sequence comparison gave insights into sequence similarity and conserved sequences, protein structure alignment and amino acid sequence comparison provided details at expression level.

Structure-based molecular analysis has now become an essential tool in clinical field for faster and more cost-efficient study as well as discovery relative to the traditional method. Among the diverse strategies considered to improve the influx of data in the field of transplantation immunology, molecular protein-peptide and protein-protein docking of HLA complexes provides important insights into their structural and chemical features (Blaney, 2012). The currently available methods and algorithms for structure-based analysis already use open-source websites like RCSB-PDB for amino acid as well as crystal structural data and HLA eplet registry for HLA eplet data.

Based on the structural knowledge of previously defined HLA complexes, antigen peptides and other immune-related proteins and peptides, it has now become easy to incorporate such biological databases as well as structural resources into clinical immunology. Schrodinger, now being the scientific leader in developing the state-of-the-art chemical simulation software used in pharmaceutical, biotechnology and material science, itself provides the user with multiple possibilities for molecular structural analysis. There is around 70 websites/software that supports in ligand, peptide and protein docking. A few has been mentioned in table 1.

Table 1: List of a few stand-alone software and web-based servers for protein-ligand and protein-protein docking and protein binding affinity analysis

Sl no.	Program & Organization	Software category	Description
1	AutoDock Vina Extended, OneAngstrom	Academic, Open source, Stand-alone	Automated docking of ligand to macromolecule (Trott & Olson, 2010)
2	CABS-dock, University of Warsaw	Open source, Stand-alone and Server	A method for flexible protein-peptide docking without prior knowledge about the binding site (Kurcinski et al., 2015)

3	FITTED	Commercial, Stand-alone	Docking program with flexibility, covalent, metalloenzyme, displaceable water considerations (Moitessier et al., 2016)
4	FlexAid, University of Sherbrooke	Open source, Stand-alone	Analysis of side chain flexibility based on surface complementarity (Gaudreault & Najmanovich, 2015)
5	Galaxy PepDock, Seoul National Univeristy	Open source, Stand-alone and Server	Protein-peptide docking based on interaction similarity (Lee et al., 2015)
6	Glide, Schrodinger	Academic, Commercial, Stand-alone	An exhaustive search-based docking program (Friesner et al., 2006)
7	HADDOCK, Center Bijvoet Center for Biomolecular Research	Academic, Open source, Server	Developed for protein-peptide and protein-protein docking (Elez et al., 2018)
8	HEX, Dave Ritchie	Open source, Server	An interactive protein docking and molecular superposition program (Macindoe et al., 2010)
9	HyperChem, Motonori Tsuji	Commercial, Stand-alone	Flexible docking combination between predicted structure-based pharmacophores and ligand-based pharmacophores (Froimowitz, 1993)
10	PRODIGY, Bonvin Lab	Academic, Open source	A collection of web services focused on the prediction of binding affinity in biological complexes as well as the identification of biological interfaces from crystallographic one (Vangone & Bonvin, 2015)
11	BindProfX, Zhang Lab	Academic, Open source, Stand-alone	Interface profile score based on conservation of homologous interfaces (Xiong et al., 2017)

12	FoldX v4, Center for Genomic Regulation	Academic, Open source	Empirical energy score based on various energy parameters (Schymkowitz et al., 2005)
13	CCharPPI, Barcelona Supercomputing Center	Academic, Open source	Integrative web server which calculates interface packing and complementarity scores, empirical potentials at various resolutions, docking potentials and composite scoring functions (Moal et al., 2015)

Knowing the fact that, inside the human body, all functions based on protein, works on the basis of structure similarity or shape-complementarity. This aids in the binding of complex proteins to its substrate molecule to perform a specific biological function or interactions, like enzyme-substrate, hormone-receptor, antibody-antigen, HLA-peptide, etc. (Bertoni et al., 2017; Gromiha, 2010; Lee et al., 2014; Litwack, 2017; Renneberg & Loroch, 2016). In case of the complex human leukocyte antigen, understanding the protein structure can provide much more insights into the limitations in transplantation immunology, like the unavailability of a computational biological system for prediction of transplantation outcomes. Even though there has been much study about HLA in relation with infection, diseases and conditions, structure-based study which specifically involves renal transplantation is very less.

In 2010, Dai et al., mentioned in his article that HLA class II, DP2 has a direct genetic link with chronic beryllium disease(CBD), a fibrotic lung disorder which is caused by beryllium (Be) exposure and characterized by granulomatous inflammation and the accumulation of Be-responsive CD4+ T cells in the lung. The group released the first structure of an HLA-DP2 molecule, an HLA allele which has been directly involved with a human disease. The structural analysis of HLA-DR-DM complex, which forms inside the phagolysosome, carried out by Pos et al., in 2012 specifically points out that the flipping of the amino acid W29 from the binding groove enables a major conformational change that position hydrophobic HLA-DR residues into the P1 amino acid pocket. This results in the release of CLIP to free the peptide binding groove of HLA DR for antigen presentation. In 2016, Li et al., published an article providing

information on class I, HLA B*58:01 existing as a protective allele against HIV-1 infection. Ooi et al., in 2017 provides mechanistic basis for dominant protection effect of HLA DR1 associated with Goodpasture's disease, a human autoimmune condition.

The impact of next generation sequencing utilized for high-resolution HLA typing as a routine for solid organ transplantation would provide valuable information, including the existence of rare alleles in the population (Smith et al., 2019). The accuracy and difficulty of prediction of relation between an HLA molecule and its target protein rely on the complexity as well as the structural annotation of both molecules. The same is the reason why docking study is very much important in this context. In clinical field the next finest step would be the involvement of state-of-the-art computational techniques which would aid in prediction of chronic conditions as well as providing the detailed analysis of mechanism of action and as a better strategy for patient survival. As much as the literature suggests, till now there is only few studies that directly link molecular docking and transplantation immunology because much of the studies aims in understating and developing an explanation for autoimmune diseases (Caillat-Zucman, 2009; Fernando, 2008). All these structural studies suggest that the understanding of the HLA structure rather than their DNA element can reveal more insights into their molecular actions. Following the structural study, simulation studies can also be carried out which would provide much clearer idea on the mechanism of action of such complex protein structures. It's a known fact that the extraction of structural information and data from amino acids has been going on for decades and has been increasing rapidly.

In 1956, surgeon JE Murray, JH Harrison and nephrologist JP Merill from Peter Bent Brigham Hospital, Boston carried out the first ever successful renal transplantation between twins without immunosuppression. The patient survived for more than 8 years. Till today, as the scientific and clinical data suggests, there has been more than 1 million renal transplantations carried out globally. The story of organ transplantation being an outstanding accomplishment in the field of treatment of end stage renal disease (ESRD), it still is an ongoing challenge. Introduction and involvement of more sophisticated computational biological techniques into the field of clinical immunology can not only aid in the identification of a better choice but also in providing with a better strategy for procedures like transplantation. The better understanding of the emergence of immune-genomics and immunoinformatics not only as a tool for simulation of immunological reactions as an aid for academics or research, rather considering it as the best choice to learn the human immune system in its full capacity in interacting with both self and non-self-molecules. However, the principal aspect limiting the success of renal transplantation still continues to be the unavailability of a perfect donor.

"Intellectuals solve the problem, genius prevents them"

- Albert Einstein

3. MATERIALS AND METHODS

The study was conducted from a cohort of 1144 transplant patients and donors (n = 572 pair). Data collection, which includes CDC-cxm between patients and donor and HLA ID of both patients-donor, has been carried out from the Transplantation Immunology and Molecular Diagnostic Laboratory, Department of Nephrology, MIMS Hospital, Calicut, India, within a period of 50 months from January 2016 to Feb 2020. The data collection was initiated after receiving approval (IEC Reg. No. ECR/01/inst/KL/2013) for data collection from the institute. Details of brain-dead or cadavers were not used for the study.

Preliminary complement dependent cell-cytotoxicity crossmatching (CDC-CXM) assay were carried out for all the samples were carried out for analyzing the presence of pre-formed antibody. Sequence-specific primer (SSP) PCR and Sequence-specific oligonucleotide (SSO) probes PCR HLA typing was performed for identifying individual specific HLA alleles. Further eplet matches/mismatches were ascertained by HLA Matchmaker for the assessment of graft survival. Molecular modeling, protein docking and biostatistical analysis has been carried out to attain the present results.

3.1 Identification of percentage of pre-formed antibody in patients using CDC-crossmatching

CDC-crossmatching is a cell viability test that helps in the detection of pre-formed antibodies in transplant recipients. This clinical test interrogates the risk that the recipient immune system will recognize a potential allograft as foreign to self, and thereby initiate inflammatory events resulting in graft damage, rejection and death. The test was first introduced in early 70s and still is considered as a gold standard for almost 75% pre-transplant clinical test carried out in India. CDC-cxm still provides direct evidence of presence of potential allo-antibodies.

The method combines recipient serum and donor lymphocytes *in vitro* and analyses the production of donor-reactive allo-antibodies from patient serum (Patel & Terasaki, 1969). This allo-antibody binds to donor cells forming Ag-Ab complexes resulting in

complement activation leading to cellular cytotoxicity. The amount of allo-antibodies production is determined by percentage scoring on cytolysis.

3.1.1 Isolation of donor lymphocytes

10 ml of donor blood collected in a heparin/EDTA-coated tube were added to 3 ml of density gradient taken in a 15 ml centrifuge tube. This was centrifuged at 2000 rpm for 20 minutes at room temperature. The spinning resulted in separation of RBC, buffy coat and plasma. The buffy coat containing lymphocytes, appeared in the middle between the RBC pellet and plasma, were transferred to a new tube. To the collected buffy coat 5 ml RPMI-1640 was added. This was centrifuged at 2000 rpm for 20 minutes. The supernatant was discarded, and pellet was washed with RPMI-1640 and repeated the spin. The supernatant was discarded and RPMI was drained. The pellet was resuspended in RPMI and used for crossmatching.

3.1.2 Crossmatching

1 µl of paraffin oil was added to all the reaction wells of a Terasaki tray. Serum was prepared in 4 dilutions; 2 µl, 1 µl, 0.5 µl and 0.25 µl and added to all the reaction wells. Internal non-reactive serum as negative control and a reactive serum as positive control were included in the test. Using Hamilton syringe 1 µl of donor lymphocytes were added to all wells including positive control and was incubated for 60 minutes. After incubation 1 µl anti human globulin (AHG) was added to all the wells to increase the sensitivity of the reaction. After incubating for 5 minutes, 5 µl of complement is added to all the wells and incubated for 2 hours, followed by the addition of 5 µl of Eosin Y to all wells and again incubated for 5 minutes. After incubation 5 µl of formalin is added to all the reaction wells. A cover glass seal is placed over the plate and incubated overnight at 2-4^{0}C.

3.2 Identification of HLA ABDR alleles of patients and donors via molecular typing

The objective has been focused on identifying the individual HLA ABDR alleles of both patients and donors by using SSP- and SSOP-PCR. Molecular HLA typing was carried out by SSP-PCR (HISTO TYPE ABDR-SSP Kit, BAG Diagnostics GmbH) and

SSOP-PCR (HISTO SPOT® SSO Kit, BAG Diagnostics GmbH) using purified DNA extracted from both patients and donors. SSP-PCR uses primer coated PCR reaction tubes complementary to HLA ABDR nucleotides, were as SSOP-PCR uses hybridization of amplicons to SSO probes fixed on the bottom of a microtiter plate (explained in review, section 2.3.3)

3.2.1 Isolation DNA from blood

From the QIAmp DNA Mini kit (QIAGEN) 20 µl of proteinase K was added to a 1.5 ml micro-centrifuge tube. To this 200 µl of sample blood was added along the wall. 200 µl of lysis buffer was added to the sample and mixed by pulse vortexing to yield a homogeneous solution. This mixture was incubated at 56^0C for 10 minutes followed by centrifugation at a low rpm to remove drops from the inside of the lid. To this homogenate 200 µl of ethanol (96%) was added and mixed by pulse vortexing. Centrifugation was repeated remove drops from the inside of the lid.

The total sample mixture was then transferred to QIAamp Mini spin column (in a 2 ml collection tube) without wetting the rim. The spin column was centrifuged at 6000 xg (8000 rpm) for 1 minute 30 seconds, RT. The tube containing the filtrate was discarded and QIAamp Mini spin column was placed in a clean 2 ml collection tube. To the spin column 500 µl of Buffer AW1 was added and centrifuged at 6000 xg for 1 minute 30 seconds. The spin column was collected and transferred to a fresh 2 ml collection tube and filtrate was discarded. This was followed by the addition of 500 µl Buffer AW2 and then centrifuged at 13000 xg (12000 rpm) for 4 minutes 20 seconds. The pellet was transferred to new a collection vial and 200 µl elution buffer was added. After 2-3 minutes the mixture was centrifuged at 6000 xg for 1 minute 30 seconds. After centrifugation the eluate was transferred to a new vial and stores at -20^0C.

3.2.2 HLA typing via SSP-PCR

The HISTO TYPE kits are used for HLA typing on molecular genetic basis. The basic material for typing with HISTO TYPE SSP kits is purified DNA samples. The test procedure is done using the sequence specific primers (SSPs). The method is based on the fact that primer extension and hence successful PCR relies on an exact match at

the 3'-end of both primers. Therefore, only if the primers entirely match the target sequence the amplification is obtained, which is subsequently visualized by agarose gel electrophoresis. The composition of the primer mixture guarantees a reliable identification of the HLA types based on the latest sequence data.

HISTO Type kits contains (i) plates/strips for the HLA typing - the pre-dropped and dried reaction mixtures consisting of allele specific primers, internal control primers (specific for the human G3PDH gene) and nucleotides. The lot number is printed on each plate/strip. (ii) PCR strips - contamination control with internal control primers and amplificate specific primers. (iii) 10x PCR buffer and (iv) strip-caps or PCR foil. Taq polymerase (KAPA Taq 5U/µL, stored at -20^{0}C) is also used. A reliable typing is guaranteed if 25-50ng DNA per reaction mix were used.

The PCR reaction was performed in 96 well primer-coated reaction tubes (Lot no.98533), were the first 24 wells contains primers for HLA A allele, the next 48 wells for HLA B allele and the remaining 24 wells for HLA DR allele. DNA from individual patients was extracted (DNA QIAmp DNA Mini kit, QIAGEN) and as mentioned in section 3.2.1. All pre-aliquot and dried reaction mixtures already contain allele-specific and control-specific primers and nucleotides. To this 25-30 ng DNA (quantified via Qubit ds DNA Quantification Kit) was added followed by vortexing. This was immediately followed by the addition in to the primer-coated PCR reaction tubes. The total reaction volume of 1020 µl contained 808 µl dH_2O, 102 µl 10x PCR buffer, 102 µl DNA and 8 µl KAPA Taq (5U/µl). From the total reaction volume of 1020 µl the amplification parameters were optimized to a final volume of 10 µl for each of 96 reaction wells. The amplification products were run in 2%, 96 well agarose gel and viewed under a UV trans-illuminator and documented. The first well of the gel is kept as negative control.

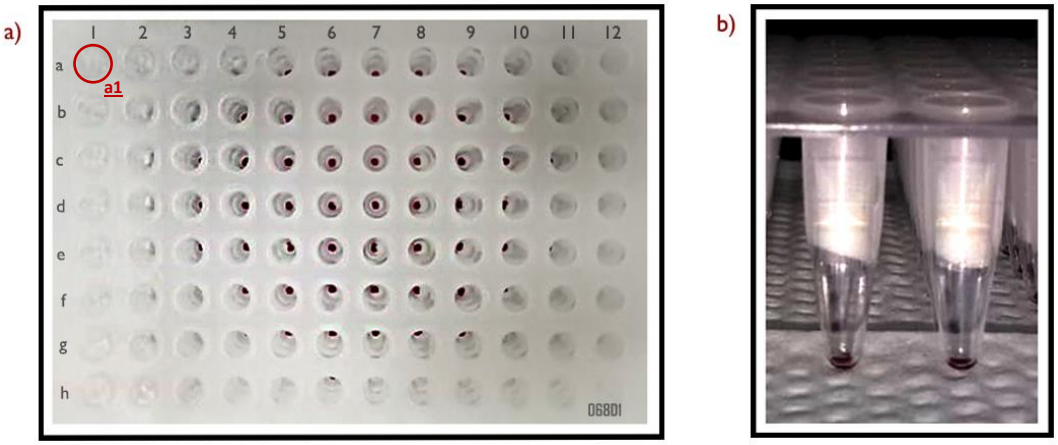


Figure 13: PCR reaction tubes for SSP-PCR containing pre-dried primer droplets coated at the bottom of 200 µl, 8x12 PCR tubes. a) Aerial view of the PCR tube (well a1 is the negative control) and b) Lateral view of the SSP-PCR tube

Program-Step	**Temp.**	**Time**	**No. of cycles**
First Denaturation	96°C	5 min	1
Denaturation	96°C	20 sec	5
Annealing + Extension	68°C	1 min	
Denaturation	96°C	20 sec	10
Annealing	64°C	50 sec	
Extension	72°C	45 sec	
Denaturation	96°C	20 sec	15
Annealing	61°C	50 sec	
Extension	72°C	45 sec	
Final Extension	72°C	5 min	1

Table 2: PCR amplification parameters for SSP HLA genotyping (HISTO Type ABDR-SSP, BAG Diagnostics GmbH)

3.2.3 HLA typing via SSOP-PCR

Sequence specific oligonucleotide probe (SSOP) hybridization helps in the detection of single nucleotide mismatch with a high degree of efficiency. SSOP-PCR is a useful tool that has the advantages of high specificity, sensitivity, and low sample size. Unlike SSP reaction the PCR method and parameters set up for SSOP-PCR is different.

For SSOP-PCR, the reagents and primers are separate for each of HLA A, HLA B and HLA DR allele for both patient and donor. HISTO SPOT® A (lot number - 967D1), B (lot number - 967D1) and DR (lot number - 967D1) allele kit contains 1100 µl master mix & 600 µl $MgCl_2$ and HISTO SPOT® reagent kit (lot number - 2009K4) contains 80 ml blocking buffer, 40 ml hybridization buffer, 100 ml stringent wash buffer, 100 ml TBS wash buffer, 36 ml substrate and 40 µl conjugate for a total of 96 reactions. The master mix contains primers, dNTPs, Taq polymerase and H_2O. For each single allele reaction 10 µl master mix, 5 µl $MgCl_2$ and 5 µl DNA was used. For identifying the allele of a single patient-donor pair 20 µl master mix, 10 µl $MgCl_2$ and10 µl DNA was used. All the reagents needed for the reaction were added to the reagent trays inside the instrument. The HLA ABDR worksheet has been loaded into the automated MR. SPOT® processor along with the 'lot number' of each allele via a barcode reader. Finally, the allele coded SSO probe containing microtiter strips were placed, the purified DNA sample was loaded to the reaction plate and the program was launched. Hybridization occurs between the amplicon of HLA A, B, DR and the SSO probes fixed on the bottom of the microtiter plate. The resulting pattern of positive probes was interpreted as genotype using HISTO SPOT® software using different worksheets for each typing.

Program-Step	Temp.	Time	No. of cycles
First Denaturation	96°C	2 min	1
Denaturation	96°C	15 sec	5
Annealing + Extension	65°C	1 min	
Denaturation	96°C	10 sec	10
Annealing	61°C	50 sec	
Extension	72°C	30 sec	
Hold	22°C	∞	

Table 3: PCR amplification parameters for SSOP HLA genotyping (HISTO SPOT® ABDR-SSO, BAG Diagnostics GmbH)

3.2.4 Identification of HLA ABDR alleles via HISTO SPOT®

HISTO MATCH HISTO SPOT® HLA AB and HLA DR (BAG Diagnostics GmbH) SSP module has been used for the interpretation SSP-PCR results and HISTO MATCH HISTO SPOT® SSO module (V 3.0.41, 2017), has been used for analysis and identification of 4-digit HLA ABDR alleles of both patient and donor. The application requires a SQL server database to store data, results and images which can be used to run both SSP and SSOP results.

For the data interpretation of SSP-PCR, each allele was selected separately (HLA A, HLA B and HLA DR) following the selection of SSP module and the lot number provided with the HLA ABDR PCR primer kit. Keeping the SSP gel image as reference the bands were traced on to the provided software window, corresponding to HLA A, HLA B and HLA DR. Each added band were seen as white highlights. The results were interpreted by HISTO MATCH using the values obtained from the image.

For analysis and interpretation of SSOP-PCR the data from MR. SPOT® processor was transferred to the HISTO MATCH software. Unlike SSP-PCR, there is no gel image for analyzing of SSO probe hybridization; rather there is an image of an Affymetrix array or a grid. After importing the HLA ABDR work lists, gridding was carried out where the grid size and positions were identified followed by spot

measurement where each spot is measured, and values are assigned for intensity and background. Positive probes are shown with a red circle in the image. Negative probes are shown with a blue circle and control probes are shown in green.

Results of both SSP-PCR and SSOP-PCR are displayed as 4-digit allelic ID following the standard HLA nomenclature method (annexure II).

3.3 HLA ABDR eplet mismatches analysis using HLA Matchmaker

HLA Matchmaker is a structurally based algorithm which considers HLA as a string of antigenic determinants represented by eplets. HLA Matchmaker work files for ABC Eplet Matching and DPDQDR Eplet Matching V2.2, 2018 was downloaded from http://www.epitopes.net/. HLA AB and HLA DR allelic pair of both patients and donors was analyzed using this algorithm and HLA ABDR allelic matches/mismatches were noted and tabulated. The 4-digit HLA ABDR allele data (n = 572) was used to identify the eplets and the mismatches between each pair of patient-donors. The program has two work files of the same algorithm. One analyses class I antigens ABC and the other is for analyzing class II antigens DPDQDR.

3.3.1 Data entry and result interpretation in HLA Matchmaker

The program makes use of the spread-sheet format of Microsoft excel. Details such as patient ID, HLA A/A, HLA B/B and HLA DRB1/DRB1 of both patient and donors were entered into the first sheet. The data can be entered in the 'enter data' sheet, filling each tab corresponding to the patient as well as the d allele. The nomenclature of HLA is strictly followed while performing the data entry. Here, only HLA AB and HLA DR alleles were analyzed as they were found to be more important over HLA C and HLA DPDQ in renal transplantation.

After data entry, the eplets are automatically generated in the 'result sheet'. This includes the number of Ab-verified, Ab-non-verified and total number of eplets for each allele of HLA AB and HLA DR. The result also gives the position number of mismatched eplets between each allele of the patient and the donor. Both ABC Eplet Matching and DPDQDR Eplet Matching V2.2 worksheets contains database which shows all the possible eplets in the alleles. In ABC Eplet Matching the database page is

EP and in DPDQDR Eplet Matching P, Q, R; DBR345-DQ Association and DQBDQA are the pages representing the database.

3.4 Analysis of structural similarity of selected HLA alleles with matching eplets using protein structure modeling

This section of the work includes the modeling of HLA DRB chains and analysis of structural variations between each chain by superimposing. The completion of structural investigation on HLA rests on the quality of the alignment of a query with a target protein. The idea of a protein structural alignment is defined as one-on-one comparison and mapping between the amino acid residues of each protein (Çamoğlu & Singh, 2007). Here, HLA DR amino acid sequences have been used for protein structural modeling. The modeled structures were super-posed to identify the areas which are structurally dissimilar, amino acid number of loops and turns, positions of α helices and β turns, etc.

Translated sequences of 8 HLA DR alleles has been selected from NCBI, namely HLA DRB1*01, *04, *07, *08, *09, *12, *14, *16, with accession numbers MN068246 (10.5 kb), AB715389 (15.1 kb), AB715392 (13.8 kb), AB715393 (16 kb), AB715399 (13.7 kb), AB715397 (13.8 kb), AB715398 (11.4 kb) respectively. The HLA DR alleles were selected based on frequency of HLA DR alleles observed in the study population, sequence availability in NCBI and increased number of eplet mismatch observed in class II HLA, analyzed in the section 3.3.1. The allele sequences were used for protein modeling using SWISS MODEL accessible via EXPASY web server https://swissmodel.expasy.org/ and structural variations were determined (Bienert et al., 2017).

3.4.1 Protein modeling using SWISS MODEL

SWISS MODEL is a fully automated protein structure homology-modeling server. The algorithm uses BLAST search and HHBlits against Uniclust30 for evolutionary related structures matching and a final number of 50 templates for modeling the desired structure (Camacho et al., 2009; Geux et al., 2009; Mirdita et al., 2017; Steinegger et al., 2019; Waterhouse et al., 2018). The validation report of the final structures along has been analyzed, noted and tabulated. Total of 8 structures

were modeled using SWISS MODEL and compared. The structures were studied for its differences at structural and amino acid level. The structural variations were studied from the validation report provide by the server. The residues found in all protein polypeptide chains of the model were displayed in an interactive sequence display. The Ramachandran plot analysis was carried out to assess the stability of the modeled structures. The percentage of torsion angles phi Φ and psi Ψ for allowed structural geometry was noted.

3.4.2 Structural variation study by superimposition

All the 8 modeled structures mentioned in the above section 3.4.1 were finally superimposed using Schrodinger Maestro 11.2, 2018, for specifying the structural variation determinants on each protein. The amino acid number, position of loops and turns, positions of α helices and β sheets has been noted and tabulated (table 5, section 4.4).

3.5 Protein docking and comparative analysis of binding affinity between HLA-Ag-TCR tri-molecular complex for the identification of compatible HLA DRB structures

The 8 HLA DR structures modeled using SWISS MODEL mentioned in section 3.4.1 were used for the protein docking study. Each structure was studied to amino acid and eplet level. The class II HLA DR structures and antigenic peptides were selected on the basis on understanding the immune mechanism taking place during an immune recognition process. In reality, a class II HLA protein presents a processed antigenic peptide, within 13-18 amino acid length, to TCR. This mechanism was simulated using the docking studies. Out of the 8 structures HLA DRB pairs having eplet mismatches and no eplet mismatches have been identified and categorized from the HLA DRB eplet mismatch data table 40-42, annexure IV. The number of amino acids, position of loops and turns, positions of α helices and β sheets helped in identifying the binding area of the HLA DR protein with an antigen peptide.

Required structural optimization was carried out with the aid of Schrodinger Maestro 11.2, 2018. The target area on each HLA DR protein was marked and docking was performed using ZDOCK server (V3.0.2) http://zdock.umassmed.edu/ (Chen et al.,

2003; Pierce et al., 2011; Pierce et al., 2014). The HLA-Ag bi-molecular complex thus formed was again docked with TCR chain, forming the HLA-Ag-TCR tri-molecular complex. The structural properties of all the molecular complexes such as percentage of non-interacting surfaces per property (NIS), no. of interatomic or interfacial contacts per property (ICs), binding energy (ΔG) and dissociation cont. (K_d) was calculated using PRODIGY server https://bianca.science.uu.nl/prodigy/.

3.5.1 Selection of peptide and TCR for HLA interaction study

To study the initial peptide interaction between HLA and antigenic peptides, natural viral peptides and CLIP (class II associated invariant chain peptide) were selected from PDB. Further, the molecular complex attained from HLA-bound antigen peptide was used to demonstrate the interaction between HLA-Ag and TCR. For this the antigen peptides were separated from its co-crystallized structures (PDB ID 1aqd, 1dlh, 1kg0, 1h15 and 1sje) (Lang et al., 2002; Mullen et al., 2002; Murthy & Stern 1997; Stern et al., 1994; Zavala-Ruiz et al., 2004). CLIP peptides were also retrieved (PDB ID 1a6a and 4x5w), for demonstrating the strength of relation between a class II HLA structure and a self-peptide (Ghosh et al., 1995; Wieczorek et al., 2016). TCR structures (PDB ID 2xna, 4udu and 3of6) were also retrieved for demonstrating the tri-molecular interaction between HLA-Ag-TCR (Pang et al., 2010; Rödström et al., 2015; Saline et al., 2010). All the TCR structures were also obtained as co-crystalized with either an HLA DR protein or an enterotoxin. The number of amino acids, structural resolution, and quality of the crystal structure were noted and tabularized.

3.5.2 Protein preparation of HLA DRB, Ag-peptides and TCR chains

All the HLA DR-Ag peptide complex were treated as representatives of donor and TCR as representative of a transplant recipient, used to demonstrate the strength of an immune reaction after transplantation. All the modeled as well as the selected structures were having resolution between 1.9 Å and 2.9 Å (table 4, section 4.4). The selected HLA DRB chains, antigen peptides and TCR chains were subjected to the addition and optimization of hydrogen bonds, removal of H_2O molecules and finally performing restrained minimization to attain the final structure for docking studies.

3.5.3 Docking study using ZDOCK

ZDOCK is a free automated Fast Fourier Transform based protein docking protein server authored and maintained by Zhiping Weng's lab (ZLAB) at the University of Massachusetts Medical School. The program searches all possible binding modes in the translational and rotational space between the 2 proteins and evaluates each pose using an energy-based scoring function. The version 3.0.2 program needs .pdb files as input. The HLA DRB chain as 'PROTEIN 1' was uploaded to the 'INPUT 1' section and a CLIP/peptide as 'PROTEIN 2' was uploaded in the 'INPUT 2' section. For ZDOCK, 'INPUT 1' was considered stationary and 'INPUT 2' was allowed to move, to create different pose. The final prepared HLA DRB chains, CLIP, Ag-peptides and TCR chains were analyzed to identify the interactive area of each chain with which the docking grid must be generated. The interactive grid of HLA DRB chain was identified to be 50 amino acid residues, lying between 30^{th} and 80^{th} amino acid residues. All the other residues were blocked. The docking was performed in such a way that each of the HLA DRB chain was first docked with the CLIP peptides and then performed docking with other Ag-peptides. The resulted HLA DRB-CLIP/Ag complexes were docked with TCR chain to from HLA-Ag-TCR tri-molecular complexes. All the results were tabulated and studied.

The docking between DRB-CLIP/Ag complexes and TCR chain was carried out for verifying the process of immune reaction between an antigen presenting HLA protein on the surface of an antigen presenting cell and T cell receptor protein on the T cell surface.

3.5.4 Binding energy analysis using PRODIGY

PRODIGY (PROtein binDIng enerGY prediction) is a collection of web services focused on the prediction of binding affinity in biological complexes as well as the identification of biological interfaces from crystallographic structures, which relies solely on the properties of the protein-protein complexes. PRODIGY server takes the structural data input as 3D structure in .pdb format. The working principle relies on the calculation of direct correlation between the numbers of interfacial contacts (ICs) in a protein-protein complex to analyze the final binding strength.

Considering that 50 amino acids were selected as the grid/binding area in class II HLA DRB and 15 amino acid as the standard length of CLIP, the total selected number of amino acids for HLA-CLIP docking were 65. The total number of amino acids in the interactive grid area for the Ag peptides was 64, 63, 65, 64 & 66 depending on the length of each peptide (table 6). The bi-molecular and tri-molecular complexes obtained after docking were analyzed for binding energy ΔG, between HLA-CLIP, HLA-Ag and HLA-Ag-TCR using PRODIGY (Kurkcuoglu et al., 2018; Vangone et al., 2015; Xue et al., 2016). To analyze the binding energy the .tar.gz compressed files were uploaded. The chain name of each protein/peptide was provided, and the uploaded structure was submitted for binding energy calculation. The value of the dissociation constant (K_d) is calculated at 37^0C. The predicted value of the binding affinity (ΔG) expressed in kcal mol^{-1} and calculated value of the dissociation constant (K_d) from percentage of NIS and no. of ICs per property, was noted and tabulated.

3.6 Biostatistical analysis on HLA ABDR eplet mismatches in relation with renal graft survival

Biostatistical analysis was carried out using SPSS V16.0, to analyze the possibility of occurrence of graft rejection in relation to the increased number of HLA ABDR eplet mismatches between a patient and a donor.

3.6.1 Study population and data analysis

Statistical analysis was performed using SPSS (Version 16.0). The statistical data were analyzed for finding the association between HLA ABDR eplet mismatches and chance of rejection of the transplanted graft. Each HLA allelic pair both of patient and donor was analyzed for number of eplet mismatches using HLA Matchmaker. The results were compared for identifying its relationship with any sort of graft rejection episode in a specific time frame.

The patients were grouped according to sex, days of survival from the date of transplantation, number of immunosuppressant medications, number of HLA AB, HLA DR eplet mismatches and present condition of the graft (surviving or rejected). The distribution of patient-donor allelic incompatibility was found using logistic regression analysis. HLA AB, HLA DR eplet mismatches and present condition of the graft were

taken as variable 1, 2 & 3 respectively. The association between broad antigen mismatches and eplet mismatches was performed using Pearson correlations (r) and analyzed for its relationship with graft rejection. Correlations were presented with P value 0.05 and 95% confidence intervals (95% CI). The results have been noted and tabulated.

4. RESULTS

The samples collected from the cohort of 1144 transplant recipients and donors (n = 572 pair) were subjected to CDC-cxm for identification of pre-formed antibody. SSP- and SSOP-PCR analysis was carried out for identification of HLA allele of both recipients and donors. Further eplet matches/mismatches were determined by HLA Matchmaker for the assessment of graft survival. This was followed by molecular modeling, protein docking and biostatistical analysis. Following are the results of the study.

4.1 Pre-formed antibody detection by CDC-crossmatching

CDC-cxm was done for the identification of cross-reacting antibody as well as pre-formed antibody in recipient serum.

4.1.1 Lymphocyte isolation from donor blood

The lymphocytes were obtained as layer of cells between the serum in the upper phase and RBC settled in the lower phase. The cells were separated using a micropipette and transferred to a fresh tube and performed crossmatching.

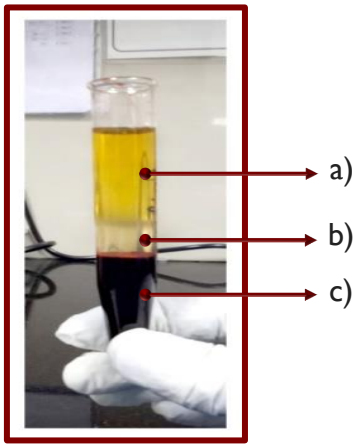


Figure 14: Images showing lymphocyte separation from donor blood after centrifugation at 2000 rpm a) upper serum layer b) middle buffy coat containing lymphocytes c) lower layer containing settled RBC

4.1.2 Crossmatching

The cells obtained after isolation and washing were subjected for antibody reaction in presence of complements. The presence of pre-formed or cross-reacting antibody leads to cell lysis. The cells are stained with eosin Y. The live cells are observed as having a clear round morphology. The result of CDC-cxm is termed negative for no cell death. Recipients with the percentage cytotoxicity less than 2 are generally suitable for transplantation. A result showing more than 15% cell death is not recommended for transplantation.

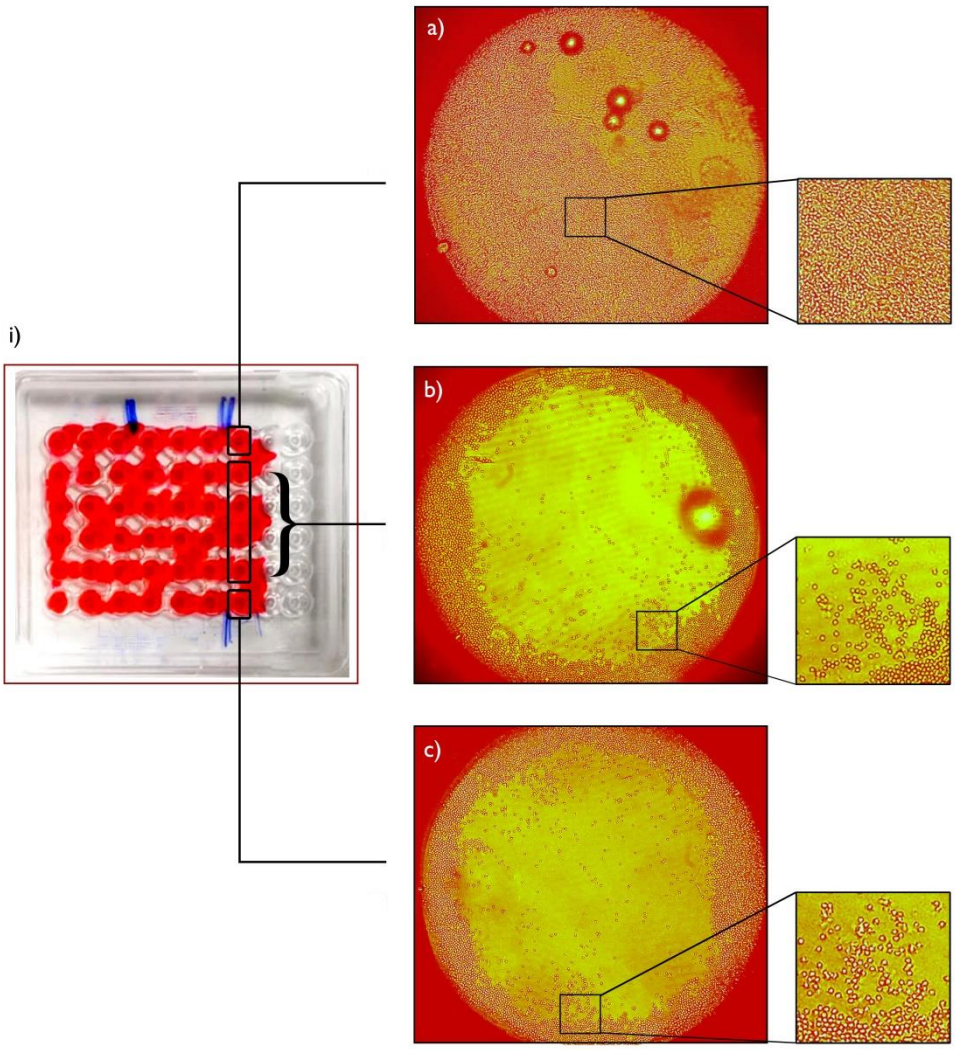


Figure 15: i) Image of CDC-crossmatch performed in a Terasaki plate after final incubation and addition of Eosin Y, a) close-up view inside internal positive control well, showing reaction between donor lymphocytes and pooled reactive serum, b) close-up view inside reaction well containing donor lymphocytes and recipient serum, c) close-up view inside negative control well (live cells) without the addition of serum.

All the cells in the positive control well were observed as dead. Reactive serum of sensitized patients was pooled and used as internal positive control. The reaction wells had a very less visible cell death. Normal lymphocytes isolated from donors without adding serum, were used as negative control, and were observed as complete live cells.

The table showing the CDC-cxm details between 572 patients and donors has been added in table 38, annexure I. Of the 572 patients subjected for CDC-crossmatching. 538 samples were CDC negative; 25 samples were AHG positive, and 9 samples showed high cell deterioration against recipient serum, having 10%, 20-30%, 40-60% and 60-80% antibody positivity against donor lymphocytes. Patient set no. 376 and 475 showed borderline CDC positivity.

4.2 HLA ABDR allele identification of donors and recipients via molecular typing

The objective focused on the identification of individual class I HLA AB and class II HLA DR alleles of donors and recipients. There were 20 different HLA A alleles, 28 different HLA B alleles and 13 HLA DRB alleles identified for 1144 individuals.

4.2.1 Isolation of DNA from blood

The DNA from both donors and patients were isolated and purified using QIAmp DNA Mini kit (QIAGEN) by column-based method, quantified using Qubit ds DNA quantification kit and stored at -20^{0}C. The purified DNA having a concentration of 25-30 ng was used for performing SSP- and SSOP-PCR analysis.

4.2.2 SSP-PCR analysis

The PCR reaction was performed in a 96 well plate in a thermal cycler (Veriti, Applied Biosystems) with the specific PCR amplification parameters provided with the HISTO Type ABDR-SSP kit. The amplified products were run in a 2%, 96-well agarose gel as described in section 3.2.2. The gel was visualized under a UV trans-illuminator. Specific bands were observed in the gel confirming the amplification of the specific

HLA ABDR alleles. A single agarose gel can only be used to run the class I HLA AB and class II HLA DR of one patient-donor sample.

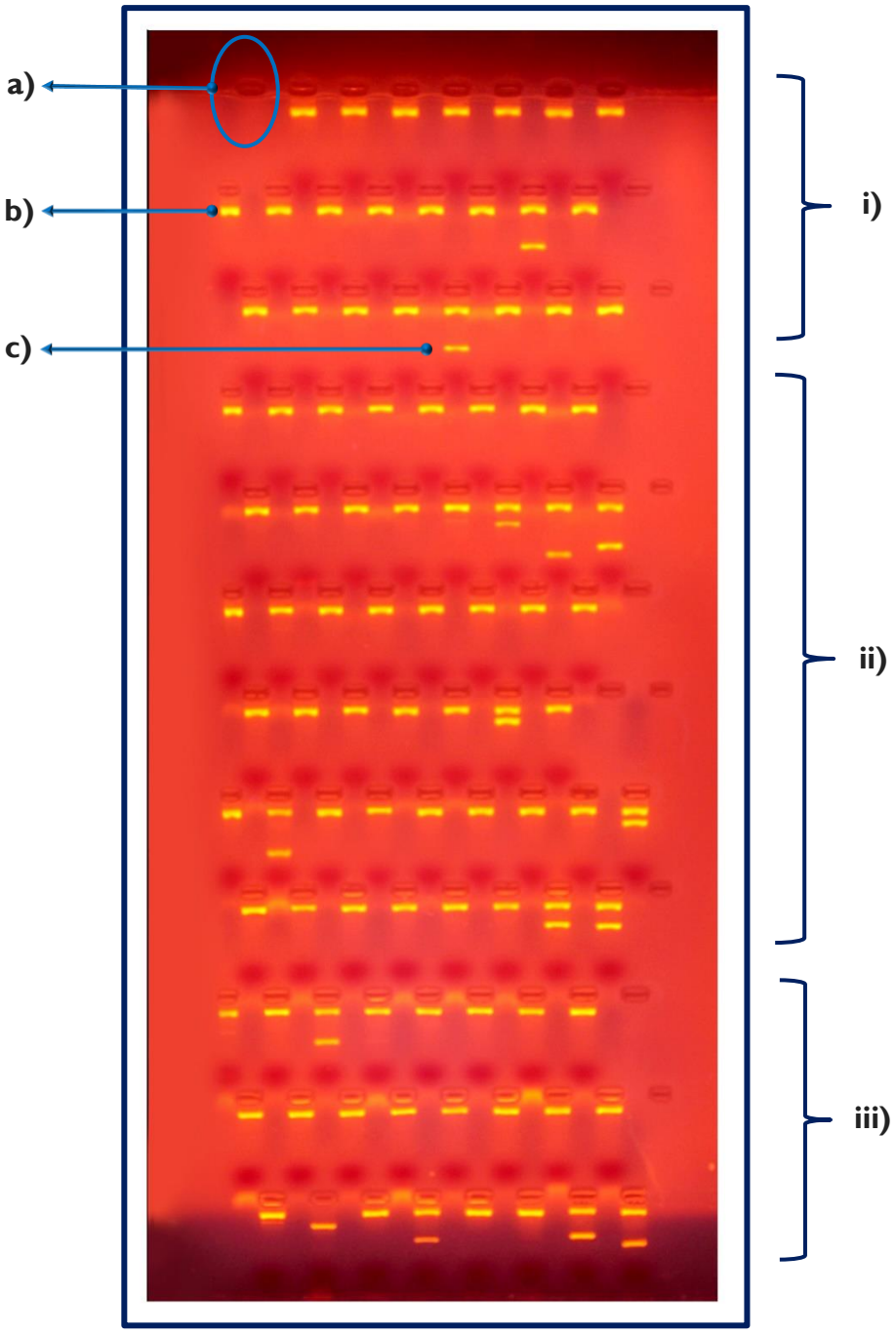


Figure 16: The gel image represents the SSP-PCR reaction between a single patient-donor pair. Image shows 96-well agarose gel after SSP-PCR run. a) negative control, b) positive control, 1070bp, c) allele specific amplification, i) specific amplified bands showing the amplification of HLA A allele in 23 wells, ii) specific amplified bands showing the amplification of HLA B allele in 48 wells and iii) specific amplified bands showing the amplification of HLA A allele in 24 wells.

In all lanes the 1070bp positive control was clearly visible. No band was visible in the negative control. Each band represents an allele which is specified by the manufacture and amplified by the pre-dried primers.

4.2.3 HLA ABDR alleles interpretation via HISTO SPOT® for SSP-PCR

Using the software database of HISTO MATCH HISTO SPOT® individual HLA ABDR alleles of both donor and recipient has been identified. The software dataset is updated every year for which each new allele would be added.

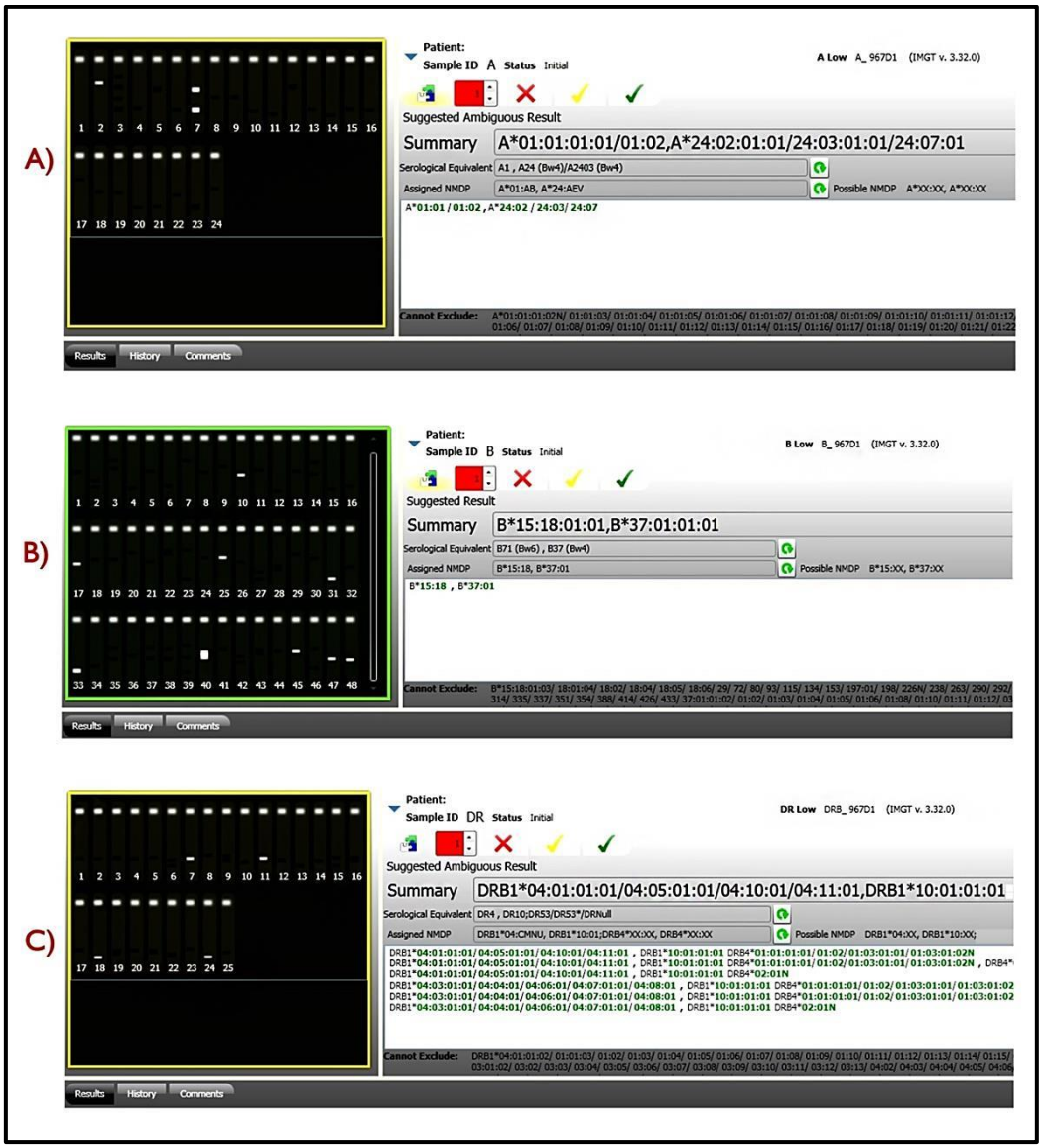


Fig 17: Image representing the interpretation of HLA ABDR allele using HISTO MATCH HISTO SPOT®, after SSP-PCR electrophoresis gel, using gel image as reference

4.2.4 SSOP-PCR analysis

The PCR reaction was performed in a 96 well thermal cycler (Veriti, Applied Biosystems) with the specific PCR amplification parameters provided with the HISTO SPOT® ABDR-SSO kit. The SSOP- reaction can be performed for multiple numbers of patients at time and the procedure is more reliable.

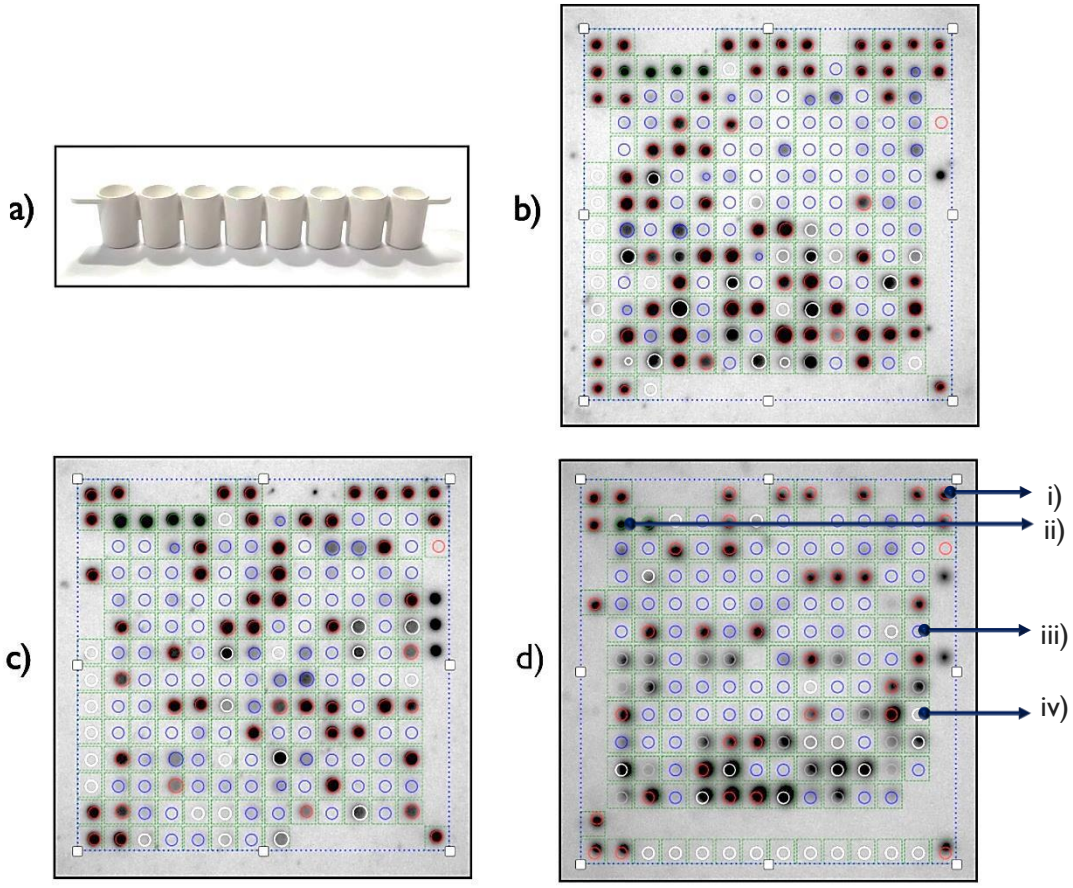


Fig 18: Image showing SSOP-PCR DOT Array performed after PCR run.

a) detachable microtitre reaction tubes coated with sequence specific oligonucleotide probes for SSOP-PCR, b) HLA A DOT Array, c) HLA B DOT Array, d) HLA DR DOT Array, i) positive probes, shown in red, ii) control probes, shown in green, iii) negative probes, shown in blue, iv) inactive probes, shown in white.

4.2.5 HLA ABDR alleles interpretation via HISTO SPOT® for SSOP-PCR

As described in section 4.2.3 was used to identify individual HLA ABDR alleles of both donor and recipient. For SSPO-PCR analysis, the DOT Array has been used to perform HISTO MATCH.

Fig 19: Image representing the interpretation of HLA ABDR allele using HISTO MATCH HISTO SPOT®, after SSOP-PCR DOT Array image as reference.

HLA ABDR 4-digit allele data of donors and patients obtained after SSP- and SSOP-PCR typing has been tabulated. Allele ID of all the patients and donor have been mentioned in table 39.1 & table 39.2 in annexure II, respectively.

4.3 Analysis of HLA ABDR eplet mismatches using HLA Matchmaker

ABC Eplet Matching and DRDQDP Eplet Matching V2.2, 2018 was downloaded from the website http://www.epitopes.net/. HLA ABDR allelic pair of both donor and recipient was analyzed using this algorithm and tabulated. Tables mentioned in annexure II lists out the ABDR alleles of all 1144 individuals, and annexure IV details i) total number of eplet match and mismatch and ii) number of the patient and donor pairs having zero eplet mismatches. The patient and donor pairs with allelic mismatch and zero eplet mismatches have been identified and discussed further.

4.3.1 Eplet mismatch analysis

HLA ABDR allele of 572 patient and donor pair (1144 individuals) was run in HLA Matchmaker and the results has been generated. The images representing each section of HLA Matchmaker worksheet and database of ABC Eplet Matching and DRDQDP Eplet Matching have been listed. The number of Ab-verifyed as well as non-verified (other) eplets was obtained from the RESULTS page of HLA Matchmaker. For conveying the process of matchmaking, the images representing the pages of HLA Matchmaker algorithm has been added in annexure III. The list of number of HLA ABDR eplet mismatches obtained after analyzing in HLA Matchmaker program has been noted and tabularized in the annexure IV. The comparative analysis between patient and donor allele pair and eplet mismatch in case of both class I HLA AB and class II HLA DR structures has been discussed in the study.

4.3.2 Analysis of relation between eplet mismatches and graft response

Each allele was studied against its number of eplets and the number of mismatched eplets between a patient and donor. The number of mismatched eplets were noted and tabularized. The amino acids present at eplet positions were analyzed and studied. A detailed breakdown on the eplets present in each HLA allele is carried out by making use of the HLA Matchmaker database. The list of patients and donors with zero class I HLA AB eplet mismatches and list of patients and donors with zero class II HLA DR eplet mismatches has been identified, tabulated, and mentioned in annexure IV, tables 40-42. Of the 572 patient and donor pair, 23 pair were having zero

class I HLA AB eplet mismatches and 46 pairs had zero class II HLA DR eplet mismatches. Patients who had allelic mismatches and zero eplet mismatches that survived for longer period have been identified and studied further.

4.4 Analysis of structural similarity of selected HLA alleles with matching eplets using protein structure modeling

The amino acid sequence of selected proteins needed for the study was retrieved from NCBI and modeled using SWISS MODEL accessible via EXPASY web server https://swissmodel.expasy.org/interactive. The details have been given below.

4.4.1 Modeling of HLA DRB alleles

In the class II HLA DRB hetero dimer complex, the functional unit is the β chain and the α chain provides the structural stability. The modeling of the 8 sequences gave 8 corresponding class II HLA DRB structures from selected templates with acceptable resolutions by the program. The number of amino acids of all the modeled structures were 190 to 202 and sequence identity was above 89, with a template resolution of 1.95 to 2.8 Å (table 4). Figure 20 represents the acquired high resolution images of HLA DRB1*01, DRB1*04, DRB1*07, DRB1*08, DRB1*09, DRB1*12, DRB1*14 and DRB1*16 modeled using SWISS MODEL.

The percentage of residues in the favored region of Ramachandran plot was observed to be in between -2 and 2 Rama-Z score. The Z-score of the structures ranged from -2.6 to -1.4. The plot images are given in figure 34 a-h, annexure V. The average number of turns in each structure was 18, no. of α helices was 3-4 and no. of β strands were 13-14. The positions of all the α helices & β strands in each HLA DRB structure has been mentioned in table 5. The modeled β chain of the class II HLA DBR showed 15-16% α helices having 29-31 amino acid residues and 37-40% β strands having 76-77 amino acid residues. The minor differences in the amino acids which has contributed to the structural variations implies to the highly polymorphic nature of HLA alleles, were the structure retains its structural similarity between individuals while exhibiting its antigenic nature.

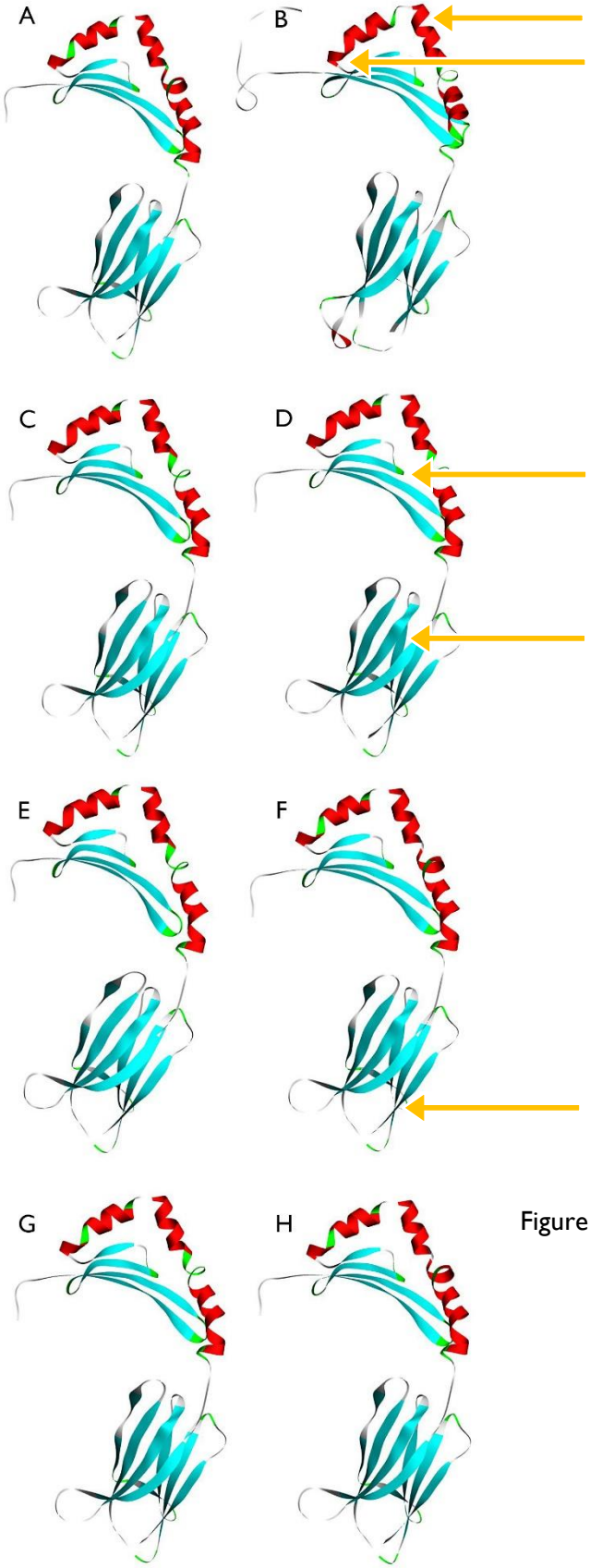


Figure 20: Image of HLA DRB1 chains modeled using SWISS MODEL

A) HLA DRB1*01,
B) HLA DRB1*04,
C) HLA DRB1*07,
D) HLA DRB1*08,
E) HLA DRB1*09,
F) HLA DRB1*12,
G) HLA DRB1*14
H) HLA DRB1*16

Table 4: Details of homology modeled HLA DRB structures

Structures modeled	No. of amino acids	No. of turns	Temp. ID	Sequence identity	Resolution (Å)
DRB1*01	190	17	3pdo.1.B	100	1.95
DRB1*04	202	16	3of6.2.B	93.14	2.80
DRB1*07	190	17	3pdo.1.B	89.90	1.95
DRB1*08	190	17	3pdo.1.B	90.40	1.95
DRB1*09	190	16	3pdo.1.B	91.41	1.95
DRB1*12	190	17	3pdo.1.B	89.39	1.95
DRB1*14	190	16	3pdo.1.B	90.40	1.95
DRB1*16	190	18	3pdo.1.B	94.95	1.95

Table 5: Positions of α helices & β strands in each HLA DRB structure

α helices			
Sl no.	**HLA ID**	**No of α helices**	**Amino acid positions**
1	DRB1*01	4	R84-N91, K94-R101, A103-T106, C108-T119
2	DRB1*04	3	R84-S92, K94-T106, C108-V115
3	DRB1*07	4	R84-N91, K94-R101, Q103-T106, C108-T119
4	DRB1*08	4	R84-N91, K94-R101, L103-T106, C108-T119
5	DRB1*09	3	R84-N91, K94-T106, C108-T119
6	DRB1*12	4	R84-N91, K94-R101, A103-T106, C108-T119
7	DRB1*14	3	R84-N91, K94-T106, C108-T119
8	DRB1*16	4	R84-N91, K94-R101, A103-T106, C108-T119
β strands			
Sl no.	**HLA ID**	**No of β strands**	**Amino acid positions**
1	DRB1*01	13	W38-F47, R52-Y61, E64-D70, E75-A78, V128-Y131, L143-Y152, E157-R162, Q165-E167, V171-S173, I177-Q178, F184-E191, Y200-E205, T214-W217
2	DRB1*04	13	E38-F47, R52-Y61, E64-D70, E75-A78, E127-Y131, L143-Y152, E157-R162, Q165-E166, V171-S173, I177-Q178, F184-E191, Y200-E205, L213-V215
3	DRB1*07	13	W38-F47, R52-Y61, E64-D70, E75-A78, E127-Y131, L143-Y152, E157-R162, Q165-E167, V171-S173, I177-Q178, F184-E191, Y200-E205, T214-W217
4	DRB1*08	13	E38-F47, R52-Y61, E64-D70, E75-A78, L127-Y131, L143-Y152, E157-R162, Q165-E167, V171-S173, I177-H178, F184-E191, Y200-E205, T214-W217

5	DRB1*09	13	L38-F47, R52-Y61, E64-D70, E75-A78, E127-Y131, L143-Y152, E157-R162, Q165-E167, V171-S173, I177-H178, F184-E191, Y200-E205, T214-W217
6	DRB1*12	13	E38-F47, R52-H61, E64-D70, E75-A78, V128-Y131, L143-Y152, E157-R162, Q165-E167, V171-S173, I177-H178, F184-E191, Y200-E205, T214-W217
7	DRB1*14	13	E38-F47, R52-H61, E64-D70, E75-A78, V128-Y131, L143-Y152, E157-R162, Q165-E167, V171-S173, I177-H178, F184-E191, Y200-E205, T214-W217
8	DRB1*16	14	W38-Q39, R42-F47, R52-Y61, E64-D70, E75-A78, V128-Y131, L143-Y152, E157-R162, Q165-E167, M171-S173, I177-H178, F184-E191, Y200-E205, T214-W217

4.4.2 Comparison of modeled HLA structures for the determination of its structural variations

All the 8 modeled HLA DR proteins were superimposed. The variations present in coils and turns were identified. The majority of the differences were found at the amino terminal as well as between the IInd and IIIrd α helices of the protein. The coils and turns in the HLA structure have been identified as areas which are more likely to be the region susceptible for polymorphism.

Among the 8 class II HLA DR structures modeled via SWISS MODEL, 75-80% showed structural similarity. Figure 21 represents the super-positioning of all 8 HLA DRB structures. As mentioned in the initial section of table 5, there were no continuous α helix in any of the structure. The α helices were situated in the regions between 84 & 119 in the structure. The minor breaks in α helix was the contribution of serine, glycine and alanine, at 92, 93 & 102 position. The class II HLA DRB1*04 structure was having a distinguishable structural difference. In the HLA DRB1*04 structure, there was an extended tail of 13 amino acids (VTLMVLSSPLALA) at the amino terminal, and a bent formed by amino acids leucine, glutamine and histidine at the 122, 123 & 124 positions. For HLA DRB1*01, HLA DRB1*07, HLA DRB1*12 & HLA DRB1*16, the loop after the IInd α helix was found to be absent. The amino acid alanine, being a shape-stabilizing residue at internal helical positions, was found at 103G/L, 104V, 105N & 106Y positions of DRB1*04, HLA DRB1*08, HLA DRB1*09, & HLA DRB1*14 structures (López-Llano et al., 2006).

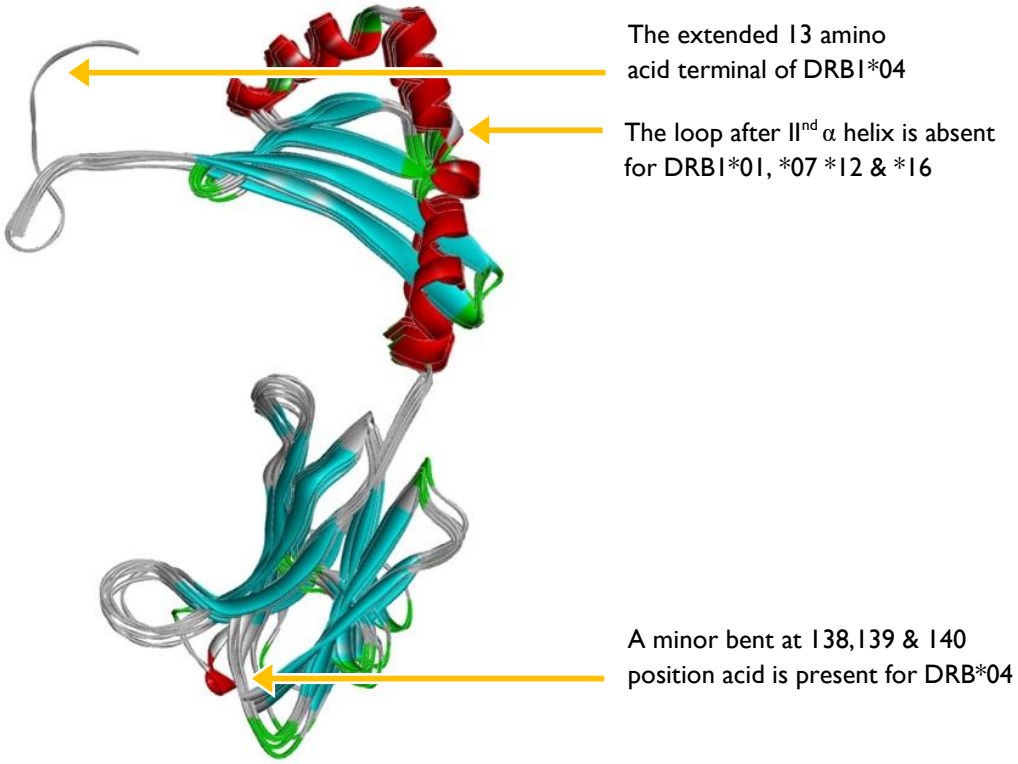


Figure 21: Image of superimposed chains of class II HLA DRB showing the minor structural variations.

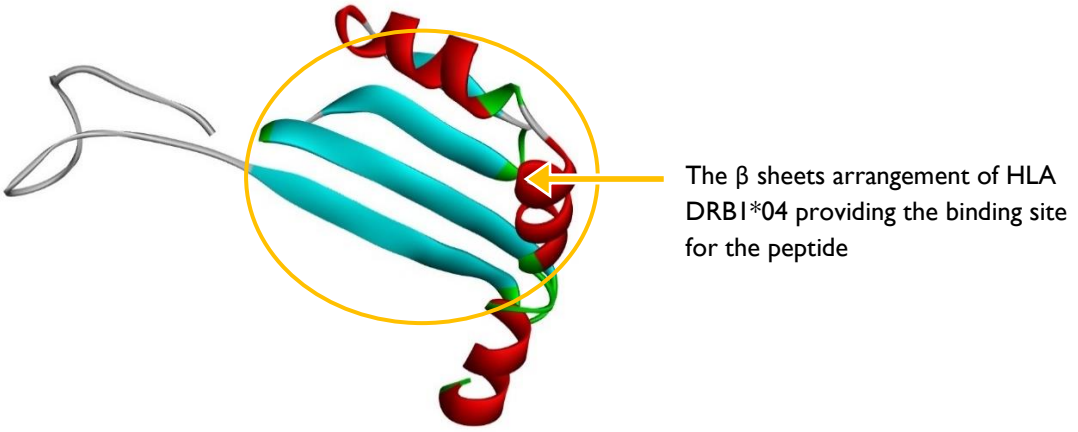


Figure 22: Aerial view of class II HLA DRB1*04 showing both α helix and β sheets which make up the binding site for the peptide.

4.4.3 Identification and comparison of eplet position in modelled HLA DRB structures

The 8 class II HLA DRB structures was analyzed for its similarity in the position of eplets. There were 16 eplets identified in total for 8 structures such as 4R/Q, 11STS, 13F, 16Y, 25R/Q, 37V, 47F, 67L, 70D, 73A, 77T, 85V/VG, 96H, 104A, 142M & 181M. Most of the eplets were present in all the structures and almost all of them were observed at the antigen binding area of the class II HLA DRB structure.

For all the structures the very first eplet was at the 4th amino acid position, either arginine, R or glutamine, Q. All the structures had eplet 4R, except HLA DRB1*07 which had 4Q. The second eplet was either 11STS (serine-threonine-serine), 13F (phenylalanine) or 16Y (tyrosine). Only the structure HLA DRB1*14 comprised the eplet 11STS. The structure HLA DRB1*01 & HLA DRB1*09 had 13F and HLA DRB1*08 & HLA DRB1*12 had the eplet 16Y. The 3rd set of eplets was 25R or 25Q. Only HLA DRB1*07 had 25Q and HLA DRB1*01, DRB1*04, DRB1*08, DRB1*09, DRB1*12 and DRB1*16 had 25R eplet. HLA DRB1*14 did not have either 25R or 25Q eplet. The 4th eplet was a less common 37YV which was present only for HLA DRB1*04 and DRB1*08, and 47F present for HLA DRB1*12. 70D (aspartic acid) eplet was common for HLA DRB1*07 DRB1*08, DRB1*12, DRB1*14 & DRB1*16. In DRB1*01 & DRB1*04, the eplet was 70Q and the eplet was absent in HLA DRB1*09. 67L (LEU) was present was DRB1*01 & DRB1*04. 73A (alanine) was absent for DRB1*07. 77T (threonine) was the next eplet which was common for all the 8 structures. The next eplet identified was 85V or 85VG (valine & glycine). HLA DRB1*07 & DRB1*12 did not contain the 85VG eplet and HLA DRB1*14 had 85V. 96H (histidine) was the next common eplet which was present in all the structures except, HLA DRB1*01 & HLA DRB1*16. In DRB1*04 the eplet was 96Y. The other less common eplets in these structures were 104A, 142M and 181M (methionine).

Comparing the results of HLA Matchmaker for the identification of common eplets in different alleles, here, the structural comparison was able to identify the eplets present at the amino acid positions as reported in the eplet database. From this data, eplet matched allelic pairs was identified.

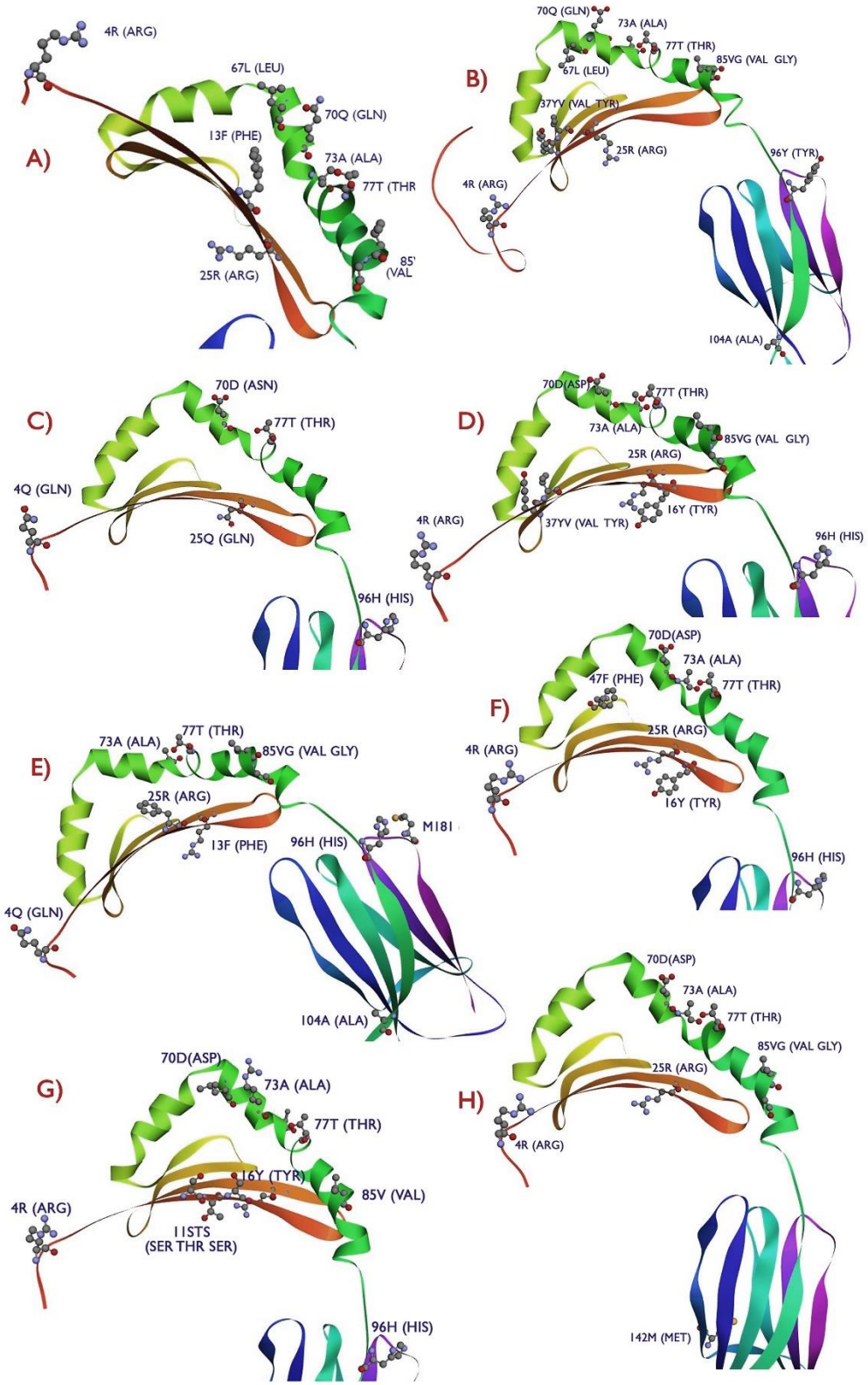


Figure 23: Images showing the eplets in each class HLA DRB structure present at the same amino acid positions, owing to its structural similarity. A) HLA DRB1*01, B) HLA DRB1*04, C) HLA DRB1*07, D) HLA DRB1*08, E) HLA DRB1*09, F) HLA DRB1*12, G) HLA DRB1*14 and H) HLA DRB1*16

4.5 Protein docking and comparative analysis of binding affinity between HLA-Ag-TCR tri-molecular complex for the identification of compatible HLA DRB structures

The 8 class II HLA DR structures namely HLA DRB1*01, *04, *07, *08, *09, *12, *14 & *16 and CLIP, Ag peptides and T cell receptors were used to perform the bimolecular and tri-molecular docking studies. The required structures other than the modeled HLA DRBs were downloaded from RCSB PDB. The details of CLIP, Ag-peptides and TCR has been provided in table 6. Each structure was visualized in Schrodinger Maestro 11.2, 2018. All the structures were separated as chains and performed the required structural adjustments and optimization. The docking was done via ZDOCK server (V3.0.2) http://zdock.umassmed.edu/ and all the resulted protein complexes were analyzed in PRODIGY server https://bianca.science.uu.nl/prodigy/ for calculating the binding energy as described in section 3.5 of materials & methods.

Table 6: Details of CLIP, Ag-peptides & TCR

Structure	Source/type	Source ID	No. of amino acids
CLIP	HLA DR3 CLIP complex	1a6a	15
	HLA DR1 CLIP complex	4x5w	15
Antigen peptides extracted from HLA complexes	HLA DRB1 endogenous peptide complex	1aqd	14
	HLA DR1 influenza peptide complex	1dlh	13
	HLA DR1 EBV gp42 peptide complex	1kg0	15
	HLA DR1 EBV DNA polymerase complex	1h15	14
	HLA DR1 HIV capsid peptide complex	1sje	16
TCR	Human T cell receptors	2xna	241
		3of6	243
		4udu	238

4.5.1 HLA-Ag and HLA-Ag-TCR docking using ZDOCK

The HLA DR structures, and antigenic peptides were selected upon understanding the immune mechanism taking place during an immune recognition process. In reality, class II HLA protein presents a processed antigenic peptide to TCR. This mechanism was simulated using the molecular docking studies via ZDOCK. The number of amino acids, position of loops/turns, positions of α helices and β sheets helped in identifying the binding area of the HLA DR protein with an antigen peptide. Required structural optimizations were carried out with the aid of Schrodinger Maestro 11.2, 2018.

The HLA-Ag i.e protein-peptide (bi-molecular) as well as HLA-Ag-TCR i.e, protein-peptide-protein (tri-molecular) docking between the modeled class II HLA DRB structures and antigen peptides was performed as mentioned in section 3.5.3. This was followed by the docking with 3 different TCR structures. The 8 modeled structures were categorized and selected based on the criteria that, allelic pairs such as DRB1*01-DRB1*14, DRB1*04-DRB1*07, DRB1*04-DRB1*14, DRB1*07-DRB1*14, DRB1*12-DRB1*14 etc., were having multiple antibody verified eplet mismatches between them and allelic pairs such as DRB1*01-DRB1*04, DRB1*01-DRB1*07, DRB1*04-DRB1*08, DRB1*07-DRB1*08, DRB1*07-DRB1*12, DRB1*07-DRB1*14 DRB1*08-DRB1*14 and DRB1*14-DRB1*16, were having zero eplet mismatches between them; table 39, annexure II & table 42, annexure IV. The simulated studies carried out helped in understanding the range of ΔG between each complex and in identifying the pattern of difference in docking between those HLA DR protein complexes having same structural eplets towards same peptide as well as same T cell receptor.

Initially, HLA DRB1*01 was docked with CLIP 1a6a (15 amino acid length), via ZDOCK. Each docking session resulted in 10 complexes. Secondly, HLA DRB1*01 was docked with antigen peptide 1aqd of length 14 amino acid. Out of the 10 complexes obtained, the complex with highest $\Delta G/K_d$ was selected to dock with 3 individual TCR chains, 2xna, 3of6 & 4udu. The binding affinity, ΔG in terms of K_d was analyzed for the resulted 10 tri-molecular complexes for each HLA-Ag-TCR complex formed between the docking with 3 TCR chains. The same procedure was followed

for the other 7 structures, HLA DRB1*04, DRB1*07, DRB1*08, DRB1*09, DRB1*12, DRB1*14 and DRB1*16.

The docking between HLA DRB1*01 with CLIP 1&2 resulted in 20 complexes: 160 in total for 8 HLA DRB structures. The resulted structure complexes between HLA DRB*01 and antigen peptide 1aqd were 10; 50 in total for 5 antigen peptides i.e., 400 in total for 8 HLA DRB structures. The docking between one HLA-Ag complex obtained from 8 HLA DRB + 5 antigen peptides, having high binding energy, with one TCR structure resulted in 40 HLA-Ag-TCR structure complexes: 120 in total for 3 TCR structures. Performing the docking studies between 8 modeled class II HLA DRB, 2 CLIP, 5 antigen peptides and 3 TCR chains gave a total of 1200 structural complexes and a final total of 1760 docked complexes. The figure 22 represents the process of selection and docking combinations of HLA with Ag-peptide and HLA-Ag with T-cell receptor.

4.5.2 Analysis of binding energy ($\Delta G/K_d$) using PRODIGY

Initially, the binding energy between DRB1*01 and CLIP 1a6a and 4x5w was assessed via PRODIGY. The binding energy ΔG and dissociation cont. K_d for all the 20 complexes were analyzed and tabulated. This was carried out to identify the baseline binding energy (ΔG) between the HLA-CLIP complexes, which revealed the basis for the effortless dissociation of CLIP from the binding area of HLA DRB. After the docking between HLA DRB1*01 and antigen peptide 1aqd, the binding affinity of the resulted 10 complexes was evaluated using PRODIGY. This helped in identifying the highest and lowest K_d values of the complexes. The complex with highest $\Delta G/K_d$ value was preferred for docking with TCR. The $\Delta G/K_d$ values for all the resulted HLA-Ag-TCR complexes were calculated and tabulated. This was repeated for all the other 7 HLA DRB structures with 2 CLIPs, 5 antigen peptides and 3 TCRs.

The consolidated table showing the $\Delta G/K_d$ value of all the 8 HLA DRB structures docked with 5 antigen peptides and 3 TCR has been giver here (tables 7-21). The compatible HLA DRB alleles with mismatched eplets identified after the analysis of $\Delta G/K_d$ value has been provided in tables 22-37. The list of percentage of non-interacting surfaces per property (NIS), interfacial contacts per property (ICs), binding

energy (ΔG) and dissociation cont. (K_d) evaluated for all the 1760 structure complexes formed between HLA DR-CLIP, HLA DR-Ag peptide and HLA DR-Ag-TCR tri-molecular complexes has been provided in the annexure V, tables 43-58 & annexure VI, tables 59-73

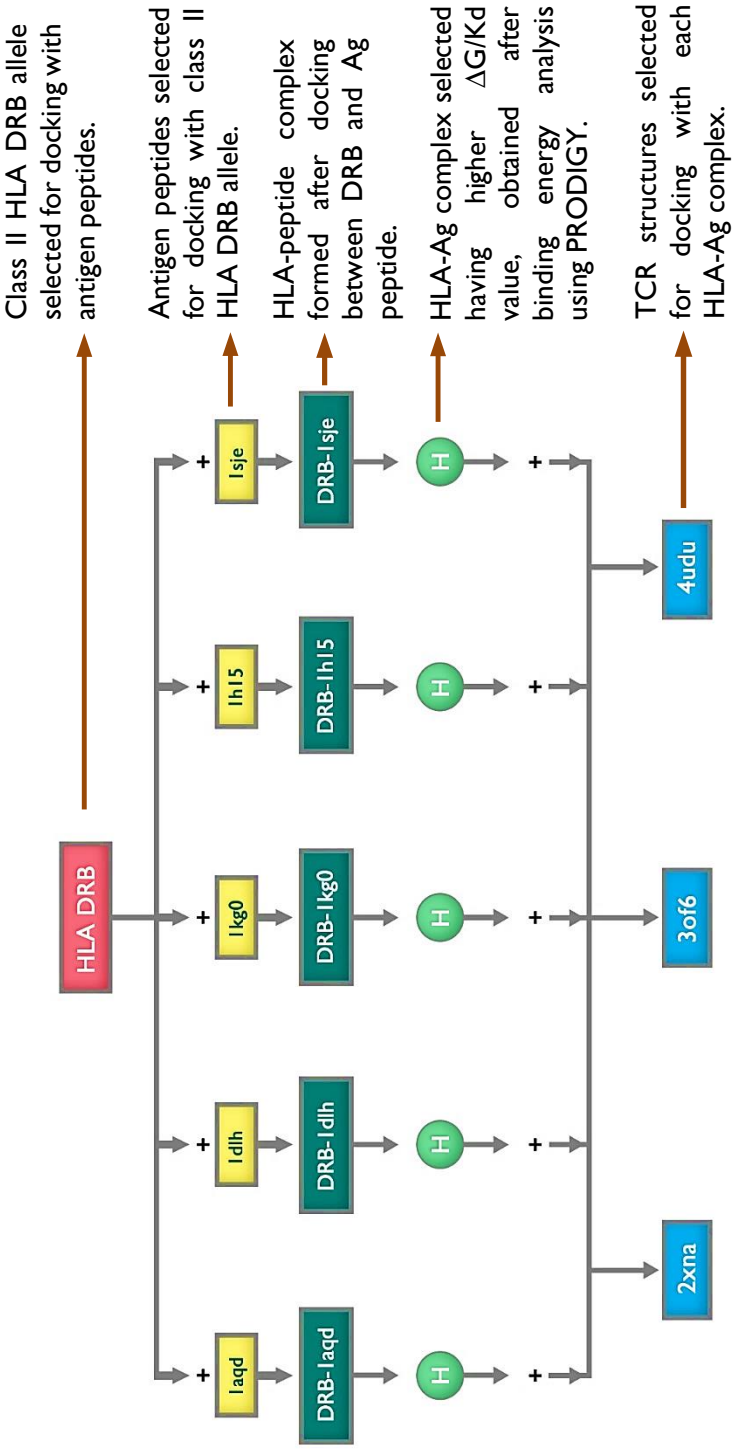


Figure 24: The illustration representing the process of selection of each class II HLA, antigen peptide and TCR structures. 'H' denotes the HLA DRB-Ag peptide complex having high $\Delta G/K_d$ value. This was the basis for selection for all the 8 modeled HLA DRB structures (HLA DRB*01, *04, *07, *08, *09, *12, *14, & *16).

Consolidated table from annexure V showing the $\Delta G/K_d$ of all the all HLA DRB-Ag structure complexes docked with TCR

Table 7: $\Delta G/K_d$ of all the 8 HLA DRB structures docked with the peptide 1aqd, complexed with TCR 2xna

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-12	3.30E-09	-11.5	7.80E-09	-12.4	1.90E-09	-11.9	3.90E-09	-12.4	1.80E-09	-10.1	8.10E-08	-12.1	3.10E-09	-11.2	1.40E-08
-9.7	1.50E-07	-11.5	7.30E-09	-11	1.90E-08	-11.5	7.80E-09	-12	3.30E-09	-9.8	1.30E-07	-10.5	3.80E-08	-10.7	2.70E-08
-9.5	2.00E-07	-10.6	3.60E-08	-10.8	2.60E-08	-10.3	5.70E-08	-11.5	7.60E-09	-9.1	3.70E-07	-10.3	5.50E-08	-10.1	8.00E-08
-9.3	2.90E-07	-10.4	4.50E-08	-10.7	2.80E-08	-10.2	6.00E-08	-11.7	5.60E-09	-9	4.70E-07	-10.3	5.90E-08	-9.9	1.00E-07
-9.2	3.10E-07	-9.1	3.80E-07	-9.6	1.70E-07	-10.1	7.80E-08	-10.1	7.10E-08	-8.8	6.40E-07	-9.8	1.20E-07	-9.7	1.50E-07
-9.2	3.40E-07	-8.7	7.50E-07	-9.1	3.90E-07	-9.8	1.20E-07	-9.7	1.50E-07	-8.8	6.00E-07	-9.8	1.30E-07	-9.5	2.00E-07
-9.1	3.50E-07	-8.5	1.00E-06	-9	4.80E-07	-9.5	2.00E-07	-9.6	1.60E-07	-8.7	7.50E-07	-9.3	3.00E-07	-9.4	2.50E-07
-8.7	7.10E-07	-8.3	1.40E-06	-7.9	2.50E-06	-9.3	2.80E-07	-9	4.30E-07	-8.5	1.10E-06	-9	4.70E-07	-9.4	2.40E-07
-8.3	3.40E-07	-8	2.30E-06	-7.7	3.60E-06	-8.9	5.50E-07	-8.6	8.50E-07	-8.5	1.00E-06	-8.6	8.00E-07	-8.1	1.80E-06
-7.2	8.80E-06	-7.5	4.80E-06	-7.7	3.60E-06	-8.1	1.90E-06	-8.5	9.60E-07	-8.2	1.70E-06	-8.1	1.90E-06	-7.7	3.90E-06

Table 8: $\Delta G/K_d$ of all the 8 HLA DRB structures docked with the peptide 1dlh, complexed with TCR 2xna

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-10.8	2.30E-08	-10	8.40E-08	-9.5	2.10E-07	-10.8	2.50E-08	-12.5	1.50E-09	-9.1	4.10E-07	-11.6	6.40E-09	-10.9	2.20E-08
-9.9	1.00E-07	-9.7	1.50E-07	-8.7	7.80E-07	-10	8.20E-08	-10.2	6.60E-08	-7.9	2.70E-06	-11.3	1.00E-08	-10.6	3.40E-08
-9.3	2.70E-07	-8.8	6.00E-07	-8.4	1.10E-06	-9.7	1.40E-07	-9.8	1.20E-07	-7.9	2.60E-06	-11.1	1.40E-08	-10.1	7.30E-08

-9.2	3.50E-07	-8.8	6.50E-07	-8.4	1.20E-06	-9.5	2.10E-07	-9.4	2.50E-07	-8.4	1.20E-06	-10.9	2.10E-08	-9.7	1.40E-07
-8.7	7.20E-07	-8.7	7.70E-07	-8.1	2.00E-06	-9.3	2.70E-07	-9.3	2.90E-07	-7.5	4.80E-06	-10.7	3.00E-08	-8.5	1.00E-06
-8.5	1.10E-06	-8.6	8.20E-07	-7.9	2.90E-06	-8.8	5.80E-07	-8.6	8.80E-07	-6.8	1.50E-05	-10.6	3.20E-08	-8.2	1.70E-06
-8.3	1.50E-06	-8.2	1.80E-06	-7.8	3.00E-06	-8.5	9.90E-07	-8.2	1.70E-06	-7.5	5.50E-06	-10.4	4.60E-08	-8	2.40E-06
-8.1	2.00E-06	-7.9	2.60E-06	-7.7	3.80E-06	-7.7	3.70E-06	-7.9	2.60E-06	-8.3	1.50E-06	-10.3	5.30E-08	-7.8	3.10E-06
-8	2.10E-06	-7.9	2.70E-06	-7.6	4.20E-06	-7.7	3.50E-06	-7.7	4.00E-06	-9.2	3.30E-07	-10	9.60E-08	-7.6	4.30E-06
-7.8	3.40E-06	-6.5	2.70E-05	-7.2	8.50E-06	-7.6	4.20E-06	-7.3	6.70E-06	-7.4	6.00E-06	-9.1	3.60E-07	-7	1.20E-05

Table 9: $\Delta G/K_d$ of all the 8 HLA DRB structures docked with the peptide 1kg0, complexed with TCR 2xna

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	**K_d**	**ΔG**	**K_d**	**ΔG**	**K_d**	**ΔG**	**K_d**	**ΔG**	**K_d**	**ΔG**	**K_d**	**ΔG**	**K_d**	**ΔG**	**K_d**
-10.7	2.70E-08	-12.2	2.60E-09	-13	6.80E-10	-13.4	3.30E-10	-12.3	2.00E-09	-10.6	3.10E-08	-11.6	6.90E-09	-12.9	7.40E-10
-10.6	3.40E-08	-11.1	1.50E-08	-10.1	7.90E-08	-11.6	6.70E-09	-10.4	4.60E-08	-9.6	1.70E-07	-10.8	2.40E-08	-10.9	2.10E-08
-10.4	4.30E-08	-10.5	3.70E-08	-9.7	1.50E-07	-11.5	7.60E-09	-10.4	4.80E-08	-9.3	2.80E-07	-10.4	4.80E-08	-10.3	5.20E-08
-9.6	1.80E-07	-10.1	7.00E-08	-9.6	1.70E-07	-10.6	3.50E-08	-10	8.40E-08	-8.7	7.20E-07	-10	9.40E-08	-9.8	1.30E-07
-8.9	5.50E-07	-10.1	7.40E-08	-9.6	1.60E-07	-10.2	6.20E-08	-9.6	1.70E-07	-8.7	7.00E-07	-9.6	1.70E-07	-9.6	1.80E-07
-8.7	7.60E-07	-9.6	1.70E-07	-9.5	2.00E-07	-10.1	7.60E-08	-9.4	2.20E-07	-8.4	1.20E-06	-9.2	3.20E-07	-9.2	3.20E-07
-8.5	1.10E-06	-9.5	1.80E-07	-9	4.30E-07	-9.6	1.80E-07	-9.2	3.50E-07	-8.4	1.10E-06	-9	4.70E-07	-8.4	1.20E-06
-8	2.40E-06	-9.4	2.20E-07	-8.1	2.00E-06	-9.2	3.30E-07	-8.5	1.10E-06	-7.8	3.00E-06	-8.8	6.60E-07	-8.1	1.90E-06
-7.3	7.10E-06	-8.3	1.40E-06	-7.8	3.30E-06	-8.4	1.30E-06	-8.1	2.00E-06	-7.5	4.80E-06	-8.5	1.10E-06	-8.1	2.10E-06
-6.8	1.70E-05	-8.1	2.00E-06	-7	1.20E-05	-8.1	2.00E-06	-7	1.20E-05	-7	1.10E-05	-7.8	3.40E-06	-7.9	2.70E-06

Table 10: ΔG/K_d of all the 8 HLA DRB structures docked with the peptide 1h15, complexed with TCR 2xna

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-11.4	8.80E-09	-11.2	1.30E-08	-11.9	4.10E-09	-11.5	7.50E-09	-12	3.50E-09	-10.9	2.00E-08	-11	1.70E-08	-10.4	5.00E-08
-10.5	4.00E-08	-11	1.80E-08	-11.5	8.30E-09	-10.5	3.90E-08	-10.9	1.90E-08	-10.3	5.90E-08	-10.4	5.00E-08	-9.9	1.00E-07
-10.3	5.70E-08	-10.4	4.50E-08	-11.4	8.70E-09	-10.4	4.40E-08	-10.1	7.90E-08	-10	8.30E-08	-10.3	5.90E-08	-9	4.30E-07
-10.2	5.90E-08	-10.4	4.50E-08	-11	1.70E-08	-9.5	2.00E-07	-10.1	8.00E-08	-9.9	9.90E-08	-10.2	6.40E-08	-9	4.70E-07
-9.7	1.60E-07	-10	8.30E-08	-10.3	5.40E-08	-9.4	2.20E-07	-9.8	1.30E-07	-9.6	1.70E-07	-9.7	1.30E-07	-8.4	1.20E-06
-9.7	1.50E-07	-9.3	2.70E-07	-10	8.90E-08	-9.2	3.10E-07	-9.5	1.90E-07	-9.5	1.90E-07	-9.4	2.30E-07	-8.3	1.50E-06
-9.2	3.40E-07	-8.6	8.10E-07	-9.5	2.10E-07	-9.1	4.10E-07	-9.2	3.40E-07	-9	4.50E-07	-9.2	3.30E-07	-8.3	1.30E-06
-8.3	1.40E-06	-8.6	8.40E-07	-9.2	3.10E-07	-8.9	5.20E-07	-9.1	4.00E-07	-8.3	1.30E-06	-8.9	5.70E-07	-7.9	2.80E-06
-7.6	4.20E-06	-8.5	1.00E-06	-9.1	4.00E-07	-8.9	5.50E-07	-8.9	5.30E-07	-7.8	3.40E-06	-8.3	1.40E-06	-7.8	3.30E-06
-7.4	5.90E-06	-8.1	2.00E-06	-8.3	1.50E-06	-7.5	5.10E-06	-7.4	6.10E-06	-7.5	5.60E-06	-8.2	1.60E-06	-7	1.10E-05

Table 11: ΔG/K_d of all the 8 HLA DRB structures docked with the peptide 1sje, complexed with TCR 2xna

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-11.9	3.90E-09	-10.2	6.10E-08	-10	9.00E-08	-14.3	8.70E-11	-11.1	1.40E-08	-11.8	4.70E-09	-11.8	5.00E-09	-11.2	1.20E-08
-10.1	8.00E-08	-10.2	7.00E-08	-9.9	1.10E-07	-12.4	1.80E-09	-10.4	4.50E-08	-10.7	3.00E-08	-11.2	1.20E-08	-11.1	1.60E-08
-10.1	7.50E-08	-10	8.60E-08	-9.6	1.70E-07	-12.2	2.40E-09	-10	9.60E-08	-9.9	1.10E-07	-9.5	1.90E-07	-10.1	7.30E-08
-10	9.60E-08	-9.1	3.90E-07	-9.3	2.60E-07	-12	3.60E-09	-8.7	7.20E-07	-9.6	1.70E-07	-9.3	2.60E-07	-9.9	9.70E-08

-9.9	1.10E-07	-9	4.30E-07	-9.3	3.00E-07	-11.4	9.50E-09	-8.2	1.60E-06	-9.3	2.60E-07	-8.8	6.20E-07	-9.8	1.20E-07
-9.3	2.90E-07	-8.9	5.70E-07	-8.7	6.80E-07	-11.3	1.10E-08	-8	2.30E-06	-8.7	7.80E-07	-8.8	6.10E-07	-9.4	2.50E-07
-9.2	3.00E-07	-8.2	1.80E-06	-8.5	9.60E-07	-10.5	4.30E-08	-7.9	2.50E-06	-8.7	7.90E-07	-8.1	2.10E-06	-9.2	3.50E-07
-9	4.80E-07	-7.9	2.90E-06	-8.2	1.80E-06	-10.4	4.30E-08	-7.8	3.10E-06	-8.6	8.30E-07	-7.8	3.20E-06	-9	4.50E-07
-8.6	8.40E-07	-7.9	2.70E-06	-8.1	2.00E-06	-10	9.40E-08	-7.8	3.10E-06	-8.2	1.80E-06	-7.8	3.00E-06	-9	4.30E-07
-8	2.50E-06	-7.6	4.20E-06	-7.9	2.50E-06	-9.4	2.30E-07	-7.7	3.80E-06	-8	2.30E-06	-7.7	3.60E-06	-8	2.20E-06

Table 12: showing the $\Delta G/K_d$ of all the 8 HLA DRB structures docked with the peptide 1aqd, complexed with TCR 3of6

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-10.3	5.20E-08	-10.4	4.50E-08	-13.1	5.50E-10	-12.3	2.10E-09	-12.2	2.70E-09	-9.6	1.70E-07	-11.7	5.50E-09	-10	9.10E-08
-10.1	7.60E-08	-10.3	5.50E-08	-11.7	5.80E-09	-11.4	9.20E-09	-11.7	5.70E-09	-9.1	4.00E-07	-10.7	2.80E-08	-10.2	6.80E-08
-9.8	1.30E-07	-10.2	6.60E-08	-11.3	1.10E-08	-11	1.60E-08	-11.1	1.50E-08	-9	4.30E-07	-11.2	1.20E-08	-10.1	7.90E-08
-9.7	1.40E-07	-10.1	8.10E-08	-10.7	2.90E-08	-10.6	3.50E-08	-10.8	2.30E-08	-8.8	5.90E-07	-10.9	2.10E-08	-9.5	2.00E-07
-9.1	3.70E-07	-10	8.20E-08	-10.7	3.10E-08	-10.4	4.60E-08	-10.8	2.60E-08	-8.1	1.90E-06	-10.1	8.10E-08	-9.2	3.10E-07
-9	4.20E-07	-9.4	2.50E-07	-10.6	3.50E-08	-9.9	9.90E-08	-10.3	5.50E-08	-8	2.30E-06	-10	9.60E-08	-9.1	4.00E-07
-9	4.40E-07	-9.4	2.30E-07	-10.1	7.70E-08	-9.4	2.50E-07	-10	9.30E-08	-7.9	2.80E-06	-10	9.30E-08	-8.9	5.40E-07
-8.9	5.60E-07	-8.2	1.60E-06	-10	8.90E-08	-8.6	8.80E-07	-9.7	1.40E-07	-7.7	3.90E-06	-9.9	1.00E-07	-8.9	5.60E-07
-8.7	7.20E-07	-8	2.20E-06	-9.9	1.10E-07	-8.4	1.20E-06	-9.5	2.10E-07	-7.5	4.90E-06	-9.7	1.50E-07	-8.7	7.90E-07
-8.1	1.80E-06	-7.3	7.50E-06	-9.4	2.30E-07	-7.2	7.80E-06	-9.4	2.50E-07	-7.3	6.80E-06	-8.9	5.40E-07	-7.8	3.20E-06

Table 13: ΔG/K_d of all the 8 HLA DRB structures docked with the peptide 1dlh, complexed with TCR 3of6

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-11.5	8.20E-09	-11	1.70E-08	-11.3	1.00E-08	-12.1	3.10E-09	-11.8	4.70E-09	-10.9	2.00E-08	-11.7	5.80E-09	-11.5	7.90E-09
-10.7	2.90E-08	-10.5	4.10E-08	-9.5	2.00E-07	-11.9	4.40E-09	-9.6	1.70E-07	-10.3	5.10E-08	-11.6	6.40E-09	-10.7	2.70E-08
-10.4	4.70E-08	-10.3	5.60E-08	-9.1	3.60E-07	-11.6	7.10E-09	-9.6	1.60E-07	-10.2	6.30E-08	-11.5	8.20E-09	-9.8	1.30E-07
-10.1	8.00E-08	-10.1	7.80E-08	-8.7	7.20E-07	-10.6	3.40E-08	-9.5	2.00E-07	-9.2	3.50E-07	-10.6	3.40E-08	-9.5	1.80E-07
-9.5	2.00E-07	-10	8.50E-08	-8.6	9.20E-07	-10.6	3.50E-08	-9.2	3.50E-07	-9.2	3.30E-07	-10.4	4.90E-08	-9	4.80E-07
-9.3	2.60E-07	-9.8	1.30E-07	-8.6	8.90E-07	-9.9	1.10E-07	-8.9	5.20E-07	-9	4.70E-07	-10.4	4.80E-08	-8.9	5.00E-07
-9.3	2.60E-07	-9.6	1.70E-07	-8.4	1.10E-06	-9.2	3.00E-07	-8.6	8.00E-07	-8.7	7.90E-07	-9.7	1.40E-07	-8.5	1.10E-06
-8.9	5.10E-07	-9.5	2.10E-07	-8.4	1.20E-06	-8.8	6.70E-07	-8.5	9.90E-07	-8.1	1.90E-06	-9.6	1.70E-07	-7.8	3.10E-06
-8.9	5.60E-07	-8.9	5.00E-07	-7.4	6.10E-06	-8.6	8.60E-07	-8.1	1.90E-06	-7.3	7.50E-06	-9.3	2.60E-07	-7.8	3.00E-06
-8.9	5.70E-07	-8.2	1.70E-06	-6.9	1.30E-05	-7.8	3.30E-06	-8.1	2.10E-06	-7	1.20E-05	-8.4	1.20E-06	-7.3	6.70E-06

Table 14: ΔG/K_d of all the 8 HLA DRB structures docked with the peptide 1kg0, complexed with TCR 3of6

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-10.7	2.70E-08	-12.2	2.60E-09	-13	6.80E-10	-12.7	1.10E-09	-11.8	5.10E-09	-10.9	2.20E-08	-11.4	9.70E-09	-13.1	5.80E-10
-10.6	3.40E-08	-11.1	1.50E-08	-10.1	7.90E-08	-11.5	7.50E-09	-11.5	8.20E-09	-10.5	3.90E-08	-10.6	3.50E-08	-11.5	7.20E-09
-10.4	4.30E-08	-10.5	3.70E-08	-9.7	1.50E-07	-10.4	4.70E-08	-10.8	2.50E-08	-9.7	1.50E-07	-10.2	6.80E-08	-10.8	2.30E-08
-9.6	1.80E-07	-10.1	7.00E-08	-9.6	1.60E-07	-10.2	6.80E-08	-10.6	3.40E-08	-9.4	2.50E-07	-9.7	1.50E-07	-10.5	3.90E-08
-8.9	5.50E-07	-10.1	7.40E-08	-9.6	1.70E-07	-10.2	6.90E-08	-10.6	3.30E-08	-9.2	3.50E-07	-9.4	2.20E-07	-10.2	6.70E-08

-8.7	7.60E-07	-9.6	1.70E-07	-9.5	2.00E-07	-9.8	1.20E-07	-10.5	4.20E-08	-8.6	8.50E-07	-9.4	2.30E-07	-9.6	1.60E-07
-8.5	1.10E-06	-9.5	1.80E-07	-9	4.30E-07	-9.6	1.70E-07	-10	8.90E-08	-8.6	9.00E-07	-8.8	6.20E-07	-9.2	3.50E-07
-8	2.40E-06	-9.4	2.20E-07	-8.1	2.00E-06	-9.4	2.40E-07	-9.5	2.10E-07	-8.5	9.80E-07	-8.8	6.20E-07	-9	4.90E-07
-7.3	7.10E-06	-8.3	1.40E-06	-7.8	3.30E-06	-9.2	3.10E-07	-9.2	3.30E-07	-8.5	1.10E-06	-8.8	6.20E-07	-8.9	5.00E-07
-6.8	1.70E-05	-8.1	2.00E-06	-7	1.20E-05	-8.9	5.30E-07	-9	4.30E-07	-8.2	1.70E-06	-8.8	6.10E-07	-8.7	7.10E-07

Table 15: $\Delta G/K_d$ of all the 8 HLA DRB structures docked with the peptide 1h15, complexed with TCR 3of6

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-9.9	1.00E-07	-11.2	1.30E-08	-12.3	2.00E-09	-10.7	3.10E-08	-12.5	1.50E-09	-10.9	2.00E-08	-12.4	2.00E-09	-11	1.70E-08
-9.7	1.40E-07	-11	1.80E-08	-10.7	2.90E-08	-10.2	6.10E-08	-10.4	5.00E-08	-10.3	5.90E-08	-12.3	2.20E-09	-10.6	3.60E-08
-9.5	1.90E-07	-10.4	4.50E-08	-10.2	6.30E-08	-9.4	2.40E-07	-10.3	5.10E-08	-10	8.30E-08	-10.7	3.00E-08	-10.2	6.90E-08
-9.4	2.50E-07	-10	8.30E-08	-10.1	7.60E-08	-9.3	2.60E-07	-9.4	2.60E-07	-9.9	9.90E-08	-10.5	3.80E-08	-10.1	7.60E-08
-9.1	4.10E-07	-9.3	2.70E-07	-9.8	1.20E-07	-9.3	2.90E-07	-9.3	2.60E-07	-9.6	1.70E-07	-10.4	4.50E-08	-9.9	1.10E-07
-9	4.50E-07	-8.9	5.50E-07	-9.6	1.80E-07	-9.3	2.60E-07	-9.2	3.10E-07	-9.5	1.90E-07	-9.4	2.40E-07	-9.8	1.20E-07
-8.8	6.00E-07	-8.6	8.10E-07	-9.3	2.90E-07	-8.9	5.10E-07	-8.8	6.20E-07	-9	4.50E-07	-9.4	2.40E-07	-9.8	1.20E-07
-8.8	6.60E-07	-8.6	8.40E-07	-8.7	7.50E-07	-8.6	8.30E-07	-8.6	8.60E-07	-8.3	1.30E-06	-9.1	3.60E-07	-9.7	1.40E-07
-8.6	9.00E-07	-8.5	1.00E-06	-8.5	1.00E-06	-8.6	8.90E-07	-8.2	1.60E-06	-7.8	3.40E-06	-8.6	8.10E-07	-9.4	2.40E-07
-8.2	1.50E-06	-8.1	2.00E-06	-8	2.20E-06	-8.6	8.70E-07	-7.7	3.60E-06	-7.5	5.60E-06	-8.3	1.30E-06	-8.9	5.10E-07

Table 16: $\Delta G/K_d$ of all the 8 HLA DRB structures docked with the peptide 1sje, complexed with TCR 3of6

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-11.9	3.90E-09	-12.9	8.40E-10	-10.3	5.50E-08	-10.7	2.70E-08	-10.6	3.30E-08	-10.7	2.80E-08	-10.4	4.40E-08	-10.9	2.20E-08
-10.1	8.00E-08	-12.7	1.10E-09	-9.4	2.30E-07	-10.6	3.10E-08	-10.3	5.20E-08	-10	8.40E-08	-9.7	1.40E-07	-10.9	2.10E-08
-10.1	7.50E-08	-10.3	5.20E-08	-8.8	6.00E-07	-10.1	7.90E-08	-8.8	6.10E-07	-9.9	9.70E-08	-9.6	1.60E-07	-9.7	1.60E-07
-10	9.60E-08	-10	8.20E-08	-8.8	6.70E-07	-10.1	7.90E-08	-8.7	7.90E-07	-9.1	3.90E-07	-9.6	1.80E-07	-9.7	1.50E-07
-9.9	1.10E-07	-9.8	1.10E-07	-8.7	7.40E-07	-10.1	7.30E-08	-8.5	1.10E-06	-8.9	5.30E-07	-9.5	1.90E-07	-9.6	1.60E-07
-9.3	2.90E-07	-9.2	3.30E-07	-8.7	7.10E-07	-9.4	2.50E-07	-8.5	9.90E-07	-8.9	5.60E-07	-9	4.70E-07	-9.5	2.00E-07
-9.2	3.00E-07	-9.1	3.80E-07	-8.5	9.80E-07	-9.4	2.30E-07	-8.3	1.40E-06	-8.5	9.40E-07	-8.8	6.70E-07	-9.5	2.00E-07
-9	4.80E-07	-8.7	7.30E-07	-8.3	1.30E-06	-9	4.30E-07	-8.1	2.10E-06	-8.3	1.30E-06	-8.5	1.10E-06	-9.2	3.50E-07
-8.6	8.40E-07	-7.8	3.30E-06	-8.1	1.80E-06	-8.8	6.20E-07	-8.1	2.00E-06	-8.2	1.70E-06	-8.5	1.10E-06	-8.8	6.60E-07
-8	2.50E-06	-7.2	8.60E-06	-7.9	2.50E-06	-8.6	8.60E-07	-7.6	4.70E-06	-7	1.20E-05	-8.2	1.60E-06	-7	1.20E-05

Table 17: $\Delta G/K_d$ of all the 8 HLA DRB structures docked with the peptide 1aqd, complexed with TCR 4udu

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-12	3.30E-09	-11.9	4.20E-09	-11.9	4.10E-09	-12.1	3.00E-09	-11	1.60E-08	-11.4	9.70E-09	-11.8	4.50E-09	-11.1	1.40E-08
-9.7	1.50E-07	-10.9	2.20E-08	-10.3	5.20E-08	-11.4	9.30E-09	-10.8	2.40E-08	-10.5	3.90E-08	-11.2	1.30E-08	-10.8	2.30E-08
-9.5	2.00E-07	-10.8	2.20E-08	-10.2	6.90E-08	-10.6	3.10E-08	-10.6	3.10E-08	-10.3	5.00E-08	-11.2	1.30E-08	-9.9	9.80E-08
-9.3	2.90E-07	-10.7	2.80E-08	-10.1	7.10E-08	-10.1	7.50E-08	-10.5	3.70E-08	-10	8.90E-08	-11	1.60E-08	-9.3	2.80E-07

-9.2	3.10E-07	-10.4	5.00E-08	-10	8.90E-08	-9.6	1.80E-07	-10.4	4.80E-08	-9.5	2.00E-07	-10.6	3.30E-08	-8.8	6.20E-07
-9.2	3.40E-07	-10.4	4.40E-08	-9.8	1.20E-07	-9.4	2.50E-07	-9.3	3.00E-07	-9.4	2.20E-07	-10.4	4.60E-08	-8.7	7.30E-07
-9.1	3.50E-07	-10.4	4.30E-08	-9.2	3.40E-07	-9.3	2.90E-07	-9.2	3.10E-07	-9.4	2.40E-07	-9	4.40E-07	-8.7	7.30E-07
-8.7	7.10E-07	-10.2	6.80E-08	-9.1	3.60E-07	-8.5	1.00E-06	-9.1	3.90E-07	-8.9	5.40E-07	-8.9	5.50E-07	-8.6	9.30E-07
-8.3	1.40E-06	-9.4	2.20E-07	-8.7	7.00E-07	-8.5	1.10E-06	-9	4.60E-07	-8.4	1.20E-06	-8.2	1.60E-06	-8.5	1.10E-06
-7.2	8.80E-06	-9.2	3.20E-07	-8.6	9.30E-07	-8	2.30E-06	-8.8	5.80E-07	-8.1	1.80E-06	-8.1	1.90E-06	-8.2	1.60E-06

Table 18: $\Delta G/K_d$ of all the 8 HLA DRB structures docked with the peptide 1dlh, complexed with TCR 4udu

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-10.4	4.80E-08	-11.5	7.60E-09	-11.4	9.60E-09	-12	3.40E-09	-11.9	4.00E-09	-11.4	9.30E-09	-11.9	3.90E-09	-10.4	4.80E-08
-9.9	1.00E-07	-10.3	5.90E-08	-11.1	1.50E-08	-11.5	7.80E-09	-10.8	2.30E-08	-11.2	1.40E-08	-10.3	5.20E-08	-10.5	4.10E-08
-9.8	1.20E-07	-10.2	5.90E-08	-10.4	4.70E-08	-10.4	4.80E-08	-10.6	3.60E-08	-11.1	1.40E-08	-9.8	1.20E-07	-10.2	6.50E-08
-9.7	1.60E-07	-9.9	1.10E-07	-10.2	6.50E-08	-10.2	6.20E-08	-10.3	5.80E-08	-10	8.30E-08	-9.6	1.60E-07	-9.7	1.40E-07
-9.7	1.50E-07	-9.9	1.00E-07	-10.2	6.40E-08	-10	8.30E-08	-10.2	6.20E-08	-9.8	1.20E-07	-9.6	1.80E-07	-9.6	1.60E-07
-8.5	1.10E-06	-9.8	1.20E-07	-9.7	1.40E-07	-9.9	1.00E-07	-10	8.70E-08	-9.4	2.40E-07	-9.1	3.90E-07	-9.5	2.00E-07
-8.5	1.00E-06	-9.8	1.20E-07	-9.7	1.40E-07	-9.1	3.80E-07	-9.9	1.10E-07	-9.2	3.50E-07	-8.7	7.50E-07	-9.2	3.40E-07
-8.5	1.10E-06	-9.7	1.60E-07	-9.2	3.10E-07	-8.9	5.50E-07	-9.7	1.50E-07	-9.2	3.20E-07	-8.1	2.10E-06	-8.9	5.20E-07
-8.1	2.00E-06	-9.4	2.30E-07	-9	4.80E-07	-8.5	1.10E-06	-9.5	1.90E-07	-8.2	1.80E-06	-7.8	3.30E-06	-8.9	5.20E-07
-7	1.10E-05	-9.2	3.10E-07	-8.7	7.40E-07	-8.3	1.50E-06	-9.4	2.50E-07	-7.8	3.00E-06	-7.6	4.20E-06	-8	2.30E-06

Table 19: $\Delta G/K_d$ of all the 8 HLA DRB structures docked with the peptide 1kg0, complexed with TCR 4udu

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-12.3	2.30E-09	-11.7	5.40E-09	-12	3.30E-09	-11.9	4.00E-09	-13.2	5.30E-10	-11.5	8.40E-09	-10.9	2.10E-08	-12.7	1.10E-09
-11.1	1.40E-08	-11.6	6.50E-09	-11.4	8.80E-09	-11.4	8.70E-09	-12.9	7.70E-10	-10.3	5.70E-08	-10.7	3.10E-08	-11.7	5.60E-09
-10.9	2.00E-08	-11.4	9.00E-09	-11.1	1.60E-08	-11.3	1.10E-08	-12.3	2.30E-09	-10.2	6.80E-08	-10.6	3.30E-08	-11.2	1.20E-08
-10.8	2.50E-08	-11.3	1.10E-08	-10.8	2.30E-08	-10.7	2.70E-08	-11.4	8.80E-09	-10	9.10E-08	-10.3	5.50E-08	-10.4	4.70E-08
-10.6	3.50E-08	-11.2	1.30E-08	-10.5	3.70E-08	-10.5	4.20E-08	-11.2	1.20E-08	-9.5	2.10E-07	-10.2	6.20E-08	-10	8.30E-08
-9.5	1.90E-07	-10.7	2.70E-08	-10.5	3.90E-08	-10.3	5.10E-08	-11.1	1.50E-08	-9.5	2.10E-07	-10	8.20E-08	-9.3	2.90E-07
-9.4	2.40E-07	-10.6	3.20E-08	-10.4	4.50E-08	-10.2	7.00E-08	-11	1.80E-08	-8.5	1.10E-06	-9.7	1.60E-07	-9.4	2.20E-07
-9	4.50E-07	-10.3	5.40E-08	-9.8	1.30E-07	-10.2	6.20E-08	-10.7	2.70E-08	-8.4	1.20E-06	-9.5	2.00E-07	-7.9	2.60E-06
-8.6	9.20E-07	-10.2	6.20E-08	-9.4	2.40E-07	-8.8	6.00E-07	-10.2	6.70E-08	-8.3	1.40E-06	-9.1	3.70E-07	-7.9	2.70E-06
-7.9	2.70E-06	-9.4	2.20E-07	-7.7	3.90E-06	-8.8	6.40E-07	-10	8.70E-08	-8.1	2.00E-06	-8.9	5.30E-07	-7.3	6.90E-06

Table 20: $\Delta G/K_d$ of all the 8 HLA DRB structures docked with the peptide 1h15, complexed with TCR 4udu

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-10.8	2.50E-08	-12.5	1.60E-09	-13.2	5.30E-10	-11.8	4.60E-09	-10.7	2.70E-08	-11.4	9.40E-09	-10.5	4.20E-08	-11.3	1.10E-08
-10.3	5.40E-08	-12.3	2.00E-09	-11.4	9.00E-09	-10.7	2.90E-08	-9.9	1.00E-07	-10.5	3.90E-08	-10.5	4.00E-08	-11.1	1.60E-08
-10.2	6.10E-08	-11.2	1.30E-08	-10.7	2.80E-08	-10.7	2.70E-08	-9.8	1.30E-07	-10.4	4.40E-08	-10.5	3.70E-08	-11	1.80E-08
-10.2	6.20E-08	-11	1.70E-08	-10.5	3.80E-08	-10.4	4.50E-08	-9.4	2.40E-07	-10.3	5.20E-08	-10.5	3.90E-08	-10.8	2.40E-08

-10.1	7.70E-08	-10.5	4.30E-08	-9.8	1.30E-07	-10.2	6.60E-08	-9.4	2.40E-07	-9.6	1.70E-07	-10.2	6.70E-08	-10.6	3.10E-08
-10.1	7.00E-08	-10.4	4.50E-08	-8.7	7.30E-07	-10	9.60E-08	-9.4	2.50E-07	-9.5	2.00E-07	-9.9	1.10E-07	-10.5	4.00E-08
-10	9.10E-08	-10.4	4.60E-08	-8.2	1.70E-06	-9.9	1.10E-07	-9.4	2.50E-07	-9.2	3.10E-07	-9.7	1.50E-07	-9.3	2.80E-07
-9.6	1.60E-07	-9.9	9.90E-08	-8	2.20E-06	-9.9	9.90E-08	-9.2	3.20E-07	-9	4.20E-07	-9.2	3.20E-07	-9	4.80E-07
-9.5	2.20E-07	-9.7	1.50E-07	-7.9	2.70E-06	-9.7	1.50E-07	-9.1	3.80E-07	-8.9	5.30E-07	-9.2	3.50E-07	-8.8	5.90E-07
-8.9	5.20E-07	-9.6	1.80E-07	-7.8	3.10E-06	-9.2	3.20E-07	-8.5	9.60E-07	-8.4	1.30E-06	-9	4.30E-07	-8.7	7.00E-07

Table 21: $\Delta G/K_d$ of all the 8 HLA DRB structures docked with the peptide 1sje, complexed with TCR 4udu

*01		*04		*07		*08		*09		*12		*14		*16	
ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d	ΔG	K_d
-10.8	2.30E-08	-11.9	4.00E-09	-8.5	1.10E-06	-12.3	2.00E-09	-12.3	2.20E-09	-12	3.50E-09	-10.6	3.50E-08	-9.8	1.30E-07
-10.3	5.90E-08	-10.9	1.90E-08	-8.4	1.20E-06	-11.3	1.00E-08	-11	1.80E-08	-11.8	4.80E-09	-9.9	9.90E-08	-9.7	1.40E-07
-9.5	2.10E-07	-10.9	2.20E-08	-8.1	2.00E-06	-10.7	3.00E-08	-9.5	2.10E-07	-10.7	3.00E-08	-9.8	1.30E-07	-9.5	2.00E-07
-9.2	3.10E-07	-10.9	2.00E-08	-7.9	2.90E-06	-10.4	4.70E-08	-8.5	1.00E-06	-10.6	3.20E-08	-9	4.40E-07	-9.4	2.20E-07
-9	4.50E-07	-10.2	6.00E-08	-7.9	2.90E-06	-9.9	1.00E-07	-8.3	1.30E-06	-10.3	5.80E-08	-8.6	9.20E-07	-9.4	2.20E-07
-8.9	5.40E-07	-9.9	1.00E-07	-7.7	3.70E-06	-8.9	4.90E-07	-8.2	1.80E-06	-9.7	1.30E-07	-8.4	1.30E-06	-8.9	5.00E-07
-8.6	8.50E-07	-9.5	2.20E-07	-7.6	4.40E-06	-8.7	7.70E-07	-8.2	1.70E-06	-9.7	1.50E-07	-8.3	1.50E-06	-8.7	7.60E-07
-8.3	1.40E-06	-8.8	5.90E-07	-7.5	5.50E-06	-8.7	7.50E-07	-8	2.30E-06	-8.4	1.20E-06	-8.2	1.60E-06	-8.6	8.10E-07
-8.2	1.70E-06	-8.7	7.90E-07	-7.3	7.70E-06	-8.4	1.10E-06	-8	2.20E-06	-8.3	1.40E-06	-7.9	2.60E-06	-8.4	1.20E-06
-7.4	5.70E-06	-7.3	7.60E-06	-7.1	9.20E-06	-8.3	1.40E-06	-7.8	3.20E-06	-8.3	1.40E-06	-7.8	3.20E-06	-8.1	1.90E-06

List of tables showing the HLA DBR pairs identified from $\Delta G/K_d$ tables 7-21 based on compatibility with eplet mismatched allele.

Table 22: HLA DRB pairs with Ag-peptide 1aqd and TCR 2xna

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*04	DRB1*01- DRB1*08	DRB1*04- DRB1*12
DRB1*01- DRB1*07	DRB1*01- DRB1*16	DRB1*09- DRB1*12
DRB1*01- DRB1*12	DRB1*04- DRB1*08	DRB1*09- DRB1*14
DRB1*01- DRB1*14	DRB1*04- DRB1*16	
DRB1*01- DRB1*16	DRB1*07- DRB1*09	
DRB1*04- DRB1*07	DRB1*07- DRB1*16	
DRB1*04- DRB1*09	DRB1*08- DRB1*12	
DRB1*04- DRB1*14	DRB1*09- DRB1*16	
DRB1*07- DRB1*08		
DRB1*07- DRB1*12		
DRB1*07- DRB1*14		
DRB1*08- DRB1*09		
DRB1*08- DRB1*14		
DRB1*08- DRB1*16		
DRB1*12- DRB1*14		
DRB1*12- DRB1*16		
DRB1*14- DRB1*16		

Table 23: HLA DRB pairs with Ag-peptide 1dlh and TCR 2xna

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*04	DRB1*01- DRB1*14	DRB1*01- DRB1*12
DRB1*01- DRB1*07	DRB1*01- DRB1*16	DRB1*04- DRB1*12
DRB1*01- DRB1*08	DRB1*04- DRB1*07	DRB1*04- DRB1*14
DRB1*01- DRB1*09	DRB1*04- DRB1*16	DRB1*07- DRB1*14
DRB1*04- DRB1*08	DRB1*07- DRB1*08	DRB1*12- DRB1*14
DRB1*04- DRB1*09	DRB1*07- DRB1*16	DRB1*14- DRB1*16
DRB1*07- DRB1*09	DRB1*08- DRB1*09	
DRB1*07- DRB1*12	DRB1*08- DRB1*12	
DRB1*08- DRB1*14	DRB1*08- DRB1*16	
DRB1*09- DRB1*14	DRB1*09- DRB1*12	
	DRB1*09- DRB1*16	
	DRB1*12- DRB1*16	

Table 24: HLA DRB pairs with Ag-peptide 1kg0 and TCR 2xna

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*04	DRB1*07- DRB1*09	
DRB1*01- DRB1*07	DRB1*07- DRB1*12	
DRB1*01- DRB1*08	DRB1*08- DRB1*12	
DRB1*01- DRB1*09	DRB1*08- DRB1*14	
DRB1*01- DRB1*12		
DRB1*01- DRB1*14		
DRB1*01- DRB1*16		

DRB1*04- DRB1*07		
DRB1*04- DRB1*08		
DRB1*04- DRB1*12		
DRB1*04- DRB1*14		
DRB1*04- DRB1*16		
DRB1*07- DRB1*08		
DRB1*07- DRB1*14		
DRB1*07- DRB1*16		
DRB1*08- DRB1*09		
DRB1*08- DRB1*16		
DRB1*09- DRB1*12		
DRB1*09- DRB1*14		
DRB1*09- DRB1*16		
DRB1*12- DRB1*14		
DRB1*12- DRB1*16		
DRB1*14- DRB1*16		

Table 25: HLA DRB pairs with Ag-peptide 1h15 and TCR 2xna

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*04	DRB1*04- DRB1*08	DRB1*07- DRB1*16
DRB1*01- DRB1*07	DRB1*07- DRB1*12	
DRB1*01- DRB1*08	DRB1*08- DRB1*16	
DRB1*01- DRB1*09	DRB1*09- DRB1*16	
DRB1*01- DRB1*12	DRB1*12- DRB1*16	
DRB1*01- DRB1*14	DRB1*14- DRB1*16	
DRB1*01- DRB1*16		
DRB1*04- DRB1*07		
DRB1*04- DRB1*09		
DRB1*04- DRB1*12		
DRB1*04- DRB1*14		
DRB1*04- DRB1*16		
DRB1*07- DRB1*08		
DRB1*07- DRB1*09		
DRB1*07- DRB1*14		
DRB1*08- DRB1*09		
DRB1*08- DRB1*12		
DRB1*08- DRB1*14		
DRB1*09- DRB1*12		
DRB1*09- DRB1*14		
DRB1*12- DRB1*14		

Table 26: HLA DRB pairs with Ag-peptide 1sje and TCR 2xna

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*04	DRB1*07- DRB1*16	DRB1*01- DRB1*16
DRB1*01- DRB1*07	DRB1*08- DRB1*16	DRB1*04- DRB1*16
DRB1*01- DRB1*08	DRB1*09- DRB1*16	
DRB1*01- DRB1*09	DRB1*12- DRB1*16	
DRB1*01- DRB1*12	DRB1*14- DRB1*16	

DRB1*01- DRB1*14		
DRB1*04- DRB1*07		
DRB1*04- DRB1*08		
DRB1*04- DRB1*09		
DRB1*04- DRB1*12		
DRB1*04- DRB1*14		
DRB1*07- DRB1*08		
DRB1*07- DRB1*09		
DRB1*07- DRB1*12		
DRB1*07- DRB1*14		
DRB1*08- DRB1*09		
DRB1*08- DRB1*12		
DRB1*08- DRB1*14		
DRB1*09- DRB1*12		
DRB1*09- DRB1*14		
DRB1*12- DRB1*14		

Table 27: HLA DRB pairs with Ag-peptide 1aqd and TCR 3of6

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*04	DRB1*01- DRB1*12	DRB1*09- DRB1*12
DRB1*01- DRB1*07	DRB1*04- DRB1*12	DRB1*12- DRB1*14
DRB1*01- DRB1*08	DRB1*07- DRB1*12	DRB1*12- DRB1*16
DRB1*01- DRB1*09	DRB1*08- DRB1*12	
DRB1*01- DRB1*14		
DRB1*01- DRB1*16		
DRB1*04- DRB1*07		
DRB1*04- DRB1*08		
DRB1*04- DRB1*09		
DRB1*04- DRB1*14		
DRB1*04- DRB1*16		
DRB1*07- DRB1*08		
DRB1*07- DRB1*09		
DRB1*07- DRB1*14		
DRB1*07- DRB1*16		
DRB1*08- DRB1*09		
DRB1*08- DRB1*14		
DRB1*08- DRB1*16		
DRB1*09- DRB1*14		
DRB1*09- DRB1*16		
DRB1*14- DRB1*16		

Table 28: HLA DRB pairs with Ag-peptide 1dlh and TCR 3of6

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*04	DRB1*01- DRB1*09	DRB1*01- DRB1*07
DRB1*01- DRB1*08	DRB1*01- DRB1*16	DRB1*01- DRB1*12
DRB1*01- DRB1*14	DRB1*04- DRB1*07	DRB1*07- DRB1*12
DRB1*04- DRB1*08	DRB1*04- DRB1*09	DRB1*04- DRB1*16
DRB1*04- DRB1*12	DRB1*07- DRB1*16	DRB1*08- DRB1*09

DRB1*04- DRB1*14	DRB1*08- DRB1*12	
DRB1*07- DRB1*08	DRB1*08- DRB1*14	
DRB1*07- DRB1*09	DRB1*09- DRB1*12	
DRB1*07- DRB1*14	DRB1*09- DRB1*16	
DRB1*08- DRB1*14	DRB1*12- DRB1*14	
DRB1*09- DRB1*14	DRB1*12- DRB1*16	
DRB1*14- DRB1*16		

Table 29: HLA DRB pairs with Ag-peptide 1kg0 and TCR 3of6

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*08	DRB1*01- DRB1*04	DRB1*07- DRB1*16
DRB1*01- DRB1*16	DRB1*01- DRB1*07	
DRB1*01- DRB1*14	DRB1*01- DRB1*09	
DRB1*04- DRB1*08	DRB1*01- DRB1*12	
DRB1*04- DRB1*09	DRB1*04- DRB1*07	
DRB1*04- DRB1*16	DRB1*04- DRB1*12	
DRB1*07- DRB1*09	DRB1*04- DRB1*14	
DRB1*07- DRB1*14	DRB1*07- DRB1*08	
DRB1*08- DRB1*09	DRB1*07- DRB1*12	
DRB1*08- DRB1*14	DRB1*08- DRB1*12	
DRB1*08- DRB1*16	DRB1*09- DRB1*12	
DRB1*09- DRB1*14		
DRB1*09- DRB1*16		
DRB1*12- DRB1*14		
DRB1*12- DRB1*16		
DRB1*14- DRB1*16		

Table 30: HLA DRB pairs with Ag-peptide 1h15 and TCR 3of6

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*04	DRB1*01- DRB1*12	DRB1*01- DRB1*14
DRB1*01- DRB1*07	DRB1*01- DRB1*16	
DRB1*01- DRB1*08	DRB1*07- DRB1*12	
DRB1*01- DRB1*09	DRB1*09- DRB1*12	
DRB1*01- DRB1*12		
DRB1*04- DRB1*07		
DRB1*04- DRB1*08		
DRB1*04- DRB1*09		
DRB1*04- DRB1*12		
DRB1*04- DRB1*16		
DRB1*07- DRB1*08		
DRB1*07- DRB1*09		
DRB1*07- DRB1*14		
DRB1*07- DRB1*16		
DRB1*08- DRB1*09		
DRB1*08- DRB1*12		
DRB1*08- DRB1*14		
DRB1*08- DRB1*16		
DRB1*09- DRB1*14		

DRB1*09- DRB1*16		
DRB1*12- DRB1*14		
DRB1*12- DRB1*16		
DRB1*14- DRB1*16		

Table 31: HLA DRB pairs with Ag-peptide 1sje and TCR 3of6

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*04	DRB1*01- DRB1*07	DRB1*04- DRB1*08
DRB1*01- DRB1*08	DRB1*01- DRB1*09	DRB1*04- DRB1*09
DRB1*01- DRB1*12	DRB1*01- DRB1*16	DRB1*04- DRB1*12
DRB1*01- DRB1*14	DRB1*04- DRB1*07	DRB1*04- DRB1*14
DRB1*07- DRB1*08	DRB1*04- DRB1*16	DRB1*07- DRB1*09
	DRB1*07- DRB1*14	DRB1*07- DRB1*12
	DRB1*07- DRB1*16	DRB1*08- DRB1*16
	DRB1*08- DRB1*09	DRB1*09- DRB1*12
	DRB1*08- DRB1*12	DRB1*12- DRB1*16
	DRB1*08- DRB1*14	
	DRB1*09- DRB1*14	
	DRB1*09- DRB1*16	
	DRB1*12- DRB1*14	
	DRB1*09- DRB1*16	

Table 32: HLA DRB pairs with Ag-peptide 1aqd and TCR 4udu

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*04	DRB1*01- DRB1*07	
DRB1*01- DRB1*09	DRB1*01- DRB1*08	
DRB1*01- DRB1*12	DRB1*01- DRB1*16	
DRB1*01- DRB1*14	DRB1*04- DRB1*08	
DRB1*04- DRB1*07	DRB1*04- DRB1*12	
DRB1*04- DRB1*09	DRB1*04- DRB1*16	
DRB1*04- DRB1*14	DRB1*12- DRB1*14	
DRB1*07- DRB1*08	DRB1*12- DRB1*16	
DRB1*07- DRB1*09	DRB1*14- DRB1*16	
DRB1*07- DRB1*12		
DRB1*07- DRB1*14		
DRB1*07- DRB1*16		
DRB1*08- DRB1*09		
DRB1*08- DRB1*12		
DRB1*08- DRB1*14		
DRB1*08- DRB1*16		
DRB1*09- DRB1*12		
DRB1*09- DRB1*14		
DRB1*09- DRB1*16		

Table 33: HLA DRB pairs with Ag-peptide 1dlh and TCR 4udu

Highly compatible	Moderate compatible	Less compatible
DRB1*04- DRB1*07	DRB1*01- DRB1*04	DRB1*01- DRB1*09
DRB1*04- DRB1*08	DRB1*01- DRB1*07	
DRB1*04- DRB1*09	DRB1*01- DRB1*08	
DRB1*04- DRB1*12	DRB1*01- DRB1*12	
DRB1*07- DRB1*09	DRB1*01- DRB1*14	
DRB1*07- DRB1*12	DRB1*01- DRB1*16	
DRB1*07- DRB1*16	DRB1*04- DRB1*14	
DRB1*08- DRB1*09	DRB1*04- DRB1*16	
DRB1*08- DRB1*12	DRB1*07- DRB1*14	
DRB1*08- DRB1*16	DRB1*08- DRB1*14	
DRB1*09- DRB1*12	DRB1*09- DRB1*14	
DRB1*09- DRB1*16		
DRB1*12- DRB1*14		
DRB1*12- DRB1*16		
DRB1*14- DRB1*16		

Table 34: HLA DRB pairs with Ag-peptide 1kg0 and TCR 4udu

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*04	DRB1*01- DRB1*12	DRB1*08- DRB1*12
DRB1*01- DRB1*07	DRB1*04- DRB1*12	DRB1*08- DRB1*16
DRB1*01- DRB1*08	DRB1*07- DRB1*12	DRB1*09- DRB1*12
DRB1*01- DRB1*09	DRB1*12- DRB1*14	DRB1*09- DRB1*16
DRB1*01- DRB1*14		DRB1*12- DRB1*16
DRB1*01- DRB1*16		DRB1*14- DRB1*16
DRB1*04- DRB1*07		
DRB1*04- DRB1*08		
DRB1*04- DRB1*09		
DRB1*04- DRB1*14		
DRB1*04- DRB1*16		
DRB1*07- DRB1*08		
DRB1*07- DRB1*09		
DRB1*07- DRB1*12		
DRB1*07- DRB1*16		
DRB1*08- DRB1*09		
DRB1*08- DRB1*14		
DRB1*09- DRB1*14		

Table 35: HLA DRB pairs with Ag-peptide 1h15 and TCR 4udu

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*04	DRB1*07- DRB1*08	DRB1*01- DRB1*07
DRB1*01- DRB1*08	DRB1*07- DRB1*09	DRB1*04- DRB1*07
DRB1*01- DRB1*09	DRB1*07- DRB1*12	DRB1*07- DRB1*14
DRB1*01- DRB1*12		DRB1*07- DRB1*16
DRB1*01- DRB1*14		
DRB1*01- DRB1*16		

DRB1*04- DRB1*08		
DRB1*04- DRB1*09		
DRB1*04- DRB1*12		
DRB1*04- DRB1*14		
DRB1*04- DRB1*16		
DRB1*08- DRB1*09		
DRB1*08- DRB1*12		
DRB1*08- DRB1*14		
DRB1*08- DRB1*16		
DRB1*09- DRB1*12		
DRB1*09- DRB1*14		
DRB1*09- DRB1*16		
DRB1*12- DRB1*14		
DRB1*12- DRB1*16		
DRB1*14- DRB1*16		

Table 36: HLA DRB pairs with Ag-peptide 1sje and TCR 4udu

Highly compatible	Moderate compatible	Less compatible
DRB1*01- DRB1*16	DRB1*01- DRB1*04	DRB1*01- DRB1*07
DRB1*04- DRB1*08	DRB1*01- DRB1*08	DRB1*01- DRB1*09
DRB1*04- DRB1*16	DRB1*01- DRB1*12	DRB1*04- DRB1*07
	DRB1*01- DRB1*14	DRB1*04- DRB1*09
	DRB1*04- DRB1*12	DRB1*04- DRB1*14
	DRB1*08- DRB1*12	DRB1*07- DRB1*08
	DRB1*08- DRB1*16	DRB1*07- DRB1*09
	DRB1*12- DRB1*14	DRB1*07- DRB1*12
	DRB1*12- DRB1*16	DRB1*07- DRB1*14
		DRB1*07- DRB1*16
		DRB1*08- DRB1*14
		DRB1*09- DRB1*12
		DRB1*09- DRB1*14
		DRB1*09- DRB1*16
		DRB1*14- DRB1*16

4.5.3 Identification of compatible HLA DRB alleles from $\Delta G/K_d$ analysis

The comparative analysis of $\Delta G/K_d$ value between the docked complexes for each HLA DRB allele structure has revealed that the energy distribution pattern of each structure bound to a peptide when docked with different TCR structures had similarities for mismatched alleles. There were 28 possible combinations between the 8 selected HLA DRB alleles. Each pair of mismatched alleles with highest compatibility based on higher and comparable $\Delta G/K_d$ values has been listed in table 7-21. A figure representing the compatibility between the various combinations of HLA DRB acquired from the data enlisted in tables 22-36, has been given below.

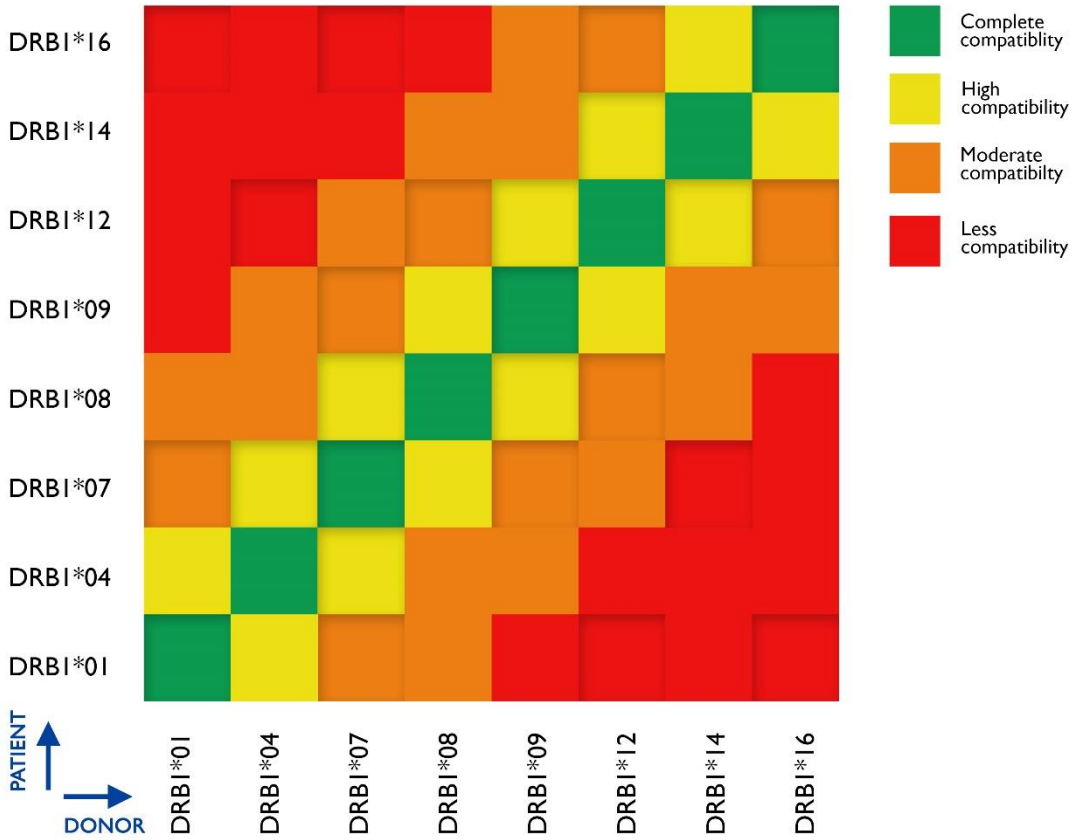


Figure 25: A consolidated pictorial illustration of table 22-36 displaying HLA compatibility between the 8 modelled HLA DRB allele. The color range represented from green to red denotes the 28 possible combinations and their compatibility between the mismatched HLA alleles.

4.6 Biostatistical analysis on HLA ABDR eplet mismatches in relation with renal graft survival

The coefficient of correlation between variables HLA AB eplet mismatch and present condition of the graft (surviving or rejected) for the total sample (n = 572) is 0.076. It shows that there is a poor correlation between the two variables since the value is near to zero. The *P*-value is 0.003 which is lower than 0.05 hence there is a significant correlation between the two variables. When comparing HLA DR eplet mismatch with present condition for the total sample, the regression coefficient is found to be -.215 which is significant at 0.01 level of significance since the significant value obtained is 0.000. This indicates a strong negative correlation existing between the two variables. When comparing the Wald statistics obtained for HLA AB (8.641) and HLA DR (74.264) eplet mismatch there was a high difference in the values. The results show an increased positive and linear correlation between the numbers of HLA DR eplet mismatches towards the graft rejection. The statistical analysis reveals that the increased number of HLA DR eplet mismatches over HLA AB eplet mismatch number can cause delayed graft rejection. HLA DR eplet mismatches are highly influential in causing graft rejection. Other variables like sex and age were taken for statistical analysis but no significant results were obtained.

Table 37: Logistic regression analysis of HLA ABDR eplet mismatches

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 1[a]	HLA AB	.076	.026	8.641	1	.003	1.079
	HLA DR	-.215	.025	74.264	1	.000	.086
	Constant	3.472	.344	101.871	1	.000	32.190
a. Variable(s) entered on step 1: HLA AB and HLA DR Data presented as correlation coefficient P-value is <0.01							

ANNEXURES

Annexure I

Table 38: List of CDC-crossmatching carried out for 572 patient and donor pair for the identification of preformed antibody

*The numbering of patient and donor pair follows 'patient set no. 1 - 572' numbering pattern in all the sections of results and discussion.

Patient set no.	CDC Results	Patient set no.	CDC Results
1	Std neg and AHG neg	287	Std neg and DTT neg
2	Std neg and AHG neg	288	Std pos (50%) & DTT pos (50%)
3	Standard negative	289	Std neg and DTT neg
4	Std neg and AHG neg	290	Std neg and DTT neg
5	Std neg and AHG neg	291	Std neg and DTT neg
6	Standard negative	292	Std neg and DTT neg
7	Std neg and AHG neg	293	Std neg and DTT neg
8	Std neg and AHG neg	294	Std neg and DTT neg
9	Std pos (50%) & AHG pos (50%)	295	Std neg and DTT neg
10	Std pos (30%) & AHG pos (30%)	296	Standard negative
11	Std neg and AHG neg	297	Std neg and DTT neg
12	Std neg and AHG neg	298	Std neg and DTT neg
13	Std neg and AHG neg	299	Std neg and DTT neg
14	Std neg and AHG neg	300	Std pos (30%) and DTT neg
15	Std neg and AHG neg	301	Std neg and DTT neg
16	Std neg and AHG neg	302	Positive
17	Std neg and AHG neg	303	Std neg and DTT neg
18	Std neg and AHG neg	304	Std neg and DTT neg
19	Std neg and AHG neg	305	Std neg and DTT neg
20	Std neg and AHG neg	306	Std neg and DTT neg
21	Std neg and AHG neg	307	Std neg and DTT neg
22	Std neg and AHG neg	308	Std neg and DTT neg
23	Std neg and AHG neg	309	Std neg and DTT neg
24	Std neg and AHG neg	310	Std neg and DTT neg
25	Std neg and AHG neg	311	Std neg and DTT neg
26	Std neg and AHG neg	312	Std neg and DTT neg
27	Std neg and AHG neg	313	Std neg and DTT neg
28	Std neg and AHG neg	314	Std neg and DTT neg
29	Std neg and AHG neg	315	Std neg and DTT neg
30	Std neg and AHG neg	316	Std neg and DTT neg
31	Standard negative	317	Std neg and DTT neg
32	Standard negative	318	Std neg and DTT neg
33	Standard negative	319	Std neg and DTT neg
34	Standard negative	320	Std neg and DTT neg
35	Std neg and AHG neg	321	Std neg and DTT neg
36	Std neg and AHG neg	322	Std neg and DTT neg
37	Standard negative	323	Std neg and DTT neg
38	Standard negative	324	Std neg and DTT neg
39	Standard negative	325	Std neg and DTT neg
40	Standard negative	326	Std neg and DTT neg
41	Standard negative	327	Std neg and DTT neg
42	Std neg and AHG neg	328	Std neg and DTT neg

43	Standard negative	329	Std neg and DTT neg
44	Standard negative	330	Std neg and DTT neg
45	Standard negative	331	Std neg and DTT neg
46	Std neg and AHG neg	332	Std neg and DTT neg
47	Std neg and AHG neg	333	Std neg and DTT neg
48	Standard negative	334	Std neg and DTT neg
49	Std neg and AHG neg	335	Negative
50	Standard negative	336	Negative
51	Standard negative	337	Negative
52	Std neg and AHG neg	338	Negative
53	Std pos (10%) & AHG pos (10%)	339	Negative
54	Standard negative	340	Negative
55	Std neg and AHG neg	341	Std pos (10%) & DTT pos (10%)
56	Std neg and AHG neg	342	Std neg and DTT neg
57	Standard negative	343	Std neg and DTT neg
58	Std neg and AHG neg	344	Std neg and DTT neg
59	Std neg and AHG neg	345	Std neg and DTT neg
60	Std neg and AHG neg	346	Std neg and DTT neg
61	Std neg and AHG neg	347	Std neg and DTT neg
62	Std neg and AHG neg	348	Std neg and DTT neg
63	Std neg and AHG neg	349	Std neg and DTT neg
64	Std neg and AHG neg	350	Std neg and DTT neg
65	Std neg and AHG neg	351	Positive
66	Std neg and AHG neg	352	Std neg and DTT neg
67	Std neg and AHG neg	353	Std neg and DTT neg
68	Std neg and AHG neg	354	Negative
69	Std neg and AHG neg	355	Std neg and DTT neg
70	Standard negative	356	Std neg and DTT neg
71	Std neg and AHG neg	357	Std neg and DTT neg
72	Std pos (80%) & AHG pos (80%)	358	Std neg and DTT neg
73	Std neg and AHG neg	359	Std neg and DTT neg
74	Std neg and AHG neg	360	Std neg and DTT neg
75	Std neg and AHG neg	361	Std neg and DTT neg
76	Std neg and AHG neg	362	Std neg and DTT neg
77	Std neg and AHG neg	363	Std neg and DTT neg
78	Std negative	364	Std neg and DTT neg
79	Std pos (60%) & AHG pos (80%)	365	Std neg and DTT neg
80	Std neg and AHG neg	366	Std neg and DTT neg
81	Standard negative	367	Std neg and DTT neg
82	Std neg and AHG neg	368	Std neg and DTT neg
83	Std neg and AHG neg	369	Std neg and DTT neg
84	Std neg and AHG neg	370	Std neg and DTT neg
85	Std neg and AHG neg	371	Std neg and DTT neg
86	Standard negative	372	Std neg and DTT neg
87	Standard negative	373	Std neg and DTT neg
88	Std neg and AHG neg	374	Std neg and DTT neg
89	Std neg and AHG neg	375	Std neg and DTT neg
90	Std neg and AHG neg	376	Borderline positive
91	Std positive (20-30%)	377	Std neg and DTT neg
92	Std neg and AHG neg	378	Std neg and DTT neg
93	Std neg and AHG neg	379	Std neg and DTT neg
94	Std neg and AHG neg	380	Std neg and DTT neg
95	Std neg and AHG neg	381	Std neg and DTT neg
96	Std neg and AHG neg	382	Std neg and DTT neg

97	Std neg and AHG neg	383	Std neg and DTT neg
98	Standard negative	384	Std neg and DTT neg
99	Std neg and AHG neg	385	Std neg and DTT neg
100	Std neg and AHG neg	386	Std neg and DTT neg
101	Std neg and AHG neg	387	Std neg and DTT neg
102	Std neg and AHG neg	388	Std neg and DTT neg
103	Std neg and AHG neg	389	Std neg and DTT neg
104	Std pos (50%) & AHG pos (50%)	390	Std neg and DTT neg
105	Std neg and AHG neg	391	Std neg and DTT neg
106	Std neg and AHG neg	392	Std neg and DTT neg
107	Std neg and AHG neg	393	Std pos (20%) & DTT pos (10%)
108	Std neg and AHG neg	394	Std neg and DTT neg
109	Std neg and AHG neg	395	Std neg and DTT neg
110	Std neg and AHG neg	396	Std neg and DTT neg
111	Std neg and AHG neg	397	Std neg and DTT neg
112	Std neg and AHG neg	398	Std neg and DTT neg
113	Std neg and AHG neg	399	Std neg and DTT neg
114	Std neg and AHG neg	400	Std neg and DTT neg
115	Std neg and AHG neg	401	Std neg and DTT neg
116	Std neg and AHG neg	402	Std neg and DTT neg
117	Std neg and AHG neg	403	Std neg and DTT neg
118	Std neg and AHG neg	404	Std neg and DTT neg
119	Std neg and AHG neg	405	Std neg and DTT neg
120	Std neg and AHG neg	406	Std neg and DTT neg
121	Std neg and AHG neg	407	Std neg and DTT neg
122	Std neg and AHG neg	408	Std neg and DTT neg
123	Std neg and AHG neg	409	Std neg and DTT neg
124	Std neg and AHG neg	410	Std neg and DTT neg
125	Std neg and AHG neg	411	Std neg and DTT neg
126	Std neg and AHG neg	412	Std neg and DTT neg
127	Std neg and AHG neg	413	Std neg and DTT neg
128	Std neg and AHG neg	414	Std neg and DTT neg
129	Std neg and AHG neg	415	Std neg and DTT neg
130	Std neg and AHG neg	416	Std neg and DTT neg
131	Std neg and AHG neg	417	Std neg and DTT neg
132	Std neg and AHG neg	418	Std neg and DTT neg
133	Std neg and AHG neg	419	Std neg and DTT neg
134	Std neg and AHG neg	420	Std neg and DTT neg
135	Std neg and AHG neg	421	Std neg and DTT neg
136	Std neg and AHG neg	422	Std neg and DTT neg
137	Std neg and AHG neg	423	Std neg and DTT neg
138	Std neg and AHG neg	424	Std neg and DTT neg
139	Std neg and AHG neg	425	Std neg and DTT neg
140	Std neg and AHG neg	426	Std neg and DTT neg
141	Std neg and AHG neg	427	Std neg and DTT neg
142	Std neg and AHG neg	428	Std neg and DTT neg
143	Std neg and AHG neg	429	Negative
144	Std neg and AHG neg	430	Negative
145	Std neg and AHG neg	431	Positive
146	Std neg and AHG neg	432	Std neg and DTT neg
147	Std neg and AHG neg	433	Std neg and DTT neg
148	Std neg and AHG neg	434	Std neg and DTT neg
149	Std neg and AHG neg	435	Std neg and DTT neg
150	Std neg and AHG neg	436	Std neg and DTT neg

151	Std neg and AHG neg	437	Std neg and DTT neg
152	Std neg and AHG neg	438	Std neg and DTT neg
153	Std neg and AHG neg	439	Negative
154	Std neg and AHG neg	440	Negative
155	Std neg and AHG neg	441	Std neg and DTT neg
156	Std neg and AHG neg	442	Std neg and DTT neg
157	Std neg and AHG neg	443	Std neg and DTT neg
158	Std neg and AHG neg	444	Std neg and DTT neg
159	Std neg and AHG neg	445	Std neg and DTT neg
160	Std neg and AHG neg	446	Std neg and DTT neg
161	Std neg and AHG neg	447	Std neg and DTT neg
162	Standard negative	448	Std neg and DTT neg
163	Std pos (10%) & AHG pos (10%)	449	Std neg and DTT neg
164	Std neg and AHG neg	450	Std neg and DTT neg
165	Std neg and AHG neg	451	Std neg and DTT neg
166	Std neg and AHG neg	452	Std neg and DTT neg
167	Std pos (30%) & AHG pos (40%)	453	Std neg and DTT neg
168	Std neg and AHG neg	454	Std neg and DTT neg
169	Std neg and AHG neg	455	Std neg and DTT neg
170	Std neg and AHG neg	456	Std neg and DTT neg
171	Std negative	457	Std neg and DTT neg
172	Std pos (30%) & DTT pos (40%)	458	Std neg and DTT neg
173	Std neg and AHG neg	459	Std neg and DTT neg
174	Std neg and AHG neg	460	Std neg and DTT neg
175	Std neg and AHG neg	461	Std neg and DTT neg
176	Std neg and AHG neg	462	Std neg and DTT neg
177	Std neg and AHG neg	463	Std neg and DTT neg
178	Std pos (60%) & DTT pos (80%)	464	Std neg and DTT neg
179	Std pos (10%) & DTT pos (20%)	465	Std neg and DTT neg
180	Std neg and AHG neg	466	Std neg and DTT neg
181	Std neg and AHG neg	467	Std neg and DTT neg
182	Std neg and AHG neg	468	Std neg and DTT neg
183	Std neg and AHG neg	469	Std neg (5%) and DTT neg (5%)
184	Std neg and AHG neg	470	Std neg and DTT neg
185	Std neg and AHG neg	471	Std neg and DTT neg
186	Std neg and AHG neg	472	Std neg and DTT neg
187	Std neg and AHG neg	473	Negative
188	Std neg and AHG neg	474	Positive
189	Std neg and AHG neg	475	Borderline positive
190	Std neg and AHG neg	476	Std neg and DTT neg
191	Std neg and AHG neg	477	Std neg and DTT neg
192	Std neg and AHG neg	478	Std neg and DTT neg
193	Std neg and AHG neg	479	Std neg and DTT neg
194	Std neg and AHG neg	480	Std neg and DTT neg
195	Std neg and AHG neg	481	Std neg and DTT neg
196	Negative	482	Positive
197	Std neg and AHG neg	483	Std neg and DTT neg
198	Std neg and AHG neg	484	Std neg and DTT neg
199	Std neg and AHG neg	485	Std neg and DTT neg
200	Std neg and AHG neg	486	Std neg and DTT neg
201	Std neg and AHG neg	487	Std neg and AHG neg
202	Std neg and AHG neg	488	Std neg and DTT neg
203	Std neg and AHG neg	489	Std neg and DTT neg
204	Std neg and AHG neg	490	Std neg and DTT neg

205	Std neg and AHG neg	491	Std pos (40%) & DTT neg
206	Std neg and AHG neg	492	Std neg and DTT neg
207	Std neg and AHG neg	493	Positive
208	Std neg and AHG neg	494	Std neg and DTT neg
209	Std neg and AHG neg	495	Std pos (20%) & DTT neg
210	Std neg and AHG neg	496	Std neg and DTT neg
211	Std neg and AHG neg	497	Std neg and DTT neg
212	Std neg and AHG neg	498	Std pos (20%) & DTT neg
213	Std neg and AHG neg	499	Std neg and DTT neg
214	Std neg and AHG neg	500	Std neg and DTT neg
215	Std neg and AHG neg	501	Std neg and DTT neg
216	Std neg and AHG neg	502	Std neg and DTT neg
217	Std neg and AHG neg	503	Std neg and DTT neg
218	Std neg and AHG neg	504	Std neg and DTT neg
219	Std neg and AHG neg	505	Std neg and DTT neg
220	Std neg and AHG neg	506	Std neg and DTT neg
221	Std neg and AHG neg	507	Std neg and DTT neg
222	Std neg and AHG neg	508	Std neg and DTT neg
223	Std neg and AHG neg	509	Std neg and DTT neg
224	Std neg and AHG neg	510	Std neg and DTT neg
225	Std neg and AHG neg	511	Std neg and DTT neg
226	Std neg and AHG neg	512	Std neg and DTT neg
227	Std neg and AHG neg	513	Std neg and DTT neg
228	Std neg and AHG neg	514	Std neg and DTT neg
229	Std neg and AHG neg	515	Std neg and DTT neg
230	Std neg and AHG neg	516	Std neg and DTT neg
231	Std neg and AHG neg	517	Std neg and DTT neg
232	Std neg and AHG neg	518	Std neg and DTT neg
233	Std neg and AHG neg	519	Std neg and DTT neg
234	Std neg and AHG neg	520	Std neg and DTT neg
235	Std neg and AHG neg	521	Std neg and DTT neg
236	Std neg and AHG neg	522	Std neg and DTT neg
237	Std neg and AHG neg	523	Std neg and DTT neg
238	Standard negative	524	Std neg and DTT neg
239	Std neg and AHG neg	525	Std neg and DTT neg
240	Std neg and AHG neg	526	Std neg and DTT neg
241	Std neg and AHG neg	527	Std neg and DTT neg
242	Std neg and AHG neg	528	Std neg and DTT neg
243	Std pos (12%) & AHG pos (12%)	529	Std neg and DTT neg
244	Std neg and DTT neg	530	Std neg and DTT neg
245	Std neg and DTT neg	531	Std neg and DTT neg
246	Std neg and DTT neg	532	Std neg and DTT neg
247	Std neg and DTT neg	533	Std neg and DTT neg
248	Std neg and DTT neg	534	Std neg and DTT neg
249	Std neg and DTT neg	535	Std neg and DTT neg
250	Std neg and DTT neg	536	Std neg and DTT neg
251	Std neg and DTT neg	537	Std neg and DTT neg
252	Std neg and DTT neg	538	Std neg and DTT neg
253	Std neg and DTT neg	539	Std neg and DTT neg
254	Std neg and DTT neg	540	Std pos (12%) & DTT neg (12%)
255	Std neg and DTT neg	541	Std neg and DTT neg
256	Std neg and DTT neg	542	Std neg and DTT neg
257	Std neg and DTT neg	543	Std neg and DTT neg
258	Std neg and DTT neg	544	Std pos (10%) & DTT pos (10%)

259	Std neg and DTT neg	545	Std neg and DTT neg
260	Std neg and DTT neg	546	Std neg and DTT neg
261	Std neg and DTT neg	547	Std neg and DTT neg
262	Std neg and DTT neg	548	Std neg and DTT neg
263	Std neg and DTT neg	549	Std pos (40%) & DTT pos (15%)
264	Std neg and DTT neg	550	Std neg and DTT neg
265	Std neg and DTT neg	551	Std neg and DTT neg
266	Std neg and DTT neg	552	Std neg and DTT neg
267	Std negative	553	Std neg and DTT neg
268	Std neg and DTT neg	554	Std neg and DTT neg
269	Std pos (20%) & DTT pos (20%)	555	Std neg and DTT neg
270	Std neg and DTT neg	556	Negative
271	Std neg and DTT neg	557	Std neg and DTT neg
272	Std neg and AHG neg	558	Std neg and DTT neg
273	Std neg and DTT neg	559	Std neg and DTT neg
274	Std negative	560	Std neg and DTT neg
275	Std neg and DTT neg	561	Std neg and DTT neg
276	Std neg and AHG neg	562	Std neg and DTT neg
277	Std negative	563	Std neg and DTT neg
278	Std neg and DTT neg	564	Std neg and DTT neg
279	Std neg and DTT neg	565	Std neg and DTT neg
280	Std neg and DTT neg	566	Std neg and DTT neg
281	Std pos (30%) & DTT neg (8%)	567	Std neg and DTT neg
282	Std neg and DTT neg	568	Std neg and DTT neg
283	Std neg and DTT neg	569	Std neg and DTT neg
284	Std neg and DTT neg	570	Std neg and DTT neg
285	Std neg and DTT neg	571	Std neg and DTT neg
286	Std neg and DTT neg	572	Std neg and DTT neg

Annexure II

Table 39: HLA ABDR 4-digit allele data of patients and donors obtained after SSP- and SSOP-PCR typing

Table 39.1: Allele ID of patients

Patient no.	A	A	B	B	DRB1	DRB1
1.	A*25:01	A*33:03	B*07:02	B*44:03	DRB1*07:01	DRB1*15:02
2.	A*24:02	A*30:01	B*13:02	B*52:01	DRB1*07:01	DRB1*07:01
3.	A*29:01	A*68:01	B*07:05	B*35:03	DRB1*13:01	DRB1*14:04
4.	A*68:01	A*68:01	B*07:05	B*52:01	DRB1*04:03	DRB1*14:04
5.	A*24:07	A*33:03	B*07:05	B*08:01	DRB1*10:01	DRB1*13:01
6.	A*33:03	A*33:03	B*40:06	B*44:03	DRB1*07:01	DRB1*07:01
7.	A*02:01	A*02:11	B*40:06	B*40:06	DRB1*14:04	DRB1*15:01
8.	A*02:02	A*68:01	B*15:18	B*41:01	DRB1*13:03	DRB1*14:04
9.	A*02:01	A*24:02	B*15:01	B*40:06	DRB1*04:04	DRB1*15:02
10.	A*24:02	A*24:02	B*07:02	B*07:02	DRB1*01:01	DRB1*01:01
11.	A*24:02	A*26:01	B*15:18	B*51:01	DRB1*08:03	DRB1*13:02
12.	A*02:01	A*24:02	B*35:01	B*57:01	DRB1*07:01	DRB1*11:01
13.	A*32:01	A*08:01	B*02:01	B*37:01	DRB1*01:01	DRB1*03:01
14.	A*03:01	A*33:03	B*35:01	B*44:03	DRB1*07:01	DRB1*07:01
15.	A*24:02	A*26:01	B*08:01	B*40:06	DRB1*14:04	DRB1*15:02
16.	A*01:01	A*31:01	B*15:02	B*51:01	DRB1*07:01	DRB1*10:01
17.	A*01:01	A*31:01	B*07:02	B*48:01	DRB1*14:04	DRB1*15:01
18.	A*03:01	A*32:01	B*27:04	B*35:01	DRB1*07:01	DRB1*14:04
19.	A*23:01	A*33:03	B*44:03	B*52:01	DRB1*03:01	DRB1*07:01
20.	A*02:01	A*11:01	B*40:06	x	DRB1*04:03	DRB1*15:01
21.	A*02:01	A*02:11	B*35:03	B*44:04	DRB1*07:01	DRB1*14:04
22.	A*03:01	A*11:01	B*51:01	B*55:02	DRB1*01:01	DRB1*13:01
23.	A*32:01	A*33:01	B*44:03	B*51:01	DRB1*07:01	DRB1*01:01
24.	A*02:01	A*29:01	B*07:05	B*52:01	DRB1*14:04	DRB1*15:02
25.	A*03:01	A*24:02	B*44:03	B*55:01	DRB1*04:01	DRB1*07:01
26.	A*02:01	A*02:01	B*07:05	B*35:03	DRB1*11:10	DRB1*14:01
27.	A*01:01	A*32:01	B*49:01	B*57:01	DRB1*04:03	DRB1*13:02
28.	A*02:07	A*24:02	B*46:01	B*51:01	DRB1*11:15	DRB1*15:02
29.	A*02:11	A*24:02	B*35:01	B*35:03	DRB1*01:01	DRB1*11:01
30.	A*01:01	A*30:01	B*37:01	B*53:01	DRB1*04:01	DRB1*10:01
31.	A*11:01	A*32:01	B*35:01	x	DRB1*11:01	DRB1*14:04
32.	A*02:01	A*03:03	B*07:02	B*15:01	DRB1*13:01	DRB1*15:01
33.	A*24:02	A*24:02	B*07:02	B*58:01	DRB1*13:02	DRB1*15:01
34.	A*11:01	A*24:02	B*07:05	B*15:01	DRB1*14:04	DRB1*15:04
35.	A*24:02	A*68:01	B*40:06	B*44:03	DRB1*07:01	DRB1*08:03
36.	A*01:01	A*02:01	B*35:03	B*57:01	DRB1*07:01	DRB1*14:04
37.	A*24:02	A*24:02	B*35:01	B*35:01	DRB1*04:10	DRB1*08:03
38.	A*03:01	A*11:01	B*15:39	B*35:01	DRB1*01:01	DRB1*07:01
39.	A*24:02	A*24:02	B*07:02	B*15:01	DRB1*03:01	DRB1*13:02
40.	A*31:01	A*33:01	B*44:03	B*51:01	DRB1*13:02	DRB1*14:04
41.	A*03:01	A*24:02	B*07:02	B*35:01	DRB1*01:01	DRB1*07:01
42.	A*11:02	A*24:02	B*51:01	B*52:01	DRB1*13:02	DRB1*15:02
43.	A*02:11	A*33:03	B*07:05	B*57:01	DRB1*14:04	DRB1*15:02

44.	A*11:02	A*33:03	B*15:02	B*44:03	DRB1*07:01	DRB1*15:01
45.	A*32:01	A*68:01	B*15:18	B*35:01	DRB1*12:02	DRB1*14:04
46.	A*24:02	A*33:03	B*14:02	B*40:06	DRB1*01:01	DRB1*04:03
47.	A*02:11	A*24:02	B*40:06	B*44:03	DRB1*01:02	DRB1*15:01
48.	A*01:01	A*30:01	B*13:02	B*57:01	DRB1*04:03	DRB1*07:01
49.	A*32:01	A*33:03	B*07:02	B*07:02	DRB1*07:01	DRB1*07:01
50.	A*02:01	A*02:11	B*40:01	B*52:01	DRB1*10:01	DRB1*15:01
51.	A*02:01	A*31:01	B*52:01	B*52:01	DRB1*01:01	DRB1*04:03
52.	A*23:01	A*24:02	B*41:01	B*52:01	DRB1*15:02	DRB1*15:02
53.	A*01:01	A*11:02	B*37:01	B*57:01	DRB1*07:01	DRB1*14:04
54.	A*11:02	A*33:03	B*35:01	B*58:01	DRB1*10:01	DRB1*15:01
55.	A*11:02	A*24:02	B*35:01	B*44:03	DRB1*01:01	DRB1*03:01
56.	A*11:02	A*68:01	B*15:18	B*35:01	DRB1*04:04	DRB1*07:01
57.	A*24:02	A*26:08	B*07:02	B*51:01	DRB1*11:01	DRB1*11:01
58.	A*01:01	A*11:02	B*15:02	B*57:01	DRB1*04:01	DRB1*13:02
59.	A*24:02	A*33:03	B*15:01	B*58:01	DRB1*07:01	DRB1*12:02
60.	A*02:01	A*02:11	B*37:01	B*58:01	DRB1*01:01	DRB1*13:01
61.	A*01:01	A*11:02	B*18:01	B*38:02	DRB1*10:01	DRB1*13:02
62.	A*24:02	A*33:03	B*38:02	B*58:01	DRB1*12:02	DRB1*15:01
63.	A*02:03	A*33:03	B*35:08	B*57:01	DRB1*13:02	DRB1*14:01
64.	A*02:11	A*24:02	B*07:05	B*15:02	DRB1*04:03	DRB1*13:01
65.	A*03:01	A*33:01	B*40:06	B*44:03	DRB1*15:01	DRB1*15:02
66.	A*01:01	A*02:01	B*13:01	B*37:01	DRB1*04:03	DRB1*07:01
67.	A*11:02	A*24:02	B*35:01	B*40:06	DRB1*07:01	DRB1*10:01
68.	A*02:01	A*32:01	B*15:18	B*44:02	DRB1*07:01	DRB1*15:02
69.	A*02:01	A*11:02	B*07:05	B*15:02	DRB1*01:01	DRB1*13:01
70.	A*02:01	A*11:02	B*35:01	B*35:01	DRB1*15:01	DRB1*15:01
71.	A*24:02	A*24:02	B*27:07	B*44:03	DRB1*01:01	DRB1*13:01
72.	A*02:01	A*11:02	B*15:01	B*52:01	DRB1*07:01	DRB1*11:01
73.	A*01:01	A*24:02	B*44:03	B*57:01	DRB1*15:01	DRB1*15:01
74.	A*11:02	A*33:03	B*07:05	B*58:01	DRB1*07:01	DRB1*07:01
75.	A*31:01	A*68:01	B*07:02	B*13:01	DRB1*09:01	DRB1*15:01
76.	A*02:01	A*33:03	B*07:02	B*58:01	DRB1*14:04	DRB1*15:04
77.	A*11:02	A*24:02	B*15:02	B*07:01	DRB1*15:01	DRB1*15:02
78.	A*24:02	A*24:02	B*07:02	B*51:06	DRB1*03:01	DRB1*07:01
79.	A*02:11	A*24:02	B*07:02	B*40:06	DRB1*01:01	DRB1*13:02
80.	A*68:03	A*74:01	B*40:06	B*51:01	DRB1*04:03	DRB1*15:01
81.	A*32:01	A*33:01	B*35:01	B*51:01	DRB1*15:02	DRB1*15:02
82.	A*02:01	A*11:02	B*15:18	B*15:18	DRB1*04:03	DRB1*11:01
83.	A*11:02	A*33:03	B*58:01	B*58:01	DRB1*04:01	DRB1*04:01
84.	A*33:03	A*68:01	B*13:01	B*58:01	DRB1*03:02	DRB1*07:01
85.	A*01:01	A*11:01	B*13:01	B*15:01	DRB1*13:02	DRB1*13:02
86.	A*01:01	A*33:03	B*44:03	B*57:01	DRB1*14:04	DRB1*14:04
87.	A*02:01	A*11:01	B*56:01	B*57:01	DRB1*04:01	DRB1*07:01
88.	A*11:01	A*24:02	B*15:02	B*15:18	DRB1*07:01	DRB1*15:01
89.	A*33:01	A*33:01	B*44:03	B*58:01	DRB1*13:07	DRB1*14:04
90.	A*24:02	A*33:01	B*40:06	B*40:06	DRB1*07:01	DRB1*13:01
91.	A*33:01	A*33:01	B*58:01	B*58:01	DRB1*07:01	DRB1*15:01
92.	A*01:01	A*03:01	B*13:01	B*37:01	DRB1*13:01	DRB1*14:04
93.	A*02:01	A*02:01	B*15:11	B*35:01	DRB1*10:01	DRB1*15:01
94.	A*02:01	A*32:01	B*07:02	B*35:01	DRB1*08:01	DRB1*13:01
95.	A*02:01	A*24:02	B*40:01	B*51:01	DRB1*04:03	DRB1*11:01
96.	A*03:01	A*24:02	B*07:02	B*52:01	DRB1*04:03	DRB1*15:01
97.	A*01:01	A*24:02	B*07:05	B*57:01	DRB1*04:01	DRB1*10:01

98.	A*03:01	A*24:02	B*13:01	B*40:06	DRB1*07:01	DRB1*15:01
99.	A*03:01	A*24:02	B*07:02	B*51:01	DRB1*01:01	DRB1*12:01
100.	A*33:01	A*68:01	B*35:0	B*52:01	DRB1*07:01	DRB1*10:01
101.	A*33:03	A*68:01	B*52:01	B*58:01	DRB1*03:01	DRB1*15:01
102.	A*02:01	A*33:03	B*07:02	B*44:03	DRB1*07:01	DRB1*15:02
103.	A*24:02	A*30:01	B*13:02	B*52:01	DRB1*07:01	DRB1*07:01
104.	A*29:01	A*68:01	B*07:05	B*35:03	DRB1*13:01	DRB1*14:04
105.	A*68:01	A*68:01	B*07:05	B*52:01	DRB1*04:03	DRB1*14:04
106.	A*24:07	A*33:03	B*07:05	B*08:01	DRB1*10:01	DRB1*13:01
107.	A*33:03	A*33:03	B*40:06	B*44:03	DRB1*07:01	DRB1*07:01
108.	A*02:01	A*02:11	B*40:06	B*40:06	DRB1*14:04	DRB1*15:01
109.	A*02:02	A*68:01	B*15:18	B*41:01	DRB1*13:03	DRB1*14:04
110.	A*02:01	A*24:02	B*15:01	B*40:06	DRB1*04:04	DRB1*15:02
111.	A*24:02	A*24:02	B*07:02	B*07:02	DRB1*01:01	DRB1*01:01
112.	A*24:02	A*26:01	B*15:18	B*51:01	DRB1*08:03	DRB1*13:02
113.	A*02:01	A*24:02	B*35:01	B*57:01	DRB1*07:01	DRB1*11:01
114.	A*32:01	A*32:01	B*08:01	B*37:01	DRB1*01:01	DRB1*03:01
115.	A*03:01	A*33:03	B*35:01	B*44:03	DRB1*07:01	DRB1*07:01
116.	A*01:01	A*31:01	B*07:02	B*48:01	DRB1*14:04	DRB1*15:01
117.	A*01:01	A*31:01	B*15:02	B*51:01	DRB1*07:01	DRB1*10:01
118.	A*24:02	A*26:01	B*08:01	B*40:06	DRB1*14:04	DRB1*15:02
119.	A*03:01	A*32:01	B*27:04	B*35:01	DRB1*07:01	DRB1*14:04
120.	A*24:02	A*33:03	B*58:01	x	DRB1*03:01	DRB1*13:02
121.	A*23:01	A*33:03	B*44:03	B*52:01	DRB1*03:01	DRB1*07:01
122.	A*02:01	A*11:01	B*40:06	x	DRB1*04:03	DRB1*15:01
123.	A*02:01	A*02:11	B*35:03	B*44:04	DRB1*07:01	DRB1*14:04
124.	A*03:01	A*11:01	B*51:01	B*55:02	DRB1*01:01	DRB1*13:01
125.	A*32:01	A*33:01	B*44:03	B*51:01	DRB1*07:01	DRB1*01:01
126.	A*02:01	A*29:01	B*07:05	B*52:01	DRB1*14:04	DRB1*15:02
127.	A*03:01	A*24:02	B*44:03	B*55:01	DRB1*04:01	DRB1*07:01
128.	A*02:01	A*02:01	B*07:05	B*35:03	DRB1*11:10	DRB1*14:01
129.	A*01:01	A*32:01	B*49:01	B*57:01	DRB1*04:03	DRB1*13:02
130.	A*02:07	A*24:02	B*46:01	B*51:01	DRB1*11:15	DRB1*15:02
131.	A*02:11	A*24:02	B*35:01	B*35:03	DRB1*01:01	DRB1*11:01
132.	A*01:01	A*30:01	B*37:01	B*53:01	DRB1*04:01	DRB1*10:01
133.	A*30:01	A*31:01	B*40:06	B*51:01	DRB1*01:01	DRB1*15:01
134.	A*11:01	A*33:01	B*35:01	B*40:06	DRB1*10:01	DRB1*15:01
135.	A*02:01	A*33:01	B*51:01	B*58:01	DRB1*03:01	DRB1*14:04
136.	A*01:01	A*33:01	B*35:01	B*44:03	DRB1*07:01	DRB1*14:04
137.	A*24:02	x	B*35:01	B*52:01	DRB1*04:03	DRB1*15:01
138.	A*01:01	x	B*15:17	B*15:18	DRB1*13:01	x
139.	A*11:01	A*32:01	B*35:01	x	DRB1*11:01	DRB1*14:04
140.	A*02:01	A*32:01	B*15:18	B*44:02	DRB1*01:01	DRB1*13:01
141.	A*02:01	A*11:02	B*07:05	B*15:02	DRB1*15:01	DRB1*15:01
142.	A*02:01	A*11:02	B*35:01	B*35:01	DRB1*01:01	DRB1*13:01
143.	A*24:02	A*24:02	B*27:07	B*44:03	DRB1*07:01	DRB1*11:01
144.	A*02:01	A*11:02	B*15:01	B*52:01	DRB1*15:01	DRB1*15:01
145.	A*01:01	A*24:02	B*44:03	B*57:01	DRB1*07:01	DRB1*07:01
146.	A*11:02	A*33:03	B*07:05	B*58:01	DRB1*09:01	DRB1*15:01
147.	A*31:01	A*68:01	B*07:02	B*13:01	DRB1*14:04	DRB1*15:04
148.	A*02:01	A*33:03	B*07:02	B*58:01	DRB1*15:01	DRB1*15:02
149.	A*11:02	A*24:02	B*15:02	B*52:01	DRB1*03:01	DRB1*07:01
150.	A*24:02	A*26:08	B*13:02	B*55:01	DRB1*01:01	DRB1*07:01
151.	A*24:02	A*24:02	B*07:02	B*51:06	DRB1*01:01	DRB1*13:02

152.	A*02:11	A*24:02	B*07:02	B*51:06	DRB1*01:01	DRB1*13:02
153.	A*68:03	A*74:01	B*40:06	B*51:01	DRB1*15:02	DRB1*15:02
154.	A*32:01	A*33:01	B*35:01	B*51:01	DRB1*04:03	DRB1*11:01
155.	A*02:01	A*11:02	B*15:18	B*15:18	DRB1*04:01	DRB1*04:01
156.	A*11:02	A*33:03	B*58:01	B*58:01	DRB1*03:08	DRB1*07:01
157.	A*33:03	A*68:01	B*13:01	B*58:01	DRB1*13:02	DRB1*13:02
158.	A*11:02	A*11:04	B*35:01	B*57:01	DRB1*07:01	DRB1*14:04
159.	A*01:01	A*11:01	B*13:01	B*15:01	DRB1*14:04	DRB1*14:04
160.	A*01:01	A*33:01	B*44:03	B*57:01	DRB1*04:01	DRB1*07:01
161.	A*02:01	A*11:01	B*56:01	B*57:01	DRB1*07:01	DRB1*15:01
162.	A*11:01	A*24:02	B*15:02	B*15:18	DRB1*13:07	DRB1*14:04
163.	A*33:01	A*33:01	B*44:03	B*58:01	DRB1*07:01	DRB1*13:01
164.	A*24:02	A*33:01	B*40:06	B*40:06	DRB1*07:01	DRB1*15:01
165.	A*33:01	A*33:01	B*58:01	B*58:01	DRB1*13:01	DRB1*14:04
166.	A*01:01	A*03:01	B*13:01	B*37:01	DRB1*10:01	DRB1*15:01
167.	A*02:01	A*02:01	B*15:11	B*35:01	DRB1*10:01	DRB1*15:01
168.	A*02:01	A*32:01	B*07:02	B*35:01	DRB1*04:03	DRB1*11:01
169.	A*24:02	A*24:08	B*55:01	B*57:01	DRB1*01:01	DRB1*07:01
170.	A*02:01	A*24:02	B*40:01	B*51:01	DRB1*04:03	DRB1*15:01
171.	A*03:01	A*24:02	B*07:02	B*52:01	DRB1*04:01	DRB1*10:01
172.	A*01:01	A*24:02	B*07:05	B*57:01	DRB1*07:01	DRB1*15:01
173.	A*03:01	A*24:02	B*13:01	B*40:06	DRB1*01:01	DRB1*12:01
174.	A*03:01	A*24:02	B*07:02	B*51:01	DRB1*07:01	DRB1*10:01
175.	A*33:01	A*68:01	B*35:01	B*52:01	DRB1*14:04	DRB1*15:01
176.	A*11:01	A*24:02	B*13:02	B*52:01	DRB1*07:01	DRB1*07:01
177.	A*01:01	A*23:01	B*08:01	B*44:03	DRB1*04:01	DRB1*07:01
178.	A*24:02	A*24:07	B*40:01	B*49:01	DRB1*13:02	DRB1*14:04
179.	A*02:01	A*33:03	B*51:01	x	DRB1*04:08	x
180.	A*02:11	A*24:02	B*07:05	B*13:01	DRB1*04:10	DRB1*15:04
181.	A*01:01	A*02:03	B*15:17	B*40:01	DRB1*08:03	DRB1*13:02
182.	A*24:02	A*33:03	B*55:01	B*58:01	DRB1*10:01	DRB1*13:02
183.	A*11:01	A*33:03	B*40:06	B*58:01	DRB1*14:04	DRB1*15:01
184.	A*01:01	A*33:03	B*44:03	B*57:01	DRB1*07:01	DRB1*15:02
185.	A*03:01	A*68:01	B*40:01	B*44:02	DRB1*04:03	DRB1*15:04
186.	A*02:01	A*02:01	B*35:01	B*58:01	DRB1*15:02	x
187.	A*02:11	A*31:01	B*40:06	B*44:03	DRB1*13:01	DRB1*15:02
188.	A*03:01	A*32:01	B*07:02	B*35:01	DRB1*11:01	DRB1*15:02
189.	A*68:01	A*68:01	B*15:01	B*55:01	DRB1*13:01	DRB1*15:02
190.	A*03:01	A*11:01	B*07:02	B*58:01	DRB1*10:01	DRB1*13:02
191.	A*02:11	A*03:01	B*51:01	B*57:01	DRB1*07:01	DRB1*14:04
192.	A*01:01	A*29:01	B*07:05	B*57:01	DRB1*14:04	DRB1*16:02
193.	A*32:01	A*33:03	B*35:03	B*52:01	DRB1*03:01	DRB1*04:03
194.	A*01:01	A*02:11	B*51:01	B*57:01	DRB1*04:03	DRB1*07:01
195.	A*24:02	A*24:02	B*35:01	B*56:01	DRB1*04:03	DRB1*15:02
196.	A*02:01	A*11:01	B*40:01	B*51:01	DRB1*04:01	DRB1*14:04
197.	A*02:11	A*01:01	B*40:06	B*44:03	DRB1*15:01	DRB1*15:02
198.	A*02:01	A*03:01	B*07:02	B*50:01	DRB1*07:01	DRB1*13:02
199.	A*02:11	A*33:03	B*40:06	B*44:03	DRB1*07:01	DRB1*15:01
200.	A*03:01	A*33:01	B*35:01	B*52:01	DRB1*07:01	DRB1*15:01
201.	A*26:01	A*26:01	B*57:01	B*57:01	DRB1*04:03	DRB1*07:01
202.	A*02:11	A*24:02	B*40:06	B*57:03	DRB1*04:03	DRB1*07:01
203.	A*01:01	A*11:01	B*52:01	B*57:01	DRB1*04:03	DRB1*15:02
204.	A*03:01	A*68:01	B*15:18	B*35:01	DRB1*13:01	DRB1*13:02
205.	A*02:01	A*02:11	B*40:01	B*58:01	DRB1*03:01	DRB1*15:01

206.	A*01:01	A*24:10	B*52:01	B*57:01	DRB1*04:03	DRB1*07:01
207.	A*01:01	A*31:01	B*15:17	B*51:01	DRB1*13:01	DRB1*13:02
208.	A*33:01	A*74:01	B*39:01	B*44:03	DRB1*13:01	DRB1*15:03
209.	A*24:02	A*32:01	B*52:01	B*35:01	DRB1*01:01	DRB1*04:03
210.	A*01:01	A*01:01	B*07:05	B*37:01	DRB1*10:01	x
211.	A*11:01	A*24:02	B*15:02	B*15:18	DRB1*04:03	DRB1*07:01
212.	A*24:02	A*24:03	B*35:03	B*58:01	DRB1*14:04	DRB1*14:04
213.	A*02:06	A*11:01	B*44:03	B*51:01	DRB1*07:01	DRB1*15:01
214.	A*02:01	A*32:01	B*35:01	B*35:03	DRB1*14:04	DRB1*15:01
215.	A*24:02	x	B*35:01	B*52:01	DRB1*04:03	DRB1*15:01
216.	A*02:11	A*11:01	B*07:05	B*13:01	DRB1*14:04	DRB1*15:01
217.	A*11:01	A*11:01	B*07:05	B*07:05	DRB1*14:04	DRB1*15:01
218.	A*11:01	A*29:02	B*35:03	B*52:01	DRB1*10:01	DRB1*13:01
219.	A*11:01	A*33:03	B*15:18	B*40:06	DRB1*13:02	DRB1*15:01
220.	A*11:01	A*26:01	B*38:01	B*44:03	DRB1*07:01	DRB1*11:01
221.	A*02:01	A*24:02	B*40:06	B*52:01	DRB1*15:01	DRB1*15:01
222.	A*01:01	A*33:01	B*14:02	B*15:18	DRB1*01:01	x
223.	A*11:01	A*24:02	B*35:01	B*07:05	DRB1*15:01	DRB1*15:01
224.	A*01:01	A*24:02	B*37:01	B*44:02	DRB1*07:01	DRB1*10:01
225.	A*03:01	A*24:02	B*35:01	B*35:01	DRB1*13:01	DRB1*14:04
226.	A*01:01	A*68:03	B*15:01	B*57:01	DRB1*12:02	DRB1*13:02
227.	A*02:11	A*32:01	B*15:18	B*15:39	DRB1*01:01	DRB1*14:04
228.	A*11:01	A*24:02	B*57:01	B*58:01	DRB1*03:01	DRB1*07:01
229.	A*02:02	A*33:03	B*14:02	B*50:01	DRB1*13:02	DRB1*15:01
230.	A*11:01	A*24:02	B*52:01	B*55:01	DRB1*04:03	DRB1*11:01
231.	A*24:07	A*33:03	B*37:01	B*52:01	DRB1*04:01	DRB1*13:01
232.	A*01:01	A*02:01	B*13:02	B*40:01	DRB1*07:01	DRB1*14:04
233.	A*24:02	A*24:02	B*07:05	B*08:01	DRB1*03:01	DRB1*15:01
234.	A*26:01	A*26:01	B*18:01	B*18:01	DRB1*11:04	DRB1*11:04
235.	A*11:01	x	B*13:01	B*35:01	DRB1*15:01	DRB1*04:03
236.	A*01:01	A*02:01	B*35:03	B*40:01	DRB1*04:04	DRB1*13:01
237.	A*31:01	A*33:03	B*04:03	B*57:01	DRB1*07:01	DRB1*07:01
238.	A*11:01	A*68:01	B*13:01	B*57:01	DRB1*07:01	DRB1*15:01
239.	A*24:02	A*31:01	B*07:05	B*40:06	DRB1*11:01	DRB1*15:01
240.	A*24:02	A*26:01	B*40:06	B*55:01	DRB1*07:01	DRB1*14:04
241.	A*11:01	A*33:03	B*07:05	B*44:03	DRB1*07:01	DRB1*14:04
242.	A*01:01	A*02:01	B*07:02	B*39:01	DRB1*07:01	DRB1*15:02
243.	A*11:01	A*31:01	B*40:06	B*52:01	DRB1*04:03	DRB1*07:01
244.	A*03:01	A*24:02	B*07:05	B*13:01	DRB1*04:05	DRB1*07:01
245.	A*11:01	A*11:01	B*13:01	B*35:03	DRB1*04:03	DRB1*15:01
246.	A*03:01	A*30:01	B*13:02	B*40:06	DRB1*07:01	DRB1*14:04
247.	A*68:01	A*68:01	B*52:01	B*78:01	DRB1*04:03	DRB1*15:02
248.	A*01:01	A*02:11	B*57:01	B*35:03	DRB1*07:01	DRB1*08:03
249.	A*33:03	A*33:03	B*07:02	B*07:02	DRB1*01:01	DRB1*15:01
250.	A*11:01	A*33:03	B*15:18	B*44:03	DRB1*07:01	DRB1*15:01
251.	A*02:01	A*11:01	B*15:18	B*40:01	DRB1*04:03	DRB1*08:03
252.	A*02:03	A*03:01	B*07:02	B*35:01	DRB1*07:01	DRB1*15:01
253.	A*01:01	A*01:01	B*44:03	B*52:01	DRB1*07:01	DRB1*13
254.	A*01:01	A*11:01	B*07:05	B*07:02	DRB1*07:01	x
255.	A*11:01	A*24:02	B*35:03	B*07:02	DRB1*15:01	DRB1*15:01
256.	A*11:01	A*33:03	B*35:01	B*58:01	DRB1*15:01	DRB1*04
257.	A*03:01	A*31:01	B*51:01	B*56:01	DRB1*07:01	DRB1*15:01
258.	A*33:03	A*68:01	B*07:02	B*55:01	DRB1*13:01	DRB1*15:01
259.	A*30:01	A*33:03	B*51:01	B*58:01	DRB1*13:01	DRB1*13:02

260.	A*01:01	A*33:03	B*44:03	B*58:01	DRB1*04:07	DRB1*08:03
261.	A*01:01	A*03:01	B*35:03	B*57:01	DRB1*03:01	DRB1*04:03
262.	A*24:02	A*68:01	B*18:01	B*58:01	DRB1*04:03	DRB1*13:01
263.	A*11:01	A*33:03	B*35:03	B*44:03	DRB1*11:01	DRB1*13:02
264.	A*03:03	A*33:03	B*35:07	B*44:04	DRB1*07:01	DRB1*08:03
265.	A*02:11	A*24:02	B*40:06	B*40:06	DRB1*07:01	DRB1*13
266.	A*24:02	A*31:01	B*35:01	B*40:01	DRB1*01:01	DRB1*08:04
267.	A*02:01	A*26:01	B*15:39	B*58:01	DRB1*13:02	DRB1*14:04
268.	A*02:11	A*11:01	B*15:18	B*44:03	DRB1*13:02	DRB1*14:04
269.	A*23:01	A*33:03	B*07:02	B*44:03	DRB1*07:01	DRB1*15:01
270.	A*02:01	A*02:01	B*18:01	B*35:03	DRB1*01:01	DRB1*15:02
271.	A*02:01	A*26:01	B*07:05	B*15:18	DRB1*08:03	DRB1*15:01
272.	A*24:07	A*31:01	B*51:01	B*52:01	DRB1*08:03	DRB1*15:01
273.	A*02:11	A*31:01	B*40:06	B*52:01	DRB1*01:01	DRB1*04:03
274.	A*02:01	A*30:02	B*35:01	B*41:01	DRB1*04:03	DRB1*08:04
275.	A*24:02	A*24:02	B*07:05	B*07:05	DRB1*03:01	DRB1*04:05
276.	A*24:02	A*33:03	B*40:06	B*44:03	DRB1*04:05	DRB1*15:01
277.	A*11:01	A*24:02	B*15:02	B*52:01	DRB1*04:08	DRB1*07:01
278.	A*01:01	A*24:02	B*15:17	B*44:03	DRB1*04:03	DRB1*10:01
279.	A*11:01	A*24:02	B*52:01	B*55:01	DRB1*07:01	DRB1*13:02
280.	A*24:02	A*24:07	B*08:01	B*18:01	DRB1*04:01	DRB1*13:01
281.	A*11:01	A*26:01	B*40:01	B*07:05	DRB1*03:01	DRB1*13:02
282.	A*02:16	A*68:01	B*15:18	B*07:05	DRB1*08:02	DRB1*14:04
283.	A*24:02	A*33:03	B*40:06	B*58:01	DRB1*11:01	DRB1*13:02
284.	A*02:01	A*24:02	B*52:01	B*52:01	DRB1*04:03	DRB1*08:04
285.	A*24:02	A*24:07	B*07:05	B*52:01	DRB1*15:01	DRB1*15:01
286.	A*24:02	A*33:03	B*07:05	B*51:01	DRB1*15:01	DRB1*04:03
287.	A*24:02	A*30:01	B*13:02	B*52:01	DRB1*04:02	DRB1*15:01
288.	A*24:02	A*26:01	B*08:01	B*44:03	DRB1*07:01	DRB1*15:01
289.	A*02:11	A*31:01	B*07:02	B*15:01	DRB1*03:01	DRB1*07:01
290.	A*11:01	A*31:01	B*37:01	B*51:01	DRB1*11:01	DRB1*11:04
291.	A*01:01	A*24:02	B*57:01	B*07:05	DRB1*01:01	DRB1*01:01
292.	A*11:01	A*11:01	B*40:06	B*40:06	DRB1*15:01	DRB1*15:01
293.	A*62:01	A*29:01	B*07:05	B*51:01	DRB1*04:01	DRB1*14:04
294.	A*11:01	A*23:01	B*40:06	B*58:01	DRB1*13:01	DRB1*15:01
295.	A*02:01	A*02:01	B*07:05	B*35:01	DRB1*01:01	DRB1*10:01
296.	A*24:02	A*68:02	B*08:01	B*51:01	DRB1*07:01	DRB1*14:04
297.	A*03:01	A*11:01	B*13:01	B*57:03	DRB1*03:01	DRB1*13:01
298.	A*02:01	A*24:02	B*51:02	B*07:05	DRB1*07:01	DRB1*15:01
299.	A*11:01	A*24:02	B*52:01	B*81:01	DRB1*14:04	DRB1*15:01
300.	A*11:01	A*24:02	B*35:01	B*40:06	DRB1*07:01	DRB1*12:01
301.	A*11:01	A*23:01	B*40:02	B*44:03	DRB1*04:10	DRB1*11:01
302.	A*02:03	A*11:01	B*38:02	B*51:01	DRB1*07:01	DRB1*14:01
303.	A*24:02	A*33:01	B*40:06	B*44:03	DRB1*01:01	DRB1*15:02
304.	A*33:01	A*68:01	B*08:01	B*35:01	DRB1*14:04	DRB1*14:04
305.	A*11:01	A*33:03	B*40:01	B*52:01	DRB1*03:01	DRB1*10:01
306.	A*33:03	A*33:03	B*13:01	B*58:01	DRB1*07:01	DRB1*07:01
307.	A*01:01	A*33:03	B*40:06	B*44:03	DRB1*13:02	**x**
308.	A*24:02	A*26:01	B*35:05	B*40:06	DRB1*07:01	DRB1*14:04
309.	A*01:01	A*01:01	B*51:01	B*51:01	DRB1*12:02	DRB1*14:04
310.	A*02:01	A*24:02	B*15:01	B*41:01	DRB1*01:01	DRB1*04:03
311.	A*24:02	A*24:02	B*35:03	B*40:06	DRB1*03:01	DRB1*07:01
312.	A*01:01	A*68:01	B*15:17	B*40:06	DRB1*07:01	DRB1*14:04
313.	A*02:01	A*11:01	B*15:10	B*57:01	DRB1*04:04	DRB1*13:02

314.	A*24:02	A*33:03	B*51:01	B*58:01	DRB1*04:03	DRB1*07:01
315.	A*02:06	A*24:02	B*15:25	B*35:01	DRB1*13:01	DRB1*13:01
316.	A*01:01	A*26:01	B*07:05	B*15:17	DRB1*08:03	DRB1*14:04
317.	A*02:01	A*33:03	B*08:01	B*40:01	DRB1*01:01	DRB1*15:01
318.	A*01:01	A*11:01	B*56:01	B*57:01	DRB1*03:01	DRB1*04:04
319.	A*11:01	A*33:03	B*44:03	B*52:01	DRB1*07:01	DRB1*12:01
320.	A*24:02	A*33:03	B*57:01	B*58:01	DRB1*04:03	DRB1*07:01
321.	A*11:01	A*24:02	B*51:01	B*58:01	DRB1*07:01	DRB1*10:01
322.	A*02:11	A*31:01	B*51:01	B*57:01	DRB1*01:01	DRB1*15:01
323.	A*01:01	A*24:02	B*48:01	B*57:01	DRB1*07:01	DRB1*12:02
324.	A*02:11	A*11:01	B*15:18	B*51:01	DRB1*12:02	DRB1*15:01
325.	A*02:01	A*11:01	B*07:05	B*07:05	DRB1*14:04	x
326.	A*32:01	A*33:03	B*44:03	B*48:01	DRB1*14:04	DRB1*15:01
327.	A*02:01	A*31:01	B*35:01	B*51:01	DRB1*07:01	DRB1*12:02
328.	A*11:01	A*33:03	B*35:01	B*58:01	DRB1*01:01	DRB1*13:01
329.	A*24:02	A*24:02	B*13:01	B*07:05	DRB1*01:01	DRB1*07:01
330.	A*23:01	A*24:02	B*44:03	B*52:01	DRB1*15:01	DRB1*08:01
331.	A*01:01	A*11:01	B*07:05	B*51:01	DRB1*07:01	DRB1*11:01
332.	A*02:03	A*23:01	B*07:02	B*41:01	DRB1*12:02	DRB1*15:01
333.	A*01:01	A*24:02	B*52:01	B*57:01	DRB1*07:01	DRB1*07:01
334.	A*03:02	A*11:01	B*35:03	B*44:03	DRB1*07:01	DRB1*13:02
335.	A*11:01	A*24:02	B*35:01	B*52:01	DRB1*07:01	DRB1*15:02
336.	A*02:01	A*02:01	B*40:06	B*51:01	DRB1*04:01	DRB1*14:04
337.	A*02:11	A*33:03	B*35:03	B*58:01	DRB1*14:01	DRB1*15:02
338.	A*24:02	A*33:03	B*18:01	B*52:01	DRB1*03:01	DRB1*14:04
339.	A*24:02	A*33:03	B*15:01	B*58:01	DRB1*13:01	DRB1*15:02
340.	A*26:01	A*31:01	B*15:18	B*27:05	DRB1*13:02	DRB1*14:04
341.	A*01:01	A*24:02	B*15:17	B*35:01	DRB1*01:01	DRB1*01:01
342.	A*03:01	A*24:07	B*15:01	B*56:01	DRB1*08:02	DRB1*12:02
343.	A*26:01	A*33:03	B*40:06	B*56:01	DRB1*04:03	DRB1*14:04
344.	A*02:01	A*03:01	B*18:01	B*40:01	DRB1*04:01	DRB1*13:01
345.	A*01:01	A*24:02	B*49:01	B*51:01	DRB1*07:01	DRB1*13:02
346.	A*03:01	A*11:01	B*07:02	B*57:01	DRB1*10:01	DRB1*15:01
347.	A*01:01	A*11:01	B*04:06	B*51:01	DRB1*04:03	DRB1*07:01
348.	A*24:02	A*26:01	B*07:02	B*51:01	DRB1*01:01	DRB1*04:03
349.	A*11:01	A*33:01	B*44:03	B*07:05	DRB1*07:01	DRB1*13:05
350.	A*24:02	A*68:01	B*15:25	B*37:01	DRB1*11:04	DRB1*11:04
351.	A*24:02	A*26:01	B*07:02	B*35:01	DRB1*04:10	DRB1*07:01
352.	A*33:03	A*33:03	B*44:03	B*58:01	DRB1*07:01	DRB1*13:02
353.	A*01:01	A*32:01	B*07:02	B*15:17	DRB1*01:01	DRB1*10:01
354.	A*02:01	A*68:01	B*15:01	B*35:01	DRB1*01:01	DRB1*13:01
355.	A*24:02	A*68:01	B*07:02	B*40:06	DRB1*15:01	DRB1*15:02
356.	A*24:02	A*31:01	B*15:01	B*51:01	DRB1*01:01	DRB1*04:01
357.	A*31:01	A*32:01	B*35:01	B*51:01	DRB1*01:01	DRB1*01:01
358.	A*02:01	A*02:06	B*51:01	B*52:01	DRB1*04:08	DRB1*15:01
359.	A*24:02	A*22:02	B*35:01	B*40:06	DRB1*04:03	DRB1*10:01
360.	A*31:01	A*33:03	B*58:01	B*27:04	DRB1*04:03	DRB1*09:01
361.	A*11:01	A*33:03	B*07:05	B*58:01	DRB1*13:02	DRB1*14:04
362.	A*11:01	A*33:03	B*07:05	B*58:01	DRB1*13:02	DRB1*14:02
363.	A*01:01	A*02:01	B*37:01	B*57:01	DRB1*07:01	DRB1*10:01
364.	A*24:02	A*26:01	B*35:01	B*37:01	DRB1*08:01	DRB1*10:01
365.	A*03:01	A*24.01	B*55:01	B*58:01	DRB1*07:01	DRB1*15:01
366.	A*03:01	A*33:03	B*35:03	B*58:01	DRB1*13:02	DRB1*15:02
367.	A*23:01	A*33:03	B*44:03	B*52:01	DRB1*07:01	DRB1*14:04

368.	A*01:01	A*26:01	B*15:39	B*35:01	DRB1*14:04	DRB1*15:01
369.	A*26:01	A*33:03	B*15:18	B*58:01	DRB1*13:01	DRB1*15:02
370.	A*26:01	A*31:01	B*07:05	B*27:04	DRB1*14:04	DRB1*15:01
371.	A*29:01	A*31:01	B*15:08	B*27:07	DRB1*07:01	DRB1*11:01
372.	A*11:01	A*31:01	B*18:01	B*51:01	DRB1*04:02	DRB1*15:01
373.	A*11:01	A*24:02	B*40:06	B*07:05	DRB1*15:01	DRB1*08:01
374.	A*01:01	A*33:01	B*37:01	B*44:02	DRB1*04:01	DRB1*10:01
375.	A*02:01	A*32:01	B*15:18	B*44:02	DRB1*01:01	DRB1*13:01
376.	A*02:01	A*11:02	B*07:05	B*15:02	DRB1*15:01	DRB1*15:01
377.	A*02:01	A*11:02	B*35:01	B*35:01	DRB1*01:01	DRB1*13:01
378.	A*24:02	A*24:02	B*27:07	B*44:03	DRB1*07:01	DRB1*11:01
379.	A*02:01	A*11:02	B*15:01	B*52:01	DRB1*15:01	DRB1*15:01
380.	A*01:01	A*24:02	B*44:03	B*57:01	DRB1*07:01	DRB1*07:01
381.	A*11:02	A*33:03	B*07:05	B*58:01	DRB1*09:01	DRB1*15:01
382.	A*31:01	A*68:01	B*07:02	B*13:01	DRB1*14:04	DRB1*15:04
383.	A*02:01	A*33:03	B*07:02	B*58:01	DRB1*15:01	DRB1*15:02
384.	A*02:01	A*31:01	B*35:01	B*51:01	DRB1*07:01	DRB1*12:02
385.	A*11:01	A*33:03	B*35:01	B*58:01	DRB1*01:01	DRB1*13:01
386.	A*24:02	A*24:02	B*13:01	B*07:05	DRB1*01:01	DRB1*07:01
387.	A*23:01	A*24:02	B*44:03	B*52:01	DRB1*15:01	DRB1*08:01
388.	A*01:01	A*11:01	B*07:05	B*51:01	DRB1*07:01	DRB1*11:01
389.	A*02:03	A*23:01	B*07:02	B*41:01	DRB1*12:02	DRB1*15:01
390.	A*01:01	A*24:02	B*52:01	B*57:01	DRB1*07:01	DRB1*07:01
391.	A*03:02	A*11:01	B*35:03	B*44:03	DRB1*07:01	DRB1*13:02
392.	A*11:01	A*24:02	B*35:01	B*52:01	DRB1*07:01	DRB1*15:02
393.	A*02:01	A*02:01	B*40:06	B*51:01	DRB1*04:01	DRB1*14:04
394.	A*02:11	A*33:03	B*35:03	B*58:01	DRB1*14:01	DRB1*15:02
395.	A*11:01	A*24:02	B*15:02	B*52:01	DRB1*04:08	DRB1*07:01
396.	A*01:01	A*24:02	B*15:17	B*44:03	DRB1*04:03	DRB1*10:01
397.	A*11:01	A*24:02	B*52:01	B*55:01	DRB1*07:01	DRB1*13:02
398.	A*24:02	A*24:07	B*08:01	B*18:01	DRB1*04:01	DRB1*13:01
399.	A*11:01	A*26:01	B*40:01	B*07:05	DRB1*03:01	DRB1*13:02
400.	A*02:16	A*68:01	B*15:18	B*07:05	DRB1*08:02	DRB1*14:04
401.	A*24:02	A*33:03	B*40:06	B*58:01	DRB1*11:01	DRB1*13:02
402.	A*02:01	A*24:02	B*52:01	B*52:01	DRB1*04:03	DRB1*08:04
403.	A*24:02	A*24:07	B*07:05	B*52:01	DRB1*15:01	DRB1*15:01
404.	A*24:02	A*33:03	B*07:05	B*51:01	DRB1*15:01	DRB1*04:03
405.	A*24:02	A*30:01	B*13:02	B*52:01	DRB1*04:02	DRB1*15:01
406.	A*24:02	A*26:01	B*08:01	B*44:03	DRB1*07:01	DRB1*15:01
407.	A*02:11	A*31:01	B*07:02	B*15:01	DRB1*03:01	DRB1*07:01
408.	A*11:01	A*31:01	B*37:01	B*51:01	DRB1*11:01	DRB1*11:04
409.	A*01:01	A*24:02	B*57:01	B*07:05	DRB1*01:01	DRB1*01:01
410.	A*11:01	A*11:01	B*40:06	B*40:06	DRB1*15:01	DRB1*15:01
411.	A*62:01	A*29:01	B*07:05	B*51:01	DRB1*04:01	DRB1*14:04
412.	A*11:01	A*23:01	B*40:06	B*58:01	DRB1*13:01	DRB1*15:01
413.	A*02:01	A*02:01	B*07:05	B*35:01	DRB1*01:01	DRB1*10:01
414.	A*24:02	A*68:02	B*08:01	B*51:01	DRB1*07:01	DRB1*14:04
415.	A*03:01	A*11:01	B*13:01	B*57:03	DRB1*03:01	DRB1*13:01
416.	A*02:01	A*24:02	B*51:02	B*07:05	DRB1*07:01	DRB1*15:01
417.	A*11:01	A*24:02	B*52:01	B*81:01	DRB1*14:04	DRB1*15:01
418.	A*11:01	A*24:02	B*35:01	B*40:06	DRB1*07:01	DRB1*12:01
419.	A*11:01	A*23:01	B*40:02	B*44:03	DRB1*04:10	DRB1*11:01
420.	A*02:03	A*11:01	B*38:02	B*51:01	DRB1*07:01	DRB1*14:01
421.	A*24:02	A*26:01	B*35:05	B*40:06	DRB1*07:01	DRB1*14:04

422.	A*01:01	A*01:01	B*51:01	B*51:01	DRB1*12:02	DRB1*14:04
423.	A*02:01	A*24:02	B*15:01	B*41:01	DRB1*01:01	DRB1*04:03
424.	A*24:02	A*24:02	B*35:03	B*40:06	DRB1*03:01	DRB1*07:01
425.	A*01:01	A*68:01	B*15:17	B*40:06	DRB1*07:01	DRB1*14:04
426.	A*02:01	A*11:01	B*15:10	B*57:01	DRB1*04:04	DRB1*13:02
427.	A*24:02	A*33:03	B*51:01	B*58:01	DRB1*04:03	DRB1*07:01
428.	A*02:06	A*24:02	B*15:25	B*35:01	DRB1*13:01	DRB1*13:01
429.	A*01:01	A*26:01	B*07:05	B*15:17	DRB1*08:03	DRB1*14:04
430.	A*02:01	A*33:03	B*08:01	B*40:01	DRB1*01:01	DRB1*15:01
431.	A*01:01	A*02:03	B*15:17	B*40:01	DRB1*08:03	DRB1*13:02
432.	A*24:02	A*33:03	B*55:01	B*58:01	DRB1*10:01	DRB1*13:02
433.	A*11:01	A*33:03	B*40:06	B*58:01	DRB1*14:04	DRB1*15:01
434.	A*01:01	A*33:03	B*44:03	B*57:01	DRB1*07:01	DRB1*15:02
435.	A*03:01	A*68:01	B*40:01	B*44:02	DRB1*04:03	DRB1*15:04
436.	A*02:01	A*02:01	B*35:01	B*58:01	DRB1*15:02	x
437.	A*02:11	A*31:01	B*40:06	B*44:03	DRB1*13:01	DRB1*15:02
438.	A*03:01	A*32:01	B*07:02	B*35:01	DRB1*11:01	DRB1*15:02
439.	A*68:01	A*68:01	B*15:01	B*55:01	DRB1*13:01	DRB1*15:02
440.	A*03:01	A*11:01	B*07:02	B*58:01	DRB1*10:01	DRB1*13:02
441.	A*02:11	A*03:01	B*51:01	B*57:01	DRB1*07:01	DRB1*14:04
442.	A*01:01	A*29:01	B*07:05	B*57:01	DRB1*14:04	DRB1*16:02
443.	A*32:01	A*33:03	B*35:03	B*52:01	DRB1*03:01	DRB1*04:03
444.	A*01:01	A*02:11	B*51:01	B*57:01	DRB1*04:03	DRB1*07:01
445.	A*24:02	A*24:02	B*35:01	B*56:01	DRB1*04:03	DRB1*15:02
446.	A*02:01	A*11:01	B*40:01	B*51:01	DRB1*04:01	DRB1*14:04
447.	A*02:11	A*01:01	B*40:06	B*44:03	DRB1*15:01	DRB1*15:02
448.	A*02:01	A*03:01	B*07:02	B*50:01	DRB1*07:01	DRB1*13:02
449.	A*02:11	A*33:03	B*40:06	B*44:03	DRB1*07:01	DRB1*15:01
450.	A*03:01	A*33:01	B*35:01	B*52:01	DRB1*07:01	DRB1*15:01
451.	A*26:01	A*26:01	B*57:01	B*57:01	DRB1*04:03	DRB1*07:01
452.	A*02:11	A*24:02	B*40:06	B*57:03	DRB1*04:03	DRB1*07:01
453.	A*01:01	A*11:01	B*52:01	B*57:01	DRB1*04:03	DRB1*15:02
454.	A*03:01	A*68:01	B*15:18	B*35:01	DRB1*13:01	DRB1*13:02
455.	A*02:01	A*02:11	B*40:01	B*58:01	DRB1*03:01	DRB1*15:01
456.	A*01:01	A*24:10	B*52:01	B*57:01	DRB1*04:03	DRB1*07:01
457.	A*01:01	A*31:01	B*15:17	B*51:01	DRB1*13:01	DRB1*13:02
458.	A*33:01	A*74:01	B*39:01	B*44:03	DRB1*13:01	DRB1*15:03
459.	A*02:01	A*11:02	B*15:18	B*15:18	DRB1*04:01	DRB1*04:01
460.	A*11:02	A*33:03	B*58:01	B*58:01	DRB1*03:08	DRB1*07:01
461.	A*33:03	A*68:01	B*13:01	B*58:01	DRB1*13:02	DRB1*13:02
462.	A*11:02	A*11:04	B*35:01	B*57:01	DRB1*07:01	DRB1*14:04
463.	A*01:01	A*11:01	B*13:01	B*15:01	DRB1*14:04	DRB1*14:04
464.	A*01:01	A*33:01	B*44:03	B*57:01	DRB1*04:01	DRB1*07:01
465.	A*02:01	A*11:01	B*56:01	B*57:01	DRB1*07:01	DRB1*15:01
466.	A*11:01	A*24:02	B*15:02	B*15:18	DRB1*13:07	DRB1*14:04
467.	A*33:01	A*33:01	B*44:03	B*58:01	DRB1*07:01	DRB1*13:01
468.	A*24:02	A*33:01	B*40:06	B*40:06	DRB1*07:01	DRB1*15:01
469.	A*33:01	A*33:01	B*58:01	B*58:01	DRB1*13:01	DRB1*14:04
470.	A*01:01	A*03:01	B*13:01	B*37:01	DRB1*10:01	DRB1*15:01
471.	A*02:01	A*02:01	B*15:11	B*35:01	DRB1*10:01	DRB1*15:01
472.	A*02:01	A*32:01	B*07:02	B*35:01	DRB1*04:03	DRB1*11:01
473.	A*24:02	A*24:08	B*55:01	B*57:01	DRB1*01:01	DRB1*07:01
474.	A*02:01	A*24:02	B*40:01	B*51:01	DRB1*04:03	DRB1*15:01
475.	A*03:01	A*24:02	B*07:02	B*52:01	DRB1*04:01	DRB1*10:01

476.	A*01:01	A*24:02	B*07:05	B*57:01	DRB1*07:01	DRB1*15:01
477.	A*03:01	A*24:02	B*13:01	B*40:06	DRB1*01:01	DRB1*12:01
478.	A*03:01	A*24:02	B*07:02	B*51:01	DRB1*07:01	DRB1*10:01
479.	A*33:01	A*68:01	B*35:01	B*52:01	DRB1*14:04	DRB1*15:01
480.	A*11:01	A*24:02	B*13:02	B*52:01	DRB1*07:01	DRB1*07:01
481.	A*01:01	A*23:01	B*08:01	B*44:03	DRB1*04:01	DRB1*07:01
482.	A*24:02	A*24:07	B*40:01	B*49:01	DRB1*13:02	DRB1*14:04
483.	A*11:01	A*24:02	B*52:01	B*81:01	DRB1*14:04	DRB1*15:01
484.	A*11:01	A*24:02	B*35:01	B*40:06	DRB1*07:01	DRB1*12:01
485.	A*11:01	A*23:01	B*40:02	B*44:03	DRB1*04:10	DRB1*11:01
486.	A*02:03	A*11:01	B*38:02	B*51:01	DRB1*07:01	DRB1*14:01
487.	A*24:02	A*33:01	B*40:06	B*44:03	DRB1*01:01	DRB1*15:02
488.	A*33:01	A*68:01	B*08:01	B*35:01	DRB1*14:04	DRB1*14:04
489.	A*11:01	A*33:03	B*40:01	B*52:01	DRB1*03:01	DRB1*10:01
490.	A*33:03	A*33:03	B*13:01	B*58:01	DRB1*07:01	DRB1*07:01
491.	A*01:01	A*33:03	B*40:06	B*44:03	DRB1*13:02	x
492.	A*24:02	A*26:01	B*35:05	B*40:06	DRB1*07:01	DRB1*14:04
493.	A*01:01	A*01:01	B*51:01	B*51:01	DRB1*12:02	DRB1*14:04
494.	A*02:01	A*24:02	B*15:01	B*41:01	DRB1*01:01	DRB1*04:03
495.	A*24:02	A*24:02	B*35:03	B*40:06	DRB1*03:01	DRB1*07:01
496.	A*01:01	A*68:01	B*15:17	B*40:06	DRB1*07:01	DRB1*14:04
497.	A*02:01	A*11:01	B*15:10	B*57:01	DRB1*04:04	DRB1*13:02
498.	A*24:02	A*33:03	B*51:01	B*58:01	DRB1*04:03	DRB1*07:01
499.	A*02:06	A*24:02	B*15:25	B*35:01	DRB1*13:01	DRB1*13:01
500.	A*01:01	A*26:01	B*07:05	B*15:17	DRB1*08:03	DRB1*14:04
501.	A*02:01	A*33:03	B*08:01	B*40:01	DRB1*01:01	DRB1*15:01
502.	A*01:01	A*02:01	B*35:03	B*40:01	DRB1*04:04	DRB1*13:01
503.	A*31:01	A*33:03	B*04:03	B*57:01	DRB1*07:01	DRB1*07:01
504.	A*11:01	A*68:01	B*13:01	B*57:01	DRB1*07:01	DRB1*15:01
505.	A*24:02	A*31:01	B*07:05	B*40:06	DRB1*11:01	DRB1*15:01
506.	A*24:02	A*26:01	B*40:06	B*55:01	DRB1*07:01	DRB1*14:04
507.	A*11:01	A*33:03	B*07:05	B*44:03	DRB1*07:01	DRB1*14:04
508.	A*33:01	A*33:01	B*44:03	B*58:01	DRB1*13:07	DRB1*14:04
509.	A*24:02	A*33:01	B*40:06	B*40:06	DRB1*07:01	DRB1*13:01
510.	A*33:01	A*33:01	B*58:01	B*58:01	DRB1*07:01	DRB1*15:01
511.	A*01:01	A*03:01	B*13:01	B*37:01	DRB1*13:01	DRB1*14:04
512.	A*02:01	A*02:01	B*15:11	B*35:01	DRB1*10:01	DRB1*15:01
513.	A*02:01	A*32:01	B*07:02	B*35:01	DRB1*08:01	DRB1*13:01
514.	A*02:01	A*24:02	B*40:01	B*51:01	DRB1*04:03	DRB1*11:01
515.	A*03:01	A*24:02	B*07:02	B*52:01	DRB1*04:03	DRB1*15:01
516.	A*01:01	A*24:02	B*07:05	B*57:01	DRB1*04:01	DRB1*10:01
517.	A*03:01	A*24:02	B*13:01	B*40:06	DRB1*07:01	DRB1*15:01
518.	A*03:01	A*24:02	B*07:02	B*51:01	DRB1*01:01	DRB1*12:01
519.	A*33:01	A*68:01	B*35:0	B*52:01	DRB1*07:01	DRB1*10:01
520.	A*33:03	A*68:01	B*52:01	B*58:01	DRB1*03:01	DRB1*15:01
521.	A*02:01	A*33:03	B*07:02	B*44:03	DRB1*07:01	DRB1*15:02
522.	A*24:02	A*30:01	B*13:02	B*52:01	DRB1*07:01	DRB1*07:01
523.	A*29:01	A*68:01	B*07:05	B*35:03	DRB1*13:01	DRB1*14:04
524.	A*68:01	A*68:01	B*07:05	B*52:01	DRB1*04:03	DRB1*14:04
525.	A*24:07	A*33:03	B*07:05	B*08:01	DRB1*10:01	DRB1*13:01
526.	A*33:03	A*33:03	B*40:06	B*44:03	DRB1*07:01	DRB1*07:01
527.	A*02:01	A*02:11	B*40:06	B*40:06	DRB1*14:04	DRB1*15:01
528.	A*02:02	A*68:01	B*15:18	B*41:01	DRB1*13:03	DRB1*14:04
529.	A*02:01	A*24:02	B*15:01	B*40:06	DRB1*04:04	DRB1*15:02

530.	A*24:02	A*24:02	B*07:02	B*07:02	DRB1*01:01	DRB1*01:01
531.	A*24:02	A*26:01	B*15:18	B*51:01	DRB1*08:03	DRB1*13:02
532.	A*02:01	A*24:02	B*35:01	B*57:01	DRB1*07:01	DRB1*11:01
533.	A*32:01	A*32:01	B*08:01	B*37:01	DRB1*01:01	DRB1*03:01
534.	A*03:01	A*33:03	B*35:01	B*44:03	DRB1*07:01	DRB1*07:01
535.	A*01:01	A*31:01	B*07:02	B*48:01	DRB1*14:04	DRB1*15:01
536.	A*01:01	A*31:01	B*15:02	B*51:01	DRB1*07:01	DRB1*10:01
537.	A*24:02	A*26:01	B*08:01	B*40:06	DRB1*14:04	DRB1*15:02
538.	A*03:01	A*32:01	B*27:04	B*35:01	DRB1*07:01	DRB1*14:04
539.	A*01:01	A*33:01	B*44:03	B*57:01	DRB1*04:01	DRB1*07:01
540.	A*02:01	A*11:01	B*56:01	B*57:01	DRB1*07:01	DRB1*15:01
541.	A*11:01	A*24:02	B*15:02	B*15:18	DRB1*13:07	DRB1*14:04
542.	A*33:01	A*33:01	B*44:03	B*58:01	DRB1*07:01	DRB1*13:01
543.	A*24:02	A*33:01	B*40:06	B*40:06	DRB1*07:01	DRB1*15:01
544.	A*33:01	A*33:01	B*58:01	B*58:01	DRB1*13:01	DRB1*14:04
545.	A*01:01	A*03:01	B*13:01	B*37:01	DRB1*10:01	DRB1*15:01
546.	A*02:01	A*02:01	B*15:11	B*35:01	DRB1*10:01	DRB1*15:01
547.	A*02:01	A*32:01	B*07:02	B*35:01	DRB1*04:03	DRB1*11:01
548.	A*24:02	A*24:08	B*55:01	B*57:01	DRB1*01:01	DRB1*07:01
549.	A*02:01	A*24:02	B*40:01	B*51:01	DRB1*04:03	DRB1*15:01
550.	A*03:01	A*24:02	B*07:02	B*52:01	DRB1*04:01	DRB1*10:01
551.	A*01:01	A*24:02	B*07:05	B*57:01	DRB1*07:01	DRB1*15:01
552.	A*03:01	A*24:02	B*13:01	B*40:06	DRB1*01:01	DRB1*12:01
553.	A*03:01	A*24:02	B*07:02	B*51:01	DRB1*07:01	DRB1*10:01
554.	A*33:01	A*68:01	B*35:01	B*52:01	DRB1*14:04	DRB1*15:01
555.	A*11:01	A*24:02	B*13:02	B*52:01	DRB1*07:01	DRB1*07:01
556.	A*01:01	A*23:01	B*08:01	B*44:03	DRB1*04:01	DRB1*07:01
557.	A*24:02	A*24:07	B*40:01	B*49:01	DRB1*13:02	DRB1*14:04
558.	A*02:01	A*33:03	B*51:01	x	DRB1*04:08	x
559.	A*02:11	A*24:02	B*07:05	B*13:01	DRB1*04:10	DRB1*15:04
560.	A*01:01	A*02:03	B*15:17	B*40:01	DRB1*08:03	DRB1*13:02
561.	A*24:02	A*33:03	B*55:01	B*58:01	DRB1*10:01	DRB1*13:02
562.	A*11:01	A*33:03	B*40:06	B*58:01	DRB1*14:04	DRB1*15:01
563.	A*01:01	A*33:03	B*44:03	B*57:01	DRB1*07:01	DRB1*15:02
564.	A*03:01	A*68:01	B*40:01	B*44:02	DRB1*04:03	DRB1*15:04
565.	A*02:01	A*02:01	B*35:01	B*58:01	DRB1*15:02	x
566.	A*24:02	A*26:01	B*35:05	B*40:06	DRB1*07:01	DRB1*14:04
567.	A*01:01	A*01:01	B*51:01	B*51:01	DRB1*12:02	DRB1*14:04
568.	A*02:01	A*24:02	B*15:01	B*41:01	DRB1*01:01	DRB1*04:03
569.	A*24:02	A*24:02	B*35:03	B*40:06	DRB1*03:01	DRB1*07:01
570.	A*01:01	A*68:01	B*15:17	B*40:06	DRB1*07:01	DRB1*14:04
571.	A*02:11	A*31:01	B*51:01	B*57:01	DRB1*04:08	DRB1*13:02
572.	A*01:01	A*24:02	B*48:01	B*57:01	DRB1*07:01	DRB1*12:02

Table 39.2: Allele ID of donors

Patient No.	A	A	B	B	DRB1	DRB1
1.	A*02:01	A*24:02	B*07:02	B*52:01	DRB1*04:03	DRB1*15:02
2.	A*11:01	A*30:01	B*13:02	B*35:01	DRB1*07:01	DRB1*15:01
3.	A*29:01	A*68:01	B*07:05	B*13:01	DRB1*14:04	DRB1*15:02
4.	A*02:01	B*26:01	B*08:01	B*40:06	DRB1*03:07	DRB1*04:03
5.	A*33:03	A*33:03	B*07:05	B*02:01	DRB1*03:01	DRB1*10:01
6.	A*24:02	A*24:03	B*15:18	B*58:01	DRB1*04:03	DRB1*13:02
7.	A*02:01	A*24:02	B*40:06	B*40:06	DRB1*14:04	DRB1*15:01
8.	A*02:02	A*68:01	B*15:18	B*41:01	DRB1*13:03	DRB1*14:04
9.	A*02:01	A*24:02	B*15:01	B*55:02	DRB1*04:04	DRB1*10:01
10.	A*11:01	A*24:02	B*07:02	B*57:01	DRB1*01:01	DRB1*07:01
11.	A*02:01	A*26:01	B*15:18	B*51:01	DRB1*04:10	DRB1*13:02
12.	A*01:01	A*24:02	B*15:17	B*35:01	DRB1*11:01	DRB1*13:02
13.	A*01:01	A*32:01	B*08:01	B*37:01	DRB1*03:01	DRB1*10:01
14.	A*02:01	A*31:01	B*40:06	B*40:06	DRB1*07:01	DRB1*15:01
15.	A*24:02	A*26:01	B*08:01	B*15:02	DRB1*12:02	DRB1*14:04
16.	A*02:01	A*24:02	B*07:02	B*37:01	DRB1*07:01	DRB1*10:01
17.	A*01:01	A*24:02	B*07:05	B*48:01	DRB1*15:01	DRB1*15:01
18.	A*02:01	A*03:01	B*02:01	B*57:01	DRB1*03:01	DRB1*15:01
19.	A*01:01	A*23:01	B*15:01	B*52:01	DRB1*03:01	DRB1*14:04
20.	A*02:01	A*02:09	B*40:06	B*58:01	DRB1*13:02	DRB1*15:01
21.	A*02:01	A*11:01	B*35:03	B*55:01	DRB1*14:04	x
22.	A*26:01	x	B*35:01	B*52:01	DRB1*07:01	DRB1*15:02
23.	A*32:01	A*33:01	B*44:03	B*51:01	DRB1*07:01	DRB1*01:01
24.	A*02:11	A*29:01	B*07:05	B*40:02	DRB1*14:04	x
25.	A*03:01	A*11:01	B*15:01	B*55:01	DRB1*04:01	DRB1*08:03
26.	A*02:01	A*24:02	B*07:05	B*07:05	DRB1*11:10	DRB1*14:01
27.	A*01:01	A*03:01	B*18:01	B*57:01	DRB1*03:01	DRB1*04:03
28.	A*01:01	A*11:01	B*40:06	B*52:01	DRB1*04:03	DRB1*15:04
29.	A*24:02	A*26:01	B*07:02	B*35:03	DRB1*11:01	DRB1*15:01
30.	A*11:01	A*31:01	B*15:01	B*15:18	DRB1*14:04	DRB1*15:01
31.	A*32:01	A*33:01	B*35:01	B*44:03	DRB1*07:01	DRB1*14:04
32.	A*24:02	A*33:01	B*40:06	B*58:01	DRB1*13:01	DRB1*15:01
33.	A*24:02	x	B*07:02	B*07:05	DRB1*15:01	DRB1*15:01
34.	A*24:02	A*24:02	B*08:01	B*15:01	DRB1*03:01	DRB1*14:04
35.	A*24:02	A*68:01	B*40:06	B*44:03	DRB1*07:01	DRB1*08:03
36.	A*24:02	A*24:02	B*39:01	B*40:06	DRB1*08:03	DRB1*13:02
37.	A*24:02	A*24:02	B*35:01	B*35:01	DRB1*04:10	DRB1*08:03
38.	A*02:01	A*24:07	B*37:01	B*52:01	DRB1*10:01	DRB1*14:04
39.	A*02:11	A*30:01	B*13:02	B*51:01	DRB1*13:02	DRB1*14:04
40.	A*11:01	A*32:01	B*35:01	B*51:01	DRB1*04:03	DRB1*07:01
41.	A*03:01	A*24:02	B*07:02	B*35:01	DRB1*01:01	DRB1*04:02
42.	A*24:02	A*33:03	B*44:03	B*51:01	DRB1*13:02	DRB1*15:02
43.	A*11:02	A*33:03	B*07:05	B*57:01	DRB1*07:01	DRB1*15:02

44.	A*11:02	A*24:02	B*15:01	B*15:02	DRB1*07:01	DRB1*15:01
45.	A*11:02	A*68:01	B*07:05	B*15:18	DRB1*04:10	DRB1*12:02
46.	A*01:01	A*33:03	B*14:02	B*15:18	DRB1*04:01	DRB1*04:03
47.	A*02:11	A*11:02	B*40:01	B*40:06	DRB1*01:02	DRB1*15:01
48.	A*03:01	A*30:01	B*13:02	B*35:01	DRB1*04:03	DRB1*14:04
49.	A*33:03	A*33:03	B*07:02	B*58:01	DRB1*07:01	DRB1*15:01
50.	A*02:01	A*02:11	B*40:01	B*52:01	DRB1*13:02	DRB1*15:01
51.	A*11:01	A*31:01	B*40:06	B*52:01	DRB1*01:01	DRB1*04:03
52.	A*01:01	A*02:01	B*15:02	B*15:17	DRB1*15:01	DRB1*15:02
53.	A*01:01	A*11:02	B*37:01	B*57:01	DRB1*07:01	DRB1*12:02
54.	A*02:01	A*11:02	B*35:01	B*40:06	DRB1*10:01	DRB1*15:01
55.	A*11:02	A*26:08	B*07:05	B*08:01	DRB1*01:01	DRB1*03:01
56.	A*11:02	A*11:02	B*40:06	B*40:06	DRB1*13:02	DRB1*15:02
57.	A*24:02	A*24:02	B*07:02	B*52:01	DRB1*14:04	DRB1*14:04
58.	A*01:01	A*11:02	B*15:02	B*57:01	DRB1*04:03	DRB1*13:02
59.	A*24:02	x	B*15:01	B*40:02	DRB1*07:01	DRB1*12:02
60.	A*02:01	A*02:11	B*37:01	B*58:01	DRB1*01:01	DRB1*04:01
61.	A*11:02	A*24:03	B*18:01	B*51:01	DRB1*10:01	DRB1*13:02
62.	A*01:01	A*24:02	B*37:01	B*38:02	DRB1*13:02	DRB1*15:01
63.	A*02:03	A*33:03	B*35:08	B*57:01	DRB1*10:01	DRB1*14:01
64.	A*24:02	A*68:01	B*07:05	B*15:18	DRB1*04:03	DRB1*13:01
65.	A*01:01	A*31:01	B*07:05	B*35:01	DRB1*04:03	DRB1*15:01
66.	A*03:01	A*24:02	B*35:01	B*52:01	DRB1*01:01	DRB1*15:01
67.	A*24:02	A*24:02	B*40:06	B*52:01	DRB1*01:01	DRB1*15:01
68.	A*03:01	A*32:01	B*15:18	B*40:06	DRB1*04:03	DRB1*15:02
69.	A*02:01	A*24:02	B*15:02	B*18:01	DRB1*01:01	DRB1*11:01
70.	A*02:01	A*33:03	B*35:01	B*44:03	DRB1*15:01	DRB1*15:01
71.	A*01:01	A*24:02	B*37:01	B*44:03	DRB1*07:01	DRB1*13:01
72.	A*02:11	A*11:02	B*15:01	B*35:03	DRB1*07:01	DRB1*10:01
73.	A*01:01	A*24:01	B*07:05	B*44:03	DRB1*15:01	DRB1*15:02
74.	A*11:02	A*24:02	B*07:05	B*44:03	DRB1*07:01	DRB1*15:01
75.	A*24:02	A*31:01	B*07:02	B*15:01	DRB1*07:01	DRB1*15:01
76.	A*30:01	A*33:03	B*40:06	B*58:01	DRB1*14:04	DRB1*15:04
77.	A*24:02	A*24:02	B*15:02	B*15:25	DRB1*14:04	DRB1*14:04
78.	A*01:01	A*24:02	B*37:01	B*40:06	DRB1*03:01	DRB1*11:04
79.	A*02:01	A*24:02	B*40:06	B*57:01	DRB1*10:01	DRB1*15:01
80.	A*11:02	A*24:02	B*44:02	B*57:01	DRB1*04:03	DRB1*07:01
81.	A*32:01	A*68:01	B*15:18	B*51:01	DRB1*04:38	DRB1*04:38
82.	A*02:01	A*11:02	B*15:18	B*15:18	DRB1*01:01	DRB1*13:01
83.	A*02:01	A*11:02	B*07:02	B*57:01	DRB1*04:01	DRB1*04:01
84.	A*02:01	A*33:03	B*58:01	B*81:01	DRB1*07:01	DRB1*07:01
85.	A*11:01	x	B*15:01	B*35:01	DRB1*13:02	DRB1*13:02
86.	A*01:01	A*02:01	B*40:01	B*57:01	DRB1*14:04	DRB1*15:01
87.	A*02:01	A*68:01	B*56:01	B*57:01	DRB1*01:01	DRB1*07:01
88.	A*11:01	A*24:02	B*15:18	B*40:06	DRB1*07:01	DRB1*15:01
89.	A*33:01	A*33:01	B*44:03	B*58:01	DRB1*13:07	DRB1*15:01
90.	A*11:02	A*33:01	B*40:01	B*44:03	DRB1*07:01	DRB1*13:01

91.	A*02:01	A*33:01	B*37:01	B*58:01	DRB1*07:01	DRB1*14:04
92.	A*01:01	A*03:01	B*13:01	B*37:01	DRB1*10:01	DRB1*13:01
93.	A*02:01	A*02:01	B*15:11	B*51:01	DRB1*10:01	DRB1*15:01
94.	A*02:01	A*11:02	B*07:02	B*37:01	DRB1*01:01	DRB1*13:01
95.	A*11:02	A*24:01	B*40:01	B*52:01	DRB1*04:03	DRB1*15:01
96.	A*01:01	A*03:01	B*07:02	B*57:01	DRB1*04:01	DRB1*04:03
97.	A*24:02	A*29:01	B*07:05	x	DRB1*07:01	DRB1*10:01
98.	A*03:01	A*68:01	B*13:01	B*52:01	DRB1*10:01	DRB1*15:01
99.	A*24:02	A*31:02	B*51:02	B*51:02	DRB1*07:01	DRB1*12:01
100.	A*33:01	A*68:01	B*35:0	B*52:01	DRB1*01:01	DRB1*07:01
101.	A*01:01	A*68:01	B*18:01	B*52:01	DRB1*13:01	DRB1*15:01
102.	A*02:01	A*24:02	B*07:02	B*52:01	DRB1*04:03	DRB1*15:02
103.	A*11:01	A*30:01	B*13:02	B*35:01	DRB1*07:01	DRB1*15:01
104.	A*29:01	A*68:01	B*07:05	B*13:01	DRB1*14:04	DRB1*15:02
105.	A*02:01	A*26:01	B*08:01	B*40:06	DRB1*03:07	DRB1*04:03
106.	A*33:03	A*33:03	B*07:05	B*08:01	DRB1*03:01	DRB1*10:01
107.	A*24:02	A*24:03	B*15:18	B*58:01	DRB1*04:03	DRB1*13:02
108.	A*02:01	A*24:02	B*40:06	B*40:06	DRB1*14:04	DRB1*15:01
109.	A*02:02	A*68:01	B*15:18	B*41:01	DRB1*13:03	DRB1*14:04
110.	A*02:01	A*24:02	B*15:01	B*55:02	DRB1*04:04	DRB1*10:01
111.	A*11:01	A*24:02	B*07:02	B*57:01	DRB1*01:01	DRB1*07:01
112.	A*02:01	A*26:01	B*15:18	B*51:01	DRB1*04:10	DRB1*13:02
113.	A*01:01	A*24:02	B*15:17	B*35:01	DRB1*11:01	DRB1*13:02
114.	A*01:01	A*32:01	B*08:01	B*37:01	DRB1*03:01	DRB1*10:01
115.	A*02:01	A*31:01	B*40:06	B*40:06	DRB1*07:01	DRB1*15:01
116.	A*01:01	A*24:02	B*07:05	B*48:01	DRB1*15:01	DRB1*15:01
117.	A*02:01	A*24:02	B*07:02	B*37:01	DRB1*07:01	DRB1*10:01
118.	A*24:02	A*26:01	B*08:01	B*15:02	DRB1*12:02	DRB1*14:04
119.	A*02:01	A*03:01	B*08:01	B*57:01	DRB1*03:01	DRB1*15:01
120.	A*24:02	A*26:01	B*55:01	B*58:01	DRB1*13:02	DRB1*14:04
121.	A*01:01	A*23:01	B*15:01	B*52:01	DRB1*03:01	DRB1*14:04
122.	A*02:01	A*02:09	B*40:06	B*58:01	DRB1*13:02	DRB1*15:01
123.	A*02:01	A*11:01	B*35:03	B*55:01	DRB1*14:04	x
124.	A*26:01	x	B*35:01	B*52:01	DRB1*07:01	DRB1*15:02
125.	A*32:01	A*33:01	B*44:03	B*51:01	DRB1*07:01	DRB1*01:01
126.	A*02:11	A*29:01	B*07:05	B*40:02	DRB1*14:04	x
127.	A*03:01	A*11:01	B*15:01	B*55:01	DRB1*04:01	DRB1*08:03
128.	A*02:01	A*24:02	B*07:05	B*07:05	DRB1*11:10	DRB1*14:01
129.	A*01:01	A*03:01	B*18:01	B*57:01	DRB1*03:01	DRB1*04:03
130.	A*01:01	A*11:01	B*40:06	B*52:01	DRB1*04:03	DRB1*15:04
131.	A*24:02	A*26:01	B*07:02	B*35:03	DRB1*11:01	DRB1*15:01
132.	A*11:01	A*31:01	B*15:01	B*15:18	DRB1*14:04	DRB1*15:01
133.	A*01:01	A*30:01	B*40:06	B*57:01	DRB1*07:01	DRB1*15:01
134.	A*01:01	A*11:01	B*35:01	B*57:01	DRB1*04:01	DRB1*10:01
135.	A*02:01	A*33:01	B*35:01	B*51:01	DRB1*03:01	DRB1*14:04
136.	A*03:01	A*01:01	B*35:01	B*50:01	DRB1*07:01	DRB1*14:04
137.	A*01:01	A*24:02	B*35:01	B*37:01	DRB1*10:01	DRB1*15:01

138.	A*01:01	A*33:01	B*15:17	B*58:01	DRB1*13:01	x
139.	A*32:01	A*33:01	B*35:01	B*44:03	DRB1*07:01	DRB1*14:04
140.	A*24:02	A*33:01	B*40:06	B*58:01	DRB1*13:01	DRB1*15:01
141.	A*24:02	x	B*07:02	B*07:05	DRB1*15:01	DRB1*15:01
142.	A*24:02	A*24:02	B*08:01	B*15:01	DRB1*03:01	DRB1*14:04
143.	A*03:01	A*31:01	B*35:01	B*51:01	DRB1*01:01	DRB1*11:01
144.	A*24:02	A*68:01	B*40:06	B*44:03	DRB1*07:01	DRB1*08:03
145.	A*24:02	A*24:02	B*39:01	B*40:06	DRB1*08:03	DRB1*13:02
146.	A*24:02	A*24:02	B*35:01	B*35:01	DRB1*04:10	DRB1*08:03
147.	A*02:01	A*24:07	B*37:01	B*52:01	DRB1*10:01	DRB1*14:04
148.	A*02:11	A*30:01	B*13:02	B*51:01	DRB1*04:03	DRB1*07:01
149.	A*11:01	A*32:01	B*35:01	B*51:01	DRB1*01:01	DRB1*04:02
150.	A*02:01	A*24:02	B*07:02	B*35:01	DRB1*13:02	DRB1*15:02
151.	A*03:01	A*24:02	B*07:02	B*35:01	DRB1*13:02	DRB1*15:02
152.	A*11:02	A*33:03	B*15:18	B*58:01	DRB1*04:03	DRB1*13:02
153.	A*24:02	A*33:03	B*44:03	B*51:01	DRB1*07:01	DRB1*15:02
154.	A*11:02	A*33:03	B*07:05	B*57:01	DRB1*07:01	DRB1*15:01
155.	A*11:02	A*24:02	B*15:01	B*15:02	DRB1*04:10	DRB1*12:02
156.	A*11:02	A*68:01	B*07:05	B*15:18	DRB1*04:01	DRB1*04:03
157.	A*01:01	A*33:03	B*14:02	B*15:18	DRB1*01:02	DRB1*15:01
158.	A*02:11	A*11:02	B*40:01	B*40:06	DRB1*04:03	DRB1*14:04
159.	A*03:01	A*30:01	B*13:02	B*35:01	DRB1*07:01	DRB1*15:01
160.	A*33:03	A*33:03	B*07:02	B*58:01	DRB1*13:02	DRB1*15:01
161.	A*02:01	A*02:11	B*40:01	B*52:01	DRB1*01:01	DRB1*04:03
162.	A*11:01	A*31:01	B*40:06	B*52:01	DRB1*15:01	DRB1*15:02
163.	A*01:01	A*02:01	B*15:02	B*15:17	DRB1*07:01	DRB1*12:02
164.	A*01:01	A*11:02	B*37:01	B*57:01	DRB1*10:01	DRB1*15:01
165.	A*02:01	A*11:02	B*35:01	B*40:06	DRB1*01:01	DRB1*03:01
166.	A*11:02	A*26:08	B*07:05	B*08:01	DRB1*13:02	DRB1*15:02
167.	A*11:02	A*11:02	B*40:06	B*40:06	DRB1*11:04	DRB1*11:04
168.	A*24:02	A*24:02	B*07:02	B*52:01	DRB1*04:03	DRB1*13:02
169.	A*01:01	A*11:02	B*15:02	B*57:01	DRB1*07:01	DRB1*12:02
170.	A*24:02	x	B*15:01	B*40:02	DRB1*01:01	DRB1*04:01
171.	A*02:01	A*02:11	B*37:01	B*58:01	DRB1*10:01	DRB1*13:02
172.	A*11:02	A*24:03	B*18:01	B*51:01	DRB1*13:02	DRB1*15:01
173.	A*01:01	A*24:02	B*37:01	B*38:02	DRB1*10:01	DRB1*14:01
174.	A*02:03	A*33:03	B*35:08	B*57:01	DRB1*04:03	DRB1*13:01
175.	A*24:02	A*68:01	B*07:05	B*15:18	DRB1*04:03	DRB1*15:01
176.	A*01:01	A*31:01	B*07:05	B*35:01	DRB1*01:01	DRB1*15:01
177.	A*03:01	A*24:02	B*35:01	B*52:01	DRB1*01:01	DRB1*15:01
178.	A*24:02	A*24:02	B*40:06	B*52:01	DRB1*04:03	DRB1*15:02
179.	A*03:01	A*32:01	B*15:18	B*40:06	DRB1*01:01	DRB1*11:01
180.	A*02:10	A*24:02	B*15:02	B*18:01	DRB1*15:01	DRB1*15:01
181.	A*02:01	A*33:03	B*35:01	B*44:03	DRB1*07:01	DRB1*13:01
182.	A*01:01	A*24:02	B*37:01	B*44:03	DRB1*07:01	DRB1*10:01
183.	A*02:11	A*11:02	B*15:01	B*35:03	DRB1*15:01	DRB1*15:02
184.	A*01:01	A*24:02	B*07:05	B*44:03	DRB1*07:01	DRB1*15:01

185.	A*11:02	A*24:02	B*07:05	B*44:03	DRB1*07:01	DRB1*15:01
186.	A*24:02	A*31:01	B*07:02	B*15:01	DRB1*14:04	DRB1*14:04
187.	A*30:01	A*33:03	B*40:06	B*58:01	DRB1*14:04	DRB1*14:04
188.	A*24:02	A*24:02	B*15:02	B*15:25	DRB1*03:01	DRB1*11:04
189.	A*26:08	A*11:02	B*55:01	B*57:01	DRB1*01:01	DRB1*14:04
190.	A*01:01	A*24:02	B*37:01	B*40:06	DRB1*10:01	DRB1*15:01
191.	A*02:01	A*24:02	B*40:06	B*57:01	DRB1*04:03	DRB1*07:01
192.	A*11:02	A*24:02	B*44:02	B*57:01	DRB1*04:38	DRB1*04:38
193.	A*32:01	A*68:01	B*15:18	B*51:01	DRB1*01:01	DRB1*13:01
194.	A*02:01	A*11:02	B*15:18	B*15:18	DRB1*04:01	DRB1*04:01
195.	A*02:01	A*11:02	B*07:02	B*57:01	DRB1*07:01	DRB1*07:01
196.	A*02:01	A*33:03	B*58:01	B*81:01	DRB1*13:02	DRB1*13:02
197.	A*02:01	A*11:04	B*13:01	B*35:01	DRB1*07:01	DRB1*14:04
198.	A*11:01	x	B*15:01	B*35:01	DRB1*14:04	DRB1*15:01
199.	A*01:01	A*02:01	B*40:01	B*57:01	DRB1*01:01	DRB1*07:01
200.	A*02:01	A*68:01	B*56:01	B*57:01	DRB1*07:01	DRB1*15:01
201.	A*11:01	A*24:02	B*15:18	B*40:06	DRB1*07:01	DRB1*15:01
202.	A*33:01	A*33:01	B*44:03	B*58:01	DRB1*07:01	DRB1*13:01
203.	A*11:02	A*33:01	B*40:01	B*44:03	DRB1*07:01	DRB1*14:04
204.	A*02:01	A*33:01	B*37:01	B*58:01	DRB1*10:01	DRB1*13:01
205.	A*01:01	A*03:01	B*13:01	B*37:01	DRB1*10:01	DRB1*15:01
206.	A*02:01	A*02:01	B*15:11	B*51:01	DRB1*01:01	DRB1*13:01
207.	A*02:01	A*11:02	B*07:02	B*37:01	DRB1*04:03	DRB1*15:01
208.	A*11:02	A*24:02	B*13:02	B*57:01	DRB1*07:01	DRB1*14:04
209.	A*11:02	A*24:02	B*40:01	B*52:01	DRB1*04:01	DRB1*04:03
210.	A*01:01	A*03:01	B*07:02	B*57:01	DRB1*07:01	DRB1*10:01
211.	A*24:02	A*29:01	B*07:05	x	DRB1*10:01	DRB1*15:01
212.	A*03:01	A*68:01	B*13:01	B*52:01	DRB1*07:01	DRB1*12:01
213.	A*24:02	A*31:02	B*51:01	B*51:02	DRB1*01:01	DRB1*07:01
214.	A*33:01	A*68:01	B*35:01	B*52:01	DRB1*01:01	DRB1*07:01
215.	A*11:01	A*24:02	B*13:02	B*52:01	DRB1*07:01	DRB1*07:01
216.	A*01:01	A*23:01	B*08:01	B*44:03	DRB1*04:01	DRB1*07:01
217.	A*66:01	A*68:01	B*52:01	B*55:01	DRB1*08:03	DRB1*15:01
218.	A*24:02	A*33:03	B*07:02	B*51:01	DRB1*04:08	DRB1*13:02
219.	A*11:01	A*24:02	B*07:05	B*07:05	DRB1*04:10	DRB1*14:04
220.	A*01:01	A*02:03	B*40:01	B*57:01	DRB1*08:03	DRB1*13:02
221.	A*33:03	A*33:03	B*58:01	B*58:01	DRB1*13:02	DRB1*14:04
222.	A*24:02	A*33:03	B*40:06	B*58:01	DRB1*15:01	DRB1*15:01
223.	A*11:01	A*33:03	B*44:03	B*07:05	DRB1*07:01	DRB1*14:04
224.	A*33:03	A*68:01	B*14:02	B*40:01	DRB1*01:02	DRB1*15:04
225.	A*02:01	A*24:02	B*40:06	B*58:01	DRB1*14:04	DRB1*15:02
226.	A*02:11	A*33:03	B*40:06	B*44:03	DRB1*13:01	DRB1*13:01
227.	A*03:01	A*32:01	B*07:02	B*35:01	DRB1*11:01	DRB1*15:02
228.	A*24:02	A*68:01	B*35:01	B*55:01	DRB1*04:03	DRB1*13:01
229.	A*11:01	A*11:02	B*58:01	B*58:01	DRB1*13:02	x
230.	A*03:01	A*11:01	B*15:02	B*57:01	DRB1*07:01	DRB1*12:02
231.	A*24:02	A*29:03	B*07:05	B*56:01	DRB1*14:04	DRB1*15:04

232.	A*01:01	A*32:01	B*35:01	B*52:01	DRB1*04:03	DRB1*15:04
233.	A*02:11	A*11:01	B*07:05	B*51:01	DRB1*04:03	DRB1*14:04
234.	A*01:01	A*24:02	B*35:01	B*38:02	DRB1*04:03	DRB1*15:04
235.	A*02:01	A*24:02	B*40:01	B*51:01	DRB1*04:01	DRB1*14:04
236.	A*33:03	A*02:11	B*40:06	B*57:03	DRB1*10:01	DRB1*15:02
237.	A*02:01	A*26:01	B*07:02	B*40:06	DRB1*07:01	DRB1*13:02
238.	A*02:11	A*33:03	B*40:06	B*44:03	DRB1*07:01	DRB1*15:01
239.	A*33:01	A*68:01	B*52:01	B*57:03	DRB1*07:01	DRB1*15:01
240.	A*02:11	A*26:01	B*07:05	B*57:01	DRB1*01:01	DRB1*04:03
241.	A*02:01	A*03:02	B*18:01	B*41:01	DRB1*04:03	DRB1*04:04
242.	A*01:01	A*11:01	B*52:01	B*57:01	DRB1*04:03	DRB1*15:02
243.	A*03:01	A*11:01	B*35:01	B*37:01	DRB1*13:01	DRB1*15:02
244.	A*01:01	A*02:01	B*40:01	B*57:01	DRB1*03:01	DRB1*07:01
245.	A*11:01	A*24:10	B*40:06	B*52:01	DRB1*04:03	DRB1*15:01
246.	A*26:01	A*31:01	B*40:01	B*56:01	DRB1*01:01	DRB1*11:01
247.	A*29:01	A*33:01	B*44:03	B*44:03	DRB1*07:01	DRB1*13:01
248.	A*24:02	A*32:01	B*35:01	B*52:01	DRB1*01:01	DRB1*04:03
249.	A*01:01	A*26:01	B*37:01	B*51:01	DRB1*04:03	DRB1*10:01
250.	A*02:01	A*11:01	B*15:02	B*40:06	DRB1*07:01	DRB1*15:01
251.	A*24:02	A*24:03	B*35:03	B*58:01	DRB1*14:04	DRB1*14:04
252.	A*02:01	A*11:01	B*07:02	B*44:03	DRB1*07:01	DRB1*10:01
253.	A*24:02	A*32:01	B*35:01	B*51:01	DRB1*01:01	DRB1*14:04
254.	A*01:01	A*24:02	B*35:01	B*37:01	DRB1*10:01	DRB1*15:01
255.	A*11:01	A*34:02	B*07:05	B*58:01	DRB1*14:04	x
256.	A*03:01	A*11:01	B*18:01	B*35:01	DRB1*13:01	DRB1*15:01
257.	A*29:02	A*29:02	B*52:01	B*52:01	DRB1*13:01	DRB1*13:01
258.	A*02:01	A*02:11	B*40:01	B*52:01	DRB1*01:01	DRB1*04:03
259.	A*11:01	A*31:01	B*04:03	B*52:01	DRB1*07:01	DRB1*15:01
260.	A*11:01	A*24:02	B*52:01	B*57:01	DRB1*07:01	DRB1*15:01
261.	A*01:01	A*68:01	B*18:01	B*15:18	DRB1*01:01	DRB1*15:01
262.	A*02:01	A*11:01	B*40:01	B*07:05	DRB1*15:01	DRB1*14:04
263.	A*01:01	A*24:02	B*37:01	B*44:02	DRB1*07:01	DRB1*10:01
264.	A*24:02	A*31:01	B*35:01	B*51:01	DRB1*15:01	DRB1*14:04
265.	A*32:01	A*68:01	B*15:17	B*58:01	DRB1*07:01	DRB1*15:02
266.	A*02:11	A*24:02	B*15:39	B*52:01	DRB1*14:04	DRB1*14:04
267.	A*01:01	A*24:02	B*08:01	B*58:01	DRB1*03:01	DRB1*01:01
268.	A*02:05	A*33:03	B*50:01	B*58:01	DRB1*13:02	DRB1*15:01
269.	A*11:01	A*24:02	B*35:03	B*44:02	DRB1*11:01	DRB1*15:01
270.	A*11:01	A*24:02	B*15:18	B*35:01	DRB1*14:04	DRB1*15:01
271.	A*01:01	A*02:11	B*13:02	B*18:01	DRB1*07:01	DRB1*08:03
272.	A*24:02	A*33:03	B*07:05	B*44:03	DRB1*07:01	DRB1*15:01
273.	A*02:01	A*26:01	B*18:01	B*40:01	DRB1*11:04	DRB1*13:01
274.	A*11:01	A*11:04	B*40:06	B*35:01	DRB1*15:01	DRB1*11:17
275.	A*01:01	A*01:01	B*15:01	B*35:03	DRB1*13:01	DRB1*13:02
276.	A*24:02	A*31:01	B*15:01	B*57:01	DRB1*07:01	DRB1*13:01
277.	A*11:01	A*11:01	B*13:01	B*51:01	DRB1*04:01	DRB1*15:01
278.	A*02:01	A*24:02	B*40:06	B*40:06	DRB1*11:01	DRB1*15:02

279.	A*24:02	A*26:01	B*52:01	B*55:01	DRB1*04:03	DRB1*07:01
280.	A*11:01	A*11:01	B*07:05	B*40:01	DRB1*04:01	DRB1*14:01
281.	A*02:01	A*32:01	B*07:02	B*48:01	DRB1*12:02	DRB1*15:02
282.	A*01:01	A*11:01	B*07:05	B*15:17	DRB1*13:02	DRB1*14:04
283.	A*02:11	A*24:02	B*07:05	B*51:01	DRB1*04:03	DRB1*04:05
284.	A*11:01	A*11:01	B*13:01	B*52:01	DRB1*04:03	DRB1*07:01
285.	A*03:01	A*33:03	B*40:06	B*44:03	DRB1*07:01	DRB1*14:04
286.	A*33:03	A*68:01	B*44:03	B*52:01	DRB1*07:01	DRB1*15:02
287.	A*02:11	A*33:03	B*35:03	B*44:03	DRB1*07:01	DRB1*08:03
288.	A*32:01	A*68:01	B*40:01	B*51:01	DRB1*10:01	DRB1*13:01
289.	A*01:01	A*33:03	B*44:03	B*57:01	DRB1*07:01	x
290.	A*02:01	A*24:02	B*15:18	B*51:01	DRB1*04:01	DRB1*04:03
291.	A*11:01	A*32:01	B*35:01	B*40:06	DRB1*11:01	DRB1*11:01
292.	A*01:01	A*68:01	B*18:01	B*52:01	DRB1*13:01	DRB1*15:01
293.	A*02:01	A*11:01	B*40:01	B*07:05	DRB1*15:01	DRB1*14:04
294.	A*01:01	A*24:02	B*37:01	B*44:02	DRB1*07:01	DRB1*10:01
295.	A*24:02	A*31:01	B*35:01	B*51:01	DRB1*15:01	DRB1*14:04
296.	A*32:01	A*68:01	B*15:17	B*58:01	DRB1*07:01	DRB1*15:02
297.	A*02:11	A*24:02	B*15:39	B*52:01	DRB1*14:04	DRB1*14:04
298.	A*01:01	A*24:02	B*08:01	B*58:01	DRB1*03:01	DRB1*01:01
299.	A*02:05	A*33:03	B*50:01	B*58:01	DRB1*13:02	DRB1*15:01
300.	A*11:01	A*24:02	B*35:03	B*44:02	DRB1*11:01	DRB1*15:01
301.	A*11:01	A*24:02	B*15:18	B*35:01	DRB1*14:04	DRB1*15:01
302.	A*01:01	A*02:11	B*13:02	B*18:01	DRB1*07:01	DRB1*08:03
303.	A*24:02	A*33:03	B*07:05	B*44:03	DRB1*07:01	DRB1*15:01
304.	A*02:01	A*26:01	B*18:01	B*40:01	DRB1*11:04	DRB1*13:01
305.	A*11:01	x	B*40:06	B*35:01	DRB1*15:01	DRB1*11:17
306.	A*01:01	A*01:01	B*15:01	B*35:03	DRB1*13:01	DRB1*13:02
307.	A*24:02	A*31:01	B*15:01	B*57:01	DRB1*07:01	DRB1*13:01
308.	A*11:01	A*11:01	B*13:01	B*51:01	DRB1*04:01	DRB1*15:01
309.	A*02:01	A*24:02	B*40:06	B*40:06	DRB1*11:01	DRB1*15:02
310.	A*24:02	A*26:01	B*52:01	B*55:01	DRB1*04:03	DRB1*07:01
311.	A*11:01	A*11:01	B*07:05	B*40:01	DRB1*04:01	DRB1*14:01
312.	A*02:01	A*32:01	B*07:02	B*48:01	DRB1*12:02	DRB1*15:02
313.	A*01:01	A*11:01	B*07:05	B*15:17	DRB1*13:02	DRB1*14:04
314.	A*02:11	A*24:02	B*07:05	B*51:01	DRB1*04:03	DRB1*04:05
315.	A*11:01	A*11:01	B*13:01	B*52:01	DRB1*04:03	DRB1*07:01
316.	A*03:01	A*33:03	B*40:06	B*44:03	DRB1*07:01	DRB1*14:04
317.	A*33:03	A*68:01	B*44:03	B*52:01	DRB1*07:01	DRB1*15:02
318.	A*02:11	A*33:03	B*35:03	B*44:03	DRB1*07:01	DRB1*08:03
319.	A*32:01	A*68:01	B*40:01	B*51:01	DRB1*10:01	DRB1*13:01
320.	A*01:01	A*33:03	B*44:03	B*57:01	DRB1*07:01	x
321.	A*02:01	A*24:02	B*15:18	B*51:01	DRB1*04:01	DRB1*04:03
322.	A*11:01	A*32:01	B*35:01	B*40:06	DRB1*07:01	DRB1*15:02
323.	A*02:01	A*11:01	B*40:01	B*07:05	DRB1*15:01	DRB1*14:04
324.	A*01:01	A*24:02	B*37:01	B*44:02	DRB1*07:01	DRB1*10:01
325.	A*01:01	A*24:02	B*35:01	B*52:01	DRB1*12:04	DRB1*13:02

326.	A*11:01	A*11:01	B*07:05	B*51:01	DRB1*04:03	DRB1*07:01
327.	A*11:01	A*24:02	B*15:05	B*35:03	DRB1*14:04	DRB1*15:01
328.	A*11:01	A*33:03	B*35:01	B*58:01	DRB1*04:02	DRB1*08:02
329.	A*02:01	A*02:01	B*07:05	B*58:01	DRB1*03:01	DRB1*15:01
330.	A*01:01	A*24:02	B*07:02	B*57:03	DRB1*14:04	DRB1*14:04
331.	A*11:01	A*24:02	B*07:02	B*13:01	DRB1*07:01	DRB1*07:01
332.	A*11:01	A*33:03	B*37:01	B*58:01	DRB1*15:02	DRB1*15:02
333.	A*01:01	A*33:03	B*44:03	B*57:01	DRB1*03:01	DRB1*10:01
334.	A*02:01	A*68:01	B*15:01	B*18:01	DRB1*04:03	DRB1*07:01
335.	A*02:01	A*33:03	B*35:03	B*44:03	DRB1*11:01	DRB1*11:01
336.	A*24:02	A*31:02	B*07:02	B*51:04	DRB1*07:01	DRB1*08:03
337.	A*02:01	A*02:11	B*07:02	B*40:06	DRB1*14:04	DRB1*15:02
338.	A*24:02	A*31:01	B*35:01	B*40:01	DRB1*01:01	DRB1*15:02
339.	A*11:01	A*24:02	B*13:01	B*51:01	DRB1*13:02	DRB1*14:04
340.	A*02:01	A*11:01	B*15:18	B*40:01	DRB1*04:10	DRB1*15:01
341.	A*24:07	A*33:03	B*07:02	B*37:01	DRB1*04:03	DRB1*15:01
342.	A*02:01	A*11:01	B*07:05	B*35:03	DRB1*01:01	DRB1*10:01
343.	A*02:01	A*11:01	B*07:05	B*40:02	DRB1*15:01	DRB1*15:01
344.	A*24:02	A*24:07	B*52:01	B*55:01	DRB1*14:04	DRB1*15:01
345.	A*02:11	A*02:11	B*35:01	B*40:06	DRB1*04:03	DRB1*13:01
346.	A*02:01	A*30:02	B*35:01	B*41:01	DRB1*08:03	DRB1*14:15
347.	A*24:02	A*33:03	B*07:05	B*57:01	DRB1*03:01	DRB1*04:05
348.	A*02:06	A*33:03	B*44:03	B*52:01	DRB1*04:03	DRB1*04:05
349.	A*11:01	A*24:02	B*07:02	B*15:02	DRB1*07:01	DRB1*15:01
350.	A*01:01	A*24:02	B*15:17	B*37:01	DRB1*10:01	DRB1*15:01
351.	A*01:01	A*24:02	B*35:03	B*40:06	DRB1*10:01	DRB1*13:02
352.	A*02:11	A*11:01	B*15:05	B*37:01	DRB1*12:01	DRB1*15:01
353.	A*11:01	A*24:02	B*27:03	B*07:05	DRB1*08:03	DRB1*10:01
354.	A*02:16	A*11:01	B*07:05	B*35:01	DRB1*11:17	DRB1*14:04
355.	A*02:01	A*24:02	B*40:06	B*51:01	DRB1*11:01	DRB1*15:01
356.	A*24:02	A*68:01	B*52:01	B*56:01	DRB1*04:03	DRB1*07:01
357.	A*23:01	A*24:07	B*13:01	B*52:01	DRB1*15:01	DRB1*16:02
358.	A*24:02	A*24:02	B*07:05	B*07:05	DRB1*04:03	DRB1*08:02
359.	A*24:02	A*24:02	B*52:01	B*58:01	DRB1*15:01	DRB1*15:01
360.	A*11:01	A*30:01	B*13:02	B*35:03	DRB1*15:01	DRB1*15:02
361.	A*02:11	A*03:01	B*07:02	B*15:01	DRB1*01:01	DRB1*07:01
362.	A*24:02	A*31:01	B*35:01	B*51:01	DRB1*04:03	DRB1*11:01
363.	A*11:01	A*24:02	B*07:05	B*07:05	DRB1*01:01	DRB1*01:01
364.	A*11:01	A*32:01	B*40:06	B*58:01	DRB1*15:01	DRB1*15:01
365.	A*24:02	A*29:01	B*07:05	B*07:05	DRB1*04:01	DRB1*14:04
366.	A*02:01	A*33:03	B*07:05	B*58:01	DRB1*04:05	DRB1*15:01
367.	A*02:01	A*33:01	B*07:02	B*35:01	DRB1*10:01	DRB1*15:01
368.	A*68:02	A*33:01	B*08:01	B*58:01	DRB1*04:03	DRB1*07:01
369.	A*02:11	A*11:01	B*13:01	B*35:03	DRB1*03:01	DRB1*03:01
370.	A*02:11	A*24:02	B*07:05	B*07:05	DRB1*04:03	DRB1*15:01
371.	A*03:02	A*11:01	B*81:01	B*58:01	DRB1*01:01	DRB1*14:04
372.	A*11:01	A*24:02	B*18:01	B*40:06	DRB1*03:01	DRB1*12:01

373.	A*11:01	A*24:02	B*40:02	B*52:01	DRB1*11:01	DRB1*14:04
374.	A*11:01	A*68:01	B*18:01	B*51:01	DRB1*04:03	DRB1*14:01
375.	A*24:02	A*31:01	B*40:06	B*39:01	DRB1*01:01	DRB1*01:01
376.	A*23:01	A*68:01	B*08:01	B*41:01	DRB1*04:03	DRB1*14:04
377.	A*11:01	A*24:02	B*52:01	B*58:01	DRB1*03:01	DRB1*14:04
378.	A*11:01	A*33:03	B*35:01	B*58:01	DRB1*07:01	DRB1*07:01
379.	A*01:01	A*33:03	B*44:03	B*51:01	DRB1*11:01	DRB1*13:02
380.	A*24:02	A*26:08	B*35:05	B*40:06	DRB1*04:08	DRB1*07:01
381.	A*24:02	A*33:03	B*51:01	B*58:01	DRB1*12:02	DRB1*14:04
382.	A*24:02	A*33:03	B*15:02	B*44:03	DRB1*03:01	DRB1*04:03
383.	A*03:01	A*24:02	B*15:18	B*40:06	DRB1*04:03	DRB1*04:05
384.	A*24:02	A*68:01	B*40:06	B*51:01	DRB1*04:03	DRB1*07:01
385.	A*02:01	A*03:01	B*35:01	B*57:01	DRB1*04:03	DRB1*04:04
386.	A*24:02	A*33:03	B*51:01	B*58:01	DRB1*07:01	DRB1*11:01
387.	A*02:06	A*11:02	B*35:01	B*40:06	DRB1*13:01	DRB1*13:02
388.	A*01:01	A*02:11	B*15:17	B*57:01	DRB1*14:04	DRB1*14:04
389.	A*02:01	A*24:02	B*35:02	B*40:01	DRB1*01:01	DRB1*07:01
390.	A*11:01	A*11:01	B*52:01	B*56:01	DRB1*04:04	DRB1*11:04
391.	A*33:03	A*33:03	B*44:03	B*44:03	DRB1*04:03	DRB1*12:01
392.	A*01:01	A*33:03	B*37:01	B*58:01	DRB1*04:03	DRB1*07:01
393.	A*01:01	A*11:01	B*18:01	B*51:01	DRB1*10:01	DRB1*13:02
394.	A*11:01	A*24:02	B*13:10	B*40:01	DRB1*04:08	DRB1*15:01
395.	A*02:01	A*24:02	B*07:02	B*48:01	DRB1*04:03	DRB1*04:03
396.	A*03:01	A*24:02	B*15:01	B*57:01	DRB1*08:03	DRB1*12:02
397.	A*11:03	A*33:03	B*27:04	B*44:03	DRB1*07:01	DRB1*11:01
398.	A*11:01	A*32:01	B*35:03	B*48:01	DRB1*04:02	DRB1*10:01
399.	A*11:01	A*24:02	B*51:01	B*57:01	DRB1*12:02	DRB1*15:01
400.	A*11:01	A*33:03	B*13:01	B*35:03	DRB1*07:01	DRB1*07:01
401.	A*11:01	A*24:02	B*13:01	B*35:01	DRB1*13:01	DRB1*15:01
402.	A*02:01	A*24:02	B*40:06	B*52:01	DRB1*08:01	DRB1*08:01
403.	A*11:01	A*24:02	B*07:05	x	DRB1*03:01	DRB1*11:01
404.	A*02:01	A*02:03	B*07:02	B*13:02	DRB1*15:01	DRB1*15:01
405.	A*11:01	A*24:02	B*57:01	B*52:01	DRB1*07:01	DRB1*07:01
406.	A*03:01	A*03:02	B*35:03	B*51:01	DRB1*04:03	DRB1*07:01
407.	A*02:01	A*24:02	B*35:01	B*52:01	DRB1*04:01	DRB1*15:02
408.	A*02:01	A*11:01	B*40:06	x	DRB1*04:01	DRB1*13:10
409.	A*24:07	A*33:03	B*08:01	B*58:01	DRB1*14:04	DRB1*15:02
410.	A*24:02	A*03:02	B*18:01	B*51:01	DRB1*03:01	DRB1*15:01
411.	A*24:02	A*33:03	B*15:01	B*51:01	DRB1*04:03	DRB1*13:01
412.	A*31:01	A*33:03	B*15:18	B*44:03	DRB1*07:01	DRB1*14:04
413.	A*01:01	A*24:02	B*15:17	B*40:01	DRB1*01:01	DRB1*13:01
414.	A*24:02	A*24:07	B*08:01	B*15:01	DRB1*03:01	DRB1*08:02
415.	A*03:01	A*26:01	B*35:01	B*40:06	DRB1*08:04	DRB1*14:04
416.	A*03:01	A*24:02	B*15:01	B*18:01	DRB1*11:01	DRB1*13:01
417.	A*01:01	A*02:01	B*40:06	B*49:01	DRB1*07:01	DRB1*15:01
418.	A*11:01	A*24:02	B*37:01	B*57:01	DRB1*10:01	DRB1*15:01
419.	A*01:01	A*26:01	B*35:01	B*51:01	DRB1*04:03	DRB1*10:01

420.	A*26:01	A*02:01	B*08:01	B*51:01	DRB1*03:01	DRB1*04:03
421.	A*24:02	A*33:01	B*35:01	B*44:03	DRB1*07:01	DRB1*13:01
422.	A*24:01	A*26:02	B*07:05	B*08:02	DRB1*01:01	DRB1*03:01
423.	A*24:02	A*68:01	B*15:25	B*37:01	DRB1*10:01	DRB1*11:04
424.	A*01:01	A*26:01	B*18:01	B*55:01	DRB1*04:03	DRB1*12:01
425.	A*24:02	A*33:03	B*44:03	B*52:01	DRB1*07:01	DRB1*15:01
426.	A*32:01	A*33:03	B*07:02	B*44:03	DRB1*07:01	DRB1*10:01
427.	A*02:01	A*02:01	B*35:01	B*40:06	DRB1*01:01	DRB1*08:04
428.	A*26:01	A*68:01	B*07:02	B*15:01	DRB1*04:08	DRB1*15:01
429.	A*03:01	A*11:01	B*07:05	B*40:06	DRB1*14:04	DRB1*15:01
430.	A*31:01	A*68:01	B*15:18	B*58:01	DRB1*07:01	DRB1*13:02
431.	A*03:01	A*24:02	B*15:01	B*40:06	DRB1*04:03	DRB1*08:04
432.	A*24:02	A*31:01	B*15:01	B*27:07	DRB1*09:01	DRB1*14:04
433.	A*11:01	A*26:01	B*15:18	B*35:01	DRB1*04:01	DRB1*15:01
434.	A*03:01	A*24:02	B*40:01	B*07:02	DRB1*04:03	DRB1*14:01
435.	A*01:01	A*02:01	B*37:01	B*57:01	DRB1*07:01	DRB1*10:01
436.	A*02:06	A*68:01	B*51:01	B*55:01	DRB1*13:01	DRB1*15:01
437.	A*02:03	A*03:01	B*07:02	B*58:01	DRB1*13:01	DRB1*15:01
438.	A*26:01	A*33:03	B*44:03	B*55:01	DRB1*07:01	DRB1*12:02
439.	A*33:03	X	B*44:03	B*58:01	DRB1*07:02	DRB1*13:02
440.	A*01:01	A*24:02	B*35:01	B*51:06	DRB1*01:01	DRB1*15:01
441.	A*02:01	A*33:03	B*35:03	B*58:01	DRB1*13:02	DRB1*14:04
442.	A*31:01	x	B*27:04	B*40:06	DRB1*14:04	DRB1*14:04
443.	A*31:01	A*33:03	B*15:08	B*35:03	DRB1*07:01	DRB1*14:04
444.	A*11:01	A*24:02	B*18:01	B*40:06	DRB1*14:04	DRB1*15:01
445.	A*02:01	A*11:01	B*51:01	B*07:05	DRB1*15:01	DRB1*14:04
446.	A*01:01	A*02:01	B*40:06	B*37:01	DRB1*15:01	DRB1*14:04
447.	A*02:01	A*24:02	B*40:06	B*51:01	DRB1*11:01	DRB1*15:01
448.	A*24:02	A*68:01	B*52:01	B*56:01	DRB1*04:03	DRB1*07:01
449.	A*23:01	A*24:07	B*13:01	B*52:01	DRB1*15:01	DRB1*16:02
450.	A*24:02	A*24:02	B*07:05	B*07:05	DRB1*04:03	DRB1*08:02
451.	A*24:02	A*24:02	B*52:01	B*58:01	DRB1*15:01	DRB1*15:01
452.	A*11:01	A*30:01	B*13:02	B*35:03	DRB1*15:01	DRB1*15:02
453.	A*02:11	A*03:01	B*07:02	B*15:01	DRB1*01:01	DRB1*07:01
454.	A*24:02	A*31:01	B*35:01	B*51:01	DRB1*04:03	DRB1*11:01
455.	A*11:01	A*24:02	B*07:05	B*07:05	DRB1*01:01	DRB1*01:01
456.	A*11:01	A*32:01	B*40:06	B*58:01	DRB1*15:01	DRB1*15:01
457.	A*24:02	A*29:01	B*07:05	B*07:05	DRB1*04:01	DRB1*14:04
458.	A*02:01	A*33:03	B*07:05	B*58:01	DRB1*04:05	DRB1*15:01
459.	A*02:01	A*33:01	B*07:02	B*35:01	DRB1*10:01	DRB1*15:01
460.	A*68:02	A*33:01	B*08:01	B*58:01	DRB1*04:03	DRB1*07:01
461.	A*02:11	A*11:01	B*13:01	B*35:03	DRB1*03:01	DRB1*03:01
462.	A*02:11	A*24:02	B*07:05	B*07:05	DRB1*04:03	DRB1*15:01
463.	A*01:01	A*23:01	B*08:01	B*44:03	DRB1*04:01	DRB1*07:01
464.	A*66:01	A*68:01	B*52:01	B*55:01	DRB1*08:03	DRB1*15:01
465.	A*24:02	A*33:03	B*07:02	B*51:01	DRB1*04:08	DRB1*13:02
466.	A*11:01	A*24:02	B*07:05	B*07:05	DRB1*04:10	DRB1*14:04

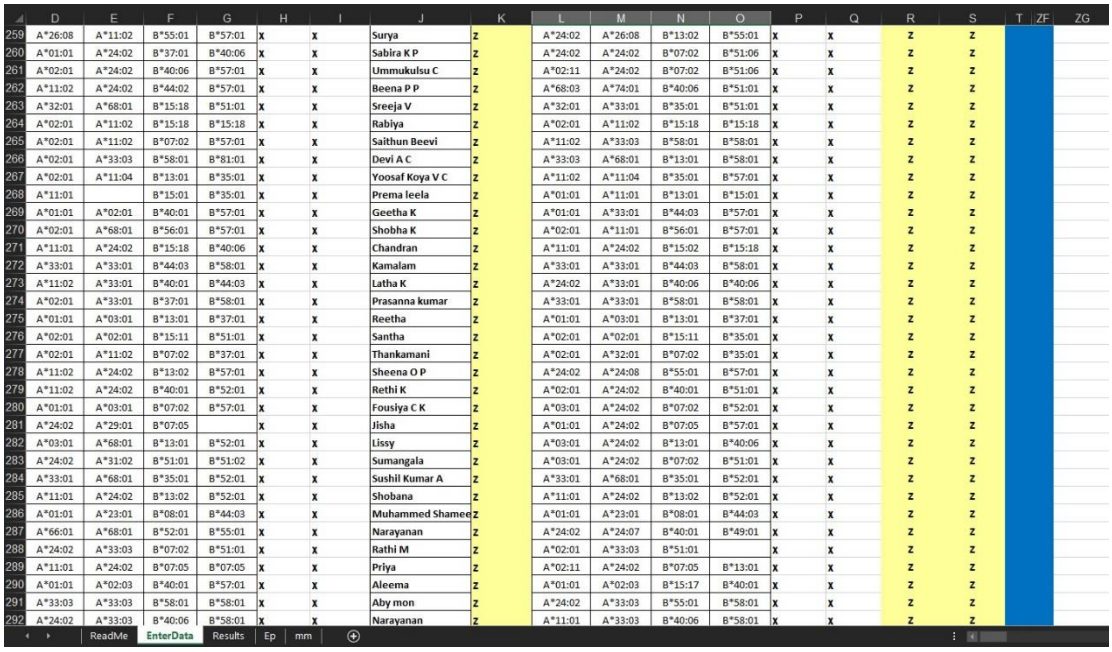
467.	A*01:01	A*02:03	B*40:01	B*57:01	DRB1*08:03	DRB1*13:02
468.	A*33:03	A*33:03	B*58:01	B*58:01	DRB1*13:02	DRB1*14:04
469.	A*24:02	A*33:03	B*40:06	B*58:01	DRB1*15:01	DRB1*15:01
470.	A*11:01	A*33:03	B*44:03	B*07:05	DRB1*07:01	DRB1*14:04
471.	A*33:03	A*68:01	B*14:02	B*40:01	DRB1*01:02	DRB1*15:04
472.	A*02:01	A*24:02	B*40:06	B*58:01	DRB1*14:04	DRB1*15:02
473.	A*02:11	A*33:03	B*40:06	B*44:03	DRB1*13:01	DRB1*13:01
474.	A*03:01	A*32:01	B*07:02	B*35:01	DRB1*11:01	DRB1*15:02
475.	A*24:02	A*68:01	B*35:01	B*55:01	DRB1*04:03	DRB1*13:01
476.	A*11:01	A*11:02	B*58:01	B*58:01	DRB1*13:02	x
477.	A*03:01	A*11:01	B*15:02	B*57:01	DRB1*07:01	DRB1*12:02
478.	A*24:02	A*29:03	B*07:05	B*56:01	DRB1*14:04	DRB1*15:04
479.	A*01:01	A*32:01	B*35:01	B*52:01	DRB1*04:03	DRB1*15:04
480.	A*02:11	A*11:01	B*07:05	B*51:01	DRB1*04:03	DRB1*14:04
481.	A*01:01	A*24:02	B*35:01	B*38:02	DRB1*04:03	DRB1*15:04
482.	A*02:01	A*24:02	B*40:01	B*51:01	DRB1*04:01	DRB1*14:04
483.	A*33:03	A*02:11	B*40:06	B*57:03	DRB1*10:01	DRB1*15:02
484.	A*02:01	A*26:01	B*07:02	B*40:06	DRB1*07:01	DRB1*13:02
485.	A*02:11	A*33:03	B*40:06	B*44:03	DRB1*07:01	DRB1*15:01
486.	A*33:01	A*68:01	B*52:01	B*57:03	DRB1*07:01	DRB1*15:01
487.	A*02:11	A*26:01	B*07:05	B*57:01	DRB1*01:01	DRB1*04:03
488.	A*02:01	A*03:02	B*18:01	B*41:01	DRB1*04:03	DRB1*04:04
489.	A*01:01	A*11:01	B*52:01	B*57:01	DRB1*04:03	DRB1*15:02
490.	A*03:01	A*11:01	B*35:01	B*37:01	DRB1*13:01	DRB1*15:02
491.	A*01:01	A*02:01	B*40:01	B*57:01	DRB1*03:01	DRB1*07:01
492.	A*11:01	A*24:10	B*40:06	B*52:01	DRB1*04:03	DRB1*15:01
493.	A*26:01	A*31:01	B*40:01	B*56:01	DRB1*01:01	DRB1*11:01
494.	A*29:01	A*33:01	B*44:03	B*44:03	DRB1*07:01	DRB1*13:01
495.	A*24:02	A*32:01	B*35:01	B*52:01	DRB1*01:01	DRB1*04:03
496.	A*01:01	A*26:01	B*37:01	B*51:01	DRB1*04:03	DRB1*10:01
497.	A*02:01	A*11:01	B*15:02	B*40:06	DRB1*07:01	DRB1*15:01
498.	A*24:02	A*24:03	B*35:03	B*58:01	DRB1*14:04	DRB1*14:04
499.	A*02:01	A*11:01	B*07:02	B*44:03	DRB1*07:01	DRB1*10:01
500.	A*24:02	A*32:01	B*35:01	B*51:01	DRB1*01:01	DRB1*14:04
501.	A*01:01	A*24:02	B*35:01	B*37:01	DRB1*10:01	DRB1*15:01
502.	A*11:01	A*34:02	B*07:05	B*58:01	DRB1*14:04	x
503.	A*03:01	A*11:01	B*18:01	B*35:01	DRB1*13:01	DRB1*15:01
504.	A*11:01	A*24:02	B*15:18	B*40:06	DRB1*07:01	DRB1*15:01
505.	A*33:01	A*33:01	B*44:03	B*58:01	DRB1*07:01	DRB1*13:01
506.	A*11:02	A*33:01	B*40:01	B*44:03	DRB1*07:01	DRB1*14:04
507.	A*02:01	A*33:01	B*37:01	B*58:01	DRB1*10:01	DRB1*13:01
508.	A*01:01	A*03:01	B*13:01	B*37:01	DRB1*10:01	DRB1*15:01
509.	A*02:01	A*02:01	B*15:11	B*51:01	DRB1*01:01	DRB1*13:01
510.	A*02:01	A*11:02	B*07:02	B*37:01	DRB1*04:03	DRB1*15:01
511.	A*11:02	A*24:02	B*13:02	B*57:01	DRB1*07:01	DRB1*14:04
512.	A*11:02	A*24:02	B*40:01	B*52:01	DRB1*04:01	DRB1*04:03
513.	A*01:01	A*03:01	B*07:02	B*57:01	DRB1*07:01	DRB1*10:01

514.	A*24:02	A*29:01	B*07:05	x	DRB1*10:01	DRB1*15:01
515.	A*03:01	A*68:01	B*13:01	B*52:01	DRB1*07:01	DRB1*12:01
516.	A*24:02	A*31:02	B*51:01	B*51:02	DRB1*01:01	DRB1*07:01
517.	A*33:01	A*68:01	B*35:01	B*52:01	DRB1*01:01	DRB1*07:01
518.	A*11:01	A*24:02	B*13:02	B*52:01	DRB1*07:01	DRB1*07:01
519.	A*01:01	A*23:01	B*08:01	B*44:03	DRB1*04:01	DRB1*07:01
520.	A*66:01	A*68:01	B*52:01	B*55:01	DRB1*08:03	DRB1*15:01
521.	A*24:02	A*33:03	B*07:02	B*51:01	DRB1*04:08	DRB1*13:02
522.	A*11:01	A*24:02	B*07:05	B*07:05	DRB1*04:10	DRB1*14:04
523.	A*01:01	A*02:03	B*40:01	B*57:01	DRB1*08:03	DRB1*13:02
524.	A*24:02	A*26:01	B*52:01	B*55:01	DRB1*04:03	DRB1*07:01
525.	A*11:01	A*11:01	B*07:05	B*40:01	DRB1*04:01	DRB1*14:01
526.	A*02:01	A*32:01	B*07:02	B*48:01	DRB1*12:02	DRB1*15:02
527.	A*01:01	A*11:01	B*07:05	B*15:17	DRB1*13:02	DRB1*14:04
528.	A*02:11	A*24:02	B*07:05	B*51:01	DRB1*04:03	DRB1*04:05
529.	A*11:01	A*11:01	B*13:01	B*52:01	DRB1*04:03	DRB1*07:01
530.	A*03:01	A*33:03	B*40:06	B*44:03	DRB1*07:01	DRB1*14:04
531.	A*33:03	A*68:01	B*44:03	B*52:01	DRB1*07:01	DRB1*15:02
532.	A*02:11	A*33:03	B*35:03	B*44:03	DRB1*07:01	DRB1*08:03
533.	A*32:01	A*68:01	B*40:01	B*51:01	DRB1*10:01	DRB1*13:01
534.	A*01:01	A*33:03	B*44:03	B*57:01	DRB1*07:01	x
535.	A*02:01	A*24:02	B*15:18	B*51:01	DRB1*04:01	DRB1*04:03
536.	A*11:01	A*32:01	B*35:01	B*40:06	DRB1*11:01	DRB1*11:01
537.	A*24:02	A*31:01	B*35:01	B*51:01	DRB1*04:03	DRB1*11:01
538.	A*11:01	A*24:02	B*07:05	B*07:05	DRB1*01:01	DRB1*01:01
539.	A*11:01	A*32:01	B*40:06	B*58:01	DRB1*15:01	DRB1*15:01
540.	A*24:02	A*29:01	B*07:05	B*07:05	DRB1*04:01	DRB1*14:04
541.	A*02:01	A*33:03	B*07:05	B*58:01	DRB1*04:05	DRB1*15:01
542.	A*02:01	A*33:01	B*07:02	B*35:01	DRB1*10:01	DRB1*15:01
543.	A*68:02	A*33:01	B*08:01	B*58:01	DRB1*04:03	DRB1*07:01
544.	A*11:01	A*32:01	B*35:01	B*40:06	DRB1*11:01	DRB1*11:01
545.	A*02:01	A*11:01	B*40:01	B*07:05	DRB1*15:01	DRB1*14:04
546.	A*01:01	A*24:02	B*37:01	B*44:02	DRB1*07:01	DRB1*10:01
547.	A*01:01	A*24:02	B*35:01	B*52:01	DRB1*12:04	DRB1*13:02
548.	A*11:01	A*11:01	B*07:05	B*51:01	DRB1*04:03	DRB1*07:01
549.	A*11:01	A*24:02	B*15:05	B*35:03	DRB1*14:04	DRB1*15:01
550.	A*11:01	A*33:03	B*35:01	B*58:01	DRB1*04:02	DRB1*08:02
551.	A*02:01	A*02:01	B*07:05	B*58:01	DRB1*03:01	DRB1*15:01
552.	A*01:01	A*24:02	B*07:02	B*57:03	DRB1*14:04	DRB1*14:04
553.	A*11:01	A*24:02	B*07:02	B*13:01	DRB1*07:01	DRB1*07:01
554.	A*11:01	A*33:03	B*37:01	B*58:01	DRB1*15:02	DRB1*15:02
555.	A*01:01	A*33:03	B*44:03	B*57:01	DRB1*03:01	DRB1*10:01
556.	A*02:01	A*68:01	B*15:01	B*18:01	DRB1*04:03	DRB1*07:01
557.	A*02:01	A*33:03	B*35:03	B*44:03	DRB1*11:01	DRB1*11:01
558.	A*24:02	A*31:02	B*07:02	B*51:04	DRB1*07:01	DRB1*08:03
559.	A*02:01	A*02:11	B*07:02	B*40:06	DRB1*14:04	DRB1*15:02
560.	A*24:02	A*31:01	B*35:01	B*40:01	DRB1*01:01	DRB1*15:02

561.	A*11:01	A*24:02	B*13:01	B*51:01	DRB1*13:02	DRB1*14:04
562.	A*02:01	A*11:01	B*15:18	B*40:01	DRB1*04:10	DRB1*15:01
563.	A*24:07	A*33:03	B*07:02	B*37:01	DRB1*04:03	DRB1*15:01
564.	A*02:01	A*11:01	B*07:05	B*35:03	DRB1*01:01	DRB1*10:01
565.	A*02:01	A*11:01	B*07:05	B*40:02	DRB1*15:01	DRB1*15:01
566.	A*24:02	A*33:03	B*51:01	B*58:01	DRB1*12:02	DRB1*14:04
567.	A*24:02	A*33:03	B*15:02	B*44:03	DRB1*03:01	DRB1*04:03
568.	A*03:01	A*24:02	B*15:18	B*40:06	DRB1*04:03	DRB1*04:05
569.	A*24:02	A*68:01	B*40:06	B*51:01	DRB1*04:03	DRB1*07:01
570.	A*02:01	A*03:01	B*35:01	B*57:01	DRB1*04:03	DRB1*04:04
571.	A*02:01	A*24:02	B*07:02	B*52:01	DRB1*04:03	DRB1*15:02
572.	A*11:01	A*30:01	B*13:02	B*35:01	DRB1*07:01	DRB1*15:01

Annexure III

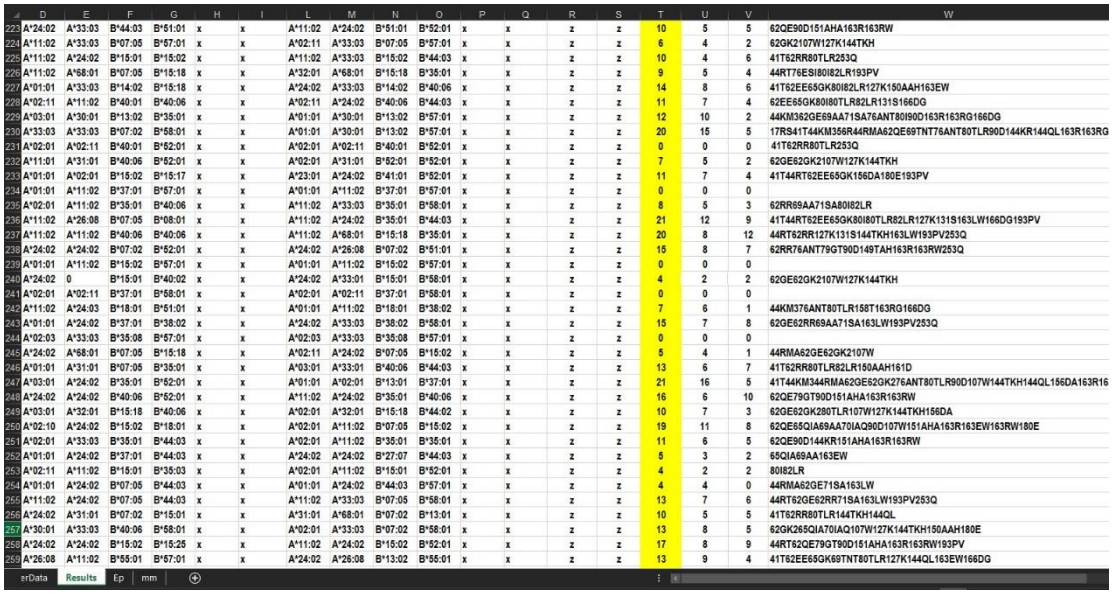
Figure 26-33 represents the interface of the HLA Matchmaker (V2.2, 2018) with which the total number of HLA ABDR eplet mismatches between a donor and a recipient has been calculated



	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	ZF	ZG
259	A*26:08	A*11:02	B*55:01	B*57:01	x	x	Surya	z	A*24:02	A*26:08	B*13:02	B*55:01	x	x	z	z			
260	A*01:01	A*24:02	B*37:01	B*40:06	x	x	Sabira K P	z	A*24:02	A*24:02	B*07:02	B*51:06	x	x	z	z			
261	A*02:01	A*24:02	B*40:06	B*57:01	x	x	Ummukulsu C	z	A*02:11	A*24:02	B*07:02	B*51:06	x	x	z	z			
262	A*11:02	A*24:02	B*44:02	B*57:01	x	x	Beena P P	z	A*68:03	A*74:01	B*40:06	B*51:01	x	x	z	z			
263	A*32:01	A*68:01	B*15:18	B*51:01	x	x	Sreeja V	z	A*32:01	A*33:01	B*35:01	B*51:01	x	x	z	z			
264	A*02:01	A*11:02	B*15:18	B*15:18	x	x	Rabiya	z	A*02:01	A*11:02	B*15:18	B*15:18	x	x	z	z			
265	A*02:01	A*11:02	B*07:02	B*57:01	x	x	Saithun Beevi	z	A*11:02	A*33:03	B*58:01	B*58:01	x	x	z	z			
266	A*02:01	A*33:03	B*58:01	B*81:01	x	x	Devi A C	z	A*33:03	A*68:01	B*13:01	B*58:01	x	x	z	z			
267	A*02:01	A*11:04	B*13:01	B*35:01	x	x	Yoosaf Koya V C	z	A*11:02	A*11:04	B*35:01	B*57:01	x	x	z	z			
268	A*11:01		B*15:01	B*35:01	x	x	Prema leela	z	A*01:01	A*11:01	B*13:01	B*15:01	x	x	z	z			
269	A*01:01	A*02:01	B*40:01	B*57:01	x	x	Geetha K	z	A*01:01	A*33:01	B*44:03	B*57:01	x	x	z	z			
270	A*02:01	A*68:01	B*56:01	B*57:01	x	x	Shobha K	z	A*02:01	A*11:01	B*56:01	B*57:01	x	x	z	z			
271	A*11:01	A*24:02	B*15:18	B*40:06	x	x	Chandran	z	A*11:01	A*24:02	B*15:02	B*15:18	x	x	z	z			
272	A*33:01	A*33:01	B*44:03	B*58:01	x	x	Kamalam	z	A*33:01	A*33:01	B*44:03	B*58:01	x	x	z	z			
273	A*11:02	A*33:01	B*40:01	B*44:03	x	x	Latha K	z	A*24:02	A*33:01	B*40:06	B*40:06	x	x	z	z			
274	A*02:01	A*33:01	B*37:01	B*58:01	x	x	Prasanna kumar	z	A*33:01	A*33:01	B*58:01	B*58:01	x	x	z	z			
275	A*01:01	A*03:01	B*13:01	B*37:01	x	x	Reetha	z	A*01:01	A*03:01	B*13:01	B*37:01	x	x	z	z			
276	A*02:01	A*02:01	B*15:11	B*51:01	x	x	Santha	z	A*02:01	A*02:01	B*15:11	B*35:01	x	x	z	z			
277	A*02:01	A*11:02	B*07:02	B*37:01	x	x	Thankamani	z	A*02:01	A*32:01	B*07:02	B*35:01	x	x	z	z			
278	A*11:02	A*24:02	B*13:02	B*57:01	x	x	Sheena O P	z	A*24:02	A*24:08	B*55:01	B*57:01	x	x	z	z			
279	A*11:02	A*24:02	B*40:01	B*52:01	x	x	Rethi K	z	A*02:01	A*24:02	B*40:01	B*51:01	x	x	z	z			
280	A*01:01	A*03:01	B*07:02	B*57:01	x	x	Fousiya C K	z	A*03:01	A*24:02	B*07:02	B*52:01	x	x	z	z			
281	A*24:02	A*29:01	B*07:05		x	x	Jisha	z	A*01:01	A*24:02	B*07:05	B*57:01	x	x	z	z			
282	A*03:01	A*68:01	B*13:01	B*52:01	x	x	Lissy	z	A*03:01	A*24:02	B*13:01	B*40:06	x	x	z	z			
283	A*24:02	A*31:02	B*51:01	B*51:02	x	x	Sumangala	z	A*03:01	A*24:02	B*07:02	B*51:01	x	x	z	z			
284	A*33:01	A*68:01	B*35:01	B*52:01	x	x	Sushil Kumar A	z	A*33:01	A*68:01	B*35:01	B*52:01	x	x	z	z			
285	A*11:01	A*24:02	B*13:02	B*52:01	x	x	Shobana	z	A*11:01	A*24:02	B*13:02	B*52:01	x	x	z	z			
286	A*01:01	A*23:01	B*08:01	B*44:03	x	x	Muhammed Shamee	z	A*01:01	A*23:01	B*08:01	B*44:03	x	x	z	z			
287	A*66:01	A*68:01	B*52:01	B*55:01	x	x	Narayanan	z	A*24:02	A*24:07	B*40:01	B*49:01	x	x	z	z			
288	A*24:02	A*33:03	B*07:02	B*51:01	x	x	Rathi M	z	A*02:01	A*33:03	B*51:01		x	x	z	z			
289	A*11:01	A*24:02	B*07:05	B*07:05	x	x	Priya	z	A*02:11	A*24:02	B*07:05	B*13:01	x	x	z	z			
290	A*01:01	A*02:03	B*40:01	B*57:01	x	x	Aleema	z	A*01:01	A*02:03	B*15:17	B*40:01	x	x	z	z			
291	A*33:03	A*33:03	B*58:01	B*58:01	x	x	Aby mon	z	A*24:02	A*33:03	B*55:01	B*58:01	x	x	z	z			
292	A*24:02	A*33:03	B*40:06	B*58:01	x	x	Narayanan	z	A*11:01	A*33:03	B*40:06	B*58:01	x	x	z	z			

ReadMe | EnterData | Results | Ep | mm

Figure 26: Image of HLA AB allele data of patients and donors entered in the HLA Matchmaker



	D	E	F	G	H	I	L	M	N	O	P	Q	R	S	T	U	V	W
225	A*24:02	A*33:03	B*44:03	B*51:01	x	x	A*11:02	A*24:02	B*51:01	B*52:01	x	x	z	z	10	5	5	62QE90D151AHA163R163RW
226	A*11:02	A*33:03	B*07:05	B*57:01	x	x	A*02:11	A*33:03	B*07:05	B*57:01	x	x	z	z	6	4	2	62GK2107W127K144TKH
227	A*11:02	A*24:02	B*15:01	B*15:02	x	x	A*11:02	A*33:03	B*15:02	B*44:03	x	x	z	z	10	4	6	41T62RR80TLR253Q
228	A*11:02	A*68:01	B*07:05	B*15:18	x	x	A*32:01	A*68:01	B*15:18	B*35:01	x	x	z	z	9	5	4	44RT76ESI80I82LR193PV
229	A*01:01	A*33:03	B*14:02	B*15:18	x	x	A*24:02	A*33:03	B*14:02	B*40:06	x	x	z	z	14	8	6	41T62EE65GK80I82LR127K150AAH163EW
230	A*02:11	A*11:02	B*40:01	B*40:06	x	x	A*02:11	A*24:02	B*40:06	B*44:03	x	x	z	z	11	7	4	62EE65GK80I80TLR82LR131S166DG
231	A*03:01	A*30:01	B*13:02	B*35:01	x	x	A*01:01	A*30:01	B*13:02	B*57:01	x	x	z	z	12	10	2	44KM362GE69AA71SA76ANT80I90D163R163RG166DG
232	A*33:03	A*33:03	B*07:02	B*58:01	x	x	A*01:01	A*30:01	B*13:02	B*57:01	x	x	z	z	20	15	5	17RS41T44KM356R44RMA62QE69TNT76ANT80TLR90D144KR144QL163R163RG
233	A*02:01	A*02:11	B*40:01	B*52:01	x	x	A*02:01	A*02:11	B*40:01	B*52:01	x	x	z	z	0	0	0	41T62RR80TLR253Q
234	A*11:01	A*31:01	B*40:06	B*62:01	x	x	A*02:01	A*31:01	B*52:01	B*62:01	x	x	z	z	7	5	2	62GE62GK2107W127K144TKH
235	A*01:01	A*02:01	B*15:02	B*15:17	x	x	A*23:01	A*24:02	B*41:01	B*52:01	x	x	z	z	11	7	4	41T44RT62EE65GK166DA180E193PV
236	A*01:01	A*11:02	B*37:01	B*57:01	x	x	A*01:01	A*11:02	B*37:01	B*57:01	x	x	z	z	0	0	0	
237	A*02:01	A*11:02	B*35:01	B*40:06	x	x	A*11:02	A*33:03	B*35:01	B*58:01	x	x	z	z	8	5	3	62RR69AA71SA80I82LR
238	A*11:02	A*26:08	B*07:05	B*08:01	x	x	A*11:02	A*24:02	B*35:01	B*44:03	x	x	z	z	21	12	9	41T44RT62EE65GK80I80TLR82LR127K131S163LW166DG193PV
239	A*11:02	A*11:02	B*40:06	B*40:06	x	x	A*11:02	A*68:01	B*15:18	B*35:01	x	x	z	z	20	8	12	44RT62RR127K131S144TKH163LW193PV253Q
240	A*24:02	A*24:02	B*07:02	B*62:01	x	x	A*24:02	A*26:08	B*07:02	B*51:01	x	x	z	z	15	8	7	62RR76ANT79GT90D149TAH163R163RW253Q
241	A*01:01	A*11:02	B*15:02	B*57:01	x	x	A*01:01	A*11:02	B*15:02	B*57:01	x	x	z	z	0	0	0	
242	A*24:02	0	B*15:01	B*40:02	x	x	A*24:02	A*33:01	B*15:01	B*58:01	x	x	z	z	4	2	2	62GE62GK2107W127K144TKH
243	A*02:01	A*02:11	B*37:01	B*58:01	x	x	A*02:01	A*02:11	B*37:01	B*58:01	x	x	z	z	0	0	0	
244	A*11:02	A*24:03	B*18:01	B*51:01	x	x	A*01:01	A*11:02	B*18:01	B*38:02	x	x	z	z	7	6	1	44KM376ANT80TLR158T163RG166DG
245	A*01:01	A*24:02	B*37:01	B*38:02	x	x	A*24:02	A*33:03	B*38:02	B*58:01	x	x	z	z	15	7	8	62GE62RR69AA71SA163LW193PV253Q
246	A*02:03	A*33:03	B*35:08	B*57:01	x	x	A*02:03	A*33:03	B*35:08	B*57:01	x	x	z	z	0	0	0	
247	A*24:02	A*68:01	B*07:05	B*15:18	x	x	A*02:11	A*24:02	B*07:05	B*15:02	x	x	z	z	5	4	1	44RMA62GE62GK2107W
248	A*01:01	A*31:01	B*07:05	B*35:01	x	x	A*03:01	A*33:01	B*40:06	B*44:03	x	x	z	z	13	6	7	41T62RR80TLR82LR150AAH161D
249	A*03:01	A*24:02	B*35:01	B*62:01	x	x	A*01:01	A*02:01	B*13:01	B*37:01	x	x	z	z	21	16	5	41T44KM344RMA62GE62GK276ANT80TLR90D107W144TKH144QL156DA163R16
250	A*24:02	A*24:02	B*40:06	B*52:01	x	x	A*11:02	A*24:02	B*35:01	B*40:06	x	x	z	z	16	6	10	62QE79GT90D151AHA163R163RW
251	A*03:01	A*32:01	B*15:18	B*40:06	x	x	A*02:01	A*32:01	B*15:18	B*44:02	x	x	z	z	10	7	3	62GE62GK280TLR107W127K144TKH156DA
252	A*02:10	A*24:02	B*15:02	B*18:01	x	x	A*02:01	A*11:02	B*07:05	B*15:02	x	x	z	z	19	11	8	62QE65QIA69AA70IAQ90D107W151AHA163R163EW163RW180E
253	A*02:01	A*33:03	B*35:01	B*44:03	x	x	A*02:01	A*11:02	B*35:01	B*35:01	x	x	z	z	11	6	5	62QE90D144KR151AHA163R163RW
254	A*01:01	A*24:02	B*37:01	B*44:03	x	x	A*24:02	A*24:02	B*27:07	B*44:03	x	x	z	z	5	3	2	65QIA69AA163EW
255	A*02:11	A*11:02	B*18:01	B*35:03	x	x	A*02:01	A*11:02	B*15:01	B*52:01	x	x	z	z	4	2	2	80I82LR
256	A*01:01	A*24:02	B*07:05	B*44:03	x	x	A*01:01	A*24:02	B*44:03	B*57:01	x	x	z	z	4	4	0	44RMA62GE71SA163LW
257	A*11:02	A*24:02	B*07:05	B*44:03	x	x	A*11:02	A*33:03	B*07:05	B*58:01	x	x	z	z	13	7	6	44RT62GE62RR71SA163LW193PV253Q
258	A*24:02	A*31:01	B*07:02	B*15:01	x	x	A*31:01	A*68:01	B*07:02	B*13:01	x	x	z	z	10	5	5	41T62RR80TLR144TKH144QL
259	A*30:01	A*33:03	B*40:06	B*58:01	x	x	A*02:01	A*33:03	B*07:02	B*58:01	x	x	z	z	13	8	5	62GK265QIA70IAQ107W127K144TKH150AAH180E
260	A*24:02	A*24:02	B*15:02	B*15:25	x	x	A*11:02	A*24:02	B*15:02	B*52:01	x	x	z	z	17	8	9	44RT62QE79GT90D151AHA163R163RW193PV
261	A*26:08	A*11:02	B*55:01	B*67:01	x	x	A*24:02	A*26:08	B*13:02	B*55:01	x	x	z	z	13	9	4	41T62EE65GK69TNT80TLR127K144QL163EW166DG

erData | Results | Ep | mm

Figure 27: Image of HLA AB eplet mismatches generated in HLA Matchmaker

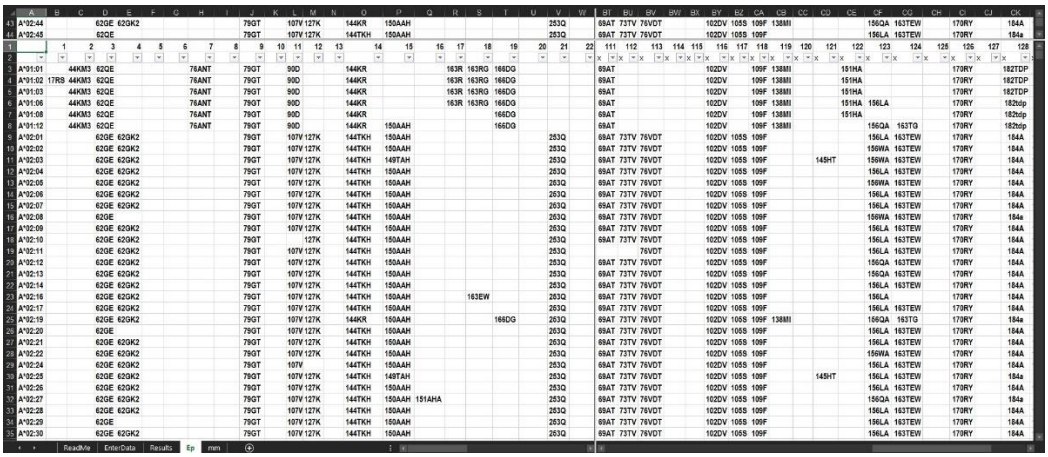
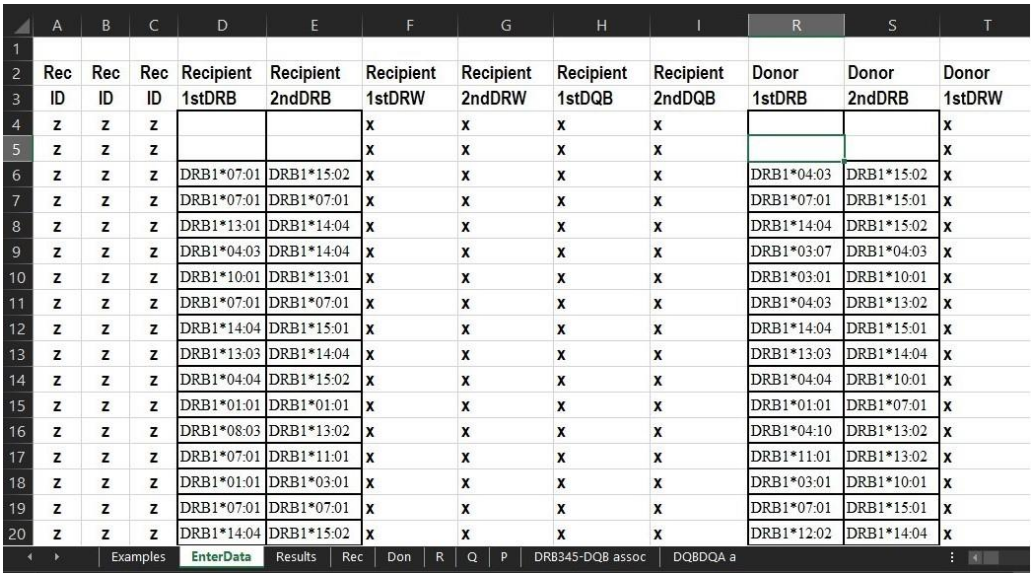
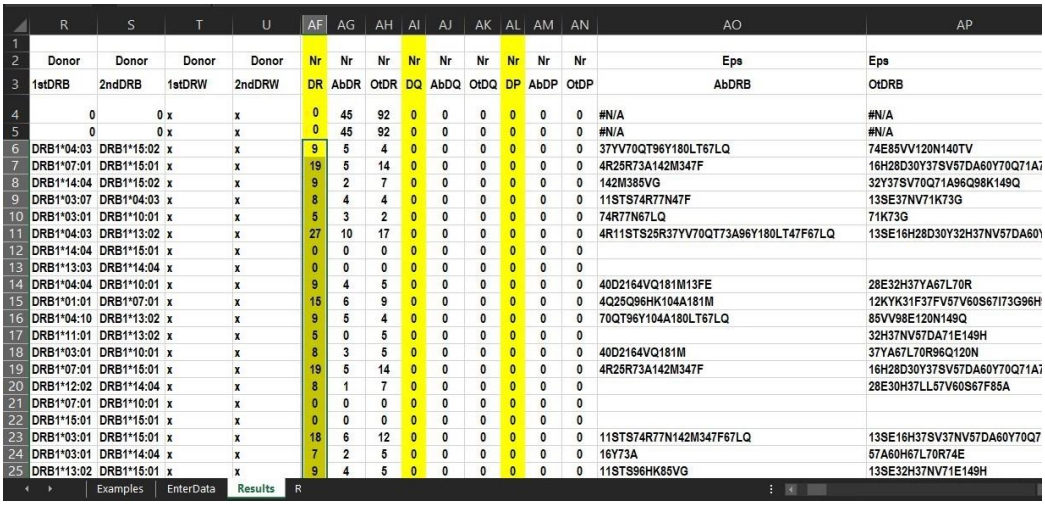


Figure 28: Image of HLA ABC eplet database in the HLA Matchmaker



	A	B	C	D	E	F	G	H	I	R	S	T
1												
2	Rec	Rec	Rec	Recipient	Recipient	Recipient	Recipient	Recipient	Recipient	Donor	Donor	Donor
3	ID	ID	ID	1stDRB	2ndDRB	1stDRW	2ndDRW	1stDQB	2ndDQB	1stDRB	2ndDRB	1stDRW
4	z	z	z			x	x	x	x			x
5	z	z	z			x	x	x	x			x
6	z	z	z	DRB1*07:01	DRB1*15:02	x	x	x	x	DRB1*04:03	DRB1*15:02	x
7	z	z	z	DRB1*07:01	DRB1*07:01	x	x	x	x	DRB1*07:01	DRB1*15:01	x
8	z	z	z	DRB1*13:01	DRB1*14:04	x	x	x	x	DRB1*14:04	DRB1*15:02	x
9	z	z	z	DRB1*04:03	DRB1*14:04	x	x	x	x	DRB1*03:07	DRB1*04:03	x
10	z	z	z	DRB1*10:01	DRB1*13:01	x	x	x	x	DRB1*03:01	DRB1*10:01	x
11	z	z	z	DRB1*07:01	DRB1*07:01	x	x	x	x	DRB1*04:03	DRB1*13:02	x
12	z	z	z	DRB1*14:04	DRB1*15:01	x	x	x	x	DRB1*14:04	DRB1*15:01	x
13	z	z	z	DRB1*13:03	DRB1*14:04	x	x	x	x	DRB1*13:03	DRB1*14:04	x
14	z	z	z	DRB1*04:04	DRB1*15:02	x	x	x	x	DRB1*04:04	DRB1*10:01	x
15	z	z	z	DRB1*01:01	DRB1*01:01	x	x	x	x	DRB1*01:01	DRB1*07:01	x
16	z	z	z	DRB1*08:03	DRB1*13:02	x	x	x	x	DRB1*04:10	DRB1*13:02	x
17	z	z	z	DRB1*07:01	DRB1*11:01	x	x	x	x	DRB1*11:01	DRB1*13:02	x
18	z	z	z	DRB1*01:01	DRB1*03:01	x	x	x	x	DRB1*03:01	DRB1*10:01	x
19	z	z	z	DRB1*07:01	DRB1*07:01	x	x	x	x	DRB1*07:01	DRB1*15:01	x
20	z	z	z	DRB1*14:04	DRB1*15:02	x	x	x	x	DRB1*12:02	DRB1*14:04	x

Figure 29: Image of HLA DRB1 allele data of patients and donors entered in HLA Matchmaker



	R	S	T	U	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP
1															
2	Donor	Donor	Donor	Donor	Nr	Nr	Nr	Nr	Nr	Nr	Nr	Nr	Nr	Eps	Eps
3	1stDRB	2ndDRB	1stDRW	2ndDRW	DR	AbDR	OtDR	DQ	AbDQ	OtDQ	DP	AbDP	OtDP	AbDRB	OtDRB
4	0	0	x	x	0	45	92	0	0	0	0	0	0	#N/A	#N/A
5	0	0	x	x	0	45	92	0	0	0	0	0	0	#N/A	#N/A
6	DRB1*04:03	DRB1*15:02	x	x	9	5	4	0	0	0	0	0	0	37YV70QT96Y180LT67LQ	74E85VV120N140TV
7	DRB1*07:01	DRB1*15:01	x	x	19	5	14	0	0	0	0	0	0	4R25R73A142M347F	16H28D30Y37SV57DA60Y70Q71A7
8	DRB1*14:04	DRB1*15:02	x	x	9	2	7	0	0	0	0	0	0	142M385VG	32Y37SV70Q71A96Q98K149Q
9	DRB1*03:07	DRB1*04:03	x	x	8	4	4	0	0	0	0	0	0	11STS74R77N47F	13SE37NV71K73G
10	DRB1*03:01	DRB1*10:01	x	x	5	3	2	0	0	0	0	0	0	74R77N67LQ	71K73G
11	DRB1*04:03	DRB1*13:02	x	x	27	10	17	0	0	0	0	0	0	4R11STS25R37YV70QT73A96Y180LT47F67LQ	13SE16H28D30Y32H37NV57DA60
12	DRB1*14:04	DRB1*15:01	x	x	0	0	0	0	0	0	0	0	0		
13	DRB1*13:03	DRB1*14:04	x	x	0	0	0	0	0	0	0	0	0		
14	DRB1*04:04	DRB1*10:01	x	x	9	4	5	0	0	0	0	0	0	40D2164VQ181M13FE	28E32H37YA67L70R
15	DRB1*01:01	DRB1*07:01	x	x	15	6	9	0	0	0	0	0	0	4Q25Q96HK104A181M	12KYK31F37FV57V60S67I73G96H
16	DRB1*04:10	DRB1*13:02	x	x	9	5	4	0	0	0	0	0	0	70QT96Y104A180LT67LQ	85VV98E120N149Q
17	DRB1*11:01	DRB1*13:02	x	x	5	0	5	0	0	0	0	0	0		32H37NV57DA71E149H
18	DRB1*03:01	DRB1*10:01	x	x	8	3	5	0	0	0	0	0	0	40D2164VQ181M	37YA67L70R96Q120N
19	DRB1*07:01	DRB1*15:01	x	x	19	5	14	0	0	0	0	0	0	4R25R73A142M347F	16H28D30Y37SV57DA60Y70Q71A7
20	DRB1*12:02	DRB1*14:04	x	x	8	1	7	0	0	0	0	0	0		28E30H37LL57V60S67F85A
21	DRB1*07:01	DRB1*10:01	x	x	0	0	0	0	0	0	0	0	0		
22	DRB1*15:01	DRB1*15:01	x	x	0	0	0	0	0	0	0	0	0		
23	DRB1*03:01	DRB1*15:01	x	x	18	6	12	0	0	0	0	0	0	11STS74R77N142M347F67LQ	13SE16H37SV37NV57DA60Y70Q7
24	DRB1*03:01	DRB1*14:04	x	x	7	2	5	0	0	0	0	0	0	16Y73A	57A60H67L70R74E
25	DRB1*13:02	DRB1*15:01	x	x	9	4	5	0	0	0	0	0	0	11STS96HK85VG	13SE32H37NV71E149H

Figure 30: Image of HLA DRB1 eplet mismatch results generated in HLA Matchmaker

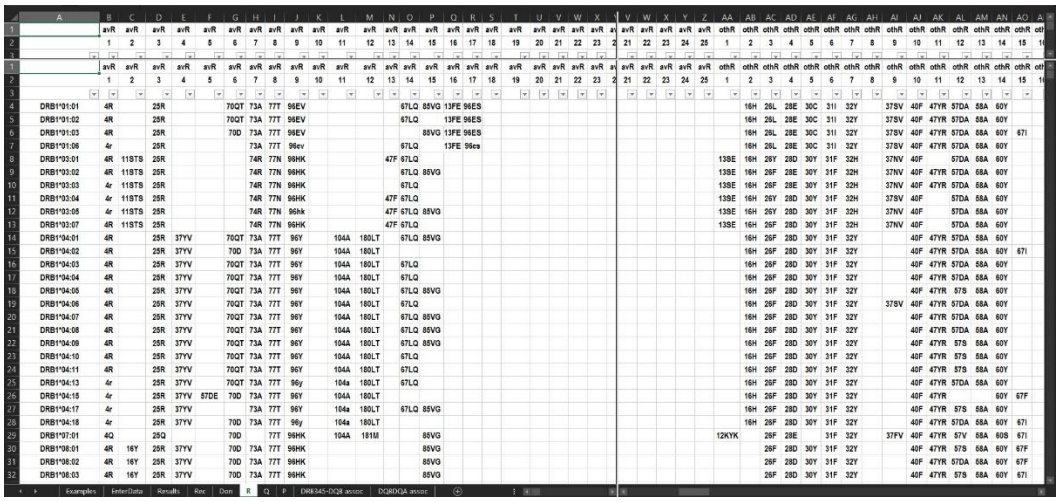


Figure 31: Image of HLA DR eplet database in the HLA Matchmaker

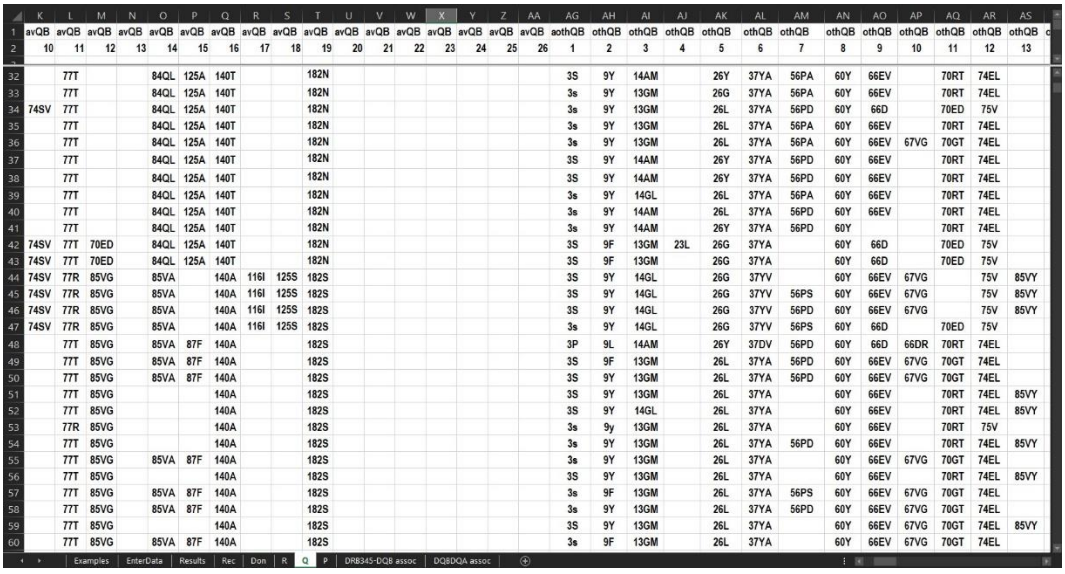


Figure 32: Image of HLA DQ eplet database in the HLA Matchmaker

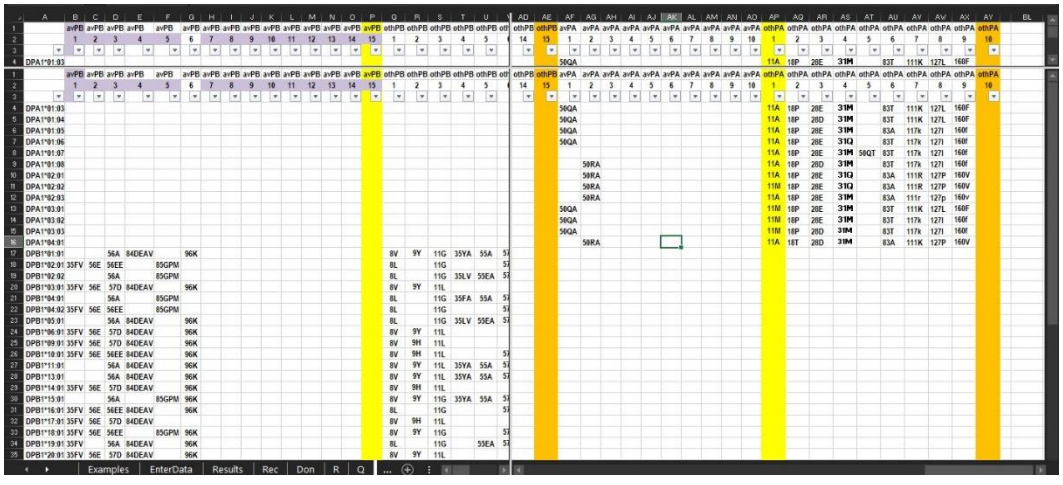


Figure 33: Image of HLA DP eplet database in the HLA Matchmaker

Annexure IV

Table 40: List of number of class I HLA AB and class II HLA DR eplet mismatches obtained after analyzing in ABC Eplet Matching and DRDQDP Eplet Matching

Patient set no.	No. of HLA AB eplet mismatches			No. of HLA DR eplet mismatches		
	Ab-verified eplets	Other eplets	Total eplets	Ab-verified eplets	Other eplets	Total eplets
1)	9	4	13	5	4	9
2)	5	5	10	5	14	19
3)	3	2	5	2	7	9
4)	8	9	17	4	4	8
5)	7	7	14	3	2	5
6)	7	7	14	10	17	27
7)	0	0	0	0	0	0
8)	0	0	0	0	0	0
9)	2	1	3	4	5	9
10)	0	0	0	6	9	15
11)	4	3	7	5	4	9
12)	5	6	11	0	5	5
13)	3	7	10	3	5	8
14)	10	7	17	5	14	19
15)	2	1	3	1	7	8
16)	10	7	17	0	0	0
17)	2	5	7	0	0	0
18)	8	8	16	6	12	18
19)	5	6	11	2	5	7
20)	7	5	12	4	5	9
21)	4	3	7	x	x	x
22)	8	11	19	5	10	15
23)	0	0	0	0	0	0
24)	6	4	10	0	0	0
25)	9	4	13	1	5	6
26)	5	3	8	0	0	0
27)	3	6	9	2	2	4
28)	11	11	22	5	5	10
29)	4	2	6	1	5	6
30)	11	4	15	4	11	15
31)	6	5	11	4	9	13
32)	9	8	17	0	0	0
33)	6	5	11	0	0	0
34)	10	10	20	4	4	8
35)	0	0	0	0	0	0
36)	18	12	30	3	10	13
37)	0	0	0	0	0	0
38)	8	6	14	3	14	17
39)	9	7	16	1	8	9
40)	5	3	8	9	11	20
41)	0	0	0	3	6	9

42)	5	5	10	0	0	0
43)	4	2	6	5	8	13
44)	5	5	10	0	0	0
45)	5	4	9	6	7	13
46)	8	6	14	0	1	1
47)	8	3	11	0	0	0
48)	10	2	12	1	7	8
49)	2	1	3	5	14	19
50)	0	0	0	3	4	7
51)	5	2	7	0	0	0
52)	7	4	11	0	1	1
53)	0	0	0	1	5	6
54)	5	3	8	0	0	0
55)	13	8	21	0	0	0
56)	8	12	20	3	11	14
57)	8	7	15	1	11	12
58)	0	0	0	0	3	3
59)	8	9	17	0	0	0
60)	0	0	0	4	3	7
61)	6	1	7	0	0	0
62)	7	8	15	2	3	5
63)	0	0	0	4	6	10
64)	4	1	5	0	0	0
65)	7	6	13	6	6	12
66)	16	5	21	5	9	14
67)	6	10	16	6	9	15
68)	8	2	10	5	4	9
69)	10	8	18	2	1	3
70)	6	5	11	0	0	0
71)	3	2	5	4	7	11
72)	2	2	4	3	8	11
73)	6	1	7	1	0	1
74)	7	6	13	5	14	19
75)	5	5	10	2	4	6
76)	8	5	13	0	0	0
77)	7	12	19	2	11	13
78)	6	6	12	3	2	5
79)	3	3	6	4	8	12
80)	7	12	19	6	8	14
81)	0	3	3	5	7	12
82)	0	0	0	3	11	14
83)	3	3	6	0	0	0
84)	5	4	9	0	0	0
85)	9	2	11	0	0	0
86)	3	2	5	2	12	14
87)	7	4	11	3	5	8
88)	1	0	1	0	0	0
89)	0	0	0	2	7	9
90)	5	2	7	0	0	0
91)	0	0	0	1	8	9
92)	0	0	0	5	6	11
93)	0	1	1	0	0	0
94)	4	4	8	5	7	12
95)	6	5	11	1	6	7

96)	6	5	11	1	1	2
97)	10	3	13	4	9	13
98)	4	6	10	3	6	9
99)	7	9	16	4	5	9
100)	0	0	0	4	4	8
101)	3	3	6	1	1	2
102)	4	3	7	5	4	9
103)	5	5	10	5	14	19
104)	3	2	5	2	7	9
105)	9	8	17	4	4	8
106)	8	5	13	3	2	5
107)	7	7	14	10	17	27
108)	0	0	0	0	0	0
109)	0	0	0	0	0	0
110)	2	1	3	4	5	9
111)	0	0	0	6	9	15
112)	4	3	7	5	4	9
113)	5	6	11	0	5	5
114)	0	0	0	3	5	8
115)	10	7	17	5	14	19
116)	2	5	7	0	0	0
117)	10	7	17	0	0	0
118)	2	1	3	1	7	8
119)	6	6	12	6	12	18
120)	x	x	x	1	8	9
121)	5	6	11	2	5	7
122)	x	x	x	4	5	9
123)	4	3	7	x	x	x
124)	x	x	x	5	10	15
125)	0	0	0	0	0	0
126)	6	4	10	x	x	x
127)	9	4	13	1	5	6
128)	5	3	8	0	0	0
129)	3	6	9	2	2	4
130)	11	11	22	5	5	10
131)	4	2	6	1	5	6
132)	11	4	15	4	11	15
133)	3	6	9	6	7	13
134)	4	9	13	6	2	8
135)	2	0	2	0	0	0
136)	5	6	11	0	0	0
137)	x	x	x	5	5	10
138)	x	x	x	x	x	x
139)	x	x	x	4	9	13
140)	8	4	12	1	3	4
141)	x	x	x	0	0	0
142)	13	13	26	3	8	11
143)	10	7	17	5	5	10
144)	12	5	17	9	16	25
145)	14	5	19	7	17	24
146)	15	17	32	7	6	13
147)	12	9	21	5	3	8
148)	7	6	13	11	14	25
149)	5	5	10	8	7	15

150)	10	3	13	3	11	14
151)	0	1	1	1	3	4
152)	11	8	19	4	4	8
153)	4	6	10	6	11	17
154)	4	4	8	4	14	18
155)	5	5	10	4	14	18
156)	6	5	11	5	3	8
157)	15	8	23	6	15	21
158)	9	4	13	5	4	9
159)	8	5	13	8	20	28
160)	13	4	17	3	12	15
161)	12	8	20	8	5	13
162)	5	3	8	2	7	9
163)	5	4	9	1	4	5
164)	8	10	18	3	6	9
165)	5	4	9	8	10	18
166)	11	6	17	3	4	7
167)	11	13	24	5	2	7
168)	8	11	19	0	5	5
169)	6	6	12	2	7	9
170)	x	x	x	4	5	9
171)	12	11	23	4	6	10
172)	12	4	16	1	6	7
173)	6	7	13	4	13	17
174)	11	8	19	7	9	16
175)	2	6	8	6	2	8
176)	12	8	20	10	16	26
177)	10	2	12	5	9	14
178)	1	4	5	7	9	16
179)	x	x	x	8	10	18
180)	9	4	13	0	1	1
181)	15	8	23	4	11	15
182)	10	9	19	3	9	12
183)	7	4	11	1	0	1
184)	6	6	12	0	1	1
185)	5	8	13	6	9	15
186)	7	4	11	2	12	14
187)	7	2	9	1	8	9
188)	12	16	28	3	6	9
189)	3	4	7	6	12	18
190)	11	8	19	1	5	6
191)	4	5	9	5	4	9
192)	10	11	21	4	4	8
193)	0	4	4	5	9	14
194)	11	3	14	0	2	2
195)	6	3	9	5	8	13
196)	8	8	16	3	4	7
197)	6	1	7	7	19	26
198)	x	x	x	2	11	13
199)	3	2	5	5	2	7
200)	7	8	15	0	0	0
201)	8	5	13	2	7	9
202)	12	6	18	2	7	9
203)	12	1	13	6	14	20

204)	4	8	12	4	10	14
205)	13	9	22	5	7	12
206)	14	6	20	5	11	16
207)	11	5	16	7	12	19
208)	5	9	14	6	16	22
209)	2	7	9	0	1	1
210)	4	2	6	x	x	x
211)	x	x	x	5	11	16
212)	7	6	13	7	15	22
213)	11	7	18	5	2	7
214)	5	1	6	11	10	21
215)	x	x	x	6	8	14
216)	14	12	26	11	10	21
217)	5	6	11	3	3	6
218)	7	7	14	6	2	8
219)	6	9	15	7	11	18
220)	7	4	11	1	8	9
221)	13	11	24	5	14	19
222)	6	5	11	x	x	x
223)	8	4	12	8	19	27
224)	16	8	24	6	11	17
225)	2	3	5	2	7	9
226)	13	7	20	0	1	1
227)	6	3	9	6	6	12
228)	8	2	10	5	4	9
229)	9	15	24	x	x	x
230)	8	6	14	4	14	18
231)	6	6	12	2	13	15
232)	12	7	19	7	11	18
233)	4	2	6	6	10	16
234)	4	7	11	6	11	17
235)	x	x	x	3	8	11
236)	11	7	18	6	9	15
237)	11	7	18	5	14	19
238)	12	9	21	0	0	0
239)	12	7	19	4	10	14
240)	6	5	11	8	9	17
241)	12	9	21	5	5	10
242)	11	11	22	5	4	9
243)	5	8	13	3	12	15
244)	7	7	14	4	8	12
245)	3	2	5	0	0	0
246)	8	4	12	9	10	19
247)	8	6	14	6	13	19
248)	13	3	16	7	10	17
249)	6	7	13	7	8	15
250)	4	4	8	0	0	0
251)	13	14	27	0	6	6
252)	5	4	9	3	6	9
253)	9	3	12	5	15	20
254)	x	x	x	8	20	28
255)	5	4	9	x	x	x
256)	7	6	13	1	1	2
257)	9	10	19	1	6	7

258)	5	10	15	10	9	19
259)	5	3	8	5	18	23
260)	8	6	14	5	15	20
261)	8	3	11	5	11	16
262)	11	7	18	2	10	12
263)	7	11	18	7	16	23
264)	5	6	11	2	15	17
265)	10	6	16	1	10	11
266)	5	7	12	0	7	7
267)	8	9	17	7	10	17
268)	8	5	13	1	7	8
269)	7	9	16	3	3	6
270)	5	6	11	2	10	12
271)	8	9	17	4	9	13
272)	5	3	8	4	9	13
273)	6	4	10	5	7	12
274)	10	10	20	4	12	16
275)	11	8	19	1	2	3
276)	5	2	7	6	13	19
277)	5	5	10	2	8	10
278)	14	5	19	6	7	13
279)	2	5	7	5	3	8
280)	9	9	18	0	7	7
281)	9	6	15	2	15	17
282)	7	9	16	2	6	8
283)	3	5	8	5	6	11
284)	9	8	17	4	9	13
285)	12	7	19	8	19	27
286)	10	8	18	6	8	14
287)	11	8	19	6	13	19
288)	12	5	17	4	10	14
289)	11	8	19	x	x	x
290)	8	7	15	5	7	12
291)	14	7	21	6	6	12
292)	4	2	6	3	6	9
293)	9	7	16	2	6	8
294)	9	7	16	8	15	23
295)	9	5	14	4	12	16
296)	8	7	15	2	9	11
297)	12	6	18	1	8	9
298)	7	9	16	8	8	16
299)	13	11	24	3	3	6
300)	1	1	2	4	13	17
301)	4	2	6	2	15	17
302)	7	9	16	2	4	6
303)	0	1	1	6	8	14
304)	3	8	11	5	11	16
305)	x	x	x	3	7	10
306)	11	8	19	5	15	20
307)	10	4	14	4	14	18
308)	9	11	20	7	11	18
309)	x	x	x	5	12	17
310)	8	3	11	5	7	12
311)	10	8	18	5	7	12

312)	13	8	21	2	13	15
313)	7	7	14	1	6	7
314)	2	4	6	0	2	2
315)	10	10	20	10	15	25
316)	16	6	22	4	9	13
317)	7	7	14	6	7	13
318)	16	7	23	6	11	17
319)	7	5	12	4	15	19
320)	6	4	10	x	x	x
321)	7	5	12	5	6	11
322)	9	5	14	6	7	13
323)	12	4	16	1	16	17
324)	10	12	22	8	11	19
325)	x	x	x	5	12	17
326)	6	12	18	11	9	20
327)	6	7	13	1	16	17
328)	0	0	0	5	5	10
329)	x	x	x	5	12	17
330)	6	2	8	0	7	7
331)	6	3	9	0	0	0
332)	14	11	25	1	0	1
333)	6	5	11	11	21	32
334)	13	7	20	5	3	8
335)	10	7	17	3	3	6
336)	5	3	8	4	11	15
337)	9	8	17	1	0	1
338)	1	3	4	6	13	19
339)	6	7	13	1	8	9
340)	8	4	12	7	10	17
341)	10	5	15	6	12	18
342)	7	4	11	8	12	20
343)	x	x	x	2	7	9
344)	11	11	22	2	12	14
345)	13	10	23	5	3	8
346)	14	7	21	4	6	10
347)	11	9	20	4	8	12
348)	15	8	23	0	1	1
349)	5	6	11	1	6	7
350)	3	9	12	6	15	21
351)	x	x	x	5	12	17
352)	x	x	x	2	9	11
353)	9	6	15	4	8	12
354)	2	4	6	3	6	9
355)	5	6	11	5	4	9
356)	3	2	5	5	9	14
357)	6	10	16	3	9	12
358)	11	12	23	3	5	8
359)	x	x	x	2	5	7
360)	7	9	16	2	7	9
361)	10	6	16	9	14	23
362)	12	8	20	5	7	12
363)	16	8	24	4	4	8
364)	x	x	x	2	5	7
365)	x	x	x	6	10	16

366)	4	3	7	6	6	12
367)	8	3	11	5	11	16
368)	11	4	15	11	9	20
369)	6	5	11	3	2	5
370)	x	x	x	6	2	8
371)	7	12	19	6	13	19
372)	4	6	10	6	13	19
373)	4	2	6	2	8	10
374)	8	4	12	2	8	10
375)	9	4	13	0	0	0
376)	16	9	25	8	13	21
377)	x	x	x	3	8	11
378)	9	6	15	0	0	0
379)	10	8	18	6	8	14
380)	9	2	11	8	9	17
381)	10	9	19	2	11	13
382)	9	9	18	9	6	15
383)	13	8	21	6	7	13
384)	5	2	7	5	8	13
385)	5	4	9	4	3	7
386)	x	x	x	4	5	9
387)	7	4	11	1	4	5
388)	10	9	19	1	8	9
389)	5	6	11	10	9	19
390)	10	4	14	11	13	24
391)	12	9	21	6	6	12
392)	7	9	16	5	4	9
393)	8	6	14	7	8	15
394)	11	9	20	6	2	8
395)	10	6	16	0	2	2
396)	9	1	10	4	12	16
397)	12	6	18	2	1	3
398)	5	6	11	4	7	11
399)	10	12	22	2	15	17
400)	9	9	18	4	10	14
401)	5	6	11	1	6	7
402)	0	0	0	1	1	2
403)	x	x	x	9	9	18
404)	10	9	19	0	0	0
405)	x	x	x	5	9	14
406)	16	10	26	5	3	8
407)	8	6	14	6	7	13
408)	x	x	x	5	10	15
409)	10	6	16	4	17	21
410)	6	2	8	5	7	12
411)	x	x	x	3	4	7
412)	17	10	27	6	16	22
413)	9	10	19	4	9	13
414)	6	10	16	6	9	15
415)	9	3	12	2	12	14
416)	11	7	18	3	7	10
417)	10	8	18	6	8	14
418)	4	4	8	4	15	19
419)	9	9	18	4	9	13

420)	5	7	12	8	5	13
421)	6	3	9	2	7	9
422)	x	x	x	9	14	23
423)	5	1	6	8	7	15
424)	10	8	18	6	6	12
425)	12	9	21	2	9	11
426)	14	7	21	6	13	19
427)	10	9	19	4	10	14
428)	11	8	19	8	11	19
429)	13	8	21	2	9	11
430)	6	8	14	7	13	20
431)	15	7	22	5	6	11
432)	6	3	9	3	15	18
433)	7	6	13	7	3	10
434)	14	6	20	6	11	17
435)	7	7	14	9	13	22
436)	1	0	1	3	7	10
437)	5	2	7	0	0	0
438)	11	6	17	5	15	20
439)	x	x	x	4	11	15
440)	10	7	17	5	8	13
441)	4	5	9	2	7	9
442)	x	x	x	0	0	0
443)	3	5	8	6	12	18
444)	13	6	19	3	13	16
445)	3	2	5	2	7	9
446)	6	9	15	2	6	8
447)	8	3	11	5	4	9
448)	8	3	11	5	3	8
449)	9	11	20	0	1	1
450)	10	17	27	6	7	13
451)	9	5	14	2	7	9
452)	12	7	19	2	7	9
453)	13	4	17	8	10	18
454)	3	7	10	7	8	15
455)	12	10	22	5	6	11
456)	8	4	12	2	7	9
457)	x	x	x	7	13	20
458)	6	3	9	7	5	12
459)	6	6	12	6	15	21
460)	6	4	10	5	2	7
461)	4	4	8	3	3	6
462)	x	x	x	7	10	17
463)	7	7	14	11	17	28
464)	12	5	17	3	11	14
465)	11	6	17	6	7	13
466)	4	4	8	6	4	10
467)	5	4	9	2	3	5
468)	10	8	18	2	11	13
469)	0	1	1	1	7	8
470)	9	2	11	6	12	18
471)	7	5	12	4	5	9
472)	5	5	10	2	13	15
473)	11	6	17	2	9	11

474)	9	8	17	5	2	7
475)	4	5	9	4	8	12
476)	13	9	22	x	x	x
477)	8	5	13	4	6	10
478)	5	6	11	3	12	15
479)	4	7	11	6	3	9
480)	7	3	10	9	17	26
481)	4	2	6	2	9	11
482)	0	2	2	6	5	11
483)	14	12	26	5	3	8
484)	12	10	22	1	8	9
485)	10	7	17	4	15	19
486)	11	7	18	2	8	10
487)	8	6	14	4	5	9
488)	3	7	10	6	8	14
489)	6	10	16	6	7	13
490)	10	6	16	6	20	26
491)	3	2	5	7	15	22
492)	5	8	13	7	10	17
493)	x	x	x	9	11	20
494)	16	8	24	7	12	19
495)	2	1	3	8	7	15
496)	9	7	16	8	8	16
497)	4	2	6	4	13	17
498)	3	7	10	1	7	8
499)	8	3	11	8	19	27
500)	16	6	22	5	10	15
501)	9	11	20	3	6	9
502)	10	6	16	x	x	x
503)	12	9	21	6	20	26
504)	9	7	16	0	0	0
505)	13	8	21	4	14	18
506)	10	7	17	0	0	0
507)	13	9	22	5	11	16
508)	9	6	15	6	10	16
509)	8	8	16	5	4	9
510)	5	6	11	5	3	8
511)	6	2	8	5	10	15
512)	6	8	14	6	3	9
513)	9	7	16	7	16	23
514)	x	x	x	5	11	16
515)	8	8	16	7	13	20
516)	14	7	21	6	12	18
517)	11	6	17	5	2	7
518)	6	6	12	4	5	9
519)	10	15	25	5	4	9
520)	2	3	5	4	5	9
521)	7	3	10	6	7	13
522)	11	6	17	9	18	27
523)	7	9	16	2	4	6
524)	3	6	9	5	8	13
525)	9	12	21	6	7	13
526)	5	4	9	6	20	26
527)	8	7	15	3	3	6

528)	3	8	11	5	4	9
529)	10	11	21	5	9	14
530)	9	6	15	7	20	27
531)	10	6	16	5	15	20
532)	8	4	12	1	4	5
533)	2	2	4	4	7	11
534)	5	5	10	x	x	x
535)	12	11	23	7	3	10
536)	6	4	10	4	5	9
537)	10	5	15	9	4	13
538)	9	12	21	5	8	13
539)	8	3	11	2	7	9
540)	x	x	x	6	10	16
541)	11	7	18	8	10	18
542)	6	2	8	4	9	13
543)	6	5	11	5	3	8
544)	4	4	8	3	3	6
545)	12	3	15	2	5	7
546)	9	12	21	5	8	13
547)	11	10	21	1	9	10
548)	8	6	14	3	6	9
549)	8	9	17	2	7	9
550)	9	8	17	3	8	11
551)	12	5	17	4	6	10
552)	5	6	11	0	9	9
553)	4	4	8	0	0	0
554)	3	7	10	1	0	1
555)	10	8	18	11	21	32
556)	18	7	25	0	2	2
557)	7	7	14	2	3	5
558)	x	x	x	6	15	21
559)	11	5	16	3	9	12
560)	14	7	21	6	10	16
561)	8	7	15	1	5	6
562)	7	4	11	6	3	9
563)	12	3	15	5	4	9
564)	7	6	13	7	8	15
565)	7	4	11	0	1	1
566)	8	5	13	1	5	6
567)	x	x	x	9	11	20
568)	8	5	13	0	1	1
569)	0	1	1	5	2	7
570)	9	6	15	5	5	10
571)	4	3	7	1	7	8
572)	12	7	19	1	11	12

Table 41: List of patients and donors with zero class I HLA AB eplet mismatches

Sl no.	No.	D/P	A1	A2	B1	B2
1	7	D	A*02:01	A*24:02	B*40:06	B*40:06
		P	A*02:01	A*02:11	B*40:06	B*40:06
2	8	D	A*02:02	A*68:01	B*15:18	B*41:01
		P	A*02:02	A*68:01	B*15:18	B*41:01
3	10	D	A*11:01	A*24:02	B*07:02	B*57:01
		P	A*24:02	A*24:02	B*07:02	B*07:02
4	23	D	A*32:01	A*33:01	B*44:03	B*51:01
		P	A*32:01	A*33:01	B*44:03	B*51:01
5	35	D	A*24:02	A*68:01	B*40:06	B*44:03
		P	A*24:02	A*68:01	B*40:06	B*44:03
6	37	D	A*24:02	A*24:02	B*35:01	B*35:01
		P	A*24:02	A*24:02	B*35:01	B*35:01
7	41	D	A*03:01	A*24:02	B*07:02	B*35:01
		P	A*03:01	A*24:02	B*07:02	B*35:01
8	50	D	A*02:01	A*02:11	B*40:01	B*52:01
		P	A*02:01	A*02:11	B*40:01	B*52:01
9	53	D	A*01:01	A*11:02	B*37:01	B*57:01
		P	A*01:01	A*11:02	B*37:01	B*57:01
10	58	D	A*01:01	A*11:02	B*15:02	B*57:01
		P	A*01:01	A*11:02	B*15:02	B*57:01
11	63	D	A*02:03	A*33:03	B*35:08	B*57:01
		P	A*02:03	A*33:03	B*35:08	B*57:01
12	82	D	A*02:01	A*11:02	B*15:18	B*15:18
		P	A*02:01	A*11:02	B*15:18	B*15:18
13	89	D	A*33:01	A*33:01	B*44:03	B*58:01
		P	A*33:01	A*33:01	B*44:03	B*58:01
14	91	D	A*02:01	A*33:01	B*37:01	B*58:01
		P	A*33:01	A*33:01	B*58:01	B*58:01
15	92	D	A*01:01	A*03:01	B*13:01	B*37:01
		P	A*01:01	A*03:01	B*13:01	B*37:01
16	100	D	A*33:01	A*68:01	B*35:01	B*52:01
		P	A*33:01	A*68:01	B*35:01	B*52:01
17	108	D	A*02:01	A*24:02	B*40:06	B*40:06
		P	A*02:01	A*02:11	B*40:06	B*40:06
18	109	D	A*02:02	A*68:01	B*15:18	B*41:01
		P	A*02:02	A*68:01	B*15:18	B*41:01
19	111	D	A*11:01	A*24:02	B*07:02	B*57:01
		P	A*24:02	A*24:02	B*07:02	B*07:02
20	114	D	A*01:01	A*32:01	B*08:01	B*37:01
		P	A*32:01	A*32:01	B*08:01	B*37:01
21	125	D	A*32:01	A*33:01	B*44:03	B*51:01
		P	A*32:01	A*33:01	B*44:03	B*51:01
22	328	D	A*11:01	A*33:03	B*35:01	B*58:01
		P	A*11:01	A*33:03	B*35:01	B*58:01
23	402	D	A*02:01	A*24:02	B*40:06	B*52:01
		P	A*02:01	A*24:02	B*52:01	B*52:01

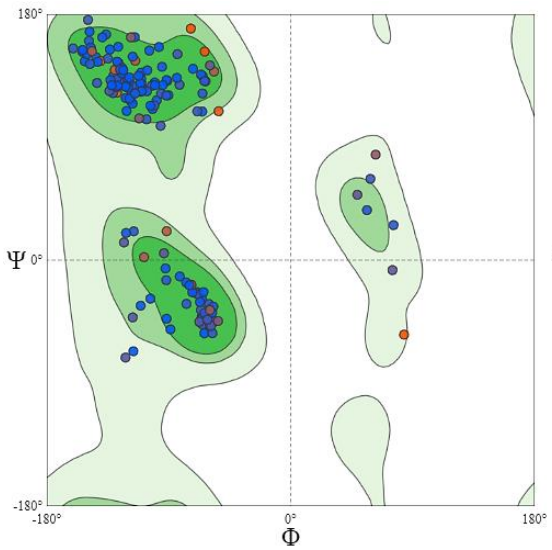
Table 42: List of patients and donors with zero class II HLA DR eplet mismatches

Sl no.	Pt. no.	D/P	DRB	DRB	Sl no.	Pt. no.	D/P	DRB	DRB
1	**7**	D	DRB1*14:04	DRB1*15:01	24	**84**	D	DRB1*07:01	DRB1*07:01
		P	DRB1*14:04	DRB1*15:01			P	DRB1*03:02	DRB1*07:01
2	**8**	D	DRB1*13:03	DRB1*14:04	25	**85**	D	DRB1*13:02	DRB1*13:02
		P	DRB1*13:03	DRB1*14:04			P	DRB1*13:02	DRB1*13:02
3	**16**	D	DRB1*07:01	DRB1*10:01	26	**88**	D	DRB1*07:01	DRB1*15:01
		P	DRB1*07:01	DRB1*10:01			P	DRB1*07:01	DRB1*15:01
4	**17**	D	DRB1*15:01	DRB1*15:01	27	**90**	D	DRB1*07:01	DRB1*13:01
		P	DRB1*14:04	DRB1*15:01			P	DRB1*07:01	DRB1*13:01
5	**23**	D	DRB1*07:01	DRB1*01:01	28	**93**	D	DRB1*10:01	DRB1*15:01
		P	DRB1*07:01	DRB1*01:01			P	DRB1*10:01	DRB1*15:01
6	**24**	D	DRB1*14:04	x	29	**100**	D	DRB1*01:01	DRB1*07:01
		P	DRB1*14:04	DRB1*15:02			P	DRB1*07:01	DRB1*10:01
7	**26**	D	DRB1*11:10	DRB1*14:01	30	**109**	D	DRB1*13:03	DRB1*14:04
		P	DRB1*11:10	DRB1*14:01			P	DRB1*13:03	DRB1*14:04
8	**32**	D	DRB1*13:01	DRB1*15:01	31	**116**	D	DRB1*15:01	DRB1*15:01
		P	DRB1*13:01	DRB1*15:01			P	DRB1*14:04	DRB1*15:01
9	**33**	D	DRB1*15:01	DRB1*15:01	32	**117**	D	DRB1*07:01	DRB1*10:01
		P	DRB1*13:02	DRB1*15:01			P	DRB1*07:01	DRB1*10:01
10	**35**	D	DRB1*07:01	DRB1*08:03	33	**125**	D	DRB1*07:01	DRB1*01:01
		P	DRB1*07:01	DRB1*08:03			P	DRB1*07:01	DRB1*01:01
11	**37**	D	DRB1*04:10	DRB1*08:03	34	**128**	D	DRB1*11:10	DRB1*14:01
		P	DRB1*04:10	DRB1*08:03			P	DRB1*11:10	DRB1*14:01
12	**42**	D	DRB1*13:02	DRB1*15:02	35	**135**	D	DRB1*03:01	DRB1*14:04
		P	DRB1*13:02	DRB1*15:02			P	DRB1*03:01	DRB1*14:04
13	**44**	D	DRB1*07:01	DRB1*15:01	36	**136**	D	DRB1*07:01	DRB1*14:04
		P	DRB1*07:01	DRB1*15:01			P	DRB1*07:01	DRB1*14:04
14	**47**	D	DRB1*01:02	DRB1*15:01	37	**141**	D	DRB1*15:01	DRB1*15:01
		P	DRB1*01:02	DRB1*15:01			P	DRB1*15:01	DRB1*15:01
15	**51**	D	DRB1*01:01	DRB1*04:03	38	**200**	D	DRB1*07:01	DRB1*15:01
		P	DRB1*01:01	DRB1*04:03			P	DRB1*07:01	DRB1*15:01
16	**54**	D	DRB1*10:01	DRB1*15:01	39	**238**	D	DRB1*07:01	DRB1*15:01
		P	DRB1*10:01	DRB1*15:01			P	DRB1*07:01	DRB1*15:01
17	**55**	D	DRB1*01:01	DRB1*03:01	40	**245**	D	DRB1*04:03	DRB1*15:01
		P	DRB1*01:01	DRB1*03:01			P	DRB1*04:03	DRB1*15:01
18	**59**	D	DRB1*07:01	DRB1*12:02	41	**250**	D	DRB1*07:01	DRB1*15:01
		P	DRB1*07:01	DRB1*12:02			P	DRB1*07:01	DRB1*15:01
19	**61**	D	DRB1*10:01	DRB1*13:02	42	**331**	D	DRB1*07:01	DRB1*07:01
		P	DRB1*10:01	DRB1*13:02			P	DRB1*07:01	DRB1*11:01
20	**64**	D	DRB1*04:03	DRB1*13:01	43	**375**	D	DRB1*01:01	DRB1*01:01
		P	DRB1*04:03	DRB1*13:01			P	DRB1*01:01	DRB1*13:01
21	**70**	D	DRB1*15:01	DRB1*15:01	44	**437**	D	DRB1*13:01	DRB1*15:01
		P	DRB1*15:01	DRB1*15:01			P	DRB1*13:01	DRB1*15:02
22	**76**	D	DRB1*14:04	DRB1*15:04	45	**442**	D	DRB1*14:04	DRB1*14:04
		P	DRB1*14:04	DRB1*15:04			P	DRB1*14:04	DRB1*16:02
23	**83**	D	DRB1*04:01	DRB1*04:01	46	**500**	D	DRB1*01:01	DRB1*14:04
		P	DRB1*04:01	DRB1*04:01			P	DRB1*08:03	DRB1*14:04

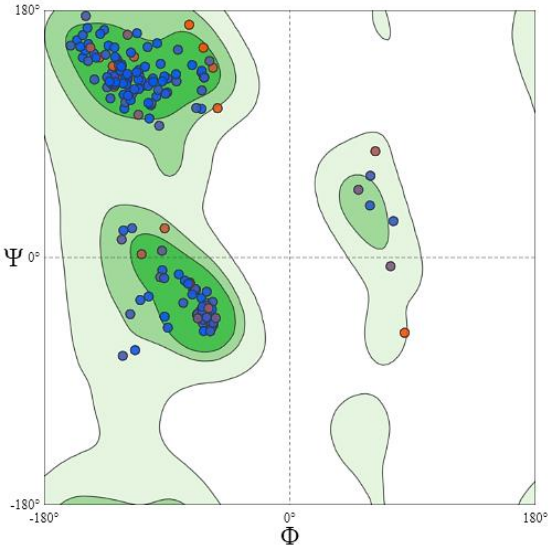
Annexure V

Figure 34 a-h represent the Ramachandran plot obtained for 8 modelled class II HLA DRB structures using SWISS MODEL. The Z score for each plot is given below.

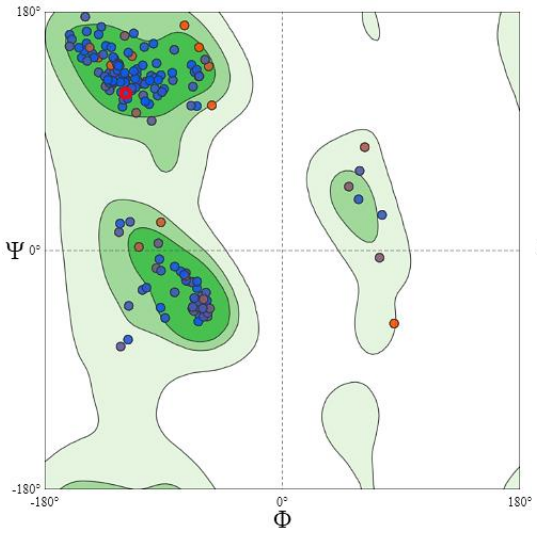
The residue backbone dihedral angles, phi Φ and psi Ψ, fall within the permitted regions for β-sheet and right-handed α-helix and a left-handed α-helix. The favored regions are shown in green, additional allowed region shown in light green, generously allowed regions are shown in pale green, and disallowed regions are in white.



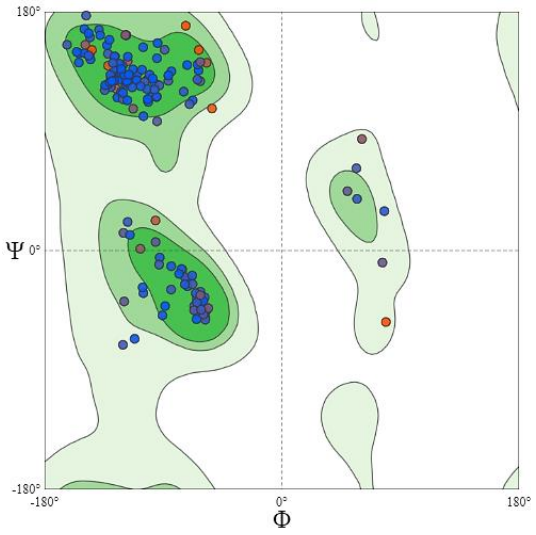
a) Z = -1.555



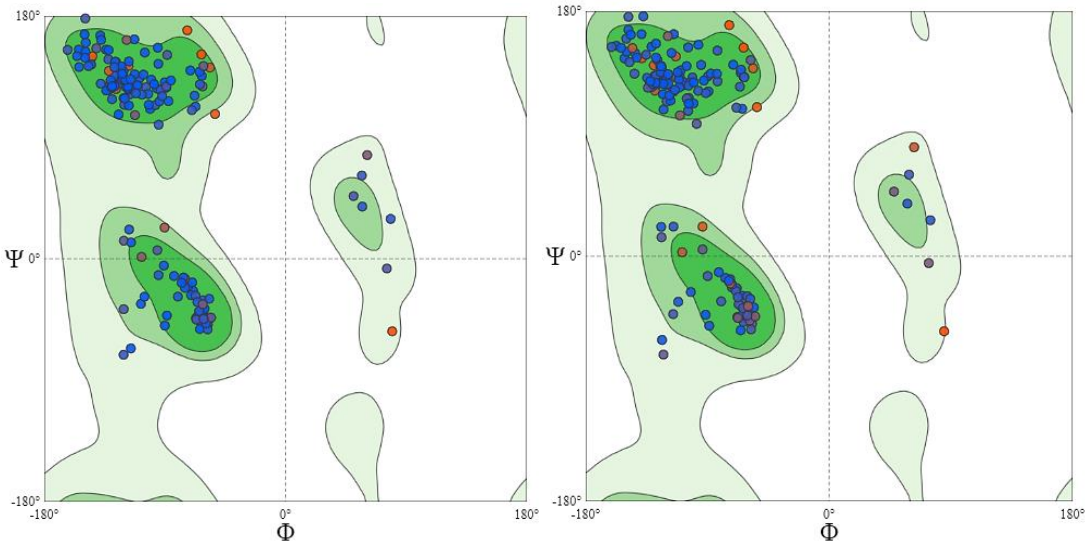
b) Z = -2.635



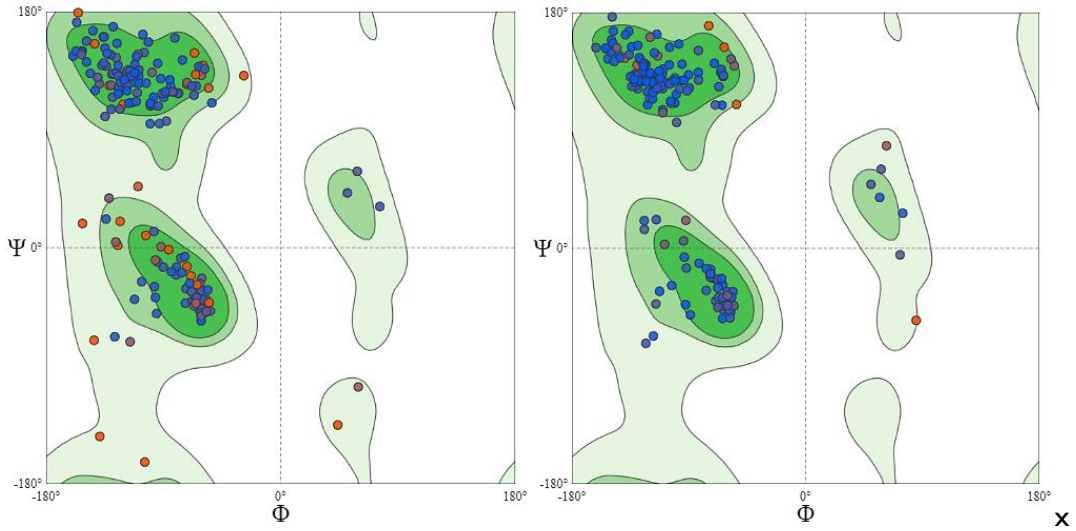
c) Z = -1.820



d) Z = -1.456



e) Z = -1.453 **f) Z = -1.682**



g) Z = -1.684 **h) Z = -1.784**

Figure 34: Ramachandran plot of the 8 modelled HLA DRB chains. a) HLA DRB1*01, b) HLA DRB1*04, c) HLA DRB1*07, d) HLA DRB1*08, e) HLA DRB1*09, f) HLA DRB1*12, g) HLA DRB1*14 and h) HLA DRB1*16

Annexure VI

Tables showing structural properties for each of the complexes formed by docking via ZDOCK, between modelled HLA DRB structures with CLIPs and Ag peptides.

Structures listed here are class II HLA DRB1*01, DRB1*04, DRB1*07, DRB1*08 HLA DRB1*09, DRB1*12, DRB1*14 and DRB1*16; CLIP - 1a6a and 4x5w and Ag peptides - 1aqd, 1dlh, 1kg0, 1h15 and 1sje.

[* PC = protein complex, NIS = non-interacting surfaces per property, ICs = no. of interatomic or interfacial contacts per property, C = charged, aP = apolar, P = polar, ΔG = binding affinity, K_d = dissociation constant]

Table 43: HLA DRB1*01 with CLIP 1a6a and 4x5w respectively

DRB1*01 + 1a6a (CLIP)							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.11	40.56	10	12	21	-7.9	2.7E-06
2	25.97	40.88	10	9	15	-7.7	4.0E-06
3	25.82	40.66	11	9	16	-7.9	2.6E-06
4	26.11	40.56	7	8	20	-7.3	7.4E-06
5	26.11	40.56	9	11	20	-8.0	2.4E-06
6	25.87	40.88	6	16	21	-8.4	1.3E-06
7	26.11	40.56	8	14	19	-8.6	8.2E-07
8	25.97	40.33	9	7	13	-7.2	8.3E-06
9	25.84	40.45	12	7	26	-7.8	3.2E-06
10	25.82	40.66	7	7	22	-6.9	1.4E-05
DRB1*01 + 4x5w (CLIP)							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.11	40.56	10	12	21	-7.9	2.7E-06
2	25.97	40.88	10	9	15	-7.7	4.0E-06
3	25.82	40.66	11	9	16	-7.9	2.6E-06
4	26.11	40.56	7	8	20	-7.3	7.4E-06
5	26.11	40.56	9	11	20	-8.0	2.4E-06
6	25.87	40.88	6	16	21	-8.4	1.3E-06
7	26.11	40.56	8	14	19	-8.6	8.2E-07
8	25.97	40.33	9	7	13	-7.2	8.3E-06
9	25.84	40.45	12	7	26	-7.8	3.2E-06
10	25.82	40.66	7	7	22	-6.9	1.4E-05

Table 44: HLA DRB1*01 with Ag peptides 1aqd, 1dlh, 1kg0, 1h15 and 1sje respectively

DRB1*01 + 1aqd							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.82	38.55	13	8	15	-8.3	1.3E-06
2	26.82	37.99	23	8	15	-9.2	3.0E-07
3	26.82	37.99	11	10	15	-8.8	6.3E-07
4	26.82	37.99	15	6	14	-8.5	1.1E-06
5	26.52	38.12	9	6	19	-7.4	5.9E-06
6	26.82	37.99	12	6	14	-8.0	2.3E-06
7	26.52	38.12	11	8	14	-8.2	1.7E-06
8	26.67	38.33	11	9	18	-8.2	1.6E-06
9	26.82	37.99	15	9	17	-8.9	5.5E-07
10	26.55	37.85	14	10	14	-9.2	3.5E-07
DRB1*01 + 1dlh							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.97	38.2	12	14	10	-9.0	4.8E-07
2	27.22	37.78	6	8	10	-7.6	4.1E-06
3	26.97	38.20	13	16	12	-9.9	1.0E-07
4	26.82	38.55	9	8	8	-7.9	2.5E-06
5	26.97	38.20	10	15	9	-9.6	1.8E-07
6	26.67	38.33	8	12	8	-8.5	9.8E-07
7	26.97	38.76	8	9	9	-7.8	3.1E-06
8	26.67	38.33	10	9	12	-8.2	1.6E-06
9	26.82	38.55	8	9	7	-8.0	2.4E-06
10	26.82	38.55	8	9	8	-8.0	2.4E-06
DRB1*01 + 1kg0							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.56	37.22	5	11	13	-7.9	2.8E-06
2	25.70	37.99	7	14	18	-8.6	8.9E-07
3	25.56	37.22	5	10	17	-7.9	2.6E-06
4	25.56	37.78	5	16	11	-8.7	7.4E-07
5	25.41	37.57	11	13	12	-8.8	6.5E-07
6	25.00	37.78	6	10	14	-7.9	2.6E-06
7	25.41	37.57	7	14	10	-8.6	8.6E-07
8	25.27	37.36	9	11	12	-8.3	1.5E-06

9	25.41	37.57	8	16	12	-9.7	1.4E-07
10	25.56	26.22	4	13	13	-8.5	1.0E-06
DRB1*01 + 1h15							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.88	38.55	17	9	19	-9.3	3.0E-07
2	26.52	38.67	13	5	10	-7.7	3.8E-06
3	26.67	38.89	15	6	21	-8.1	1.8E-06
4	27.37	37.99	17	8	14	-9.1	4.1E-07
5	26.67	38.89	16	7	14	-8.5	1.1E-06
6	26.52	38.67	13	2	12	-7.0	1.2E-05
7	26.52	38.67	12	4	10	-7.4	6.5E-06
8	26.67	38.89	15	7	22	-8.5	1.1E-06
9	27.07	38.12	13	3	15	-7.2	9.0E-06
10	26.67	38.89	12	5	21	-7.7	3.7E-06
DRB1*01 + 1sje							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.11	40.56	14	8	19	-8.0	2.4E-06
2	26.11	40.56	7	13	16	-8.4	1.2E-06
3	26.52	40.33	5	13	12	-7.4	5.9E-06
4	26.23	40.44	9	11	15	-8.1	2.1E-06
5	26.37	40.66	7	9	16	-7.3	6.6E-06
6	25.97	40.33	10	7	13	-7.3	7.0E-06
7	26.23	40.44	6	6	10	-6.5	2.5E-05
8	26.26	40.22	17	9	13	-8.5	9.5E-07
9	26.37	40.66	11	12	19	-6.5	2.6E-05
10	26.23	40.44	6	8	10	-8.5	9.8E-07

Table 45: HLA DRβ 04 with CLIP 1a6a and 4x5w respectively

DRB1*04 + 1a6a (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.00	41.67	13	9	16	-8.1	1.8E-06
2	25.39	41.97	16	4	20	-7.2	8.4E-06
3	24.87	41.97	9	4	19	-6.4	3.2E-05
4	25.13	41.88	15	5	17	-7.3	7.3E-06
5	25.26	41.74	14	4	12	-7.2	9.1E-06

6	25.39	41.45	12	4	16	-7.0	1.2E-05
7	24.87	41.97	8	5	15	-7.0	1.2E-05
8	24.87	41.97	7	8	15	-6.9	1.4E-05
9	24.87	42.33	24	9	21	-8.9	4.9E-07
10	24.87	41.97	18	8	16	-9.7	7.8E-07
DRB1*04 + 4x5w (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.39	41.45	9	13	26	-8.2	1.8E-06
2	24.87	41.45	14	10	23	-8.4	1.1E-06
3	25.00	41.67	11	10	23	-8.2	1.8E-06
4	25.26	41.24	7	7	21	-6.6	2.1E-05
5	24.87	41.45	9	4	20	-6.6	2.3E-05
6	25.00	40.82	10	12	21	-8.5	1.0E-06
7	25.39	41.45	11	9	21	-7.7	3.6E-06
8	25.00	40.82	13	14	18	-8.8	6.7E-07
9	25.39	40.93	10	16	15	-9.2	3.1E-07
10	24.87	41.45	14	8	24	-7.5	5.3E-06

Table 46: HLA DRB1*04 with Ag peptides 1aqd, 1dlh, 1kg0, 1h15 and 1sje respectively

DRB1*04 + 1aqd							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.52	39.58	21	1	15	-7.3	6.7E-06
2	25.79	39.47	16	2	18	-7.3	7.7E-06
3	25.52	39.58	19	3	15	-7.8	3.2E-06
4	25.79	39.47	19	2	21	-7.6	4.1E-06
5	25.52	39.58	15	3	11	-7.3	7.2E-06
6	25.39	39.38	14	4	12	-8.2	1.7E-06
7	25.65	39.79	13	5	16	-7.8	3.3E-06
8	25.52	39.58	16	0	14	-6.8	1.6E-05
9	25.65	39.27	20	4	19	-8.3	1.3E-06
10	25.52	39.06	8	3	11	-6.7	1.6E-05
DRB1*04 + 1dlh							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.77	39.18	8	11	4	-8.5	1.1E-06
2	25.53	39.89	12	3	13	-6.7	1.8E-05

3	25.79	39.47	10	3	15	-6.5	2.7E-05
4	25.65	39.79	13	7	6	-8.3	1.3E-06
5	25.52	39.58	12	7	6	-8.0	2.3E-06
6	25.93	39.68	6	13	10	-8.6	8.7E-07
7	25.79	39.47	9	11	9	-8.8	6.4E-07
8	26.18	39.27	12	15	6	-9.9	1.1E-07
9	25.65	39.79	9	4	8	-6.7	2.0E-05
10	25.52	39.06	8	13	6	-9.0	4.8E-07
DRB1*04 + 1kg0							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	24.74	38.95	10	16	15	-8.8	6.2E-07
2	24.61	38.74	9	9	10	-8.1	1.8E-06
3	24.61	38.74	10	15	14	-9.5	2.0E-07
4	24.74	38.95	9	14	18	-9.3	2.7E-07
5	24.48	38.54	11	19	14	-10.7	3.0E-08
6	24.61	39.27	5	11	15	-8.2	1.7E-06
7	24.48	39.06	4	8	16	-7.2	8.6E-06
8	24.74	38.95	7	21	15	-9.8	1.2E-07
9	24.61	39.27	9	13	14	-9.1	4.2E-07
10	24.61	38.74	11	12	15	-8.9	5.0E-07
DRB1*04 + 1h15							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.52	40.10	17	2	14	-7.6	4.7E-06
2	25.79	40.00	20	2	12	-7.7	3.5E-06
3	25.52	40.10	17	2	12	-7.5	5.5E-06
4	25.93	40.21	20	2	15	-8.1	2.1E-06
5	25.79	40.00	16	4	18	-7.9	2.7E-06
6	26.04	40.10	23	2	20	-8.0	2.3E-06
7	25.79	40.00	23	2	16	-8.4	1.2E-06
8	25.79	40.00	15	4	14	-7.8	3.2E-06
9	25.79	40.00	13	1	19	-6.8	1.6E-05
10	26.46	40.21	25	7	15	-9.3	2.6E-07
DRB1*04 + 1sje							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.13	41.54	12	5	20	-7.0	6.9E-06
2	25.13	41.88	13	4	16	-7.1	5.8E-06
3	25.00	41.67	11	10	16	-8.2	1.0E-06

4	25.00	42.19	13	6	22	-7.3	4.6E-06
5	25.13	41.88	12	5	18	-7.0	7.6E-06
6	25.13	41.88	13	3	23	-6.5	1.6E-05
7	24.21	42.63	16	12	22	-9.0	2.7E-07
8	25.00	42.19	12	2	22	-6.4	2.2E-05
9	25.13	41.88	14	4	19	-7.1	5.7E-06
10	25.65	41.88	12	5	21	-7.2	5.3E-06

Table 47: HLA DRB1*07 with CLIP 1a6a and 4x5w respectively

DRB1*07 + 1a6a (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	24.58	41.90	7	7	27	-7.4	6.2E-06
2	24.86	41.44	5	6	25	-6.7	1.8E-05
3	24.73	41.76	8	2	18	-6.5	2.8E-05
4	24.59	41.53	14	7	19	-7.6	4.5E-06
5	25.14	41.31	7	10	26	-7.6	4.3E-06
6	24.59	42.08	7	6	25	-7.1	9.4E-06
7	24.73	41.76	2	9	19	-6.6	2.3E-05
8	24.73	41.76	0	9	23	-6.6	2.3E-05
9	24.86	41.44	6	10	22	-7.7	3.5E-06
10	24.73	41.76	4	7	20	-6.7	1.8E-05
DRB1*07 + 4x5w (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	24.46	41.30	8	5	23	-6.8	1.6E-05
2	24.73	41.21	10	10	23	-8.1	2.0E-06
3	24.59	40.98	12	9	18	-7.9	2.5E-06
4	24.59	40.98	8	5	17	-6.6	2.1E-05
5	24.86	40.88	7	8	19	-7.6	4.6E-06
6	24.46	41.30	6	6	15	-7.0	1.2E-05
7	24.59	40.98	7	6	20	-7.0	1.1E-05
8	24.73	40.66	3	10	21	-7.4	6.1E-06
9	24.31	41.44	12	5	19	-7.4	6.4E-06
10	24.18	41.76	15	6	24	-7.7	3.9E-06

Table 48: HLA DRB1*07 with Ag peptides 1aqd, 1dlh, 1kg0, 1h15 and 1sje respectively

DRB1*07 + 1aqd							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.70	38.55	16	4	25	-7.6	4.4E-06
2	25.56	38.89	22	5	15	-8.6	9.0E-07
3	25.41	39.23	12	7	21	-8.0	2.3E-06
4	25.27	39.56	7	3	17	-6.4	2.9E-05
5	25.56	38.89	11	5	16	-7.8	3.4E-06
6	25.41	39.23	7	3	17	-6.6	2.3E-05
7	25.41	39.23	7	10	21	-7.9	2.8E-06
8	25.41	39.23	9	4	16	-6.9	1.3E-05
9	25.56	38.89	23	6	22	-9.2	3.3E-07
10	25.56	39.44	15	10	23	-8.2	1.6E-06
DRB1*07 + 1dlh							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.41	39.78	12	19	11	-10.3	5.3E-08
2	25.27	39.56	10	16	12	-9.7	1.5E-07
3	25.14	39.66	10	13	7	-8.8	6.1E-07
4	25.41	39.78	8	3	14	-6.6	2.3E-05
5	25.41	39.78	6	3	15	-6.4	3.2E-05
6	25.27	39.56	8	3	11	-6.2	3.9E-05
7	25.56	39.44	6	6	10	-6.8	1.6E-05
8	25.56	39.44	12	3	19	-6.9	1.3E-05
9	25.41	39.23	12	3	19	-6.8	1.6E-05
10	25.27	39.56	7	1	13	-6.0	6.0E-05
DRB1*07 + 1kg0							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	24.31	38.12	4	7	13	-7.4	6.6E-06
2	24.18	38.46	5	8	14	-7.6	4.2E-06
3	24.18	37.91	3	7	13	-7.1	9.7E-06
4	24.04	38.25	5	6	17	-9.7	1.4E-07
5	24.18	38.46	1	10	15	-7.4	6.1E-06
6	24.04	38.8	5	13	14	-8.5	9.7E-07
7	24.18	38.46	4	9	16	-7.8	3.4E-06
8	24.18	38.46	3	9	12	-7.7	4.0E-06

9	24.18	38.46	4	7	11	-7.3	7.1E-06
10	24.04	38.80	3	8	14	-7.4	6.2E-06
DRB1*07 + 1h15							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.41	39.78	13	4	16	-7.4	6.1E-06
2	25.00	40.56	12	7	14	-7.9	2.7E-06
3	25.41	39.78	14	3	17	-7.1	1.0E-05
4	25.41	39.78	15	3	26	-7.6	4.7E-06
5	25.70	39.66	15	4	21	-8.0	2.4E-06
6	25.41	39.78	4	4	19	-6.5	2.6E-05
7	25.41	39.23	21	7	21	-8.9	5.4E-07
8	24.86	40.88	10	6	17	-7.2	7.9E-06
9	25.27	40.11	20	2	21	-7.8	3.2E-06
10	25.41	39.78	9	2	20	-6.6	2.1E-05
DRB1*07 + 1sje							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	24.46	41.85	8	6	27	-7.1	9.9E-06
2	24.73	41.21	8	10	26	-7.5	5.1E-06
3	24.73	41.21	8	9	21	-7.1	1.0E-05
4	24.73	41.76	3	7	22	-6.4	3.0E-05
5	24.31	41.99	11	4	27	-7.0	1.1E-05
6	24.44	41.67	7	8	30	-6.9	1.3E-05
7	24.86	41.44	5	8	21	-6.9	1.4E-05
8	24.59	41.53	5	6	22	-6.6	2.0E-05
9	24.86	41.44	6	6	19	-6.6	2.1E-05
10	24.86	41.44	8	1	21	-5.8	8.2E-05

Table 49: HLA DRB1*08 with CLIP 1a6a and 4x5w respectively

DRB1*08 + 1a6a (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.41	39.78	11	9	19	-8.3	1.3E-06
2	25.56	39.44	14	9	19	-8.3	1.4E-06
3	25.56	39.44	12	8	19	-8.1	2.1E-06
4	25.56	39.44	7	6	17	-7.4	6.3E-06
5	25.56	39.44	7	9	26	-8.0	2.4E-06
6	25.27	39.56	5	9	18	-7.2	8.2E-06

7	25.27	39.56	5	8	16	-7.0	1.2E-05
8	25.00	40.00	8	12	18	-8.3	1.3E-06
9	25.41	39.78	14	9	21	-8.7	7.1E-07
10	25.56	39.44	13	7	22	-8.1	1.9E-06
DRB1*08 + 4x5w (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.41	38.67	8	10	21	-8.2	1.7E-06
2	25.41	38.67	5	9	22	-7.8	3.0E-06
3	25.28	38.76	15	13	27	-9.5	2.1E-07
4	25.14	39.11	14	8	19	-8.5	1.1E-06
5	25.41	39.23	10	6	17	-7.4	6.4E-06
6	25.70	39.11	12	12	26	-9.1	3.8E-07
7	25.56	38.89	10	8	22	-7.8	3.3E-06
8	25.41	38.67	15	11	24	-9.0	4.4E-07
9	25.00	38.33	19	14	31	-10.2	6.3E-08
10	25.14	39.66	13	7	18	-8.2	1.6E-06

Table 50: HLA DRB1*08 with Ag peptides 1aqd, 1dlh, 1kg0, 1h15 and 1sje respectively

DRB1*08 + 1aqd							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.97	37.02	11	5	14	-7.8	3.4E-06
2	26.11	37.22	13	8	19	-8.9	5.5E-07
3	25.70	37.43	21	8	17	-10.0	9.2E-08
4	26.11	37.22	15	7	16	-8.4	1.3E-06
5	25.97	37.02	21	7	16	-9.1	3.7E-07
6	26.14	36.93	19	1	21	-9.7	1.4E-07
7	26.11	37.22	19	4	22	-8.3	1.4E-06
8	25.70	36.87	14	5	4	-8.4	1.2E-06
9	26.26	36.87	13	7	18	-8.6	8.6E-07
10	25.97	37.02	8	8	18	-8.2	1.5E-06
DRB1*08 + 1dlh							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.40	37.08	16	15	12	-10.5	4.2E-08
2	26.36	36.87	15	14	11	-9.9	1.0E-07
3	26.11	37.22	13	15	8	-9.8	1.3E-07

4	26.11	37.22	10	11	8	-8.4	1.2E-06
5	26.26	37.43	15	13	12	-9.9	1.1E-07
6	26.26	37.43	10	9	10	-7.9	2.8E-06
7	26.26	37.43	9	7	12	-7.8	3.1E-06
8	25.56	37.22	9	7	11	-8.1	1.8E-06
9	26.11	37.22	11	16	13	-9.8	1.2E-07
10	26.11	37.22	3	12	12	-8.1	1.9E-06
DRB1*08 + 1kg0							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	24.73	36.26	6	13	16	-8.9	5.2E-07
2	25.00	36.11	9	21	14	-10.7	2.8E-08
3	24.86	35.91	12	19	17	-10.8	2.4E-08
4	24.86	36.46	10	19	20	-10.3	5.3E-08
5	25.00	36.11	8	15	17	-9.7	1.3E-07
6	24.44	36.67	10	14	16	-9.3	2.7E-07
7	25.00	36.11	8	14	17	-9.1	3.6E-07
8	24.73	36.26	3	15	17	-8.9	5.6E-07
9	25.00	36.11	9	11	15	-8.6	8.0E-07
10	25.00	36.11	9	19	17	-10.2	6.8E-08
DRB1*08 + 1h15							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.56	37.22	14	7	14	-8.7	7.0E-07
2	25.41	37.02	14	7	16	-8.7	7.4E-07
3	25.70	37.43	21	7	16	-9.6	1.8E-07
4	25.97	37.57	14	8	17	-8.7	6.8E-07
5	26.11	37.22	16	5	21	-8.2	1.6E-06
6	26.26	37.43	23	2	11	-8.6	8.0E-07
7	26.11	37.78	14	5	17	-8.3	1.4E-06
8	25.97	37.57	18	8	20	-9.2	3.1E-07
9	25.97	37.57	18	18	21	-9.1	3.6E-07
10	26.11	37.22	10	4	18	-7.6	4.6E-06
DRB1*08 + 1sje							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	24.73	39.56	10	10	23	-8.1	1.9E-06
2	25.00	39.44	15	13	23	-9.5	2.1E-07
3	25.14	39.11	14	10	23	-8.8	6.0E-07
4	25.99	39.55	10	18	27	-10.0	8.3E-08

5	25.27	39.56	9	7	26	-7.4	6.5E-06
6	25.14	39.34	9	12	21	-8.3	1.5E-06
7	25.56	40.00	7	10	24	-7.5	5.0E-06
8	25.14	39.34	12	12	21	-8.8	5.8E-07
9	25.14	39.11	11	10	22	-8.5	9.7E-07
10	25.56	39.44	17	8	26	-8.6	8.0E-07

Table 51: HLA DRB1*09 with CLIP 1a6a and 4x5w respectively

DRB1*09 + 1a6a (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.78	41.53	9	7	14	-7	1.2E-05
2	27.07	41.44	4	9	19	-6.7	1.9E-05
3	26.92	41.76	10	8	18	-7.3	6.7E-06
4	26.63	41.85	4	7	18	-6.6	2.1E-05
5	26.92	41.76	8	10	19	-7.5	5.3E-06
6	26.92	41.76	7	9	20	-7.4	5.6E-06
7	26.92	41.21	7	9	18	-7	1.2E-05
8	26.92	41.76	17	11	18	-8.8	6.2E-07
9	26.82	41.9	19	9	24	-8.4	1.1E-06
10	26.78	42.08	14	10	16	-8	2.5E-06
DRB1*09 + 4x5w (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.78	40.98	8	7	12	-7.3	7.7E-06
2	26.78	40.98	9	16	20	-9.3	2.8E-07
3	26.11	41.67	19	5	23	-7.6	4.5E-06
4	27.22	41.11	10	12	23	-7.8	3.0E-06
5	26.78	41.53	16	10	19	-8.4	1.3E-06
6	26.92	40.66	9	7	22	-7.4	6.0E-06
7	26.92	40.66	14	11	17	-8.4	1.1E-06
8	26.78	40.98	7	8	13	-7.2	8.4E-06
9	26.11	41.11	21	9	16	-9.1	3.9E-07
10	26.78	40.98	9	6	15	-6.7	2.0E-05

Table 52: HLA DRB1*09 with Ag peptides 1aqd, 1dlh, 1kg0, 1h15 and 1sje respectively

DRB1*09 + 1aqd							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.37	39.11	21	6	18	-8.8	6.3E-07
2	27.07	39.23	17	5	12	-8.4	1.2E-06
3	27.53	38.76	21	8	14	-9.2	3.3E-07
4	27.32	39.34	11	7	10	-7.6	4.4E-06
5	27.37	39.11	17	4	14	-7.7	3.4E-06
6	27.47	39.01	15	11	17	-9.1	3.6E-07
7	27.47	39.01	10	9	13	-8.1	2.0E-06
8	27.78	38.89	20	5	15	-8.2	1.8E-06
9	27.32	39.34	9	7	11	-7.4	6.0E-06
10	27.32	38.8	11	5	13	-7.1	9.1E-06
DRB1*09 + 1dlh							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.62	39.23	8	7	7	-7	1.2E-05
2	27.32	39.34	10	11	9	-8	2.2E-06
3	26.82	39.66	14	11	10	-8.8	6.2E-07
4	27.32	39.34	9	7	10	-7.1	9.7E-06
5	27.78	38.89	13	8	12	-7.5	5.5E-06
6	27.32	39.34	11	10	7	-8.4	1.2E-06
7	27.47	39.01	13	17	13	-10.1	7.4E-08
8	27.93	39.11	15	11	9	-8.8	6.6E-07
9	27.32	39.34	9	9	9	-7.5	5.5E-06
10	27.32	39.34	12	15	14	-9.6	1.7E-07
DRB1*09 + 1kg0							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.82	40.22	19	7	16	-8.8	6.4E-07
2	27.62	39.78	10	8	21	-7.6	4.3E-06
3	27.47	39.56	20	6	16	-8.2	1.6E-06
4	27.32	39.89	15	1	13	-7.2	8.3E-06
5	27.17	39.67	9	6	10	-7	1.1E-05
6	27.78	39.44	10	3	19	-6.9	1.4E-05
7	27.78	39.44	10	6	21	-7.2	8.5E-06
8	27.47	39.56	20	4	12	-8.1	1.8E-06

9	27.47	39.56	16	3	17	-7.1	9.3E-06
10	27.12	39.55	11	4	20	-7.9	2.9E-06
DRB1*09 + 1h15							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.32	39.34	10	11	9	-8.1	1.9E-06
2	27.78	38.89	9	12	9	-8	2.4E-06
3	27.32	39.34	9	9	11	-7	1.2E-05
4	27.32	39.34	9	13	8	-8.5	1.1E-06
5	27.07	39.23	20	8	8	-8.9	5.5E-07
6	26.82	40.22	15	12	12	-9	4.3E-07
7	27.62	39.23	8	3	8	-6.4	3.2E-05
8	27.32	39.34	7	10	8	-7.7	3.8E-06
9	27.47	39.01	8	4	8	-6.8	1.7E-05
10	28.09	38.76	13	14	8	-8.9	5.3E-07
DRB1*09 + 1sje							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.92	41.76	15	4	21	-7.1	9.6E-06
2	27.07	41.44	6	5	18	-6.5	2.7E-05
3	26.67	41.11	14	4	20	-7.3	7.5E-06
4	26.67	41.67	19	5	26	-7.9	2.7E-06
5	25.82	41.76	20	1	10	-7	1.2E-05
6	26.92	41.21	11	7	20	-7.4	6.0E-06
7	26.78	41.53	7	9	19	-7.1	9.4E-06
8	27.07	41.44	10	6	17	-6.9	1.3E-05
9	25.82	41.76	17	4	10	-7.3	7.5E-06
10	27.07	41.44	9	6	20	-6.8	1.6E-05

Table 53: HLA DRB1*12 with CLIP 1a6a and 4x5w respectively

DRB1*12 + 1a6a (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.37	39.01	11	5	15	-7.6	4.2E-06
2	26.37	39.01	14	4	15	-7.7	3.7E-06
3	26.23	39.89	14	6	15	-7.7	3.6E-06
4	26.23	39.34	8	5	13	-7.4	6.3E-06
5	26.09	39.67	14	4	10	-7.3	6.8E-06
6	26.23	39.34	13	3	17	-7	1.1E-05

7	25.27	40.66	13	9	14	-7.8	3.2E-06
8	26.23	39.34	6	4	10	-6.7	2.0E-05
9	26.23	39.34	8	5	7	-6.9	1.4E-05
10	25.27	40.11	13	8	16	-7.5	5.3E-06
DRB1*12 + 4x5w (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.23	39.34	13	3	16	-7	1.1E-05
2	26.23	38.25	10	5	15	-7.2	8.3E-06
3	26.23	39.34	13	5	17	-7.5	5.1E-06
4	26.09	38.59	8	5	10	-7.2	8.9E-06
5	26.09	39.13	11	4	11	-7.1	9.3E-06
6	26.37	38.46	10	5	15	-7.2	7.8E-06
7	26.37	38.46	15	3	11	-7.6	4.5E-06
8	26.23	38.8	8	5	14	-7.1	9.8E-06
9	26.37	37.91	8	5	14	-7	1.2E-05
10	26.09	38.59	6	5	9	-7.1	1.1E-05

Table 54: HLA DRB1*12 with Ag peptides 1aqd, 1dlh, 1kg0, 1h15 and 1sje respectively

DRB1*12 + 1aqd							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.22	37.22	21	9	15	-9.9	9.8E-08
2	27.07	36.46	15	3	12	-8	2.5E-06
3	27.07	37.02	20	6	15	-8.6	8.0E-07
4	27.07	36.46	19	4	12	-8.5	1.1E-06
5	27.07	36.46	14	3	10	-8.2	1.6E-06
6	26.78	36.61	11	3	8	-7.3	7.3E-06
7	26.67	36.67	11	11	14	-9.4	2.4E-07
8	26.67	37.22	21	5	15	-8.9	5.2E-07
9	27.22	36.67	16	2	13	-8.3	1.3E-06
10	26.63	37.5	8	6	10	-7.4	5.9E-06
DRB1*12 + 1dlh							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.07	36.46	11	14	10	-9.7	1.5E-07
2	27.07	37.02	9	10	6	-8.5	9.4E-07

3	27.07	36.46	8	4	10	-7.1	1.0E-05
4	26.78	37.16	8	7	8	-7.5	5.2E-06
5	27.22	37.22	9	4	12	-7.3	6.9E-06
6	26.92	36.81	11	15	11	-9.7	1.3E-07
7	26.78	37.7	5	13	5	-8.5	1.1E-06
8	26.67	37.22	11	11	8	-9.1	3.9E-07
9	26.92	37.36	10	6	5	-7.4	6.0E-06
10	26.63	37.5	7	4	7	-6.7	2.0E-05
DRB1*12 + 1kg0							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.07	36.46	10	8	8	-8.3	1.4E-06
2	26.37	37.36	8	8	9	-8.4	1.2E-06
3	27.22	36.67	8	4	10	-7.2	8.0E-06
4	26.78	37.16	8	6	7	-7.4	6.4E-06
5	26.78	37.7	9	2	8	-6.6	2.1E-05
6	26.92	36.81	8	11	8	-8.6	8.1E-07
7	27.22	36.67	11	3	13	-7.1	9.7E-06
8	26.78	37.16	6	5	8	-6.8	1.5E-05
9	27.07	37.02	8	6	12	-7.4	5.6E-06
10	26.92	36.81	9	5	12	-7.2	8.7E-06
DRB1*12 + 1h15							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.37	37.91	13	8	11	-8.6	8.4E-07
2	26.92	37.36	17	1	15	-7.6	4.7E-06
3	26.37	37.91	10	8	14	-8.4	1.2E-06
4	26.37	37.91	12	7	15	-8.2	1.7E-06
5	26.78	37.16	12	6	16	-8.1	1.8E-06
6	26.78	37.16	13	4	9	-7.6	4.3E-06
7	26.92	36.81	7	2	11	-6.7	1.9E-05
8	26.78	37.16	18	4	10	-8.1	1.9E-06
9	26.23	38.25	15	7	19	-8.3	1.5E-06
10	26.92	37.91	12	9	14	-8.8	6.6E-07
DRB1*12 + 1sje							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.09	39.67	4	4	14	-6.2	4.0E-05
2	26.52	39.23	8	3	11	-6.6	2.1E-05
3	26.23	39.34	14	5	17	-7.1	9.6E-06

4	25.54	39.67	18	10	13	-9	4.8E-07
5	26.09	39.67	6	3	15	-6.5	2.6E-05
6	26.09	39.13	5	4	14	-6.3	3.4E-05
7	25.56	39.44	14	11	16	-8.9	5.0E-07
8	26.23	38.8	4	4	16	-6.6	2.3E-05
9	25.68	39.89	4	16	18	-8.2	1.7E-06
10	26.23	39.34	5	3	13	-6.1	4.6E-05

Table 55: HLA DRB1*14 with CLIP 1a6a and 4x5w respectively

DRB1*14 + 1a6a (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.52	38.67	15	6	19	-8.1	1.9E-06
2	26.52	38.67	16	5	19	-8.0	2.4E-06
3	26.52	38.67	11	5	14	-7.3	7.4E-06
4	26.67	38.33	14	5	17	-7.7	3.6E-06
5	26.67	38.33	17	7	16	-8.3	1.5E-06
6	26.52	38.67	14	9	29	-8.8	6.4E-07
7	26.52	38.12	12	10	19	-8.4	1.1E-06
8	26.52	38.67	11	10	17	-8.2	1.6E-06
9	26.37	38.46	11	6	14	-7.7	3.9E-06
10	26.37	38.46	15	4	15	-7.9	2.7E-06
DRB1*14 + 4x5w (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.52	38.12	18	8	21	-9.1	4.1E-07
2	25.70	37.99	19	11	22	-9.8	1.3E-07
3	26.82	37.99	17	9	23	-9.3	2.9E-07
4	26.23	38.25	10	6	23	-7.8	3.1E-06
5	26.52	38.12	16	7	19	-8.1	2.1E-06
6	26.67	37.78	19	6	18	-8.9	5.0E-07
7	26.37	38.46	11	3	18	-6.8	1.6E-05
8	26.37	38.46	14	6	17	-8.0	2.4E-06
9	26.37	37.91	14	6	16	-8.0	2.4E-06
10	26.52	38.67	15	7	22	-8.3	1.3E-06

Table 56: HLA DRB1*14 with Ag peptides 1aqd, 1dlh, 1kg0, 1h15 and 1sje respectively

DRB1*14 + 1aqd							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.22	36.11	14	6	17	-8.7	7.7E-07
2	27.22	36.11	16	6	20	-8.9	5.5E-07
3	27.22	36.11	16	4	14	-8.2	1.6E-06
4	27.07	35.91	15	5	15	-8.3	1.4E-06
5	27.07	35.91	15	5	16	-8.5	1.0E-06
6	27.22	36.11	18	4	23	-8.2	1.6E-06
7	27.37	35.75	18	0	25	-7.5	5.4E-06
8	27.07	35.91	24	5	13	-9.3	2.7E-07
9	27.22	36.11	15	1	21	-7.4	5.6E-06
10	27.37	35.75	25	1	19	-8.5	1.0E-06
DRB1*14 + 1dlh							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.37	35.75	14	12	9	-9.5	2.0E-07
2	27.37	36.87	14	7	13	-8.3	1.5E-06
3	27.37	36.31	14	9	15	-8.5	9.9E-07
4	27.37	36.31	14	13	9	-10.0	8.8E-08
5	27.37	36.31	12	4	13	-7.4	6.2E-06
6	27.37	36.31	12	16	7	-10.5	4.0E-08
7	27.37	36.31	13	5	9	-8.0	2.3E-06
8	26.97	37.08	17	17	11	-10.6	3.2E-08
9	27.22	36.11	8	11	7	-8.9	5.1E-07
10	27.53	35.96	14	11	9	-9.6	1.7E-07
DRB1*14 + 1kg0							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.68	35.52	10	13	18	-9.5	2.0E-07
2	25.97	35.36	11	13	16	-9.6	1.7E-07
3	25.97	34.81	13	17	17	-10.9	2.0E-08
4	25.97	35.36	13	3	16	-10.2	6.6E-08
5	25.68	35.52	7	10	17	-8.7	7.0E-07
6	25.82	35.16	6	9	16	-8.1	2.1E-06
7	25.82	35.16	8	9	13	-8.5	9.4E-07

8	26.11	35.00	10	14	15	-9.9	1.1E-07
9	25.68	34.97	5	9	14	-7.8	3.1E-06
10	25.11	35.00	9	13	18	-9.5	1.9E-07
DRB1*14 + 1h15							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.22	36.67	19	1	21	-8.1	1.9E-06
2	27.37	36.87	20	2	22	-8.0	2.2E-06
3	26.11	37.78	17	9	13	-9.6	1.7E-07
4	27.22	36.11	18	2	19	-8.2	1.7E-06
5	27.22	36.67	15	3	20	-7.9	2.7E-06
6	27.07	36.46	17	1	17	-7.5	5.1E-06
7	26.82	37.43	18	4	18	-8.1	2.1E-06
8	26.67	37.22	19	5	22	-8.4	1.1E-06
9	26.82	37.43	20	6	17	-9.0	4.6E-07
10	26.97	36.52	16	4	20	-8.8	6.7E-07
DRB1*14 + 1sje							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.70	39.11	12	8	23	-8.1	1.4E-06
2	26.37	38.46	13	7	24	-8.0	2.3E-06
3	26.37	39.01	13	4	23	-7.4	6.0E-06
4	26.52	38.12	11	4	20	-7.3	7.6E-06
5	26.67	38.33	15	3	16	-7.6	4.6E-06
6	25.56	39.44	9	3	14	-7.0	1.2E-05
7	26.37	39.01	11	6	14	-7.7	3.9E-06
8	26.52	38.67	6	11	11	-8.1	1.8E-06
9	26.52	38.67	15	2	21	-7.3	7.2E-06
10	29.67	38.33	19	4	15	-7.9	2.7E-06

Table 57: HLA DRB1*16 with CLIP 1a6a and 4x5w respectively

DRB1*16 + 1a6a (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.11	40	10	10	23	-7.7	3.5E-06
2	26.11	40.56	10	7	15	-7.1	9.1E-06
3	26.4	39.89	13	7	24	-8.1	1.9E-06
4	25.97	40.33	7	7	21	-7.1	9.7E-06
5	26.26	40.22	9	5	21	-6.9	1.3E-05

6	26.11	40.56	6	15	22	-8.2	1.7E-06
7	25.82	40.11	9	4	13	-6.7	1.9E-05
8	26.67	40	8	10	23	-7.6	4.7E-06
9	26.52	39.78	8	10	24	-7.7	3.6E-06
10	25.97	40.33	7	8	23	-7.3	6.7E-06
DRB1*16 + 4x5w (CLIP)							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.11	40	10	6	16	-7.1	9.5E-06
2	26.52	39.78	11	6	22	-7.3	7.0E-06
3	26.11	39.44	9	7	22	-7.5	5.5E-06
4	26.11	40	12	5	18	-7.6	4.6E-06
5	26.37	39.01	6	7	12	-7.5	5.3E-06
6	26.11	39.44	8	6	19	-7	1.1E-05
7	26.26	39.66	10	8	21	-7.9	2.6E-06
8	25.82	39.56	8	6	15	-7.1	9.1E-06
9	26.11	39.44	8	7	18	-7.5	4.8E-06
10	26.11	39.44	11	4	14	-7.1	1.0E-05

Table 58: HLA DRB1*16 with Ag peptides 1aqd, 1dlh, 1kg0, 1h15 and 1sje respectively

DRB1*16 + 1aqd							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.82	37.99	14	7	16	-8.3	1.4E-06
2	26.82	37.43	22	6	15	-9	4.6E-07
3	26.55	37.29	18	7	16	-9.1	4.0E-07
4	26.52	37.57	9	6	19	-7.7	3.6E-06
5	26.82	37.99	11	9	15	-8.6	9.1E-07
6	26.82	37.43	13	4	13	-7.7	3.5E-06
7	26.67	37.78	10	7	14	-7.9	2.8E-06
8	26.82	37.43	21	5	13	-8.8	6.7E-07
9	26.82	37.43	15	8	18	-8.8	6.7E-07
10	26.82	37.43	17	3	17	-7.6	4.3E-06
DRB1*16 + 1dlh							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.97	37.64	14	13	11	-9	4.2E-07
2	27.22	37.78	8	5	11	-7.2	9.0E-06

3	26.82	37.99	11	7	9	-8	2.2E-06
4	26.82	37.99	13	16	13	-10	9.3E-08
5	27.37	37.43	10	5	10	-7.4	6.1E-06
6	26.82	37.99	9	9	9	-8.2	1.7E-06
7	26.97	38.2	8	9	9	-7.9	2.6E-06
8	26.82	37.99	9	8	8	-8	2.5E-06
9	26.82	37.99	10	11	8	-8.5	9.6E-07
10	26.97	38.2	16	5	10	-7.9	2.6E-06
DRB1*16 + 1kg0							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.22	37.78	9	7	10	-7.7	3.7E-06
2	27.12	37.85	13	15	10	-9.3	2.6E-07
3	27.37	37.99	16	16	13	-10.4	4.8E-08
4	26.97	37.64	11	7	13	-8.3	1.5E-06
5	26.55	38.42	18	12	10	-9.9	1.0E-07
6	26.82	37.99	11	12	9	-8.7	7.7E-07
7	26.97	38.2	10	5	8	-7.4	6.0E-06
8	27.37	37.99	10	5	7	-7.3	7.2E-06
9	26.97	37.64	13	11	11	-9.2	3.4E-07
10	26.97	37.64	8	6	7	-7.4	5.6E-06
DRB1*16 + 1h15							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.67	38.33	15	6	21	-8.3	1.3E-06
2	26.52	38.12	13	5	11	-7.8	3.3E-06
3	26.82	37.99	15	2	17	-7.3	7.3E-06
4	26.67	38.33	12	2	13	-7	1.1E-05
5	26.97	38.2	16	6	13	-8.3	1.3E-06
6	27.22	37.78	10	2	13	-6.8	1.7E-05
7	26.52	38.12	12	4	12	-7.5	5.5E-06
8	26.67	38.33	10	4	18	-7.3	7.2E-06
9	26.82	37.99	16	2	17	-7.3	7.2E-06
10	27.37	37.99	21	5	14	-8.8	6.5E-07
DRB1*16 + 1sje							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.26	40.22	17	6	18	-7.9	2.9E-06
2	26.26	40.22	6	13	18	-8.3	1.3E-06
3	26.37	40.11	7	9	16	-7.4	5.6E-06

4	26.52	39.78	9	11	11	-7.9	2.9E-06
5	26.26	40.22	13	8	19	-8.2	1.6E-06
6	26.11	40	12	6	12	-7.4	5.9E-06
7	26.11	40	11	10	17	-7.9	2.5E-06
8	25.97	40.33	5	3	21	-5.8	8.E-05
9	25.82	40.11	9	12	15	-8.3	1.4E-06
10	25.84	40.45	20	6	20	-8.4	1.3E-06

Annexure VII

Tables showing structural properties for each of the complexes formed by docking via ZDOCK, between HLA DRB-Ag complexes and TCR chain which forms the tri-molecular protein complexes.

Structures listed here are HLA DRB1*01, DRB1*04, DRB1*07, DRB1*08, DRB1*09, DRB1*12, DRB1*14 and DRB1*16, each bound with antigen peptides 1aqd, 1dlh, 1kg0, 1h15 and 1sje (having highest ΔG within the 10 complexes), docked with TCR chains 2xna, 3of6 and 4udu.

[* PC = protein complex, NIS = non-interacting surfaces per property, ICs = no. of interatomic or interfacial contacts per property, C = charged, aP = apolar, P = polar, ΔG = binding affinity, K_d = dissociation constant]

Table 59: HLA DRB-1aqd complex (having highest values within the 10 complexes) with TCR 2xna.

HLA DRB1*01-1aqd (PC-10) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37°C
	C	aP	C-aP	P-aP	aP-aP		
1	26.72	36.36	30	18	21	-12	3.3E-09
2	26.85	36.71	17	9	14	-8.7	7.1E-07
3	26.56	36.86	7	13	7	-9.2	3.1E-07
4	26.49	37.76	17	13	7	-9.1	3.5E-07
5	26.43	36.78	13	11	16	-9.5	2.0E-07
6	25.56	36.86	14	12	16	-9.7	1.5E-07
7	25.2	36.9	3	5	6	-7.2	8.8E-06
8	26.36	36.96	5	8	10	-9.2	3.4E-07
9	26.37	36.81	16	6	11	-8.3	3.4E-07
10	26.63	36.41	11	12	5	-9.3	2.9E-07
HLA DRB*04-1aqd (PC-9) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37°C
	C	aP	C-aP	P-aP	aP-aP		
1	26.46	37.83	13	22	15	-11.5	7.80E-09
2	26.53	37.4	14	21	19	-11.5	7.30E-09
3	25.86	37.47	22	13	15	-10.4	4.50E-08
4	26.32	37.11	12	8	11	-8	2.30E-06
5	26.39	37.2	14	10	17	-9.1	3.80E-07
6	26.39	37.47	7	9	13	-7.5	4.80E-06
7	26.53	37.4	15	18	11	-10.6	3.60E-08
8	26.18	37.17	11	9	11	-8.3	1.40E-06
9	25.78	37.24	16	4	14	-8.7	7.50E-07
10	26.46	37.04	17	8	17	-8.5	1.00E-06

HLA DRB*07-1aqd (PC-9) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.89	37.87	9	19	12	-9.6	1.7E-07
2	26.09	37.23	9	16	10	-9	4.8E-07
3	25.74	37.8	10	7	7	-7.7	3.6E-06
4	25.81	37.37	14	19	16	-10.7	2.8E-08
5	25.68	37.84	13	11	14	-7.9	2.5E-06
6	25.54	37.90	9	23	10	-11	1.9E-08
7	26.02	37.67	5	14	13	-9.1	3.9E-07
8	25.61	37.47	17	17	12	-10.8	2.6E-08
9	26.23	37.43	7	5	2	-7.7	3.6E-06
10	26.02	37.4	13	28	7	-12.4	1.9E-09
HLA DRB*08-1aqd (PC-3) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.43	36.51	21	18	22	-11.9	3.9E-09
2	25.89	36.51	28	9	14	-10.3	5.7E-08
3	26.22	37.76	12	16	18	-9.3	2.8E-07
4	25.8	36.7	10	7	7	-8.1	1.9E-06
5	26.15	36.66	9	13	15	-9.5	2.0E-07
6	25.54	36.68	21	11	21	-10.2	6.0E-08
7	26.01	36.73	19	19	11	-11.5	7.8E-09
8	26.15	36.39	11	14	10	-10.1	7.8E-08
9	26.08	36.85	15	14	14	-9.8	1.2E-07
10	26.09	36.68	15	11	16	-8.9	5.5E-07
HLA DRB1*09-1aqd (PC-1) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.9	37.5	15	22	15	-11.7	5.6E-09
2	26.9	37.5	11	14	14	-8.6	8.5E-07
3	27.25	37.33	24	19	25	-11.5	7.6E-09
4	27.03	37.57	14	24	18	-12	3.3E-09
5	26.83	37.4	11	14	9	-8.5	9.6E-07
6	26.83	37.67	9	16	10	-9.0	4.3E-07
7	26.81	37.27	10	15	10	-9.7	1.5E-07
8	27.17	37.5	15	17	16	-9.6	1.6E-07
9	26.95	37.47	15	26	15	-12.4	1.8E-09
10	27.05	37.7	10	21	10	-10.1	7.1E-08

HLA DRB*12-1aqd (PC-1) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.81	36.46	14	13	19	-10.1	8.1E-08
2	26.81	36.46	9	10	12	-9	4.7E-07
3	27.1	36.31	19	10	18	-9.8	1.3E-07
4	26.34	36.83	15	10	18	-8.8	6.4E-07
5	26.68	36.66	8	11	12	-8.7	7.5E-07
6	26.34	36.83	10	12	14	-9.1	3.7E-07
7	26.54	36.73	9	10	9	-8.5	1.1E-06
8	26.88	36.56	8	8	8	-8.2	1.7E-06
9	26.74	36.63	10	8	12	-8.5	1.0E-06
10	26.74	36.63	10	9	10	-8.8	6.0E-07
HLA DRB*14-1aqd (PC-8) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.61	36.02	18	11	20	-10.3	5.5E-08
2	26.83	35.77	31	13	24	-12.1	3.1E-09
3	26.67	35.73	7	10	7	-8.6	8.0E-07
4	26.81	35.92	21	10	14	-9.8	1.3E-07
5	27.03	35.95	9	17	13	-10.5	3.8E-08
6	26.61	36.56	15	16	15	-10.3	5.9E-08
7	26.60	35.9	12	6	17	-8.1	1.9E-06
8	26.74	36.1	12	12	15	-9.8	1.2E-07
9	27.1	36.04	14	14	15	-9.3	3.0E-07
10	26.81	35.92	7	13	5	-9	4.7E-07
HLA DRB*16-1aqd (PC-4) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.42	36.93	19	10	22	-9.4	2.5E-07
2	26.47	36.9	6	7	9	-7.7	3.9E-06
3	26.34	37.1	17	12	17	-9.4	2.4E-07
4	26.47	36.9	19	11	19	-10.1	8.0E-08
5	26.34	36.56	17	13	12	-9.9	1.0E-07
6	26.13	36.8	13	4	9	-8.1	1.8E-06
7	26.47	36.63	18	9	13	-9.7	1.5E-07
8	26.76	36.76	21	11	13	-10.7	2.7E-08
9	26.54	36.73	17	17	13	-11.2	1.4E-08
10	26.47	36.36	19	6	13	-9.5	2.0E-07

Table 60: HLA DRB-1dlh complex (having highest values within the 10 complexes) with TCR 2xna.

HLA DRB*01-1dlh (PC-3) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.72	37.19	16	10	6	-9.9	1.0E-07
2	26.92	36.26	25	11	13	-10.8	2.3E-08
3	25.95	37.3	12	6	4	-8.7	7.2E-07
4	26.29	36.86	9	10	4	-9.2	3.5E-07
5	26.85	36.71	10	8	7	-8.1	2.0E-06
6	26.49	37.03	1	5	3	-7.8	3.4E-06
7	26.9	36.41	14	6	2	-8.5	1.1E-06
8	25.89	37.06	8	5	4	-8	2.1E-06
9	26.5	37.16	12	9	9	-9.3	2.7E-07
10	26.47	36.9	13	4	2	-8.3	1.5E-06
HLA DRB*04-1dlh (PC-8) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.92	37.43	18	6	6	-9.7	1.5E-07
2	25.85	37.6	16	2	5	-8.2	1.8E-06
3	25.86	37.87	12	7	5	-8.6	8.2E-07
4	26.05	38.16	16	11	12	-8.8	6.0E-07
5	26.05	37.11	14	4	6	-8.7	7.7E-07
6	26.03	37.63	2	3	3	-6.5	2.7E-05
7	26.12	37.99	16	9	10	-8.8	6.5E-07
8	26.3	37.24	7	7	2	-7.9	2.6E-06
9	26.05	37.89	20	11	7	-10	8.4E-08
10	25.59	38.12	10	5	4	-7.9	2.7E-06
HLA DRB*07-1dlh (PC-1) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.20	37.8	9	4	4	-7.7	3.8E-06
2	25.61	37.74	13	7	6	-8.4	1.1E-06
3	25.07	38.13	9	5	4	-7.9	2.9E-06
4	25.68	37.57	11	5	6	-8.1	2.0E-06
5	25.8	37.77	9	5	5	-7.8	3.0E-06
6	25.34	37.74	7	6	4	-7.6	4.2E-06
7	25.8	37.5	10	8	4	-8.7	7.8E-07

8	25.27	37.77	18	8	5	-9.5	2.1E-07
9	25.94	37.7	11	8	4	-8.4	1.2E-06
10	26.02	37.4	10	5	6	-7.2	8.5E-06
HLA DRB*08-1dlh (PC-1) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.16	36.78	16	17	12	-10.8	2.5E-08
2	25.88	36.93	10	6	8	-7.6	4.2E-06
3	26.36	36.96	9	17	12	-10	8.2E-08
4	25.88	36.93	8	12	4	-7.7	3.7E-06
5	26.43	36.78	13	12	7	-8.8	5.8E-07
6	26.58	36.99	16	9	8	-8.5	9.9E-07
7	26.16	36.78	14	15	7	-9.5	2.1E-07
8	26.36	36.96	15	12	14	-9.3	2.7E-07
9	26.08	36.83	8	7	7	-7.7	3.5E-06
10	26.92	36.81	15	17	11	-9.7	1.4E-07
HLA DRB1*09-1dlh (PC-7) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.61	37.9	17	8	5	-9.3	2.9E-07
2	26.67	37.6	5	12	5	-7.7	4.0E-06
3	27.25	37.6	19	16	9	-10.2	6.6E-08
4	26.68	37.47	16	9	3	-8.2	1.7E-06
5	26.88	37.37	22	22	15	-12.5	1.5E-09
6	26.93	37.6	12	14	11	-8.6	8.8E-07
7	27.01	36.9	10	19	15	-9.4	2.5E-07
8	26.6	37.5	6	10	4	-7.3	6.7E-06
9	27.01	37.17	13	20	19	-9.8	1.2E-07
10	26.86	37.5	8	8	9	-7.9	2.6E-06
HLA DRB1*12-1dlh (PC-2) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.76	37.03	6	19	5	-9.1	4.1E-07
2	26.56	36.86	15	8	7	-7.9	2.7E-06
3	26.68	37.2	5	18	7	-7.9	2.6E-06
4	27.17	36.14	16	10	11	-8.4	1.2E-06
5	27.03	36.22	14	7	9	-7.5	4.8E-06
6	26.81	36.19	10	6	6	-6.8	1.5E-05
7	26.68	36.93	3	14	5	-7.5	5.5E-06

8	26.76	37.3	7	17	6	-8.3	1.5E-06
9	26.83	36.59	12	14	8	-9.2	3.3E-07
10	27.1	36.31	13	7	9	-7.4	6.0E-06
HLA DRB*14-1dlh (PC-8) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.05	36.61	12	18	14	-10	9.6E-08
2	26.83	36.04	9	17	6	-10.6	3.2E-08
3	26.61	36.02	23	5	12	-9.1	3.6E-07
4	26.85	37.53	10	19	11	-10.3	5.3E-08
5	26.98	36.51	14	23	12	-11.3	1.E-08
6	26.98	36.51	10	21	3	-11.1	1.4E-08
7	26.98	35.69	27	15	18	-11.6	6.4E-09
8	26.92	35.99	25	11	8	-10.7	3.E-08
9	26.83	36.31	17	17	11	-10.9	2.1E-08
10	26.56	36.59	21	14	12	-10.4	4.6E-08
HLA DRB1*16-1dlh (PC-5) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.17	36.96	5	15	6	-7.8	3.1E-06
2	27.1	36.59	15	19	18	-10.9	2.2E-08
3	27.4	36.71	11	22	12	-10.6	3.4E-08
4	26.98	36.51	12	16	13	-9.7	1.4E-07
5	27.1	36.59	12	17	15	-10.1	7.3E-08
6	26.95	36.66	4	15	6	-8.2	1.7E-06
7	26.98	36.78	7	13	11	-7.6	4.3E-06
8	27.1	36.86	2	14	10	-8.5	1.0E-06
9	27.17	36.68	5	12	6	-8	2.4E-06
10	26.61	37.1	10	5	5	-7.0	1.2E-05

Table 61: HLA DRB-1kg0 complex (having highest values within the 10 complexes) with TCR 2xna.

HLA DRB*01-1kg0 (PC-9) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	24.93	37.53	18	5	6	-9.6	1.8E-07
2	25.07	37.6	13	2	5	-8	2.4E-06
3	25.46	37.8	20	14	8	-10.6	3.4E-08
4	25.07	37.73	12	6	7	-8.5	1.1E-06

5	25.26	37.89	23	11	7	-10.7	2.7E-08
6	25.26	37.5	16	3	6	-8.7	7.6E-07
7	25.13	37.7	15	4	6	-8.9	5.5E-07
8	25.26	37.63	5	4	4	-7.3	7.1E-06
9	25	37.5	23	11	6	-10.4	4.3E-08
10	25.65	37.7	9	7	2	-6.8	1.7E-05

HLA DRB*04-1kg0 (PC-5) + 2xna

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.73	37.4	21	28	12	-12.2	2.6E-09
2	25.93	37.04	9	22	12	-10.1	7.E-08
3	25.13	37.7	23	15	12	-11.1	1.5E-08
4	25.59	37.47	19	18	13	-10.1	7.4E-08
5	25.13	37.57	16	8	9	-9.4	2.2E-07
6	25.53	37.37	15	15	10	-9.5	1.8E-07
7	25.72	37.27	3	19	9	-8.1	2.E-06
8	25	37.63	19	12	12	-10.5	3.7E-08
9	24.93	37.27	16	8	9	-9.6	1.7E-07
10	25.26	37.5	10	13	3	-8.3	1.4E-06

HLA DRB*07-1kg0 (PC-4) + 2xna

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.82	36.96	8	25	13	-9.6	1.7E-07
2	25.33	37.07	4	16	7	-7.8	3.3E-06
3	25.68	37.03	15	15	14	-9.5	2.E-07
4	25.2	37.14	8	5	4	-7	1.2E-05
5	25.4	37.17	8	21	11	-9.7	1.5E-07
6	25.47	37.53	10	13	7	-8.1	2.E-06
7	25.34	37.06	29	28	19	-13	6.8E-10
8	25	36.83	16	14	6	-10.1	7.9E-08
9	25.4	37.17	8	19	13	-9	4.3E-07
10	25.54	37.1	9	20	8	-9.6	1.6E-07

HLA DRB*08-1kg0 (PC-3) + 2xna

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.61	35.97	9	20	12	-10.2	6.2E-08
2	26.03	35.89	26	26	33	-13.4	3.3E-10
3	25.89	35.97	17	24	9	-11.5	7.6E-09
4	25.88	36.12	12	19	8	-9.6	1.8E-07
5	26.03	35.62	18	25	25	-11.6	6.7E-09

6	25.95	35.95	7	15	10	-8.4	1.3E-06
7	25.74	35.66	14	17	11	-10.1	7.6E-08
8	25.47	35.92	10	14	5	-9.2	3.3E-07
9	25.53	35.9	2	13	2	-8.1	2.E-06
10	26.02	36.04	19	17	11	-10.6	3.5E-08

HLA DRB1*09-1kg0 (PC-6) + 2xna

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.56	38.21	11	13	4	-8.1	2.0E-06
2	26.92	37.91	15	29	16	-12.3	2.0E-09
3	26.83	37.94	11	21	15	-10.4	4.6E-08
4	26.92	37.64	25	14	22	-10.4	4.8E-08
5	26.42	38.27	8	9	6	-7.0	1.2E-05
6	26.76	38.38	13	20	12	-9.4	2.2E-07
7	26.76	38.38	14	15	10	-9.6	1.7E-07
8	27.05	37.98	13	16	11	-10	8.4E-08
9	26.9	38.04	14	16	12	-9.2	3.5E-07
10	26.61	37.9	7	11	5	-8.5	1.1E-06

HLA DRB1*12-1kg0 (PC-6) + 2xna

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.9	35.87	25	10	10	-10.6	3.1E-08
2	26.47	36.36	13	9	5	-8.7	7.2E-07
3	26.54	35.92	12	6	7	-8.4	1.2E-06
4	26.22	36.49	19	8	5	-9.6	1.7E-07
5	26.47	36.36	9	6	5	-7.5	4.8E-06
6	26.53	36.07	7	8	7	-7.8	3.0E-06
7	26.49	35.95	15	7	7	-8.7	7.0E-07
8	26.42	36.12	17	7	5	-8.4	1.1E-06
9	26.56	36.31	23	8	4	-9.3	2.8E-07
10	26.47	36.36	7	5	5	-7.0	1.1E-05

HLA DRB*14-1kg0 (PC-3) + 2xna

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.36	35.33	15	19	8	-10.8	2.4E-08
2	25.88	35.58	6	11	3	-9.6	1.7E-07
3	26.16	35.42	17	11	10	-11.6	6.9E-09
4	26.34	35.48	23	18	8	-8.8	6.6E-07
5	26.06	35.37	8	11	4	-8.5	1.1E-06
6	25.6	35.73	3	7	4	-9.2	3.2E-07

7	25.75	35.23	7	11	5	-10.4	4.8E-08
8	26.23	34.97	22	11	13	-10	9.4E-08
9	25.87	35.2	22	11	10	-9	4.7E-07
10	26.27	35.66	6	11	3	-7.8	3.4E-06
HLA DRB1*16-1kg0 (PC-3) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.4	36.99	15	15	14	-9.6	1.8E-07
2	26.98	37.33	7	14	9	-8.1	1.9E-06
3	26.98	37.06	16	22	12	-10.9	2.1E-08
4	27.27	37.19	13	22	12	-10.3	5.2E-08
5	26.9	36.96	12	7	10	-7.9	2.7E-06
6	27.05	37.16	19	15	10	-9.8	1.3E-07
7	26.92	37.09	18	25	22	-12.9	7.4E-10
8	26.98	37.06	17	12	8	-9.2	3.2E-07
9	26.7	37.33	15	8	7	-8.4	1.2E-06
10	26.27	37.27	9	11	4	-8.1	2.1E-06

Table 62: HLA DRB-1h15 complex (having highest values within the 10 complexes) with TCR 2xna.

HLA DRB*01-1h15 (PC-1) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.76	37.03	10	7	4	-7.4	5.9E-06
2	27.2	37.09	13	22	12	-11.4	8.8E-09
3	26.9	37.23	19	11	7	-9.7	1.6E-07
4	26.85	36.99	15	10	10	-9.2	3.4E-07
5	27.12	36.99	15	18	18	-9.7	1.5E-07
6	26.63	36.68	15	15	7	-10.5	4.E-08
7	26.98	37.33	22	13	10	-10.3	5.7E-08
8	26.83	36.86	14	6	6	-8.3	1.4E-06
9	27.12	37.26	17	16	10	-10.2	5.9E-08
10	26.68	37.2	10	8	4	-7.6	4.2E-06
HLA DRB*04-1h15 (PC-10) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.26	38.2	21	14	18	-10	8.3E-08
2	26.47	38.5	22	18	17	-11	1.8E-08
3	26.44	38.22	8	9	13	-8.1	2.E-06

4	26.46	38.1	17	8	11	-8.5	1.E-06
5	26.53	38.2	12	23	13	-11.2	1.3E-08
6	26.18	38.22	11	13	8	-8.6	8.1E-07
7	26.25	38.32	12	10	13	-8.6	8.4E-07
8	26.46	38.36	19	15	18	-10.4	4.5E-08
9	26.25	38.06	16	10	19	-10.4	4.5E-08
10	25.92	38.48	16	10	15	-9.3	2.7E-07
HLA DRB*07-1h15 (PC-7) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.89	37.6	16	19	11	-11.4	8.7E-09
2	26.02	37.13	22	16	16	-11	1.7E-08
3	26.15	37.74	10	12	3	-9.1	4.E-07
4	25.34	37.74	16	14	16	-9.5	2.1E-07
5	26.09	37.77	20	20	17	-11.9	4.1E-09
6	26.15	37.74	23	9	9	-10	8.9E-08
7	26.01	37.53	15	11	13	-9.2	3.1E-07
8	25.75	37.4	21	18	22	-11.5	8.3E-09
9	26.02	37.67	19	15	13	-10.3	5.4E-08
10	26.02	37.94	18	8	3	-8.3	1.5E-06
HLA DRB*08-1h15 (PC-3) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.95	36.76	13	10	12	-9.2	3.1E-07
2	25.88	36.66	15	9	7	-9.4	2.2E-07
3	25.88	36.39	14	8	8	-9.1	4.1E-07
4	25.82	36.68	10	8	19	-8.9	5.2E-07
5	26.08	36.83	12	9	13	-8.9	5.5E-07
6	26.17	36.91	19	19	6	-11.5	7.5E-09
7	26.43	36.78	8	3	7	-7.5	5.1E-06
8	26.43	36.51	12	15	8	-10.4	4.4E-08
9	25.75	36.59	14	10	15	-9.5	2.E-07
10	25.95	36.76	16	13	8	-10.5	3.9E-08
HLA DRB1*09-1h15 (PC-1) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.36	38.04	20	8	17	-9.8	1.3E-07
2	26.98	37.6	15	8	7	-9.1	4.0E-07
3	26.83	37.67	17	4	9	-7.4	6.1E-06
4	26.56	37.94	21	17	10	-12	3.5E-09

5	26.78	37.98	18	13	10	-10.1	7.9E-08
6	26.43	38.15	22	15	16	-10.1	8.0E-08
7	26.63	37.77	21	10	17	-9.2	3.4E-07
8	26.27	38.07	16	8	9	-8.9	5.3E-07
9	26.43	38.15	15	11	9	-9.5	1.90E-07
10	26.43	37.87	18	14	10	-10.9	1.9E-08
HLA DRB1*12-1h15 (PC-1) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.76	37.03	16	16	7	-10.9	2.0E-08
2	26.08	36.83	14	10	13	-8.3	1.3E-06
3	26.27	36.73	14	12	10	-10	8.3E-08
4	26.2	36.63	11	9	8	-9.0	4.5E-07
5	26.01	37.00	17	9	8	-9.5	1.9E-07
6	26.34	36.83	11	12	9	-9.6	1.7E-07
7	26.54	36.73	7	6	4	-7.5	5.6E-06
8	26.4	36.53	21	11	12	-10.3	5.9E-08
9	26.61	36.83	8	17	4	-9.9	9.9E-08
10	26.2	37.17	14	4	4	-7.8	3.4E-06
HLA DRB*14-1h15 (PC-3) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.42	36.39	21	9	13	-10.2	6.4E-08
2	26.43	36.78	19	16	10	-11	1.7E-08
3	26.49	36.76	11	11	4	-9.2	3.3E-07
4	26.13	36.8	13	6	4	-8.2	1.6E-06
5	26.06	36.97	8	7	2	-8.3	1.4E-06
6	26.49	36.49	18	9	9	-10.3	5.9E-08
7	25.94	36.90	13	8	11	-8.9	5.7E-07
8	26.22	36.49	16	9	9	-9.4	2.3E-07
9	26.63	36.41	19	8	7	-9.7	1.3E-07
10	26.36	36.96	22	11	8	-10.4	5.E-08
HLA DRB1*16-1h15 (PC-10) + 2xna							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.76	37.03	18	13	8	-10.4	5.0E-08
2	26.83	36.86	6	6	7	-7.8	3.3E-06
3	26.56	36.86	11	7	7	-7.9	2.8E-06
4	26.83	36.86	9	9	6	-8.3	1.5E-06
5	27.03	36.76	11	8	9	-8.3	1.3E-06

6	27.32	36.89	12	14	7	-9.9	1.0E-07
7	27.12	36.71	15	11	11	-9	4.3E-07
8	26.76	37.03	11	10	7	-9	4.7E-07
9	26.68	37.2	10	5	5	-7	1.1E-05
10	26.61	37.1	15	6	6	-8.4	1.2E-06

Table 63: HLA DRB-1sje complex (having highest values within the 10 complexes) with TCR 2xna.

HLA DRB*01-1sje (PC-10) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.12	39.05	14	16	18	-10	9.6E-08
2	25.93	39.15	15	16	18	-10.1	8.E-08
3	25.65	39.01	15	15	11	-10.1	7.5E-08
4	25.98	39.37	18	10	9	-9	4.8E-07
5	26.05	38.95	14	12	19	-9.3	2.9E-07
6	25.99	38.73	27	19	24	-11.9	3.9E-09
7	26.05	38.95	16	7	11	-8	2.5E-06
8	26.32	39.21	10	17	9	-9.2	3.E-07
9	25.85	38.9	11	17	12	-9.9	1.1E-07
10	25.52	39.06	13	11	10	-8.6	8.4E-07
HLA DRB*04-1sje (PC-7) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.46	39.11	12	19	15	-10.2	6.1E-08
2	25.33	39.31	9	16	14	-9	4.3E-07
3	25.26	39.21	8	17	10	-9.1	3.9E-07
4	25.26	39.06	14	9	9	-7.6	4.2E-06
5	25.59	39.05	11	9	12	-7.9	2.9E-06
6	25.2	39.37	11	13	7	-8.9	5.7E-07
7	25.19	38.96	10	10	10	-8.2	1.8E-06
8	25.73	38.73	18	14	16	-10	8.6E-08
9	25.39	39.27	10	8	13	-7.9	2.7E-06
10	25.53	38.95	22	15	26	-10.2	7.E-08
HLA DRB*07-1sje (PC-2) + 2xna							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.33	38.40	9	10	10	-8.5	9.6E-07
2	25.40	38.50	12	12	6	-9.3	2.6E-07

3	25.27	38.56	11	11	12	-8.7	6.8E-07
4	25.27	38.56	10	8	12	-8.2	1.8E-06
5	25.33	38.40	18	14	16	-9.9	1.1E-07
6	25.74	38.61	14	11	10	-9.3	3.E-07
7	25.41	38.65	20	8	17	-9.6	1.7E-07
8	25.27	38.56	17	13	17	-10	9.E-08
9	25.81	38.17	12	7	14	-7.9	2.5E-06
10	25.67	38.24	11	8	16	-8.1	2.E-06

HLA DRB*08-1sje (PC-4) + 2xna

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.02	36.77	20	25	28	-12.4	1.8E-09
2	26.65	37.36	15	21	28	-10.5	4.3E-08
3	26.23	37.98	17	22	23	-11.3	1.1E-08
4	26.58	36.99	19	15	25	-10.0	9.4E-08
5	26.87	36.57	16	22	33	-12.0	3.6E-09
6	26.65	37.64	18	26	24	-12.2	2.4E-09
7	26.50	37.70	13	22	16	-10.4	4.3E-08
8	26.87	36.57	26	29	35	-14.3	8.7E-11
9	26.50	37.43	8	16	23	-9.4	2.3E-07
10	26.59	36.57	21	20	47	-11.4	9.5E-09

HLA DRB1*09-1sje (PC-1) + 2xna

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.54	38.87	13	10	14	-8	2.3E-06
2	26.88	38.44	6	10	8	-7.8	3.1E-06
3	26.47	38.77	8	12	8	-7.7	3.8E-06
4	26.9	38.04	9	22	28	-10.4	4.5E-08
5	26.76	38.38	15	21	25	-11.1	1.4E-08
6	26.95	38.54	19	17	13	-8.7	7.2E-07
7	26.61	38.44	14	12	12	-8.2	1.6E-06
8	26.9	38.86	13	18	22	-10	9.6E-08
9	26.33	38.83	12	7	7	-7.9	2.5E-06
10	26.54	38.61	9	12	9	-7.8	3.1E-06

HLA DRB1*12-1sje (PC-7) + 2xna

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.36	37.23	15	19	17	-11.8	4.7E-09
2	26.08	37.37	14	13	10	-9.6	1.7E-07
3	26.08	37.37	11	14	11	-9.3	2.6E-07

4	25.47	37.8	15	8	8	-8.7	7.8E-07
5	26.29	36.86	13	13	13	-9.9	1.1E-07
6	25.74	37.53	17	7	8	-8.7	7.9E-07
7	26.36	37.77	14	26	14	-10.7	3.0E-08
8	25.6	37.6	10	8	7	-8	2.3E-06
9	25.95	37.57	13	8	11	-8.2	1.8E-06
10	25.74	37.8	9	11	16	-8.6	8.3E-07

HLA DRB*14-1sje (PC-8) + 2xna

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.13	37.33	13	11	12	-9.3	2.6E-07
2	26.2	37.43	12	10	12	-8.8	6.2E-07
3	26.47	37.17	8	8	19	-8.1	2.1E-06
4	26.4	37.33	13	4	13	-7.7	3.6E-06
5	26.26	37.67	7	8	7	-7.8	3.2E-06
6	26.83	37.13	14	25	22	-11.8	5.E-09
7	26.4	37.33	7	8	9	-7.8	3.E-06
8	26.47	37.43	7	12	11	-8.8	6.1E-07
9	26.06	37.50	15	12	10	-9.5	1.9E-07
10	26.61	36.83	24	16	32	-11.2	1.2E-08

HLA DRB1*16-1sje (PC-8) + 2xna

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.34	37.9	11	15	14	-9.8	1.2E-07
2	26.42	37.47	15	10	15	-9.2	3.5E-07
3	26.56	37.94	10	20	21	-10.1	7.3E-08
4	26.63	38.04	11	23	14	-11.1	1.6E-08
5	26.42	38.01	16	14	14	-9.4	2.5E-07
6	26.49	37.84	11	14	14	-9	4.5E-07
7	26.34	37.9	10	8	10	-8	2.2E-06
8	26.29	37.94	8	15	16	-9	4.3E-07
9	26.34	37.9	21	19	26	-11.2	1.2E-08
10	26.42	38.01	10	17	16	-9.9	9.7E-08

Table 64: HLA DRB-1aqd complex (having highest values within the 10 complexes) with TCR 3of6.

HLA DRB*01-1aqd (PC-10) + 3of6							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.45	38.02	20	12	16	-10.1	7.6E-08
2	26.23	37.98	17	9	10	-9.8	1.3E-07
3	26.58	37.53	16	7	11	-8.9	5.6E-07
4	26.37	37.91	22	7	11	-9.7	1.4E-07
5	26.37	37.64	14	12	20	-9.0	4.2E-07
6	26.65	37.64	14	9	14	-8.1	1.8E-06
7	26.50	37.98	24	10	9	-10.3	5.2E-08
8	26.52	37.85	14	8	10	-9.0	4.4E-07
9	26.50	37.70	17	8	8	-8.7	7.2E-07
10	26.58	37.81	20	11	21	-9.1	3.7E-07
HLA DRB*04-1aqd (PC-9) + 3of6							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.99	38.73	19	15	25	-10.4	4.5E-08
2	25.98	38.58	15	4	13	-8.0	2.2E-06
3	25.98	38.85	18	15	25	-10.3	5.5E-08
4	25.98	39.11	8	10	16	-8.2	1.6E-06
5	25.99	38.73	19	14	23	-10.2	6.6E-08
6	26.13	38.93	20	12	12	-10.0	8.2E-08
7	25.99	38.46	19	11	18	-9.4	2.5E-07
8	26.05	38.68	15	14	21	-10.1	8.1E-08
9	25.98	39.11	6	8	15	-7.3	7.5E-06
10	26.26%	38.73	17	10	11	-9.4	2.3E-07
HLA DRB*07-1aqd (PC-9) + 3of6							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.96	38.80	14	18	13	-10.0	8.9E-08
2	25.89	38.69	10	21	15	-10.7	2.9E-08
3	25.89	38.96	12	21	19	-10.7	3.1E-08
4	25.96	38.52	16	16	14	-10.1	7.7E-08
5	25.90	38.84	10	21	23	-9.9	1.1E-07
6	25.75	38.75	9	17	16	-9.4	2.3E-07
7	25.96	38.52	16	19	29	-10.6	3.5E-08

8	26.17	38.57	22	27	20	-13.1	5.5E-10
9	25.82	38.74	26	17	12	-11.7	5.8E-09
10	25.75	39.02	17	21	15	-11.3	1.1E-08
HLA DRB*08-1aqd (PC-3) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.10	37.64	17	19	23	-11.4	9.2E-09
2	26.04	38.23	24	23	18	-12.3	2.1E-09
3	26.23	37.70	10	6	16	-7.2	7.8E-06
4	26.10	37.36	12	12	17	-8.6	8.8E-07
5	26.23	37.43	18	12	17	-9.9	9.9E-08
6	25.75	37.94	18	15	20	-10.4	4.6E-08
7	26.09	37.77	14	11	17	-9.4	2.5E-07
8	26.23	37.43	13	10	16	-8.4	1.2E-06
9	25.82	38.04	14	16	21	-10.6	3.5E-08
10	26.17	37.74	16	18	20	-11.0	1.6E-08
HLA DRB1*09-1aqd (PC-1) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.12	38.36	9	20	19	-10	9.3E-08
2	26.63	38.86	12	17	20	-9.5	2.1E-07
3	27.05	38.25	13	21	19	-10.8	2.3E-08
4	27.12	38.63	19	18	29	-10.8	2.6E-08
5	26.78	38.8	13	22	13	-10.3	5.5E-08
6	26.37	39.29	18	23	13	-12.2	2.7E-09
7	26.78	38.8	11	19	15	-9.7	1.4E-07
8	26.8	38.67	17	25	29	-11.7	5.7E-09
9	27.12	38.36	13	25	25	-11.1	1.5E-08
10	26.9	38.86	18	15	12	-9.4	2.5E-07
HLA DRB*12-1aqd (PC-1) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.9	37.5	16	6	12	-8.8	5.9E-07
2	26.56	38.21	11	7	15	-7.5	4.9E-06
3	26.56	37.94	10	7	16	-7.7	3.9E-06
4	26.63	37.5	15	8	9	-9	4.3E-07
5	26.49	38.11	11	8	13	-7.9	2.8E-06
6	26.63	37.77	17	12	17	-9.6	1.7E-07
7	26.76	37.57	14	10	17	-9.1	4.0E-07

8	26.49	38.11	9	9	15	-8	2.3E-06
9	26.68	38.01	10	9	11	-8.1	1.9E-06
10	26.49	38.11	9	6	13	-7.3	6.8E-06
HLA DRB*14-1aqd (PC-8) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.83	36.86	17	17	23	-10.7	2.8E-08
2	27.05	37.43	13	20	15	-11.2	1.2E-08
3	26.49	37.57	14	15	12	-10.0	9.6E-08
4	26.83	37.13	14	14	25	-10.0	9.3E-08
5	26.61	37.10	13	10	22	-8.9	5.4E-07
6	26.83	37.13	16	18	26	-10.9	2.1E-08
7	26.61	37.37	15	14	17	-10.1	8.1E-08
8	26.83	36.86	16	12	19	-9.7	1.5E-07
9	26.68	36.93	14	14	13	-9.9	1.E-07
10	27.05	36.61	25	17	28	-11.7	5.5E-09
HLA DRB*16-1aqd (PC-4) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.42	37.74	16	13	19	-10	9.1E-08
2	26.42	38.01	13	11	16	-9.1	4.0E-07
3	26.42	38.01	13	12	21	-9.5	2.0E-07
4	26.36	38.04	23	11	23	-10.2	6.8E-08
5	26.34	37.9	9	17	18	-10.1	7.9E-08
6	26.09	38.04	19	8	16	-9.2	3.1E-07
7	26.34	37.9	17	7	13	-8.9	5.4E-07
8	26.34	38.17	9	11	14	-8.7	7.9E-07
9	26.56	37.67	14	9	19	-8.9	5.6E-07
10	26.42	38.01	6	8	14	-7.8	3.2E-06

Table 65: HLA DRB-1dlh complex (having highest values within the 10 complexes) with TCR 3of6.

HLA DRB*01-1dlh (PC-3) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.65	38.46	13	11	10	-8.9	5.7E-07
2	26.87	37.67	24	10	9	-10.7	2.9E-08
3	26.65	37.91	16	6	14	-9.3	2.6E-07
4	26.80	38.40	14	14	12	-9.3	2.6E-07

5	27.02	37.60	17	22	19	-11.5	8.2E-09
6	26.78	38.52	13	14	10	-8.9	5.1E-07
7	26.78	37.70	13	12	14	-9.5	2.E-07
8	26.72	38.02	16	19	19	-10.1	8.E-08
9	26.85	38.08	15	10	8	-8.9	5.6E-07
10	26.70	37.87	23	10	9	-10.4	4.7E-08
HLA DRB*04-1dlh (PC-8) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.26	38.99	17	17	22	-10.5	4.1E-08
2	26.46	38.89	14	16	16	-9.5	2.1E-07
3	26.19	39.15	19	12	16	-9.6	1.7E-07
4	26.13	39.47	22	15	12	-11.0	1.7E-08
5	26.39	39.05	11	18	12	-9.8	1.3E-07
6	26.19	39.15	13	16	15	-10.0	8.5E-08
7	26.40	39.20	14	19	14	-10.1	7.8E-08
8	26.01	39.14	20	14	9	-10.3	5.6E-08
9	26.33	39.10	18	12	13	-8.9	5.E-07
10	26.39	39.05	12	11	11	-8.2	1.7E-06
HLA DRB*07-1dlh (PC-1) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.89	38.69	15	9	12	-8.6	8.9E-07
2	25.89	38.96	8	8	13	-7.4	6.1E-06
3	25.81	39.25	10	14	9	-8.4	1.1E-06
4	25.88	39.08	12	12	13	-8.4	1.2E-06
5	25.96	38.80	21	6	11	-8.6	9.2E-07
6	26.03	38.90	21	12	13	-9.5	2.E-07
7	25.97	38.67	21	22	13	-11.3	1.E-08
8	25.88	39.08	6	6	9	-6.9	1.3E-05
9	26.02	39.02	14	11	11	-9.1	3.6E-07
10	25.82	38.86	15	11	13	-8.7	7.2E-07
HLA DRB*08-1dlh (PC-1) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.52	37.85	9	22	13	-10.6	3.4E-08
2	26.58	38.08	10	18	13	-9.2	3.E-07
3	25.89	38.15	11	12	6	-8.8	6.7E-07
4	26.23	38.25	13	15	12	-9.9	1.1E-07
5	26.29	37.94	11	8	5	-8.6	8.6E-07

6	26.37	37.91	26	20	16	-11.6	7.1E-09
7	26.43	37.87	12	21	12	-10.6	3.5E-08
8	26.37	38.19	17	23	16	-12.1	3.1E-09
9	26.30	38.36	11	9	10	-7.8	3.3E-06
10	26.72	38.02	15	26	14	-11.9	4.4E-09

HLA DRB1*09-1dlh (PC-7) + 3of6

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.03	38.92	12	8	13	-8.1	1.9E-06
2	26.81	38.61	13	12	16	-8.1	2.1E-06
3	26.76	38.38	18	9	12	-8.5	9.9E-07
4	26.88	38.71	13	19	10	-9.6	1.7E-07
5	26.83	38.75	12	14	13	-9.2	3.5E-07
6	26.81	38.87	9	20	9	-9.6	1.6E-07
7	26.83	38.48	23	10	14	-9.5	2.0E-07
8	26.83	38.48	17	10	16	-8.9	5.2E-07
9	27.2	38.46	19	26	15	-11.8	4.7E-09
10	27.17	38.04	13	13	13	-8.6	8.0E-07

HLA DRB1*12-1dlh (PC-2) + 3of6

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.7	37.87	10	24	8	-10.3	5.1E-08
2	26.76	38.11	8	16	9	-9.2	3.5E-07
3	26.68	37.74	9	7	9	-7	1.2E-05
4	26.63	37.77	16	14	15	-9.2	3.3E-07
5	26.9	37.23	12	20	21	-10.2	6.3E-08
6	26.85	37.81	13	24	11	-10.9	2.0E-08
7	26.61	37.9	2	14	7	-8.7	7.9E-07
8	26.68	38.01	9	8	5	-7.3	7.5E-06
9	26.61	37.9	4	13	6	-8.1	1.9E-06
10	26.68	37.74	10	14	6	-9	4.7E-07

HLA DRB*14-1dlh (PC-8) + 3of6

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.72	38.02	17	21	11	-11.7	5.8E-09
2	26.78	37.43	17	11	20	-9.3	2.6E-07
3	26.58	38.08	17	11	10	-9.7	1.4E-07
4	26.58	38.08	12	20	12	-10.6	3.4E-08
5	26.78	37.98	18	10	11	-9.6	1.7E-07
6	27.07	37.29	18	22	23	-11.6	6.4E-09

7	26.72	37.74	22	14	16	-10.4	4.9E-08
8	26.65	37.64	16	14	17	-10.4	4.8E-08
9	26.56	37.94	7	9	4	-8.4	1.2E-06
10	26.45	38.02	17	22	12	-11.5	8.2E-09
HLA DRB1*16-1dlh (PC-5) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.7	37.87	15	23	14	-11.5	7.9E-09
2	26.56	38.21	8	12	12	-8.5	1.1E-06
3	26.78	38.25	13	17	12	-9.8	1.3E-07
4	26.78	37.98	17	11	12	-8.9	5.0E-07
5	26.83	37.94	10	7	5	-7.3	6.7E-06
6	27.22	37.78	22	19	15	-10.7	2.7E-08
7	27.05	38.25	13	9	5	-7.8	3.1E-06
8	26.92	37.91	17	15	14	-9.5	1.8E-07
9	26.98	37.87	10	8	6	-7.8	3.0E-06
10	26.83	37.94	12	15	10	-9	4.8E-07

Table 66: HLA DRB-1kg0 complex (having highest values within the 10 complexes) with TCR 3of6.

HLA DRB*01-1kg0 (PC-9) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	24.93	37.53	18	5	6	-9.6	1.8E-07
2	25.07	37.60	13	2	5	-8.0	2.4E-06
3	25.46	37.80	20	16	8	-10.6	3.4E-08
4	25.07	37.73	12	6	7	-8.5	1.1E-06
5	25.26	37.89	23	11	7	-10.7	2.7E-08
6	25.26	37.50	16	3	6	-8.7	7.6E-07
7	25.13	37.70	15	4	6	-8.9	5.5E-07
8	25.26	37.63	5	4	4	-7.3	7.1E-06
9	25.00	37.50	23	11	6	-10.4	4.3E-08
10	25.65	37.70	9	7	2	-6.8	1.7E-05
HLA DRB*04-1kg0 (PC-5) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.73	37.40	21	28	12	-12.2	2.6E-09
2	25.93	37.04	9	22	12	-10.1	7.E-08
3	25.13	37.70	23	15	12	-11.1	1.5E-08

4	25.59	37.47	19	18	13	-10.1	7.4E-08
5	25.13	37.57	16	18	13	-9.4	2.2E-07
6	25.53	37.37	15	15	10	-9.5	1.8E-07
7	25.72	37.27	3	19	9	-8.1	2.E-06
8	25.00	37.63	19	12	12	-10.5	3.7E-08
9	24.93	37.27	16	8	7	-9.6	1.7E-07
10	25.26	37.50	10	13	3	-8.3	1.4E-06
HLA DRB*07-1kg0 (PC-4) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.82	36.96	8	25	13	-9.6	1.7E-07
2	25.33	37.07	4	16	7	-7.8	3.3E-06
3	25.68	37.03	15	15	14	-9.5	2.E-07
4	25.20	37.14	8	5	4	-7.0	1.2E-05
5	25.40	37.17	8	21	11	-9.7	1.5E-07
6	25.47	37.5	10	13	7	-8.1	2.E-06
7	25.34	37.06	29	28	19	-13.0	6.8E-10
8	25.00	36.83	16	14	6	-10.1	7.9E-08
9	25.40	37.17	8	19	13	-9.0	4.3E-07
10	25.54	37.10	9	20	8	-9.6	1.6E-07
HLA DRB*08-1kg0 (PC-3) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.89	37.06	10	25	14	-10.2	6.9E-08
2	25.61	37.06	8	22	15	-9.6	1.7E-07
3	25.75	37.13	3	21	8	-9.2	3.1E-07
4	25.54	37.23	19	24	11	-11.5	7.5E-09
5	25.82	37.23	9	24	17	-10.4	4.7E-08
6	25.54	37.23	7	19	9	-9.4	2.4E-07
7	25.82	37.50	13	16	7	-9.8	1.2E-07
8	25.82	37.23	11	20	16	-10.2	6.8E-08
9	25.68	37.43	20	29	13	-12.7	1.1E-09
10	25.68	37.30	9	14	4	-8.9	5.3E-07
HLA DRB1*09-1kg0 (PC-6) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.94	38.89	18	23	18	-11.5	8.2E-09
2	26.94	39.17	24	21	19	-11.8	5.1E-09
3	26.92	39.01	14	21	14	-10.6	3.4E-08
4	26.52	39.5	15	18	12	-9.5	2.1E-07

5	26.8	38.95	18	17	12	-10.6	3.3E-08
6	26.85	39.18	17	24	13	-10.8	2.5E-08
7	26.72	39.39	17	19	18	-10	8.9E-08
8	26.37	39.56	16	13	6	-9	4.3E-07
9	27	38.57	12	24	25	-10.5	4.2E-08
10	26.8	38.67	22	10	10	-9.2	3.3E-07
HLA DRB1*12-1kg0 (PC-6) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.76	37.03	18	20	10	-10.9	2.2E-08
2	26.43	37.87	16	10	13	-9.4	2.5E-07
3	26.68	37.74	15	5	5	-9.2	3.5E-07
4	26.56	37.67	19	7	9	-8.5	9.8E-07
5	26.78	36.89	21	6	13	-8.6	8.5E-07
6	26.56	37.67	18	5	12	-8.5	1.1E-06
7	26.58	37.53	17	17	11	-10.5	3.9E-08
8	26.98	37.33	22	9	15	-9.7	1.5E-07
9	26.68	37.47	11	6	6	-8.6	9.0E-07
10	26.49	37.57	9	9	11	-8.2	1.7E-06
HLA DRB*14-1kg0 (PC-3) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.43	36.51	12	25	11	-10.6	3.5E-08
2	26.36	36.68	12	19	14	-10.2	6.8E-08
3	26.02	36.86	19	22	7	-11.4	9.7E-09
4	26.16	36.24	23	7	10	-9.4	2.2E-07
5	26.30	36.16	18	6	14	-8.8	6.2E-07
6	26.16	36.24	16	6	7	-8.8	6.2E-07
7	26.29	36.59	21	5	9	-8.8	6.2E-07
8	26.09	36.68	8	18	5	-9.7	1.5E-07
9	26.22	36.76	10	13	4	-8.8	6.1E-07
10	26.30	35.89	19	8	13	-9.4	2.3E-07
HLA DRB1*16-1kg0 (PC-3) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.82	38.55	15	18	14	-10.5	3.9E-08
2	27.35	37.85	21	17	12	-10.8	2.3E-08
3	26.8	38.67	20	12	13	-9.6	1.6E-07
4	27.05	37.98	20	6	17	-8.9	5.0E-07
5	27.2	38.19	10	26	25	-11.5	7.2E-09

6	26.56	38.48	11	14	8	-9.2	3.5E-07
7	27.02	38.44	19	32	25	-13.1	5.8E-10
8	27.27	38.02	13	19	22	-10.2	6.7E-08
9	26.9	38.04	21	6	11	-9	4.9E-07
10	26.9	38.04	18	5	12	-8.7	7.1E-07

Table 67: HLA DRB-1h15 complex (having highest values within the 10 complexes) with TCR 3of6.

HLA DRB*01-1h15 (PC-1) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.78	37.98	18	9	14	-9.4	2.5E-07
2	27.00	38.02	18	12	21	-9.5	1.9E-07
3	26.85	38.36	18	7	10	-8.2	1.5E-06
4	26.85	38.08	19	5	9	-9.0	4.5E-07
5	26.80	38.12	24	11	15	-9.9	1.E-07
6	26.72	38.02	18	6	9	-9.1	4.1E-07
7	26.65	38.46	14	10	9	-8.8	6.E-07
8	26.70	38.15	12	10	8	-8.6	9.E-07
9	27.00	38.29	20	9	11	-9.7	1.4E-07
10	26.65	38.46	17	8	11	-8.8	6.6E-07
HLA DRB*04-1h15 (PC-10) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.26	38.20	21	14	18	-10.0	8.3E-08
2	26.47	38.50	22	18	17	-11.0	1.8E-08
3	26.44	38.22	8	9	13	-8.1	2.E-06
4	26.46	38.10	17	8	11	-8.5	1.E-06
5	26.53	38.20	12	23	13	-11.2	1.3E-08
6	26.18	38.22	11	13	8	-8.6	8.1E-07
7	26.25	38.32	12	10	13	-8.6	8.4E-07
8	26.46	38.36	19	15	18	-10.4	4.5E-08
9	26.25	38.06	16	10	19	-8.9	5.5E-07
10	25.92	38.48	16	10	15	-9.3	2.7E-07
HLA DRB*07-1h15 (PC-7) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.48	38.50	25	20	19	-12.3	2.E-09
2	25.47	39.30	14	16	17	-10.1	7.6E-08

3	25.95	38.92	20	8	15	-9.6	1.8E-07
4	25.95	38.65	13	7	17	-8.0	2.2E-06
5	25.54	38.86	19	14	16	-10.2	6.3E-08
6	25.89	38.69	23	6	10	-8.7	7.5E-07
7	25.95	38.65	15	9	21	-8.5	1.E-06
8	25.54	38.86	19	9	16	-9.3	2.9E-07
9	25.41	39.07	12	15	20	-9.8	1.2E-07
10	25.55	38.74	19	16	18	-10.7	2.9E-08
HLA DRB*08-1h15 (PC-3) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.23	37.70	15	8	10	-8.6	8.9E-07
2	25.90	37.74	24	13	21	-10.7	3.1E-08
3	26.23	37.70	17	13	16	-9.3	2.6E-07
4	26.30	38.08	13	15	13	-9.4	2.4E-07
5	26.30	37.53	20	10	20	-9.3	2.9E-07
6	26.09	38.04	11	12	13	-9.3	2.6E-07
7	26.02	37.94	12	10	12	-8.6	8.3E-07
8	26.30	37.81	15	15	11	-10.2	6.1E-08
9	26.30	37.53	13	12	15	-8.9	5.1E-07
10	26.30	37.81	17	9	10	-8.6	8.7E-07
HLA DRB1*09-1h15 (PC-1) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.72	39.12	34	15	26	-12.5	1.5E-09
2	26.56	39.3	13	7	16	-7.7	3.6E-06
3	26.7	38.69	22	9	14	-9.3	2.6E-07
4	26.63	39.13	17	7	13	-8.8	6.2E-07
5	26.65	38.74	22	7	13	-8.6	8.6E-07
6	26.36	39.13	16	6	9	-8.2	1.6E-06
7	26.63	38.86	20	9	10	-9.2	3.1E-07
8	26.58	39.18	29	11	16	-10.3	5.1E-08
9	26.65	39.01	18	14	12	-9.4	2.6E-07
10	26.63	38.86	27	8	10	-10.4	5.0E-08
HLA DRB1*12-1h15 (PC-1) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.76	37.03	16	16	7	-10.9	2.0E-08
2	26.08	36.83	14	10	13	-8.3	1.3E-06
3	26.27	36.73	14	12	10	-10	8.3E-08

4	26.2	36.63	11	9	8	-9	4.5E-07
5	26.01	37	17	9	8	-9.5	1.9E-07
6	26.34	36.83	11	12	9	-9.6	1.7E-07
7	26.54	36.73	7	6	4	-7.5	5.6E-06
8	26.4	36.53	21	11	12	-10.3	5.9E-08
9	26.61	36.83	8	17	4	-9.9	9.9E-08
10	26.2	37.17	14	4	4	-7.8	3.4E-06
HLA DRB*14-1h15 (PC-3) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.29	37.94	19	8	10	-8.6	8.1E-07
2	26.58	37.81	24	10	6	-9.4	2.4E-07
3	26.43	37.60	26	15	21	-10.7	3.E-08
4	26.65	37.64	20	15	7	-10.5	3.8E-08
5	26.65	37.91	21	20	10	-12.3	2.2E-09
6	26.37	37.91	28	12	16	-10.4	4.5E-08
7	26.36	37.77	24	9	14	-9.4	2.4E-07
8	26.67	37.22	32	17	21	-12.4	2.E-09
9	26.50	37.98	14	13	13	-9.1	3.6E-07
10	26.58	37.81	12	8	21	-8.3	1.3E-06
HLA DRB1*16-1h15 (PC-10) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.12	38.08	17	12	13	-9.4	2.4E-07
2	26.85	38.08	12	12	8	-9.8	1.2E-07
3	26.59	38.23	25	12	25	-11	1.7E-08
4	26.92	38.19	24	11	12	-10.2	6.9E-08
5	26.87	38.23	24	14	21	-10.6	3.6E-08
6	26.8	38.4	22	13	14	-10.1	7.6E-08
7	26.85	38.36	15	10	11	-8.9	5.1E-07
8	26.65	38.19	16	13	10	-9.9	1.1E-07
9	26.7	37.87	23	7	10	-9.8	1.2E-07
10	26.65	38.46	20	13	12	-9.7	1.4E-07

Table 68: HLA DRB-1sje complex (having highest values within the 10 complexes) with TCR 3of6.

HLA DRB*01-1sje (PC-10) + 3of6							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.12	39.05	14	16	18	-10.0	9.6E-08
2	25.93	39.15	15	16	18	-10.1	8.E-08
3	25.65	39.01	15	15	11	-10.1	7.5E-08
4	25.98	39.37	18	10	9	-9.0	4.8E-07
5	26.05	38.95	14	12	19	-9.3	2.9E-07
6	25.99	38.73	27	19	24	-11.9	3.9E-09
7	26.05	38.95	16	7	11	-8.0	2.5E-06
8	26.32	39.21	10	17	9	-9.2	3.E-07
9	25.85	38.90	11	17	12	-9.9	1.1E-07
10	25.52	39.06	13	11	10	-8.6	8.4E-07
HLA DRB*04-1sje (PC-7) + 3of6							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.47	40.11	21	29	35	-12.7	1.1E-09
2	25.53	40.43	14	15	12	-9.8	1.1E-07
3	25.00	40.43	15	6	11	-7.8	3.3E-06
4	25.46	40.32	10	15	10	-9.2	3.3E-07
5	24.59	40.54	25	11	13	-10.3	5.2E-08
6	24.53	40.53	24	8	8	-10.0	8.2E-08
7	25.61	39.89	20	27	31	-12.9	8.4E-10
8	25.27	40.16	14	13	18	-8.7	7.3E-07
9	25.33	40.63	4	12	14	-7.2	8.6E-06
10	25.40	40.74	19	11	12	-9.1	3.8E-07
HLA DRB*07-1sje (PC-2) + 3of6							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	25.96	39.34	4	25	21	-10.3	5.5E-08
2	25.41	39.73	10	12	15	-8.8	6.E-07
3	25.82	39.40	8	14	26	-8.7	7.4E-07
4	25.34	39.89	14	10	15	-8.8	6.7E-07
5	25.61	39.89	14	10	15	-8.7	7.1E-07
6	25.54	39.67	23	5	10	-8.3	1.3E-06
7	25.34	39.89	9	9	13	-7.9	2.5E-06

8	25.54	39.78	8	10	10	-8.1	1.8E-06
9	25.47	39.84	14	9	17	-8.5	9.8E-07
10	25.75	39.45	19	14	19	-9.4	2.3E-07
HLA DRB*08-1sje (PC-4) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.39	38.61	19	20	21	-10.7	2.7E-08
2	26.45	38.57	8	15	19	-9.4	2.5E-07
3	26.67	38.33	17	17	28	-10.6	3.1E-08
4	26.52	38.40	6	18	23	-8.8	6.2E-07
5	26.24	38.67	13	18	19	-10.1	7.9E-08
6	26.23	39.07	7	12	15	-10.1	7.9E-08
7	26.67	38.33	18	16	24	-10.1	7.3E-08
8	26.59	38.50	6	20	21	-9.4	2.3E-07
9	26.23	38.80	5	17	11	-9.0	4.3E-07
10	26.45	38.57	8	15	19	-8.6	8.6E-07
HLA DRB1*09-1sje (PC-1) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.36	39.95	11	13	12	-8.3	1.4E-06
2	26.7	39.51	12	11	17	-8.7	7.9E-07
3	26.9	39.67	13	9	19	-7.6	4.7E-06
4	26.5	39.62	12	14	20	-8.5	1.1E-06
5	26.78	39.34	13	12	16	-8.8	6.1E-07
6	26.85	39.45	14	21	16	-10.3	5.2E-08
7	26.43	39.78	13	11	14	-8.1	2.1E-06
8	26.29	40.11	17	6	13	-8.1	2.0E-06
9	26.63	39.95	23	5	10	-8.5	9.9E-07
10	27.12	39.45	26	12	18	-10.6	3.3E-08
HLA DRB1*12-1sje (PC-7) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.95	38.92	10	13	20	-8.5	9.4E-07
2	26.1	38.46	15	24	33	-10.7	2.8E-08
3	25.89	38.96	17	11	13	-9.1	3.9E-07
4	26.09	38.86	13	12	12	-8.9	5.3E-07
5	26.09	38.86	15	17	14	-9.9	9.7E-08
6	26.02	38.48	22	5	14	-8.9	5.6E-07
7	26.09	38.59	16	11	21	-8.3	1.3E-06
8	25.81	39.25	14	6	9	-8.2	1.7E-06

9	25.96	38.8	30	9	13	-10	8.4E-08
10	25.96	38.8	14	6	15	-7	1.2E-05
HLA DRB*14-1sje (PC-8) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.56	38.21	15	14	27	-9.7	1.4E-07
2	26.49	38.38	12	15	25	-9.5	1.9E-07
3	26.49	38.38	10	10	13	-8.5	1.1E-06
4	26.63	38.59	13	18	18	-10.4	4.4E-08
5	26.42	38.54	10	10	18	-8.5	1.1E-06
6	26.63	38.04	14	14	25	-9.6	1.6E-07
7	26.42	38.54	10	9	12	-8.2	1.6E-06
8	26.56	38.21	16	12	20	-9.6	1.8E-07
9	26.63	38.04	12	12	20	-8.8	6.7E-07
10	26.42	38.54	9	14	19	-9.0	4.7E-07
HLA DRB1*16-1sje (PC-8) + 3of6							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.29	39.3	10	18	28	-9.7	1.6E-07
2	25.95	39.46	12	22	21	-10.9	2.2E-08
3	26.5	39.07	16	14	18	-8.8	6.6E-07
4	26.02	39.3	23	11	11	-9.5	2.0E-07
5	25.95	39.46	18	19	19	-10.9	2.1E-08
6	26.43	38.96	16	13	25	-9.2	3.5E-07
7	26.37	38.74	20	15	19	-9.7	1.5E-07
8	26.22	39.46	6	9	20	-7	1.2E-05
9	25.95	39.19	11	17	23	-9.5	2.0E-07
10	25.81	39.52	14	16	17	-9.6	1.6E-07

Table 69: HLA DRB-1aqd complex (having highest values within the 10 complexes) with TCR 4udu.

HLA DRB*01-1aqd (PC-10) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.72	36.36	30	18	21	-12.0	3.3E-09
2	26.85	36.71	17	9	14	-8.7	7.1E-07
3	26.56	36.86	7	13	7	-9.2	3.1E-07
4	26.49	36.76	17	9	7	-9.1	3.5E-07
5	26.43	36.78	13	11	16	-9.5	2.E-07

6	26.56	36.86	14	12	16	-9.7	1.5E-07
7	26.20	36.90	9	5	6	-7.2	8.8E-06
8	26.36	36.96	13	8	10	-9.2	3.4E-07
9	26.37	36.81	18	6	11	-8.3	1.4E-06
10	26.63	36.41	11	12	5	-9.3	2.9E-07
HLA DRB*04-1aqd (PC-9) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.08	37.80	17	15	28	-10.4	4.4E-08
2	27.15	38.17	27	17	14	-11.9	4.2E-09
3	26.81	37.80	25	15	19	-10.9	2.2E-08
4	27.22	37.74	22	16	22	-10.8	2.2E-08
5	27.49	37.74	23	14	14	-10.4	5.E-08
6	27.57	37.84	19	17	17	-10.7	2.8E-08
7	27.08	37.80	16	16	13	-10.2	6.8E-08
8	27.01	37.70	15	14	17	-9.4	2.2E-07
9	26.88	37.37	25	12	24	-10.4	4.3E-08
10	26.74	37.97	20	7	20	-9.2	3.2E-07
HLA DRB*07-1aqd (PC-9) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.80	37.85	17	13	15	-9.8	1.2E-07
2	26.85	37.53	12	15	16	-9.1	3.6E-07
3	27.15	37.95	24	19	15	-11.9	4.1E-09
4	26.80	37.57	18	8	14	-8.7	7.E-07
5	26.65	37.91	12	16	15	-10.0	8.9E-08
6	27.27	37.47	23	14	13	-10.2	6.9E-08
7	26.85	37.81	9	15	10	-9.2	3.4E-07
8	27.07	37.85	21	15	8	-10.1	7.1E-08
9	26.72	38.02	13	18	15	-10.3	5.2E-08
10	26.78	37.70	8	13	11	-8.6	9.3E-07
HLA DRB*08-1aqd (PC-3) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.42	36.84	14	18	24	-10.6	3.1E-08
2	26.84	37.01	23	18	20	-11.4	9.3E-09
3	27.17	36.97	19	20	24	-12.1	3.E-09
4	27.37	37.15	14	15	14	-10.1	7.5E-08
5	26.85	36.99	13	7	17	-8.5	1.E-06
6	27.05	36.89	13	6	13	-8.5	1.1E-06

7	27.35	37.02	14	10	15	-9.6	1.8E-07
8	26.85	36.99	10	7	18	-8.0	2.3E-06
9	26.67	36.94	18	12	11	-9.4	2.5E-07
10	27.12	36.99	17	8	20	-9.3	2.9E-07
HLA DRB1*09-1aqd (PC-1) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	28.18	37.57	15	20	24	-10.4	4.8E-08
2	28.18	37.85	9	15	16	-9	4.6E-07
3	28.21	37.71	17	17	19	-10.6	3.1E-08
4	28.02	37.36	10	16	19	-9.2	3.1E-07
5	27.93	37.71	20	15	18	-10.8	2.4E-08
6	27.86	37.88	24	16	21	-10.5	3.7E-08
7	28.18	37.57	9	16	17	-9.3	3.0E-07
8	28.02	37.64	7	15	13	-8.8	5.8E-07
9	27.93	37.71	21	19	25	-11	1.6E-08
10	27.65	37.71	15	12	17	-9.1	3.9E-07
HLA DRB*12-1aqd (PC-) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.87	36.34	16	11	25	-9.5	2.0E-07
2	27.82	36.64	21	8	21	-9.4	2.2E-07
3	27.87	36.61	12	7	12	-8.4	1.2E-06
4	27.95	36.44	23	11	20	-10.3	5.0E-08
5	27.82	36.91	31	14	22	-11.4	9.7E-09
6	27.87	36.61	12	7	14	-8.1	1.8E-06
7	28.25	36.29	18	13	23	-10	8.9E-08
8	27.67	36.71	20	9	21	-9.4	2.4E-07
9	27.6	37.16	15	8	15	-8.9	5.4E-07
10	27.62	37.02	21	15	15	-10.5	3.9E-08
HLA DRB*14-1aqd (PC-8) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.67	36.44	15	7	18	-8.9	5.5E-07
2	27.78	36.67	24	15	18	-11.0	1.6E-08
3	27.62	36.46	26	12	13	-10.6	3.3E-08
4	28.10	36.64	21	20	18	-11.8	4.5E-09
5	27.72	36.14	11	6	12	-8.1	1.9E-06
6	28.02	36.54	13	18	11	-11.2	1.3E-08
7	28.10	36.36	29	10	11	-11.2	1.3E-08

8	27.47	36.54	17	15	15	-10.4	4.6E-08
9	27.72	36.14	10	10	13	-9.0	4.4E-07
10	27.60	36.34	11	7	17	-8.2	1.6E-06
HLA DRB*16-1aqd (PC-4) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol-1)**	**K_d (M) at 37°C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.32	37.16	18	10	23	-9.3	2.8E-07
2	27.45	36.96	10	10	15	-8.7	7.3E-07
3	27.25	36.78	14	5	17	-8.2	1.6E-06
4	27.45	37.23	9	10	18	-8.6	9.3E-07
5	27.32	37.16	18	7	19	-8.8	6.2E-07
6	27.67	36.71	24	12	24	-11.1	1.4E-08
7	27.6	36.61	18	5	16	-8.7	7.3E-07
8	27.75	37.09	24	14	16	-10.8	2.3E-08
9	27.37	36.86	18	4	15	-8.5	1.1E-06
10	27.47	36.54	21	9	21	-9.9	9.8E-08

Table 70: HLA DRB-1dlh complex (having highest values within the 10 complexes) with TCR 4udu.

HLA DRB*01-1dlh (PC-3) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol-1)**	**K_d (M) at 37°C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.42	37.67	19	12	9	-9.9	1.E-07
2	27.37	37.71	16	15	10	-9.8	1.2E-07
3	27.67	36.99	17	10	7	-9.7	1.6E-07
4	27.62	37.57	9	10	13	-8.5	1.1E-06
5	27.47	37.36	10	8	14	-8.1	2.E-06
6	27.40	37.53	10	7	11	-7.0	1.1E-05
7	27.40	37.53	17	6	10	-8.5	1.E-06
8	27.55	37.19	17	11	7	-9.7	1.5E-07
9	27.82	36.91	5	13	16	-8.5	1.1E-06
10	27.65	37.43	20	14	8	-10.4	4.8E-08
HLA DRB*04-1dlh (PC-8) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol-1)**	**K_d (M) at 37°C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.27	38.24	15	16	19	-10.3	5.9E-08
2	27.15	38.44	12	17	19	-9.9	1.1E-07
3	27.35	38.34	17	20	19	-11.5	7.6E-09
4	27.15	38.44	18	12	17	-9.4	2.3E-07

5	27.54	38.24	13	13	11	-9.2	3.1E-07
6	27.69	37.90	16	14	12	-9.8	1.2E-07
7	27.15	38.17	16	15	15	-10.2	5.9E-08
8	27.01	37.97	15	13	17	-9.7	1.6E-07
9	27.57	38.65	17	15	11	-9.9	1.E-07
10	27.42	38.17	19	12	12	-9.8	1.2E-07

HLA DRB*07-1dlh (PC-1) + 4udu

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.15	37.95	24	16	13	-11.1	1.5E-08
2	27.22	37.78	23	14	11	-10.2	6.5E-08
3	27.35	37.85	16	16	11	-10.2	6.4E-08
4	26.94	38.33	16	14	8	-9.7	1.4E-07
5	27.20	37.91	17	13	17	-9.0	4.8E-07
6	27.00	38.02	16	15	15	-9.2	3.1E-07
7	26.58	38.63	22	13	9	-10.4	4.7E-08
8	27.22	37.78	25	17	13	-11.4	9.6E-09
9	26.85	38.08	19	7	10	-8.7	7.4E-07
10	27.27	38.57	21	14	10	-9.7	1.4E-07

HLA DRB*08-1dlh (PC-1) + 4udu

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.37	37.43	23	20	12	-11.5	7.8E-09
2	27.55	36.91	10	12	9	-8.3	1.5E-06
3	27.47	36.81	10	13	7	-9.1	3.8E-07
4	27.62	37.02	11	10	7	-8.5	1.1E-06
5	27.70	36.84	15	13	12	-8.9	5.5E-07
6	27.58	36.77	14	17	18	-10.2	6.2E-08
7	27.42	37.12	15	16	9	-10.0	8.3E-08
8	27.45	36.97	26	18	17	-12.0	3.4E-09
9	27.27	36.91	11	16	7	-10.4	4.8E-08
10	27.09	37.15	20	13	9	-9.9	1.E-07

HLA DRB1*09-1dlh (PC-7) + 4udu

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	28.1	37.74	22	14	8	-10.3	5.8E-08
2	28.3	36.81	24	7	14	-9.5	1.9E-07
3	27.98	37.67	27	18	12	-11.9	4.0E-09
4	28.06	37.5	25	15	13	-10.6	3.6E-08
5	27.95	38.08	16	14	8	-10.2	6.2E-08

6	28.3	37.64	17	16	7	-10	8.7E-08
7	28.18	37.57	22	16	11	-10.8	2.3E-08
8	27.95	37.53	17	15	16	-9.7	1.5E-07
9	28.14	37.43	18	16	15	-9.9	1.1E-07
10	27.75	37.64	20	8	10	-9.4	2.5E-07

HLA DRB1*12-1dlh (PC-2) + 4udu

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.5	36.94	21	13	11	-11.1	1.4E-08
2	27.62	37.02	22	13	15	-10	8.3E-08
3	28.02	36.81	7	17	11	-9.2	3.5E-07
4	27.35	37.02	14	14	6	-9.8	1.2E-07
5	28.02	37.09	8	11	7	-7.8	3.0E-06
6	28.13	37.33	14	26	13	-11.4	9.3E-09
7	27.55	36.91	20	7	10	-9.4	2.4E-07
8	27.87	37.16	10	17	8	-9.2	3.2E-07
9	28.33	36.67	13	19	11	-11.2	1.4E-08
10	27.6	36.61	13	7	6	-8.2	1.8E-06

HLA DRB*14-1dlh (PC-8) + 4udu

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.98	37.12	16	12	13	-9.6	1.6E-07
2	27.82	36.36	9	5	20	-7.6	4.2E-06
3	27.78	37.22	12	5	8	-7.8	3.3E-06
4	27.75	36.54	16	5	7	-8.7	7.5E-07
5	27.78	36.94	15	11	13	-9.1	3.9E-07
6	27.07	37.29	26	6	6	-10.3	5.2E-08
7	28.29	36.69	18	11	14	-9.6	1.8E-07
8	27.82	36.36	19	12	11	-9.8	1.2E-07
9	27.32	36.90	28	12	16	-11.9	3.9E-09
10	27.55	37.19	11	7	11	-8.1	2.1E-06

HLA DRB1*16-1dlh (PC-5) + 4udu

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.95	36.99	10	19	11	-10.4	4.8E-08
2	28.02	37.09	8	14	8	-8.9	5.2E-07
3	27.9	37.02	23	7	10	-9.6	1.6E-07
4	28.13	37.33	17	19	14	-10.2	6.5E-08
5	27.87	36.89	9	12	9	-8.9	5.2E-07
6	27.86	37.33	22	14	15	-10.5	4.1E-08

7	28.18	37.02	19	11	9	-9.5	2.0E-07
8	27.78	37.22	14	14	11	-9.7	1.4E-07
9	27.95	36.99	7	12	5	-8	2.3E-06
10	28.18	36.74	12	14	14	-9.2	3.4E-07

Table 71: HLA DRB-1kg0 complex (having highest values within the 10 complexes) with TCR 4udu.

HLA DRB*01-1kg0 (PC-9) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	25.94	38.24	34	7	9	-11.1	1.4E-08
2	26.08	37.63	22	6	10	-9.5	1.9E-07
3	25.61	38.27	26	7	9	-10.6	3.5E-08
4	26.02	37.67	24	21	13	-12.3	2.3E-09
5	26.20	37.97	10	7	8	-7.9	2.7E-06
6	25.87	38.40	24	6	9	-9.4	2.4E-07
7	25.88	38.01	29	8	7	-10.9	2.E-08
8	26.13	37.60	12	7	6	-8.6	9.2E-07
9	26.33	38.03	20	5	7	-9.0	4.5E-07
10	26.01	38.34	14	16	5	-10.8	2.5E-08
HLA DRB*04-1kg0 (PC-5) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.34	37.63	21	20	17	-10.7	2.7E-08
2	26.56	37.94	22	20	17	-11.4	9.E-09
3	25.74	37.80	32	9	11	-11.6	6.5E-09
4	25.80	38.03	23	10	6	-9.4	2.2E-07
5	26.54	37.80	10	19	9	-10.3	5.4E-08
6	26.74	37.70	17	19	15	-10.2	6.2E-08
7	26.88	37.63	20	19	15	-11.3	1.1E-08
8	26.03	37.26	30	14	12	-11.7	5.4E-09
9	26.63	37.77	24	16	12	-10.6	3.2E-08
10	26.56	37.67	22	18	11	-11.2	1.3E-08
HLA DRB*07-1kg0 (PC-4) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.17	38.02	29	19	7	-12.0	3.3E-09
2	26.50	37.16	10	19	10	-10.5	3.7E-08

3	26.45	37.47	22	17	6	-11.4	8.8E-09
4	26.37	37.09	13	25	16	-11.1	1.6E-08
5	26.45	37.74	21	15	4	-10.4	4.5E-08
6	26.37	37.36	20	19	12	-10.8	2.3E-08
7	26.43	37.06	9	23	19	-10.5	3.9E-08
8	26.36	37.23	6	12	7	-7.7	3.9E-06
9	26.50	37.43	7	12	7	-9.4	2.4E-07
10	26.23	37.43	12	17	14	-9.8	1.3E-07

HLA DRB*08-1kg0 (PC-3) + 4udu

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.45	36.36	14	20	20	-10.2	7.E-08
2	26.45	36.09	19	21	16	-11.9	4.E-09
3	26.72	36.36	13	19	8	-10.5	4.2E-08
4	26.39	36.67	17	21	15	-11.3	1.1E-08
5	26.72	36.09	10	12	10	-8.8	6.E-07
6	26.85	36.16	5	15	15	-8.8	6.4E-07
7	26.59	36.57	23	15	14	-10.3	5.1E-08
8	26.82	36.59	22	20	15	-11.4	8.7E-09
9	26.80	36.46	20	15	11	-10.2	6.2E-08
10	26.80	35.91	14	19	12	-10.7	2.7E-08

HLA DRB1*09-1kg0 (PC-6) + 4udu

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.45	38.38	21	21	12	-11.4	8.8E-09
2	28.29	38.1	20	28	17	-13.2	5.3E-10
3	27.93	38.83	22	18	10	-11.1	1.5E-08
4	28.29	38.66	18	25	13	-12.3	2.3E-09
5	28.01	38.94	19	18	12	-10.7	2.7E-08
6	27.81	38.48	26	21	18	-12.9	7.7E-10
7	28.13	38.16	19	17	18	-10.2	6.7E-08
8	27.73	38.66	17	16	11	-10	8.7E-08
9	27.81	38.48	25	16	16	-11.2	1.2E-08
10	27.55	38.57	15	21	12	-11	1.8E-08

HLA DRB1*12-1kg0 (PC-6) + 4udu

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.67	36.71	17	8	9	-8.1	2.0E-06
2	27.05	37.16	24	6	7	-10.2	6.8E-08
3	27.52	36.24	10	9	12	-8.3	1.4E-06

4	27.52	36.51	12	4	9	-8.4	1.2E-06
5	27.79	36.24	18	3	8	-8.5	1.1E-06
6	27.82	36.91	19	14	13	-9.5	2.1E-07
7	27.52	36.78	17	10	8	-10	9.1E-08
8	27	36.91	19	11	10	-10.3	5.7E-08
9	28.02	36.54	16	23	16	-11.5	8.4E-09
10	27.32	36.89	22	5	6	-9.5	2.1E-07
HLA DRB*14-1kg0 (PC-3) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.25	35.69	20	12	6	-10.2	6.2E-08
2	26.94	35.56	19	14	7	-9.7	1.6E-07
3	27.27	35.81	15	18	4	-10.7	3.1E-08
4	27.35	35.08	18	12	7	-10.9	2.1E-08
5	27.15	35.73	12	14	5	-8.9	5.3E-07
6	27.00	35.81	17	14	6	-9.1	3.7E-07
7	26.92	35.99	12	20	16	-10.0	8.2E-08
8	27.12	35.07	17	20	16	-9.5	2.E-07
9	27.35	35.36	17	17	9	-10.6	3.3E-08
10	26.72	35.81	24	7	8	-10.3	5.5E-08
HLA DRB1*16-1kg0 (PC-3) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	28.25	36.84	20	14	10	-9.4	2.2E-07
2	27.95	37.26	6	5	6	-7.3	6.9E-06
3	28.17	37.18	24	23	20	-12.7	1.1E-09
4	27.95	37.26	9	8	5	-7.9	2.6E-06
5	27.93	37.15	18	17	12	-10.4	4.7E-08
6	27.95	37.26	7	8	6	-7.9	2.7E-06
7	27.93	37.43	18	14	16	-9.3	2.9E-07
8	28.05	37.68	20	19	17	-11.2	1.2E-08
9	28.33	37.22	20	14	9	-10	8.3E-08
10	27.7	37.12	17	21	13	-11.7	5.6E-09

Table 72: HLA DRB-1h15 complex (having highest values within the 10 complexes) with TCR 4udu.

HLA DRB*01-1h15 (PC-1) + 4udu							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.78	37.50	19	10	14	-9.6	1.6E-07
2	27.89	37.46	20	13	14	-10.3	5.4E-08
3	27.93	37.15	25	10	14	-10.1	7.7E-08
4	27.86	37.33	15	13	11	-10.2	6.1E-08
5	27.86	37.33	19	13	14	-10.1	7.E-08
6	27.93	37.43	21	10	12	-10.8	2.5E-08
7	27.93	37.43	20	12	17	-10.0	9.1E-08
8	28.06	37.22	21	5	9	-8.9	5.2E-07
9	27.78	37.50	20	10	14	-10.2	6.2E-08
10	27.98	37.12	21	6	15	-9.5	2.2E-07
HLA DRB*04-1h15 (PC-10) + 4udu							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.49	38.27	16	16	25	-10.4	4.5E-08
2	27.76	38.54	17	17	20	-10.5	4.3E-08
3	27.76	38.27	17	17	15	-10.4	4.6E-08
4	27.45	38.59	29	19	18	-12.3	2.E-09
5	27.17	39.13	35	16	15	-12.5	1.6E-09
6	27.69	38.71	21	11	13	-9.6	1.8E-07
7	27.10	39.02	26	16	12	-11.0	1.7E-08
8	27.54	38.50	16	13	21	-9.7	1.5E-07
9	27.17	38.32	34	11	19	-11.2	1.3E-08
10	27.42	38.44	18	11	12	-9.9	9.9E-08
HLA DRB*07-1h15 (PC-7) + 4udu							
PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.54	37.71	30	18	20	-13.2	5.3E-10
2	27.20	37.09	18	2	16	-7.9	2.7E-06
3	27.12	37.81	19	3	11	-8.2	1.7E-06
4	27.12	37.53	20	5	14	-8.7	7.3E-07
5	27.00	37.19	22	5	14	-10.5	3.8E-08
6	26.80	37.57	10	14	13	-9.8	1.3E-07
7	26.98	37.33	7	10	20	-7.8	3.1E-06

8	26.33	38.10	30	13	16	-11.4	9.E-09
9	26.33	37.82	26	11	13	-10.7	2.8E-08
10	26.90	37.77	18	3	12	-8.0	2.2E-06
HLA DRB*08-1h15 (PC-3) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.15	37.12	17	12	14	-10.0	9.6E-08
2	26.89	37.25	33	14	17	-11.8	4.6E-09
3	27.15	36.84	19	8	15	-9.2	3.2E-07
4	27.42	36.57	15	14	16	-9.9	1.1E-07
5	27.15	36.84	19	10	16	-9.9	9.9E-08
6	26.74	37.33	26	10	13	-10.4	4.5E-08
7	27.50	37.22	20	16	11	-10.7	2.9E-08
8	26.97	37.08	22	14	15	-10.7	2.7E-08
9	26.94	36.94	21	11	14	-10.2	6.6E-08
10	27.02	37.05	23	8	19	-9.7	1.5E-07
HLA DRB1*09-1h15 (PC-1) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.42	38.23	25	5	10	-9.1	3.8E-07
2	27.9	38.12	16	14	10	-9.9	1.0E-07
3	27.5	38.33	22	9	10	-9.4	2.4E-07
4	27.7	38.23	21	9	9	-9.8	1.3E-07
5	27.7	37.95	27	4	12	-9.4	2.4E-07
6	27.7	37.95	20	7	18	-9.4	2.5E-07
7	27.78	38.33	21	13	6	-10.7	2.7E-08
8	27.9	38.12	23	4	9	-9.2	3.2E-07
9	27.82	38.02	21	5	7	-9.4	2.5E-07
10	27.82	38.29	17	5	9	-8.5	9.6E-07
HLA DRB1*12-1h15 (PC-1) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.53	37.08	27	15	14	-11.4	9.4E-09
2	27.47	36.81	20	4	9	-9.2	3.1E-07
3	27.07	37.29	18	12	7	-10.5	3.9E-08
4	27.4	36.99	23	7	11	-9.6	1.7E-07
5	27.2	37.36	20	6	7	-9.5	2.0E-07
6	27.0	37.19	29	5	7	-10.4	4.4E-08
7	26.92	37.36	22	5	16	-9.0	4.2E-07
8	27.2	37.36	21	10	11	-10.3	5.2E-08

9	27.6	36.89	19	2	8	-8.4	1.3E-06
10	27.4	36.99	15	7	9	-8.9	5.3E-07
HLA DRB*14-1h15 (PC-3) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.15	37.12	20	7	11	-9.7	1.5E-07
2	27.15	37.12	29	6	10	-10.5	4.2E-08
3	27.35	36.46	37	3	10	-10.5	4.E-08
4	27.47	36.81	19	4	10	-9.0	4.3E-07
5	27.35	37.02	23	7	8	-9.2	3.2E-07
6	27.35	36.74	29	4	7	-9.9	1.1E-07
7	26.94	37.22	18	12	8	-10.5	3.7E-08
8	27.42	36.84	25	10	9	-10.5	3.9E-08
9	27.47	36.81	19	5	8	-9.2	3.5E-07
10	27.30	37.33	20	9	5	-10.2	6.7E-08
HLA DRB1*16-1h15 (PC-10) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.89	37.46	33	12	16	-11.3	1.1E-08
2	27.9	37.02	17	7	15	-8.7	7.0E-07
3	27.86	37.33	25	11	12	-10.5	4.0E-08
4	27.7	37.4	21	6	22	-9	4.8E-07
5	27.73	37.54	27	12	12	-10.8	2.4E-08
6	27.45	37.82	26	12	13	-11.1	1.6E-08
7	27.78	37.22	22	6	13	-9.3	2.8E-07
8	27.86	37.33	27	12	12	-11	1.8E-08
9	27.5	37.5	20	5	19	-8.8	5.9E-07
10	27.73	37.25	24	12	17	-10.6	3.1E-08

Table 73: HLA DRB-1sje complex (having highest values within the 10 complexes) with TCR 4udu.

HLA DRB*01-1sje (PC-10) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.47	39.57	34	7	9	-10.8	2.3E-08
2	27.01	39.30	18	9	16	-8.6	8.5E-07
3	27.13	39.36	17	10	8	-9.0	4.5E-07
4	26.86	39.36	13	6	14	-7.4	5.7E-06
5	27.01	39.04	14	11	20	-8.3	1.4E-06

6	26.54	38.87	22	6	10	-9.2	3.1E-07
7	27.08	39.41	17	6	13	-8.2	1.7E-06
8	26.15	39.62	26	7	9	-10.3	5.9E-08
9	27.08	39.41	20	12	14	-9.5	2.1E-07
10	26.93	39.47	11	13	13	-8.9	5.4E-07
HLA DRB*04-1sje (PC-7) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	26.61	39.25	14	15	15	-9.9	1.E-07
2	26.15	39.62	18	16	29	-10.2	6.E-08
3	26.49	39.46	19	16	29	-10.9	1.9E-08
4	25.74	39.95	34	7	9	-10.9	2.2E-08
5	26.27	39.41	16	11	14	-8.8	5.9E-07
6	26.33	39.63	12	6	18	-7.3	7.6E-06
7	26.33	39.63	21	10	14	-9.5	2.2E-07
8	26.49	39.46	28	19	26	-11.9	4.E-09
9	26.40	39.47	18	9	8	-8.7	7.9E-07
10	26.54	39.68	22	17	15	-10.9	2.E-08
HLA DRB*07-1sje (PC-2) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**Ap**	**C-Ap**	**P-Ap**	**Ap-Ap**		
1	26.56	38.75	12	6	19	-7.6	4.4E-06
2	26.70	38.69	16	5	14	-7.9	2.9E-06
3	26.63	38.86	10	5	18	-7.1	9.2E-06
4	26.70	38.69	13	5	20	-7.5	5.5E-06
5	26.70	38.42	10	8	18	-7.7	3.7E-06
6	26.36	38.86	11	8	17	-7.9	2.9E-06
7	27.07	38.12	11	11	30	-8.4	1.2E-06
8	26.63	38.59	16	8	12	-8.5	1.1E-06
9	26.56	38.75	17	6	17	-8.1	2.E-06
10	26.36	38.86	13	4	21	-7.3	7.7E-06
HLA DRB*08-1sje (PC-4) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.50	37.22	9	19	21	-10.4	4.7E-08
2	27.50	37.50	10	19	24	-9.9	1.E-07
3	27.58	37.88	7	14	22	-8.4	1.1E-06
4	27.35	37.85	8	14	20	-8.7	7.7E-07
5	27.09	37.99	11	11	15	-8.7	7.5E-07

6	27.50	37.78	6	17	23	-8.9	4.9E-07
7	27.25	37.92	34	17	20	-12.3	2.E-09
8	27.27	37.74	8	11	17	-8.3	1.4E-06
9	27.17	37.82	26	13	21	-10.7	3.E-08
10	27.58	37.33	14	25	30	-11.3	1.E-08

HLA DRB1*09-1sje (PC-1) + 4udu

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.82	38.57	17	8	19	-8.5	1.0E-06
2	27.75	38.46	13	7	16	-8	2.3E-06
3	27.6	38.8	18	6	12	-8	2.2E-06
4	27.67	38.9	18	5	17	-8.2	1.8E-06
5	27.47	39.01	17	6	18	-8.2	1.7E-06
6	27.67	39.18	14	9	17	-8.3	1.3E-06
7	27.98	38.5	16	8	17	-7.8	3.2E-06
8	28.09	38.76	17	22	27	-11	1.8E-08
9	28.49	38.27	11	19	28	-9.5	2.1E-07
10	27.86	38.72	28	20	21	-12.3	2.2E-09

HLA DRB1*12-1sje (PC-7) + 4udu

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	26.65	37.91	16	14	28	-9.7	1.3E-07
2	27.0	37.74	21	15	20	-10.3	5.8E-08
3	27.61	37.18	19	29	45	-12.0	3.5E-09
4	27.07	37.57	19	17	15	-10.6	3.2E-08
5	27.58	37.6	15	26	37	-11.8	4.8E-09
6	27.35	37.57	10	14	30	-9.7	1.5E-07
7	26.85	37.81	13	9	22	-8.3	1.4E-06
8	26.65	37.91	16	6	19	-8.3	1.4E-06
9	27.0	37.74	18	16	32	-10.7	3.0E-08
10	27.12	37.81	8	11	24	-8.4	1.2E-06

HLA DRB*14-1sje (PC-8) + 4udu

PC no	NIS per property (%)		ICs per property (no.)			ΔG (kcal mol^{-1})	K_d (M) at 37^{0}C
	C	aP	C-aP	P-aP	aP-aP		
1	27.75	36.81	15	15	26	-9.9	9.9E-08
2	27.90	36.74	17	17	30	-10.6	3.5E-08
3	27.52	37.60	17	6	14	-8.6	9.2E-07
4	27.52	37.60	14	6	16	-8.4	1.3E-06
5	27.52	37.60	17	5	13	-8.2	1.6E-06
6	27.55	37.19	15	12	33	-9.8	1.3E-07

7	27.52	37.60	15	6	10	-8.3	1.5E-06
8	27.52	37.33	8	8	17	-7.8	3.2E-06
9	27.45	37.77	14	5	9	-7.9	2.6E-06
10	27.25	37.60	15	10	16	-9.0	4.4E-07
HLA DRB1*16-1sje (PC-8) + 4udu							
PC no	**NIS per property (%)**		**ICs per property (no.)**			**ΔG (kcal mol^{-1})**	**K_d (M) at 37^{0}C**
	C	**aP**	**C-aP**	**P-aP**	**aP-aP**		
1	27.62	37.85	13	11	23	-8.9	5.0E-07
2	27.27	38.57	20	13	14	-9.7	1.4E-07
3	27.55	38.29	19	13	29	-9.4	2.2E-07
4	27.62	37.85	15	13	24	-9.5	2.0E-07
5	27.62	37.85	10	11	22	-8.6	8.1E-07
6	27.62	38.12	11	8	23	-8.4	1.2E-06
7	27.42	38.5	14	7	22	-8.1	1.9E-06
8	27.2	38.46	16	13	28	-9.4	2.2E-07
9	27.4	38.36	11	11	19	-8.7	7.6E-07
10	27.2	38.19	16	15	26	-9.8	1.3E-07

Annexure VIII

List of transplanted patients who experienced renal graft rejection within the period of study (Jan 2016 to Feb 2020, 50 months)

Table 74: Patient and donor having mismatched HLA A/B/DR allele pair which resulted in graft rejection

Sl no.	Pt. No.	D/P	A1	A2	B1	B2	DRB1	DRB1	Date of Tx	Date of GR	Total days
1	2	P	A*24:02	A*30:01	B*13:02	B*52:01	DRB1*07:01	DRB1*07:01	08-05-16	20-07-16	74
		D	A*11:01	A*30:01	B*13:02	B*35:01	DRB1*07:01	DRB1*15:01			
2	14	P	A*03:01	A*33:03	B*35:01	B*44:03	DRB1*07:01	DRB1*07:01	22-05-16	14-02-17	269
		D	A*02:01	A*31:01	B*40:06	B*40:06	DRB1*07:01	DRB1*15:01			
3	36	P	A*01:01	A*02:01	B*35:03	B*57:01	DRB1*07:01	DRB1*14:04	17-06-16	19-12-16	186
		D	A*24:02	A*24:02	B*39:01	B*40:06	DRB1*08:03	DRB1*13:02			
4	48	P	A*01:01	A*30:01	B*13:02	B*57:01	DRB1*04:03	DRB1*07:01	12-07-16	14-03-17	246
		D	A*03:01	A*30:01	B*13:02	B*35:01	DRB1*04:03	DRB1*14:04			
5	85	P	A*01:01	A*11:01	B*13:01	B*15:01	DRB1*13:02	DRB1*13:02	31-07-16	08-04-17	252
		D	A*11:01	x	B*15:01	B*35:01	DRB1*13:02	DRB1*13:02			
6	107	P	A*33:03	A*33:03	B*40:06	B*44:03	DRB1*07:01	DRB1*07:01	18-09-16	19-12-16	124
		D	A*24:02	A*24:03	B*15:18	B*58:01	DRB1*04:03	DRB1*13:02			
7	119	P	A*03:01	A*32:01	B*27:04	B*35:01	DRB1*07:01	DRB1*14:04	10-01-17	10-04-17	91
		D	A*02:01	A*03:01	B*08:01	B*57:01	DRB1*03:01	DRB1*15:01			
8	130	P	A*02:07	A*24:02	B*46:01	B*51:01	DRB1*11:15	DRB1*15:02	05-02-17	06-06-17	122
		D	A*01:01	A*11:01	B*40:06	B*52:01	DRB1*04:03	DRB1*15:04			
9	143	P	A*24:02	A*24:02	B*27:07	B*44:03	DRB1*07:01	DRB1*11:01	19-02-17	20-12-17	305
		D	A*03:01	A*31:01	B*35:01	B*51:01	DRB1*01:01	DRB1*11:01			
10	159	P	A*01:01	A*11:01	B*13:01	B*15:01	DRB1*14:04	DRB1*14:04	02-04-17	19-10-17	201
		D	A*03:01	A*30:01	B*13:02	B*35:01	DRB1*07:01	DRB1*15:01			
11	167	P	A*02:01	A*02:01	B*15:11	B*35:01	DRB1*10:01	DRB1*15:01	12-05-17	05-04-18	321
		D	A*11:02	A*11:02	B*40:06	B*40:06	DRB1*11:04	DRB1*11:04			

12	**206**	P	A*01:01	A*24:10	B*52:01	B*57:01	DRB1*04:03	DRB1*07:01	09-07-17	02-11-17	117
		D	A*02:01	A*02:01	B*15:11	B*51:01	DRB1*01:01	DRB1*13:01			
13	**258**	P	A*33:03	A*68:01	B*07:02	B*55:01	DRB1*13:01	DRB1*15:01	20-08-17	20-11-17	93
		D	A*02:01	A*02:11	B*40:01	B*52:01	DRB1*01:01	DRB1*04:03			
14	**274**	P	A*02:01	A*30:02	B*35:01	B*41:01	DRB1*04:03	DRB1*08:04	17-09-17	28-12-17	103
		D	A*11:01	A*11:04	B*40:06	B*35:01	DRB1*15:01	DRB1*11:17			
15	**315**	P	A*02:06	A*24:02	B*15:25	B*35:01	DRB1*13:01	DRB1*13:01	08-10-17	17-02-18	133
		D	A*11:01	A*11:01	B*13:01	B*52:01	DRB1*04:03	DRB1*07:01			
16	**326**	P	A*32:01	A*33:03	B*44:03	B*48:01	DRB1*14:04	DRB1*15:01	05-01-18	05-09-18	244
		D	A*11:01	A*11:01	B*07:05	B*51:01	DRB1*04:03	DRB1*07:01			
17	**345**	P	A*01:01	A*24:02	B*49:01	B*51:01	DRB1*07:01	DRB1*13:02	09-02-18	17-07-18	159
		D	A*02:11	A*02:11	B*35:01	B*40:06	DRB1*04:03	DRB1*13:01			
18	**389**	P	A*02:03	A*23:01	B*07:02	B*41:01	DRB1*12:02	DRB1*15:01	25-03-18	13-06-18	81
		D	A*02:01	A*24:02	B*35:02	B*40:01	DRB1*01:01	DRB1*07:01			
19	**412**	P	A*11:01	A*23:01	B*40:06	B*58:01	DRB1*13:01	DRB1*15:01	06-05-18	08-08-18	95
		D	A*31:01	A*33:03	B*15:18	B*44:03	DRB1*07:01	DRB1*14:04			
20	**429**	P	A*01:01	A*26:01	B*07:05	B*15:17	DRB1*08:03	DRB1*14:04	01-06-18	26-09-18	118
		D	A*03:01	A*11:01	B*07:05	B*40:06	DRB1*14:04	DRB1*15:01			
21	**463**	P	A*01:01	A*11:01	B*13:01	B*15:01	DRB1*14:04	DRB1*14:04	10-01-19	15-03-19	65
		D	A*01:01	A*23:01	B*08:01	B*44:03	DRB1*04:01	DRB1*07:01			
22	**490**	P	A*01:01	A*33:03	B*40:06	B*44:03	DRB1*13:02	x	11-04-19	20-06-19	71
		D	A*03:01	A*11:01	B*35:01	B*37:01	DRB1*13:01	DRB1*15:02			
23	**503**	P	A*31:01	A*33:03	B*04:03	B*57:01	DRB1*07:01	DRB1*07:01	30-05-19	14-08-19	77
		D	A*03:01	A*11:01	B*18:01	B*35:01	DRB1*13:01	DRB1*15:01			
24	**519**	P	A*33:01	A*68:01	B*35:0	B*52:01	DRB1*07:01	DRB1*10:01	15-06-19	30-08-19	77
		D	A*01:01	A*23:01	B*08:01	B*44:03	DRB1*04:01	DRB1*07:01			
25	**555**	P	A*11:01	A*24:02	B*13:02	B*52:01	DRB1*07:01	DRB1*07:01	10-08-19	12-10-19	64
		D	A*01:01	A*33:03	B*44:03	B*57:01	DRB1*03:01	DRB1*10:01			

Annexure IX

1. Images of modeled class II HLA DRB*01, *04, *07, *08, *09, *12, *14 and *16 structures docked with CLIP.

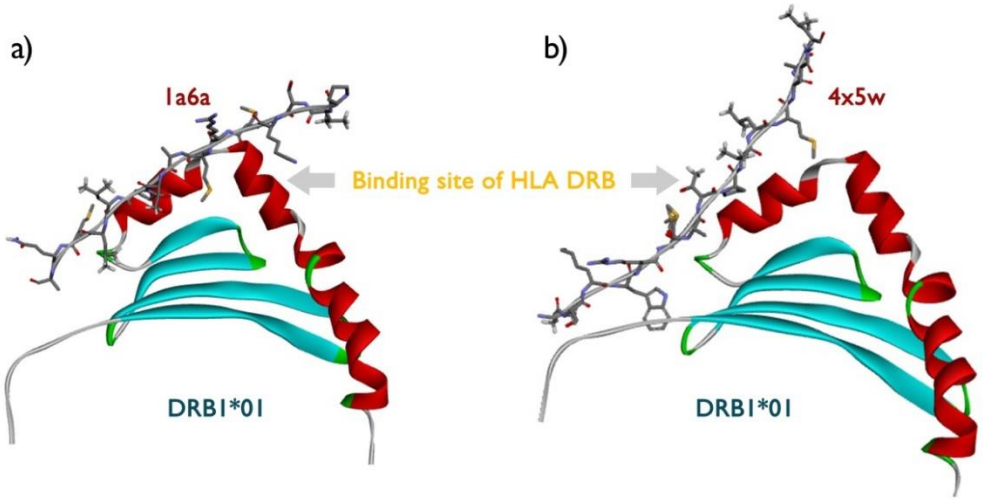


Fig 35: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*01 with a) 1a6a CLIP and b) 4x5w CLIP.

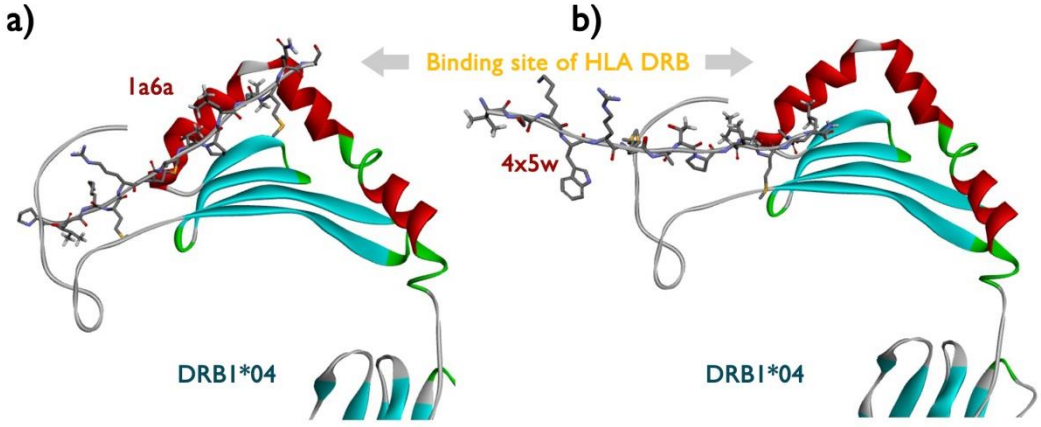


Fig 36: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*04 with a) 1a6a CLIP and b) 4x5w CLIP.

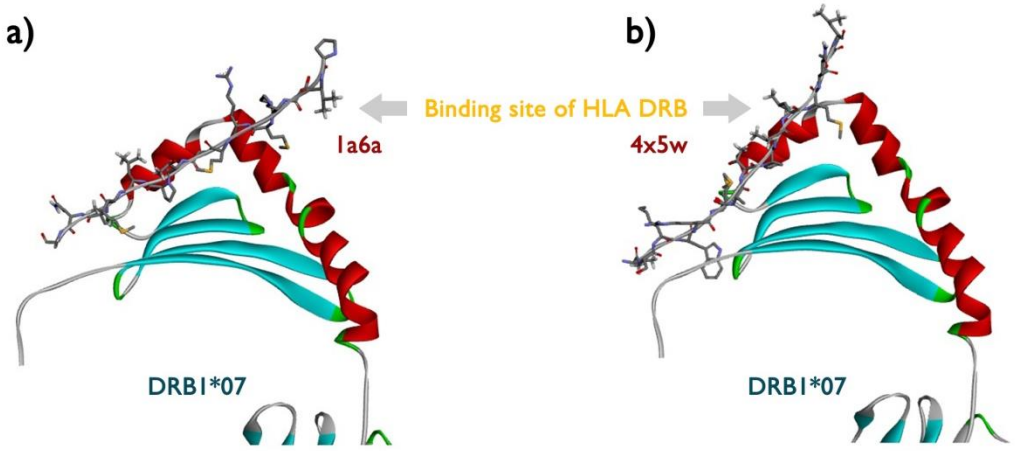


Fig 37: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*07 with a) 1a6a CLIP and b) 4x5w CLIP.

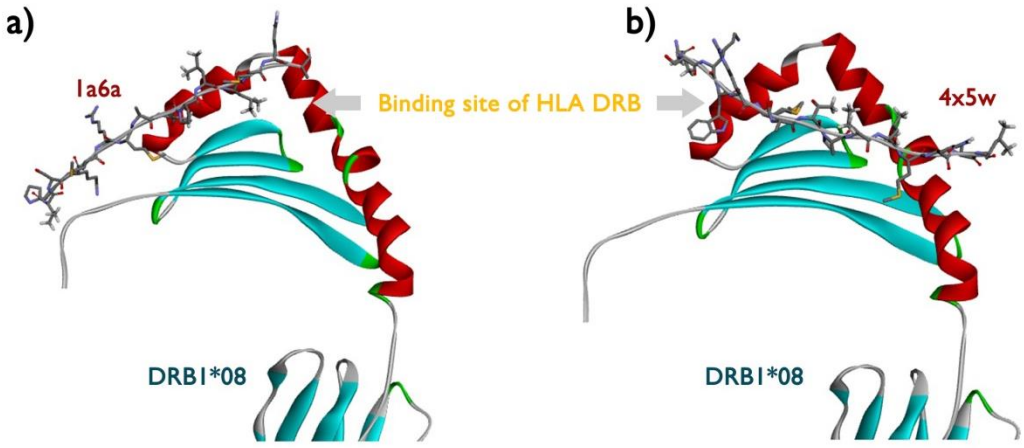


Fig 38: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*08 with a) 1a6a CLIP and b) 4x5w CLIP.

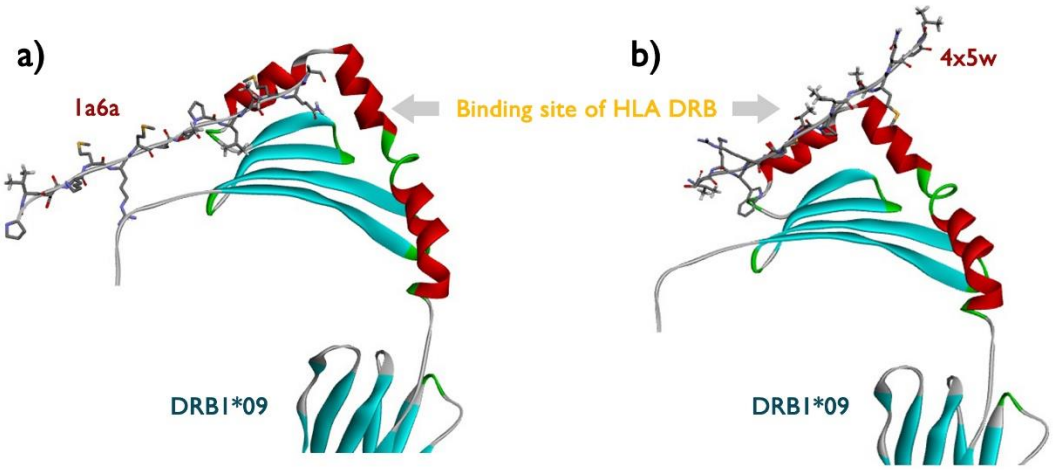


Fig 39: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*09 with a) 1a6a CLIP and b) 4x5w CLIP.

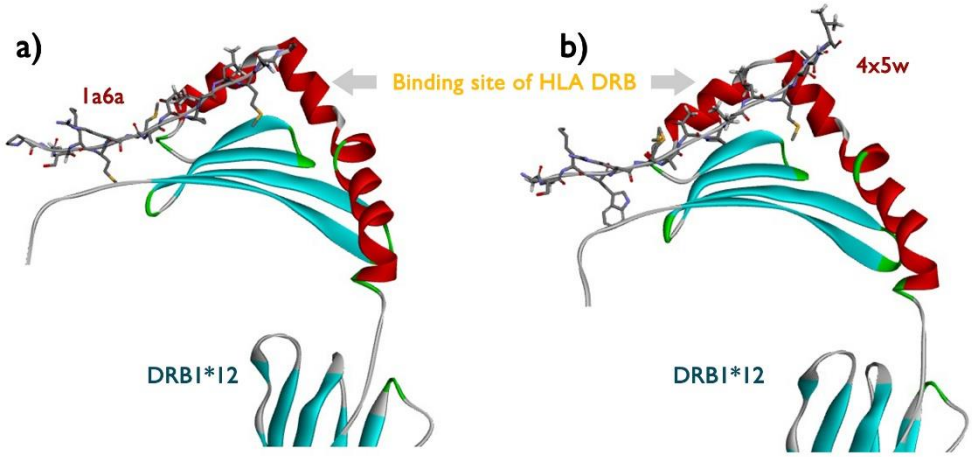


Fig 40: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*12 with a) 1a6a CLIP and b) 4x5w CLIP.

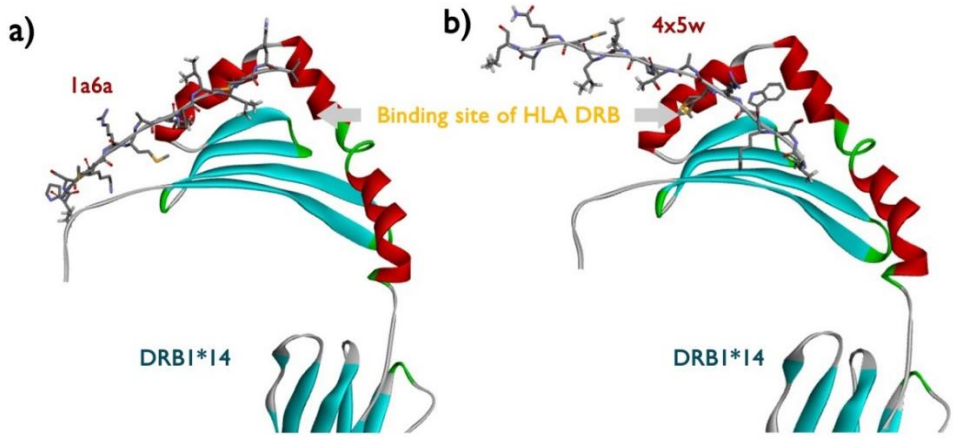


Fig 41: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*14 with a) 1a6a CLIP and b) 4x5w CLIP.

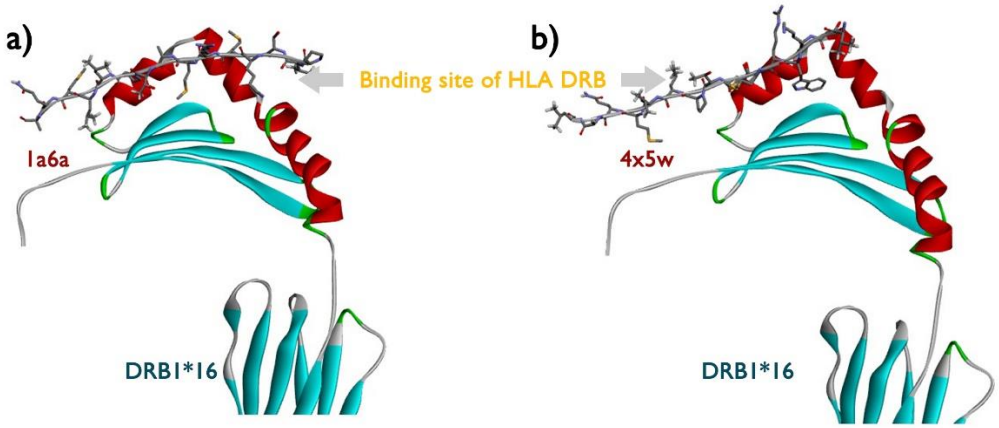


Fig 42: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*16 with a) 1a6a CLIP and b) 4x5w CLIP.

2. Images of modeled class II HLA DRB*01, *04, *07, *08, *09, *12, *14 and *16 structures docked with 5 antigen peptides.

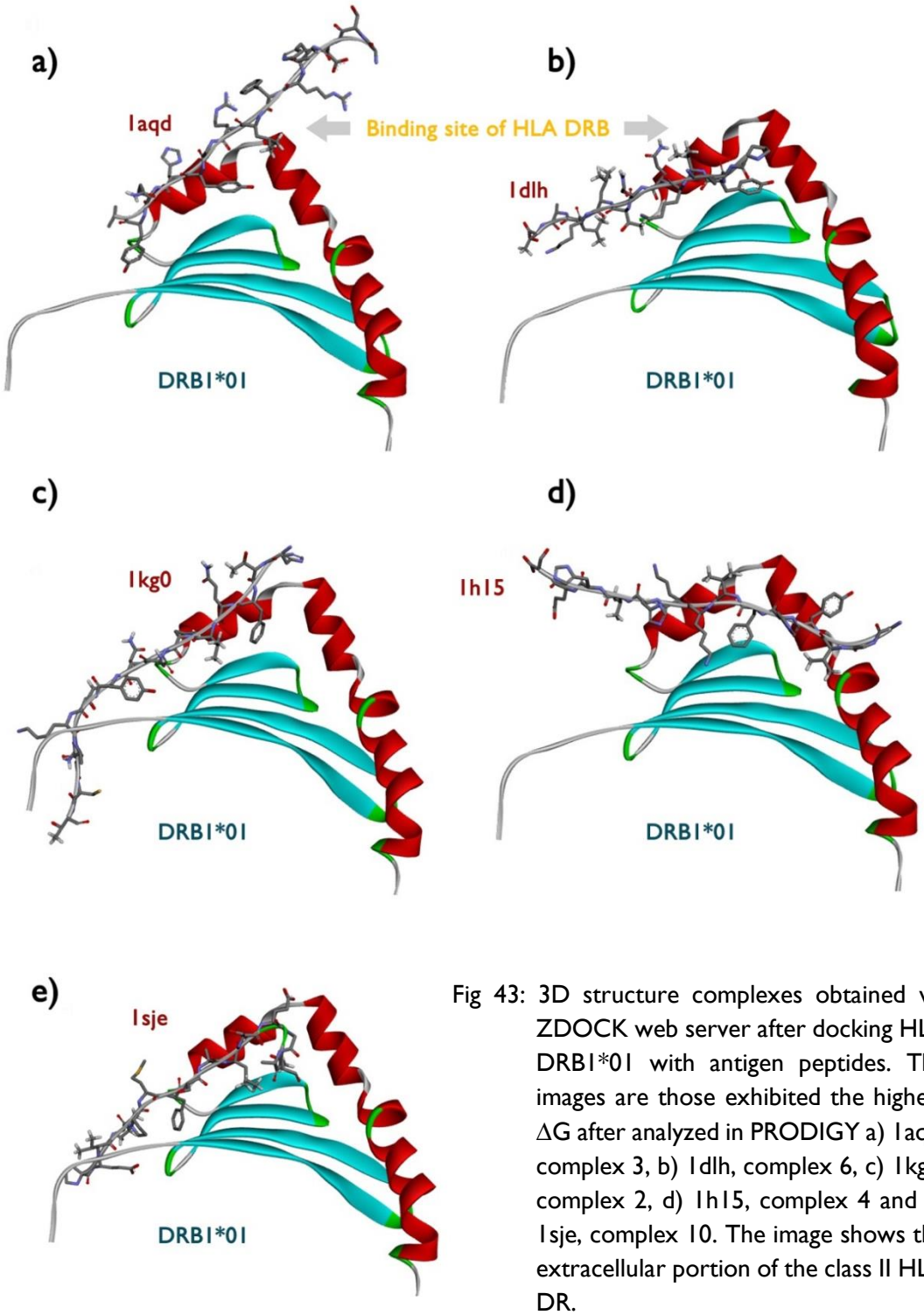


Fig 43: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*01 with antigen peptides. The images are those exhibited the highest ΔG after analyzed in PRODIGY a) 1aqd, complex 3, b) 1dlh, complex 6, c) 1kg0, complex 2, d) 1h15, complex 4 and e) 1sje, complex 10. The image shows the extracellular portion of the class II HLA DR.

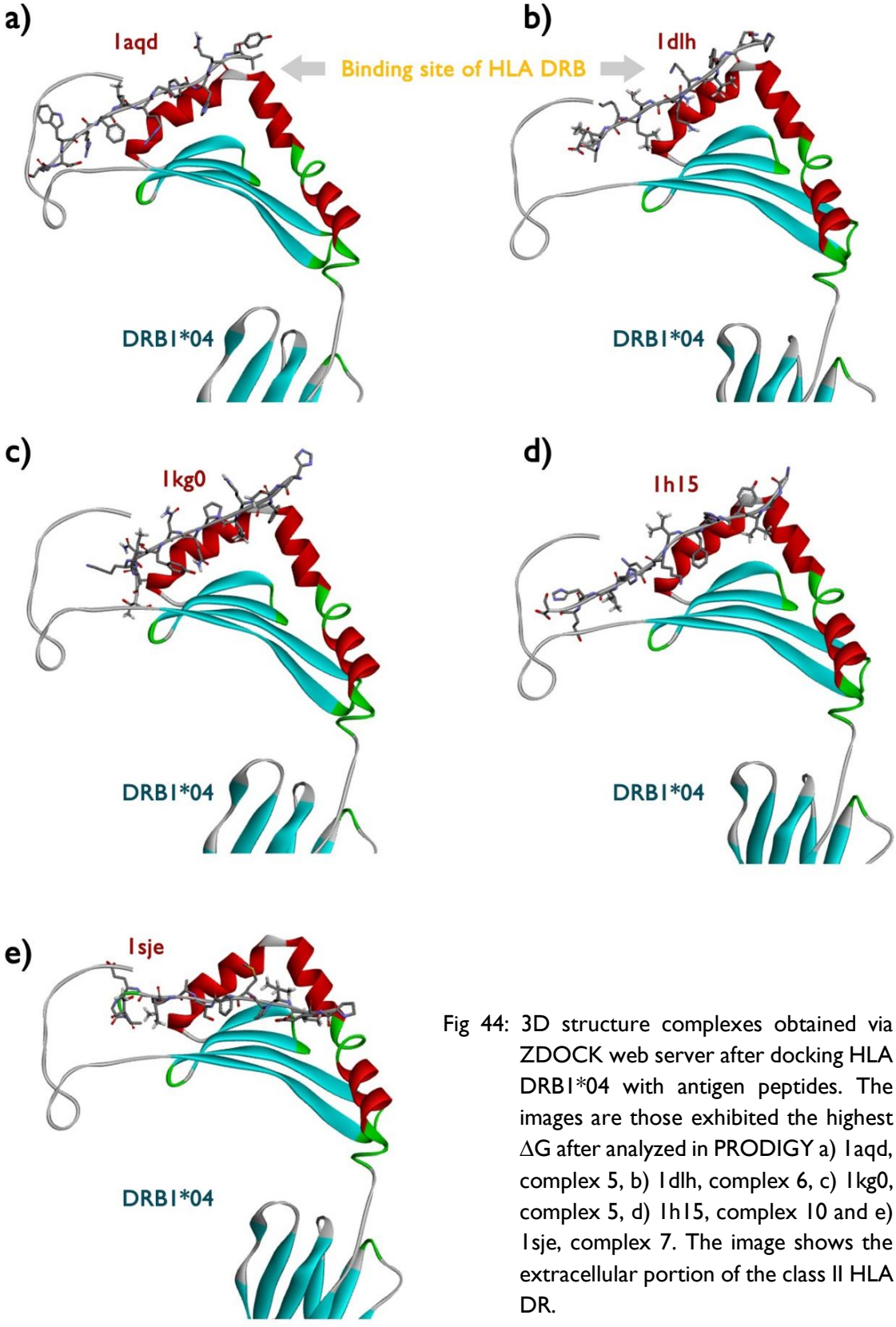


Fig 44: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*04 with antigen peptides. The images are those exhibited the highest ΔG after analyzed in PRODIGY a) 1aqd, complex 5, b) 1dlh, complex 6, c) 1kg0, complex 5, d) 1h15, complex 10 and e) 1sje, complex 7. The image shows the extracellular portion of the class II HLA DR.

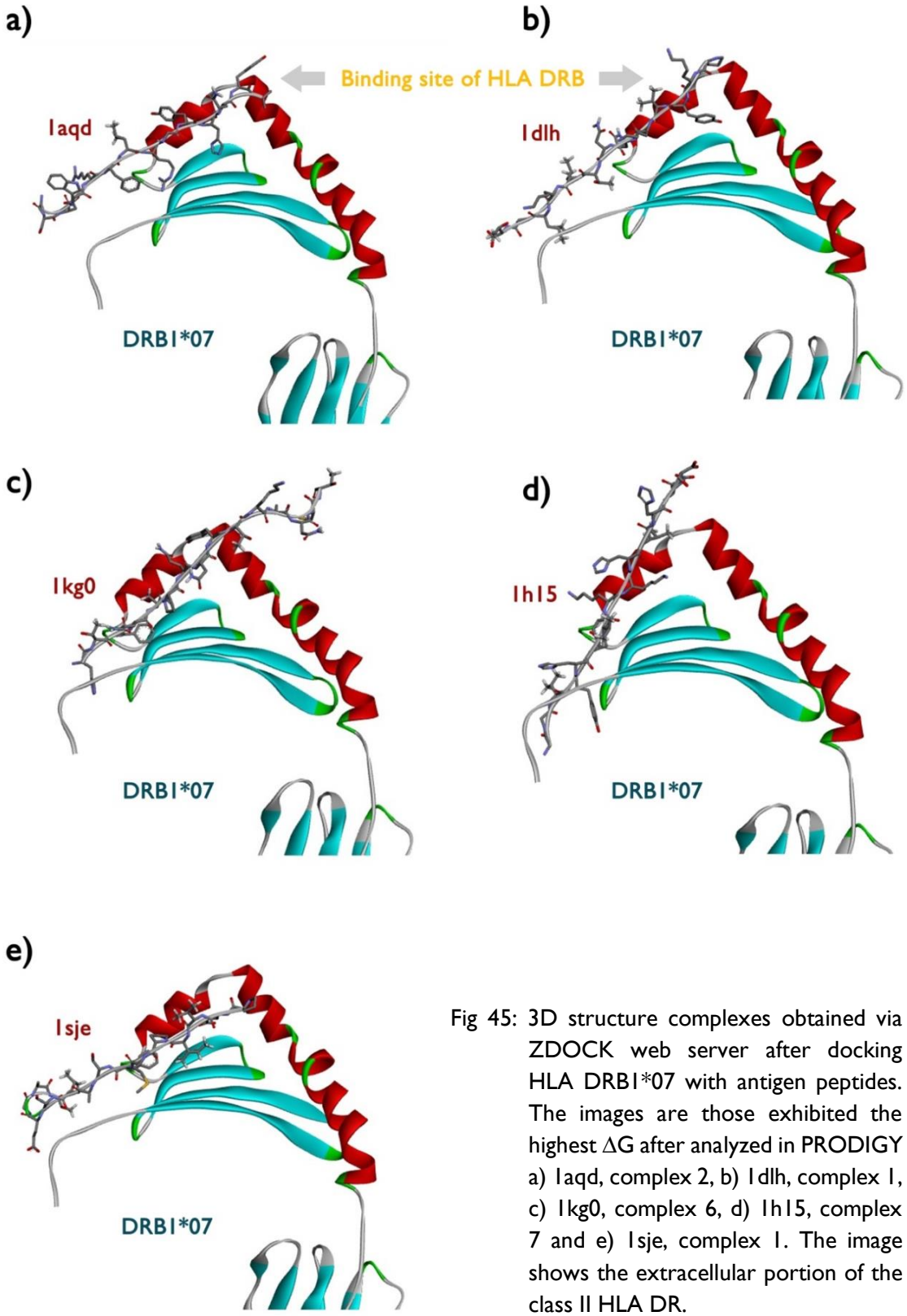


Fig 45: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*07 with antigen peptides. The images are those exhibited the highest ΔG after analyzed in PRODIGY a) 1aqd, complex 2, b) 1dlh, complex 1, c) 1kg0, complex 6, d) 1h15, complex 7 and e) 1sje, complex 1. The image shows the extracellular portion of the class II HLA DR.

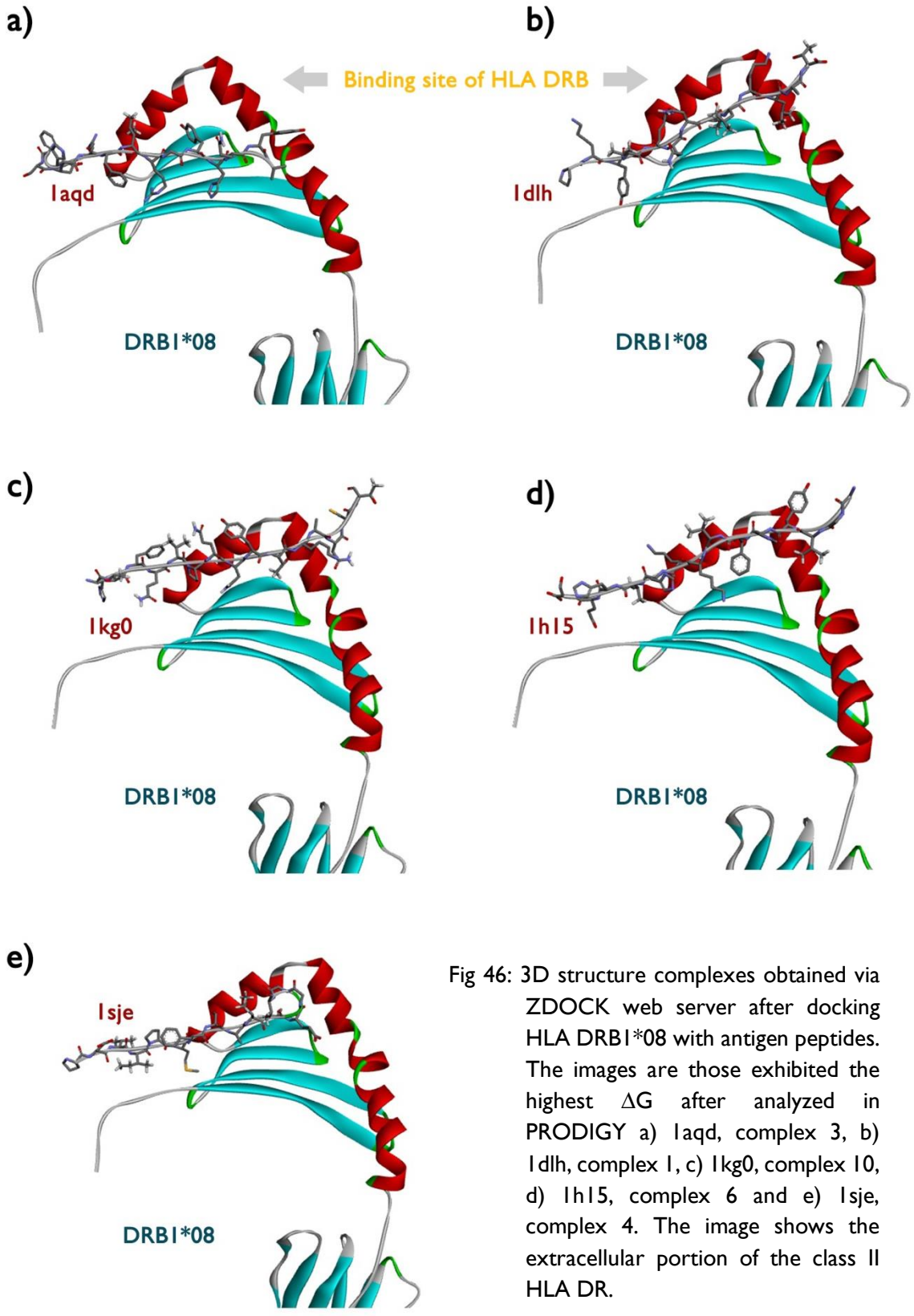


Fig 46: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*08 with antigen peptides. The images are those exhibited the highest ΔG after analyzed in PRODIGY a) 1aqd, complex 3, b) 1dlh, complex 1, c) 1kg0, complex 10, d) 1h15, complex 6 and e) 1sje, complex 4. The image shows the extracellular portion of the class II HLA DR.

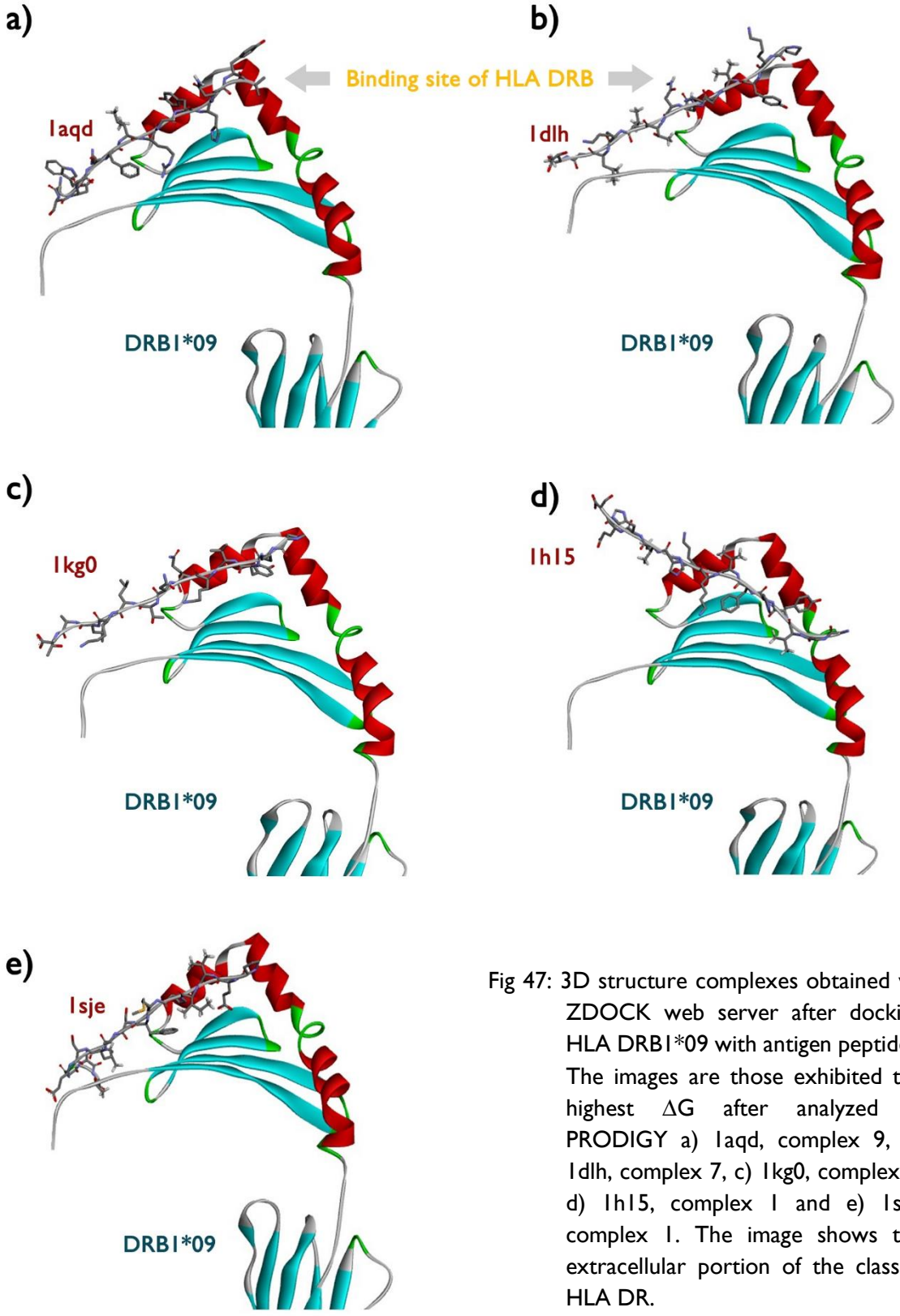


Fig 47: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*09 with antigen peptides. The images are those exhibited the highest ΔG after analyzed in PRODIGY a) 1aqd, complex 9, b) 1dlh, complex 7, c) 1kg0, complex 1, d) 1h15, complex 1 and e) 1sje, complex 1. The image shows the extracellular portion of the class II HLA DR.

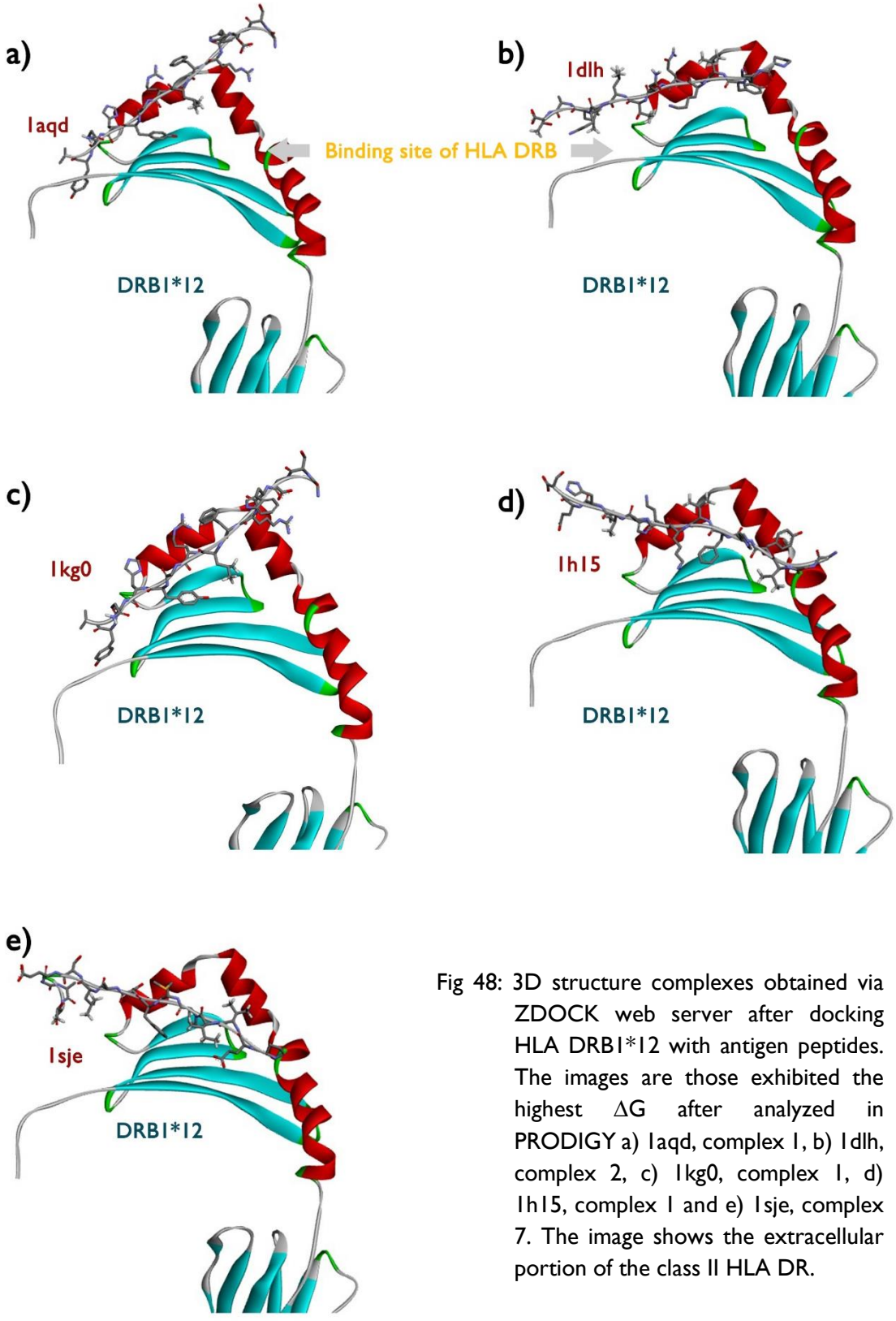


Fig 48: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*12 with antigen peptides. The images are those exhibited the highest ΔG after analyzed in PRODIGY a) 1aqd, complex 1, b) 1dlh, complex 2, c) 1kg0, complex 1, d) 1h15, complex 1 and e) 1sje, complex 7. The image shows the extracellular portion of the class II HLA DR.

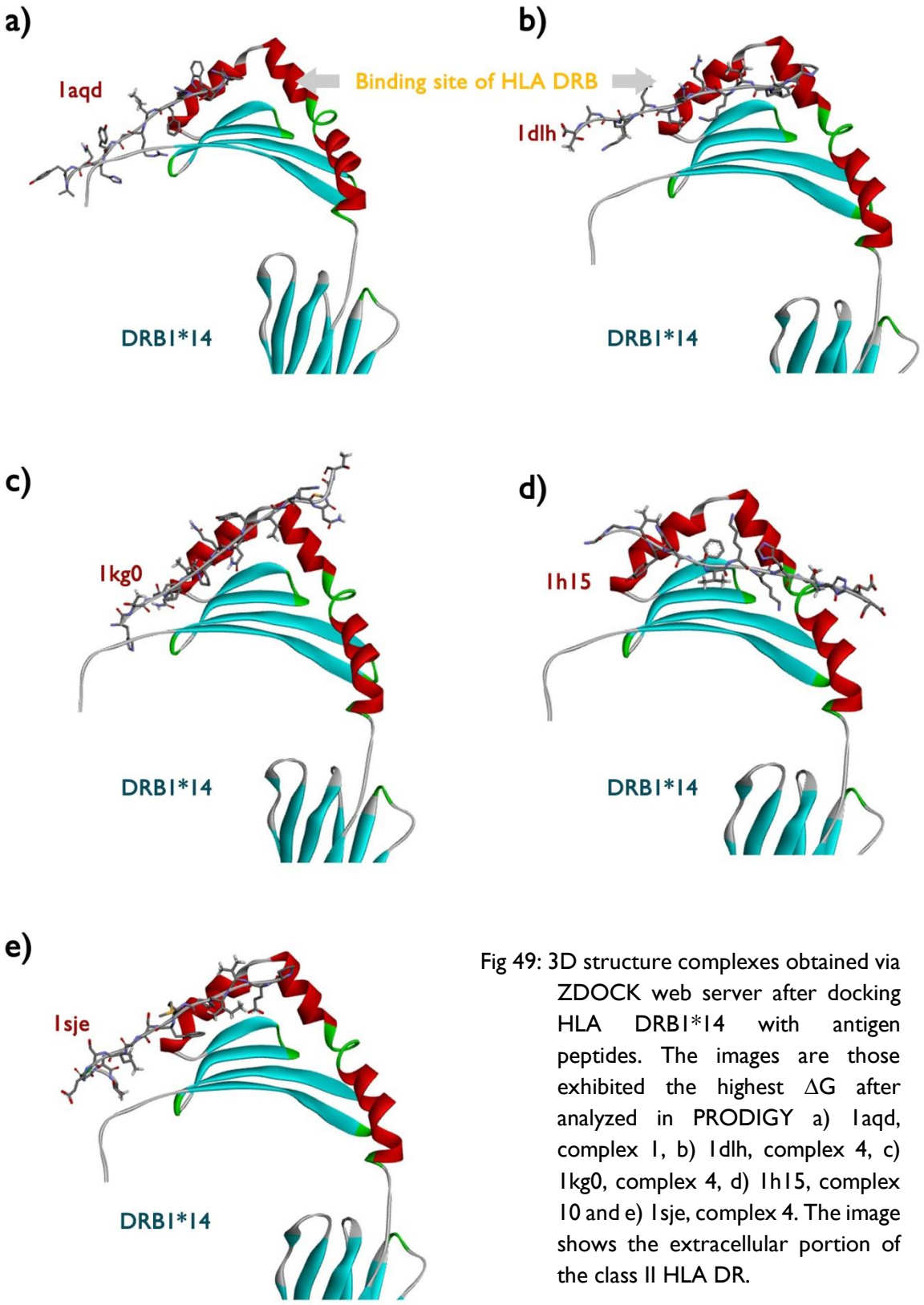


Fig 49: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*14 with antigen peptides. The images are those exhibited the highest ΔG after analyzed in PRODIGY a) 1aqd, complex 1, b) 1dlh, complex 4, c) 1kg0, complex 4, d) 1h15, complex 10 and e) 1sje, complex 4. The image shows the extracellular portion of the class II HLA DR.

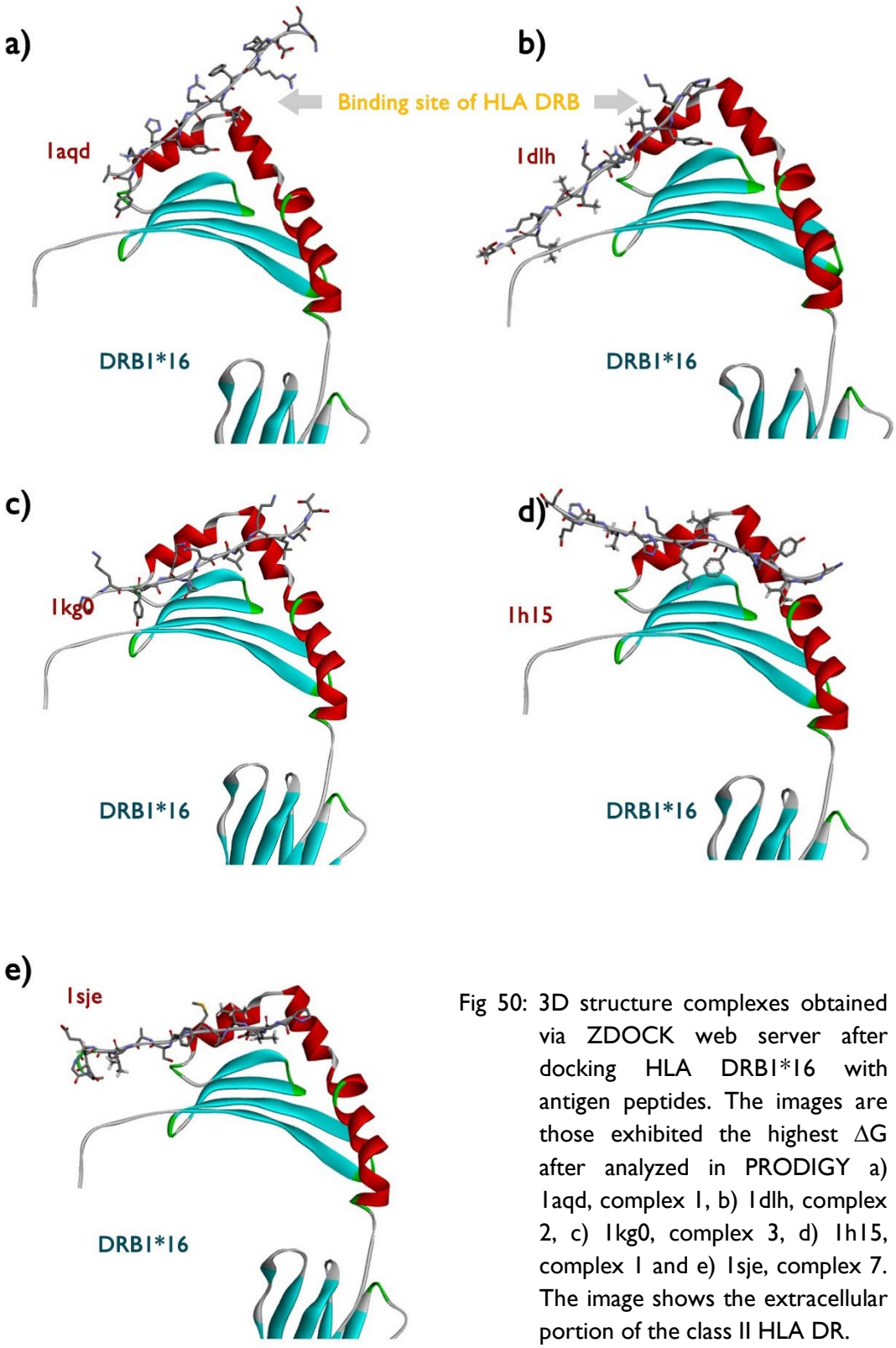


Fig 50: 3D structure complexes obtained via ZDOCK web server after docking HLA DRB1*16 with antigen peptides. The images are those exhibited the highest ΔG after analyzed in PRODIGY a) 1aqd, complex 1, b) 1dlh, complex 2, c) 1kg0, complex 3, d) 1h15, complex 1 and e) 1sje, complex 7. The image shows the extracellular portion of the class II HLA DR.

3. Images of class II HLA DRB*01, *04, *07, *08, *09, *12, *14 and *16 structures and Ag peptide complex docked with 3 TCR chain

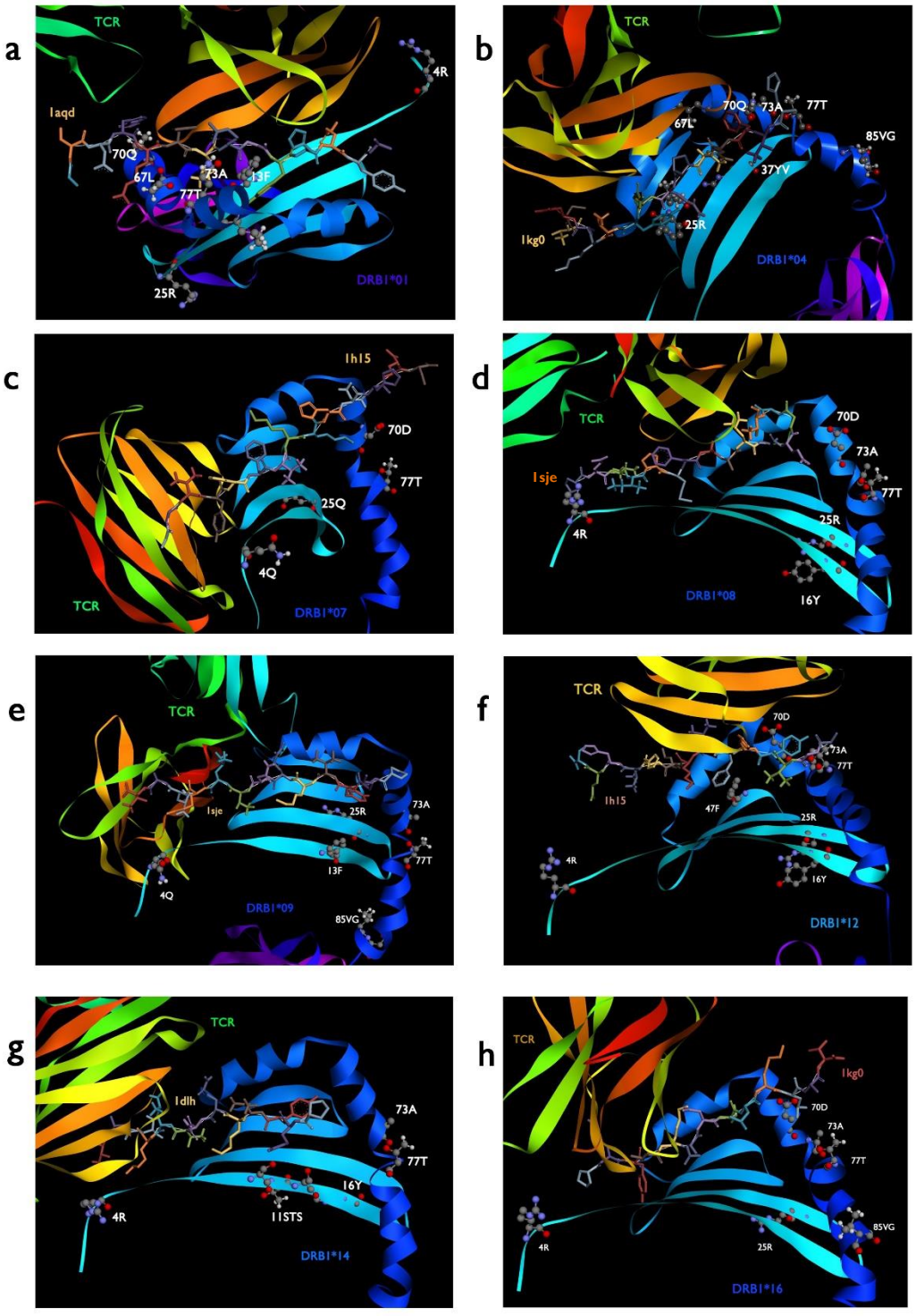


Fig 51: 3D structure complexes obtained via ZDOCK web server after docking HLA-Ag complex with TCR. a) HLA DRB1*01+1aqd+2xna, b) DBR1*04+1kg0+2xna, c) DRB1*07+1h15+3of6, d) DRB1*08+1sje+4udu, e) DRN1*09+1sje+3of6, f) DRB1*12+1h15+4udu, g) DRB1*14+1dlh+3of6 and h) DRB1*16+1kg0+3of6

5. DISCUSSIONS

The results obtained from HLA ABDR allele identification, HLA ABDR eplet mismatch analysis and protein-protein docking studies carried out with HLA DRB, CLIP, Ag-peptide and HLA-Ag-TCR are elaborately discussed here. The diversity among HLA ABDR alleles were studied. Those allelic pair with zero eplet mismatch was identified from mismatch analysis. The relation between HLA ABDR eplet mismatches and increased chance of graft survival was studied in detail. A few of HLA DR alleles was selected to demonstrate the compatibility between eplet matched alleles. The selected modeled HLA DRB structures was used to perform bi-molecular as well as tri-molecular docking and the analysis of binding energy was carried out in the basis of $\Delta G/K_d$ which represents the strength of binding as well as the dissociation energy between the docked complexes.

The study population data collected from the Transplantation & Molecular Diagnostic Lab, Aster MIMS, Calicut, between the period of Jan 2016 and Oct 2018, included a total of 1144 individuals (572 patient and donor). The group showed a very divergent allelic distribution. There were 20 different HLA A alleles, 28 different HLA B alleles and 13 HLA DRB alleles identified for 1144 individuals. The most recurrent allele, from highest to lowest, in class I HLA type A was A*24, A*02, A*11, A*33 & A*01, and the least distributed allele were HLA-A*08, A*22, A*25 A*34, A*62, A*66 and A*74. Similarly, in case of class I HLA type B the most frequent allele was HLA-B*07, B*40, B*35, B*15, B*44, B*51, B*52, B*58 & B*42, and the least frequent alleles were HLA B*78, B*46, B*53, B*02, B*04, B*39, B*50, B*81, B*14 & B*49. The allele distribution of class II HLA DR was less when compared to class I HLA alleles as there were only a few alleles in the study group. The most common HLA DR allele type was HLA-DRB1*15, DRB1*07, DRB1*04, DRB1*14 & DRB1*13 and the least common alleles were HLA-DRB1*16 & DRB1*09. In our study, HLA-A*08, A*22, A*25, HLA-B*78, B*46, B*53, B*02, HLA-DRB1*16 & DRB1*09 is considered rare as their occurrences in the total study population was less than 10 loci and a few of the alleles were not detected in the population taken for this study.

5.1 Interpretation of HLA ABDR eplet matches and mismatches of patient and donor via HLA Matchmaker

Evaluating the 572 patient and donor allele pairs tabulated in annexure II, the total number of patient and donor with full matched HLA ABDR alleles was 6 (patient and donor set no. 8, 23, 35, 37, 109 & 125) and half matched for either one or two allele was 306 and complete allele mismatch was 260. The term 'full matched' allele specifies a complete match between maternal and paternal alleles of the 2 HLA allele classes, class I AB, and class II DR, between a patient and donor. The term 'half matched' allele indicates either one or two of the alleles, of both classes, being not matched between the patient and donor. For the analysis of matched and mismatched allelic pairs of patient and donor, 8 allele combinations were studied, i) full matched HLA ABDR, ii) matched HLA A and mismatched HLA BDR, iii) matched HLA B and mismatched HLA ADR, iv) matched HLA DR and mismatched HLA AB, v) matched HLA AB, mismatched HLA DR vi) matched HLA ADR, mismatched HLA B, vii) matched HLA BDR, mismatched HLA A, and finally viii) full mismatched HLA ABDR. Here, a random number of the patient and donor pairs having full/half allelic match as well as mismatched and non-mismatched eplets were selected from table 39.1 & 39.2 of annexure II and table 40-42 of annexure IV. The comparative analysis between patient and donor allele pair and eplet mismatch in case of both class I HLA AB and class II HLA DR structures, is discussed below.

5.1.1 Acceptable HLA ABDR allelic mismatches and lower number of eplet mismatches

Considering the 6 different cases of half allelic mismatches explained earlier, multiple number of patients survived for more than 1500 days (4 years) were found to be having eplet mismatch less than 10 and most of them being zero (table 10, annexure IV). Taking some examples from the data table; scenario I - the patient and donor set no. 7 have a half-matched HLA A allele (HLA-A*02:01 & HLA-A*24:02) and full matched HLA B and HLA DR allele. This half-matched allelic pair was having zero eplet mismatches and the patient showed a survival period of more than 1480 days. Scenario II - the patient and donor set no. 17 has a half-matched HLA A (A*24:02 & A*31:01) and HLA DR allele (DRB1*14:01 & DRB1*15:01), and full matched HLA B

allele and patient and donor set no. 90 has a half-matched HLA A allele (A*11:01 and A*24:01). Both patient sets had 7 A and zero DR eplet mismatches. These grafts survived for more than 1625 days. Scenario III - the patient and donor set no. 50 has a half-matched DR allele, (HLA DRB1*13:01 & DRB1*10:01) having 6 DR eplet mismatches also survived for a longer period. This clearly indicated 2 possibilities, i) the presence of identical eplets in both alleles of patient and donor and ii) the chance of existence of acceptable allelic mismatches between non-identical HLA alleles. In both cases the long-term survival of the graft or the reduced chances of an early graft rejection might be a result of the presence of those identical eplets, which aided in its structural conformation as well as its similarity.

5.1.2 Increased number of HLA DR eplet mismatches and graft rejection

Some of the patients faced early graft loss. The analysis of the allele as well as eplets of the patient and donor suggested that there existed non-acceptable allelic mismatches as well as an increased number of eplet mismatches between both HLA AB and DR alleles (table 40, annexure IV). The patient and donor set no. 40, having complete ABDR allele mismatch, had 8 eplet mismatches between AB alleles, A*11:01/32:01, A*31:01/33:01 & B*35:01/51:01, B*44:03/51:01, and 20 eplet mismatches between DRB1*04:03/ 07:01 & DRB1*13:02/14:04. The patient survived only for 124 days, after the date of transplant. The patient and donor set no. 233 had 6 AB eplet mismatches and 16 DR eplet mismatches between A*02:11/11:01, A*24:02/24:02, B*07:05/51:01, B*07:05/08:01 and DRB1*04:03/14:04 DRB1*03:01/ 15:01, the graft rejected within 140 days of transplant. In case of patient and donor set no. 526, having the allele HLA A*02:01/32:01, A*33:03/33:03, B*07:02/48:01, B*40:06/44:03 and DRB1*12:02/15:02, DRB1*07:01/07:01 had 9 AB and 26 DR eplet mismatches. The graft survived for a few months only. The eplet analysis on these HLA DR alleles indicated that the increased number of HLA DR eplet mismatch is most likely to have caused the genetic/immunological reaction which led to the graft rejection. This has been further analyzed and confirmed biostatistical methods.

Section 4.6 explains the statistical correlation result between increased number of class II HLA DR eplet mismatches and renal graft outcome. The occurrence of rejection was confirmed by analysis of urine creatinine and renal biopsy.

There are reports confirming the direct correlation between variances in amino acids sharing the same position in an allo-HLA allele with immunogenicity, which also shows the increasing association between higher immunogenic response (antibody response) and mismatch per amino acid between the alleles (Kosmoliaptsis et al., 2011). The precise characterization of the immunogenicity of each eplets mismatch can lead to the identification of acceptable mismatches within the wide range of existing HLA alleles (Tambur et al., 2014). In 2015, Ruth Sapir-Pichhadze and team have published an article stating that there is a direct correlation between high number of HLA DRDQ eplet mismatches with transplant glomerulopathy (TG), a morphological lesion characterized by basilar membrane disruption in the glomerular region (Hass, 2011). This article being the first to link patient and donor compatibility at eplet level coined the fact that the sum of HLA DRDQ eplet mismatch is a clear risk factor for TG.

5.1.3 Patient and donors with zero HLA ABDR eplet mismatches

The total number of patient and donors with zero HLA AB eplet mismatch was 23 out of 572. In case of patient set no. 7, 10, 91, 108, 111, 114 and 402 from the table 40, annexure IV, there are multiple occurrences of allelic mismatches in HLA A and B allele for which we are to expect corresponding eplet mismatches. But all of them are found to have zero HLA AB eplet mismatches. As discussed earlier in section 5.1.1, there are mismatched alleles which showed zero eplet mismatches.

In case of patient set no. 7, the mismatched allele of patient is HLA A*02:11 and that of the donor is A*24:02. Patient set no. 10 the mismatched allele of the patient is HLA A*24:02 and that of donor is A*11:01, the allele of the patient is HLA B*07:02 and that of the donor is B*57:01. Patient set no. 91, the allele of patient is HLA A*33:01 and that of donor is A*02:01, the allele of HLA B of donor is B*37:01 and that of patient is B*58:01. Patient set no. 108 the donor allele of HLA A is A*24:02 and that of patient is A*02:11. Patient set no. 111 the HLA A allele of donor is A*11:01 and

that of patient is A*24:02, the HLA B allele of donor is B*57:01 and that of the patient B*07:02. Patient set no. 114 the HLA A allele of donor is A*01:01 and that of patient is A*32:01. Patient set no. 402 the HLA B allele of donor is B*40:06 and that of patient is A*52:01.

The total number of patient and donor pair with zero HLA DR eplet mismatch was 46 out of 572. Patient set no. 17, 33, 84, 116, 331, 375, 442 and 500 from the table 40, annexure IV, were observed to be having allelic mismatches either for single or for both alleles. Patient set no 17 the HLA DR allele of donor is DRB1*15:01 and the recipient is DRB1*14:04. Patient set no 33 the HLA DR allele of donor is DRB1*15:01 and the recipient is DRB1*13:02. Patient set no 84 the HLA DR allele of donor is DRB1*07:01 and the recipient is DRB1*03:02. Patient set no 116 the HLA DR allele of donor is DRB1*15:01 and the recipient is DRB1*14:04. Patient set no 331 the HLA DR allele of donor is DRB1*07:01 and the recipient is DRB1*11:01. Patient set no 375 the HLA DR allele of donor is DRB1*01:01 and the recipient is DRB1*13:01. Patient set no 442 the HLA DR allele of donor is DRB1*14:04 and the recipient is DRB1*16:02. Patient set no 500 HLA DR allele of donor is DRB1*01:01 and the recipient is DRB1*08:03.

5.1.4 Existence of shared eplets between HLA ABDR eplet mismatches

HLA matching at eplet or amino acid level delivers promising opportunities. The first article published by Rene J. Duquesnoy in 2001, laid the basic groundwork for eplet mismatch identification and eplet based selection between both sensitized and unrelated donors. Duquesnoy and his team has contributed more than 60 articles stating the relation between different scenarios in solid organ transplantation with HLA allelic match as well as HLA eplet matches and how a clinical expert can use the same in the betterment of donor selection criteria. Today the HLA eplet match and mismatch analysis has been employed in heart, liver and renal transplantations. But, identifying acceptable mismatches for sensitized patients as well as finding a healthier mismatched donor for non-sensitized patients via HLA Eplet Matching, lacks the experimental identification of clinically relevant eplets (Duquesnoy, 2017). These experiments bridge the gap between the antibody-verified eplets and those which exist

as theoretical entities, were no antibody information is available, by providing structural data to the amino acid level (Duquesnoy & Marrari, 2017).

Here, the analysis of eplets in different alleles highlighted the existence of shared eplets between allele mismatched individuals. Even when there is a complete mismatch between both class I and II HLA ABDR alleles the position of eplets sharing the same space in the three-dimensional structure of the protein resulted in the formation of HLA protein complex with eplets in same position as the allo-allele. The presence of such HLA alleles with similar eplets can be considered as close relatives which are molded as a result of evolutionary polymorphism. Such individuals carrying different allele with lower number of eplet mismatches can be considered for transplantation because this results in an inferior chance of chronic graft rejection. While considering the amount of broad antigen/HLA mismatches for investigating the possibility for a graft rejection, understanding whether they have eplets shared in the same position in 3D space can reduce the risk of rejection as there is a possibility for the eplet matched HLA allele to mimic the structural conformation of the recipient allele. Our study further analyzed this via protein-peptide-protein, tri-molecular docking.

Our findings provide the first insight of the possibility of choosing unrelated donors with different allele having matched HLA ABDR eplets in connection with HLA structural information, as a better option for renal transplantation. The analysis of amino acids and eplets at structural level provides the best possible evidence of structural compatibility between eplet matched HLA alleles supporting the existing reports which explains the selection of donors having acceptable eplet mismatches for renal transplantation.

5.2 Interpretation of binding affinity of all docked complexes via PRODIGY

It is known that majority of the critical cellular activities relies on specific protein-protein interactions and the characterization of such molecular interactions is fundamental for understanding the mechanism underlying its functions (Mintseris et al., 2007; Vangone & Bovin, 2015; Vangone et al., 2019). During the past 2 decades, several types of improved computational methods for analysis of protein surface

interactions and binding energy predictions have been developed, which mostly depend on surface complementarity and electrostatics (Cheng et al., 2012; Hou et al., 2015). According to Launay et al., 2017, protein interaction takes places through interfacial interactions having specific surface properties, which are not usually considered in global structural comparison. While relying on localized structural comparison which is restricted to the evaluation of a large number of physical or interfacial interactions between two complementary atomic contacts, the measurement of the equilibrium dissociation constant K_d is a significant parameter to elucidate the dynamic surface interactions (Launay et al., 2017; Visscher et al., 2015). Equilibrium dissociation constant K_d is a measure of binding affinity, which provides the significant information about how strong a specific molecular interaction is. Smaller the K_d value greater the binding affinity between the investigated complexes. Naturally, the tremendous diversity of cellular processes in the vast evolutionary timescale the K_d values span more than 11 orders of magnitude, i.e., the higher mM to lower fM concentrations. K_d values obtained greater than $1x10^{-6}$ implies appreciable binding affinity in case of protein-protein complexes and above $1x10^{-9}$ is considered as a strong binding or need high energy to dissociate them (Kastritis et al., 2011; Kastritis et al., 2014; Visscher et al., 2015).

According to the existing reports, CLIP must be released from the peptide binding site in the HLA DRB protein structure in order to accommodate the incoming processed antigen peptide via endosomal pathway, having 13-18 amino acid length (Chaturvedi et al., 2000; Sette et al., 1995; Thayer et al., 1999). The K_d value obtained for docking between all selected HLA DRB with 2 different CLIP structures revealed the weak affinity between the selected bio-molecular structures. Of the 20 structures obtained after docking between a single HLA DRB and CLIP, 80% of the protein complexes showed lower K_d values suggesting the facile dissociation of the CLIP from class II HLA DRB.

5.2.1 Analysis of $\Delta G/K_d$ between HLA-CLIP complexes

The average percentage of non-interacting surfaces per property for the resulted complexes formed between CLIP and class II HLA DRB structures was

approximately between 66.3 and 66.9, which is the sum of its charged (C) and apolar (aP) amino acids. Surfaces per property simply expresses the minimal interactive area (5.5 Å) which is needed to from an appreciable interfacial contact between 2 peptides or the initial folding in case of protein secondary structure formation. The NIS percentages indicated that only 21.5 - 21.9 interfacial contacts (ICs) interacts effectively with the selected grid area and constitute for the low binding affinity between the two biomolecules. The summary of different types of ICs like charged-apolar (C-aP), poplar-apolar (P-aP) and apolar-apolar (aP-aP) interaction, obtained from the study is presented in annexure V, tables 12, 14, 16, 18, 20, 22, 24 & 26. The lower number of interacting interfacial amino acids resulted in lower K_d thus facilitating the dissociation of CLIP from HLA DRB. The K_d value ranged between $1.2x10^{-5}$ and $9.1x10^{-6}$ exhibiting low dissociation cont. which enabled the peptide to be dissociated easily.

5.2.2 Analysis of $\Delta G/K_d$ between HLA-Ag peptide complexes

The ΔG values obtained for 400 docked HLA-Ag peptide complexes (5 peptides, 10 complex each; total 400 complexes for 8 HLA DRB structures) ranged between -5.8 and -10.9 kcal/mol and the K_d value ranged between $1.3x10^{-5}$ to $9.8x\ 10^{-8}$, showing low to moderate association between the two biomolecular structures. The low binding energy is due to the low number of ICs like charged-apolar (C-aP) and poplar-apolar (P-aP) or due to high number of apolar-apolar (aP-aP) interaction formed between the peptide and HLA DRB which is evident from table 16. For example, DRB1*07+1aqd complex 8, DRB1*07+1dlh complex 8 and DRB1*07+1sje complex 6 of annexure V, table 16. An evident increase in percentage of interacting surfaces or ICs in case of HLA-Ag peptide binding was observed which resulted in higher negative ΔG values. The results have been tabulated in annexure V, tables 13, 15, 17, 19, 21, 23, 25 & 27.

5.2.3 Analysis of $\Delta G/K_d$ between HLA-Ag-TCR tri-molecular complexes

For the analysis, interpretation and identification of the binding affinity in term of K_d between the tri-molecular complexes, all the HLA DRB-Ag peptide complexes

docked with same TCR were compared between each other. The data enlisted in table 28-32 contains the list of all the 8 HLA DRB structures docked with 5 Ag-peptide and TCR - 2xna; table 33-37 contains the list of all the 8 HLA DRB structures docked with 5 Ag-peptides and the TCR - 3of6 and tables 38-42 contains the list of all the 8 HLA DRB structures docked with 5 Ag-peptides and the TCR - 4udu. The image showing the process of selection of each structure for docking has been represented in Fig 22. This was carried out by identifying those pairs of HLA DRBs having comparable $\Delta G/K_d$ values (K_d values with lesser than 10^{-1} difference between respective complexes). Those complexes with difference in K_d values more than 10^{-2} and 10^{-3} was considered as moderate compatible and less compatible respectively. The changes observed in ΔG values substantiate this statement. The data summary has been listed in tables 43-56 of annexure VII. Of the 1200 HLA-Ag-TCR tri-molecular complexes obtained, those HLA DRB pairs categorized as compatible the analysis of each tri-molecular complex revealed that there exists an 80-90% similarity in $\Delta G/K_d$ values within the 10 docked complexes i.e., out of 10, 8 to 9 complexes showed negligible difference in $\Delta G/K_d$ values. This also points out the fact that these compatible HLA DBR pair might share the same eplets too. From the data tabulated in annexure II and IV, and comparison with the data tabulated in annexure IV, V and VI, it was observed that the binding affinity for tri-molecular complexes in case of those HLA pair observed to be having zero eplet mismatches came under those HLA DRB pair listed as comparable with very low or only negligible difference in $\Delta G/K_d$ values. Whereas the K_d values of tri-molecular protein complexes simulated in case of eplet mismatched HLA pair differed evidently with each class II HLA DR. All the possible combinations of HLA DR pairs have been studies and tabulated.

To further understand the role of peptide in class II HLA presentation and TCR recognition of both peptide and HLA DR, the peptide in HLA-Ag peptide complex was blocked before docking with TCR during the simulation study. The tri-molecular complexes with masked peptides displayed distinct changes in the $\Delta G/K_d$ value with each HLA DR and TCR following the same pattern of low to high $\Delta G/K_d$ values similar to the non-blocked docking session. Here the HLA-Ag-TCR tri-molecular complexes produced comparable results independent of the peptide.

To summarize, after the recognition of the peptide presence in the cellular compartment, the pre-assembly of the α and β chain of class II HLA occurs in the endoplasmic reticulum assembling the hetero dimeric structure. The structure is stabilized by the equalization of attractive and repulsive forces between the α chain and the β chain. Here the α chain assists in the conformation & structural stability and the β chain acts as the functional component in antigen presentation. The structural eplets, present in the antigen binding site provides the structural stability for the whole HLA structure complex. Presence of different amino acids or change of amino acids which make up these eplets causes changes in the HLA structural conformation, there by altering the shape complementarity. Presence of same eplets in the donor HLA can mock the structural conformation of self-HLA to an extent to which it can present the peptide in a similar manner. Here, the TCR might recognize the donor HLA as self-HLA. In other way, TCR might be unable to differentiate between donor and self HLA DR; another point of view in the docking study. The probability of graft rejection from such eplet combinations was observed to be far less when compared to eplet mismatched pairs.

5.3 Biostatistical analysis on HLA ABDR eplet mismatches in relation with renal graft survival

This collaborative study is conducted within a local population based on the data provided by the collaborative institute. The use of computational and statistical approach has been utilized for analyzing HLA allelic data obtained by HLA typing using SSP- and SSOP-PCR. The analysis of 572 renal transplant candidates and their donor was carried out within period of 50 months, form Jan 2016 to Feb 2020. The presence of alleles like, class I HLA A*24, A*02, B*07, B*40, class II HLA DRB1*15 & DRB1*07 was found to be frequently occurring in the population and the comparative analysis of eplet mismatches between the patient and donor was statistically studied.

The study was conducted to understand the existence of relation between HLA ABDR eplet mismatches between patient and donor case of renal transplantation and the chance of having a single event of renal graft rejection. The information about locus specific eplet mismatches can be used to predict the potential chance of having the

possibility of renal graft rejection. Previous studies have attempted to address the occurrence of common eplet load between a renal transplant patient and donor pair in case of specific kidney diseases (Do Nguyen et al., 2016; Neal et al., 2011; Sapir-Pichhadze et al., 2015). With the knowledge from earlier and recent reports, analysis of HLA eplet mismatches via matchmaker algorithm and statistical analysis using the HLA allelic data, here we have discussed the existence of correlation between eplet level mismatches and eplet load between patient and donor HLA AB and HLA DR allele and outcome of renal transplantation, within a local population. Furthermore, early studies involving transplant patients who underwent renal transplantation exhibited a higher occurrence of postoperative complications, such as, late acute rejection, infections, etc.

6. SUMMARY & CONCLUSIONS

The present study has been focused to ascertain an ideal strategy for selecting unrelated individuals as potential donors for renal transplantation by analyzing the number of eplet mismatches and structural variations, that each individual possesses, thus eliminating the possibility of an undesired immune reaction observed in our population. Here, HLA ABDR alleles were identified via HLA typing by SSP- & SSOP-PCR, HLA Matchmaker analysis for eplet mismatch identification between HLA AB and HLA DR alleles, protein modeling of selected 8 HLA DRB structures, protein docking between HLA-CLIP, HLA-Ag and HLA-Ag-TCR for the identification of compatible HLA DR structural pairs, and biostatistical analysis for finding the correlation between increased HLA DR eplet mismatch and renal graft outcome, was performed for a total of 572 patient and donor pair.

In the diverge allelic population selected for our study there were 20 different HLA A alleles, 28 different HLA B alleles and 13 HLA DRB alleles. The highest distributed allele of class I HLA A was A*24, A*02, A*11, A*33 & A*01, HLA B were B*07, B*40, B*35, B*15, B*44, B*51, B*52, B*58 & B*42 and class II HLA DR were HLA DRB1*15, DRB1*07, DRB1*04, DRB1*14 & DRB1*13. In our study, all the 3 allelic groups had rare allele types like, HLA-A*08, A*22, A*25, HLA-B*78, B*46, B*53, B*02, HLA-DRB1*16 & DRB1*09. The occurrences of these alleles in the total study population were found to be less than 10 loci and a few of the alleles were not detected in the population taken for this study. The analysis of the allele as well as eplets of the patient and donor who faced early graft loss suggested that there existed non-acceptable allelic mismatches as well as an increased number of eplet mismatches between both HLA AB and DR alleles. The eplet analysis on these HLA DR alleles indicated that the increased number of HLA DR eplet mismatch might have caused the immune response which led to the graft rejection. Here, the analysis of eplets in different alleles highlighted the existence of shared eplets between allele mismatched individuals. Both class I and II HLA ABDR alleles who share the position of eplets in the same space in the three-dimensional structure of the protein resulted in the formation of HLA protein complex with eplets in same position as the allo-allele. Our findings provide

the first insight of the possibility of choosing unrelated donors with different allele having matched HLA ABDR eplets in connection with HLA structural information, as a better option for renal transplantation.

The study establishes that class II HLA DRB structures which share same eplets between each other can present an antigen peptide in a similar energy ($\Delta G/K_d$) pattern despite of the peptide involved. Further simplifying, the co-dominantly expressing self-HLA structure with a set of structural eplets on the antigen binding site can be mimicked with a donor HLA DRB structure, having the same set of structural eplets on its antigen binding site. In our study, the difference obtained in the $\Delta G/K_d$ values in case of eplet matched and mismatched HLA DRB pairs substantiates this interpretation. There was an appreciable number of interfacial contacts between the eplet matched HLA DRB structures which were comparable. This can also depend on the amino acid present in the structural eplets. HLA-Ag docking and HLA-Ag complex presentation to TCR was discussed in the study as this was the principal event taking place during an immunological reaction after transplantation. The comparison between eplet matched and mismatched class II HLA DR using bi-molecular and tri-molecular protein docking, the results revealed that the HLA-Ag complexes with similar eplets showed same degree of energy in antigen presentation to TCR. The outcome of our study was parallel with those patients who faced graft rejection. Among the other clinical explanations, the HLA DR alleles of the patients with high number of eplet mismatch was observed to be having graft rejection. The statistical study corelated with the results of HLA Matchmaker and analysis of eplet mismatches correlated with the tri-molecular docking study.

During the study, an error in the HLA Matchmaker was observed which aided to the fact that Matchmaker database should be updated with clinical data of Ab-verified eplets. Duquesnoy et al., in 2019 and Bezstarosti in 2022, has added that HLA Matchmaker has not been validated enough to be used directly in clinical level study as there exists theoretical eplets too. Looking through another perspective of the scenario, studies on the pattern recognition capability of human T cell receptor to HLA-Ag bi-molecular complex can also be taken into concern, which can be added as

a future study, which might reveal the ability of human TCR in recollecting the binding pattern to the residual binding site within the HLA-Ag complex.

Our study bridges the gap between eplet number and graft survival by structural biological analysis. The study discussed, in detail, the reason for the existence relation between low HLA eplet mismatch number and higher possibility of graft survival. Thus, through our study we were able to identify compatible HLA DR allelic pairs which can be selected as potential donor alleles for renal transplantation, which would reduce the chance of possible chronic graft rejection.

- Partial results from the study has been published in International Journal for Research in Applied Science and Engineering Technology, 2023

7. RECOMMENDATIONS FOR FUTURE STUDIES

The present study fulfils the criteria for carrying out and delivering impactful research. The study aided in better understanding of HLA and its compatibility between patient and donor, based on structural similarity for the better survival of the transplanted organ. The study explored the intriguing world of immunoinformatics and its boundless use in the field of transplantation immunology. The identification of HLA compatibility based on structural similarity can be taken into consideration while formulating the clinical protocol for renal transplantation, thus benefiting the society by aiding in better survival period of the graft and reducing the extensive use of immunosuppressants. The interaction of patient-donor HLA-Ag-TCR can also be studied through continuous monitoring of patients after transplantation which would provide us with better information on the corresponding TCR which interacts with a specific HLA-Ag complex. Looking through another perspective of the scenario, studies on the pattern recognition capability of human T cell receptor to HLA-Ag bi-molecular complex can also be taken into concern, which can be added as a future study, which might reveal the ability of human TCR in recollecting the binding pattern to the residual binding site within the HLA-Ag complex. This study was conducted from a minor local population. The study, if extended to a large population through institutional collaboration, a detailed database of compatible HLA alleles can be formulated and made use for selecting potential donors for renal transplantation. The same can be furthermore evaluated based on physicochemical properties and taken into consideration for HLA-Ag-TCR tri-molecular studies revealing the pattern recognition ability of human T cell receptor.

8. REFERENCES

Abou-Jaoudé, M., El Hage, S., Akiki, D., & Araman, R. (2021). Effect of donor-to-recipient HLA matching in low-immunological risk kidney transplant recipients without induction therapy on acute rejection, graft survival, infections, and surgical complications at 3 years: The road towards new recommendations. *Transplant Immunology*, *69*, 101490.

Adebiyi, O., Umukoro, P., Sharfuddin, A., Taber, T., Chen, J., Lane, K. A., Li, X., Goggins, W., & Yaqub, M. S. (2021). Patient and Graft Survival Outcomes During 2 Eras of Immunosuppression Protocols in Kidney Transplantation: Indiana University Retrospective Cohort Experience. Transplantation Proceedings,

Afzali, B., Lombardi, G., & Lechler, R. I. (2008). Pathways of major histocompatibility complex allorecognition. *Current Opinion in Organ Transplantation*, *13*(4).

Ahn, K., Angulo, A., Ghazal, P., Peterson, P. A., Yang, Y., & Früh, K. (1996). Human cytomegalovirus inhibits antigen presentation by a sequential multistep process. *Proceedings of the National Academy of Sciences*, *93*(20), 10990-10995.

Alelign, T., Ahmed, M. M., Bobosha, K., Tadesse, Y., Howe, R., & Petros, B. (2018). Kidney transplantation: the challenge of human leukocyte antigen and its therapeutic strategies. *Journal of immunology research*, *2018*.

Argani, H. (2019). Anti-HLA antibody: the role of epitopes in organ transplantation. *Exp Clin Transplant*, *17*(Suppl 1), 38-42.

Ayala García, M. A., González Yebra, B., López Flores, A. L., & Guaní Guerra, E. (2012). The Major Histocompatibility Complex in Transplantation. *Journal of Transplantation*, *2012*, 842141. https://doi.org/10.1155/2012/842141

Ayna, T., Ciftci, H., Isitmangil, G., Gurtekin, M., & Carin, M. (2011). Flow cytometric crossmatching and panel-reactive antibodies in chronic renal failure patients. Transplantation proceedings,

Barker, C. F., & Markmann, J. F. (2013). Historical overview of transplantation. *Cold Spring Harbor perspectives in medicine*, *3*(4), a014977.

Bartl, S., & Weissman, I. L. (1994). Isolation and characterization of major histocompatibility complex class IIB genes from the nurse shark. *Proceedings of the National Academy of Sciences*, *91*(1), 262-266.

Baumgart, M., Moos, V., Schuhbauer, D., & Müller, B. (1998). Differential expression of major histocompatibility complex class II genes on murine macrophages associated with T cell cytokine profile and protective/suppressive effects. *Proceedings of the National Academy of Sciences*, *95*(12), 6936-6940.

Benichou, G., & Thomson, A. (2009). Direct versus indirect allorecognition pathways: on the right track. *American journal of transplantation: official journal of the American Society of Transplantation and the American Society of Transplant Surgeons*, *9*(4), 655.

Bertoni, M., Kiefer, F., Biasini, M., Bordoli, L., & Schwede, T. (2017). Modeling protein quaternary structure of homo-and hetero-oligomers beyond binary interactions by homology. *Scientific reports*, *7*(1), 1-15.

Bezstarosti, S., Kramer, C. S., Claas, F. H., de Fijter, J. W., Reinders, M. E., & Heidt, S. (2022). Implementation of molecular matching in transplantation requires further characterization of both immunogenicity and antigenicity of individual HLA epitopes. *Human Immunology*, *83*(3), 256-263.

Bienert, S., Waterhouse, A., De Beer, T. A., Tauriello, G., Studer, G., Bordoli, L., & Schwede, T. (2017). The SWISS-MODEL Repository—new features and functionality. *Nucleic acids research*, *45*(D1), D313-D319.

Black, C. K., Termanini, K. M., Aguirre, O., Hawksworth, J. S., & Sosin, M. (2018). Solid organ transplantation in the 21st century. *Annals of translational medicine*, *6*(20).

Blaney, J. (2012). A very short history of structure-based design: how did we get here and where do we need to go? *Journal of computer-aided molecular design*, *26*(1), 13-14.

Blum, J. S., Wearsch, P. A., & Cresswell, P. (2013). Pathways of antigen processing. *Annual review of immunology*, *31*, 443.

Boulesteix, A.-L., Wilson, R., & Hapfelmeier, A. (2017). Towards evidence-based computational statistics: lessons from clinical research on the role and design of real-data benchmark studies. *BMC Medical Research Methodology*, *17*(1), 1-12.

Bub, C. B., Martinelli, B. M., Avelino, T. M., Gonçalez, A. C., Barjas-Castro, M. d. L., & Castro, V. (2013). Platelet antibody detection by flow cytometry: an effective method to evaluate and give transfusional support in platelet refractoriness. *Revista brasileira de hematologia e hemoterapia*, *35*, 252-255.

Bunce, M., & Welsh, K. I. (1994). Rapid DNA typing for HLA-C using sequence-specific primers (PCR-SSP): identification of serological and non-serologically defined HLA-C alleles including several new alleles. *Tissue antigens*, *43*(1), 7-17.

Busch, R., Doebele, R. C., Patil, N. S., Pashine, A., & Mellins, E. D. (2000). Accessory molecules for MHC class II peptide loading. *Current opinion in immunology*, *12*(1), 99-106.

Caillat-Zucman, S. (2009). Molecular mechanisms of HLA association with autoimmune diseases. *Tissue antigens*, *73*(1), 1-8.

Calabia-Linares, C., Robles-Valero, J., de la Fuente, H., Perez-Martinez, M., Martín-Cofreces, N., Alfonso-Pérez, M., Gutierrez-Vázquez, C., Mittelbrunn, M., Ibiza, S., & Urbano-Olmos, F. R. (2011). Endosomal clathrin drives actin accumulation at the immunological synapse. *Journal of cell science*, *124*(5), 820-830.

Camacho, C., Coulouris, G., Avagyan, V., Ma, N., Papadopoulos, J., Bealer, K., & Madden, T. L. (2009). BLAST+: architecture and applications. *BMC bioinformatics*, *10*(1), 1-9.

Çamoğlu, O., & Singh, A. K. (2007). Protein Structure Comparison and Classification. In *Computational Methods for Protein Structure Prediction and Modeling* (pp. 147-180). Springer.

Cao, K., Chopek, M., & Fernandez-Vina, M. (1999). High and intermediate resolution DNA typing systems for class I HLA-A, B, C genes by hybridization with sequence-specific oligonucleotide probes (SSOP). *Reviews in immunogenetics*, *1*(2), 177-208.

Chalasani, G., Li, Q., Konieczny, B. T., Smith-Diggs, L., Wrobel, B., Dai, Z., Perkins, D. L., Baddoura, F. K., & Lakkis, F. G. (2004). The allograft defines the type of rejection (acute versus chronic) in the face of an established effector immune response. *The Journal of Immunology*, *172*(12), 7813-7820.

Chaturvedi, P., Hengeveld, R., Zechel, M. A., Lee-Chan, E., & Singh, B. (2000). The functional role of class II-associated invariant chain peptide (CLIP) in its ability to variably modulate immune responses. *International immunology*, *12*(6), 757-765.

Chen, R., Li, L., & Weng, Z. (2003). ZDOCK: an initial-stage protein-docking algorithm. *Proteins: Structure, Function, and Bioinformatics*, *52*(1), 80-87.

Chen, X., & Jensen, P. E. (2008). MHC class II antigen presentation and immunological abnormalities due to deficiency of MHC class II and its associated genes. *Experimental and molecular pathology*, *85*(1), 40-44.

Cheng, T., Li, Q., Zhou, Z., Wang, Y., & Bryant, S. H. (2012). Structure-based virtual screening for drug discovery: a problem-centric review. *The AAPS journal*, *14*(1), 133-141.

Chinen, J., & Buckley, R. H. (2010). Transplantation immunology: solid organ and bone marrow. *Journal of Allergy and Clinical Immunology*, *125*(2), S324-S335.

Choi, J., & Chandraker, A. (2019). Immunologic Risk Assessment and Approach to Immunosuppression Regimen in Kidney Transplantation. *Clinics in Laboratory Medicine*, *39*(4), 643-656.

Chou, C.-L., Mirshahidi, S., Su, K. W., Kim, A., Narayan, K., Khoruzhenko, S., Xu, M., & Sadegh-Nasseri, S. (2008). Short peptide sequences mimic HLA-DM functions. *Molecular immunology*, *45*(7), 1935-1943.

Chou, C.-L., & Sadegh-Nasseri, S. (2000). HLA-DM recognizes the flexible conformation of major histocompatibility complex class II. *The Journal of experimental medicine*, *192*(12), 1697-1706.

Church, H. J., Brammeier, K. L., Petty, J., Mercer, J., Tylee, K. L., Ghosh, A., Jones, S. A., & Wynn, R. F. (2022). Graft rejection and spontaneous recovery in mucopolysaccharidosis type I post-HSCT. *Molecular Genetics and Metabolism*, *135*(2), S32-S33.

Claas, F. H., & Heidt, S. (2017). Epitope-based HLA matching: a useful strategy with many shortcomings to overcome. *Transplantation*, *101*(8), 1744-1745.

Cresswell, P. (1996). Invariant chain structure and MHC class II function. *Cell*, *84*(4), 505-507.

Crux, N. B., & Elahi, S. (2017). Human leukocyte antigen (HLA) and immune regulation: how do classical and non-classical HLA alleles modulate immune response to human immunodeficiency virus and hepatitis C virus infections? *Frontiers in immunology*, *8*, 832.

Dai, S., Murphy, G. A., Crawford, F., Mack, D. G., Falta, M. T., Marrack, P., Kappler, J. W., & Fontenot, A. P. (2010). Crystal structure of HLA-DP2 and implications for chronic beryllium disease. *Proceedings of the National Academy of Sciences*, *107*(16), 7425-7430.

Delves, P. J., & Roitt, I. M. (1998). *Encyclopedia of immunology*. Academic Press.

DeVos, J. M., Gaber, A. O., Knight, R. J., Land, G. A., Suki, W. N., Gaber, L. W., & Patel, S. J. (2012). Donor-specific HLA-DQ antibodies may contribute to poor graft outcome after renal transplantation. *Kidney international*, *82*(5), 598-604.

Dhanda, S. K., Usmani, S. S., Agrawal, P., Nagpal, G., Gautam, A., & Raghava, G. P. (2017). Novel in silico tools for designing peptide-based subunit vaccines and immunotherapeutics. *Briefings in bioinformatics*, *18*(3), 467-478.

Do Nguyen, H. T., Wong, G., Chapman, J. R., McDonald, S. P., Coates, P. T., Watson, N., Russ, G. R., D'Orsogna, L., & Lim, W. H. (2016). The association between broad antigen HLA mismatches, eplet HLA mismatches and acute rejection after kidney transplantation. *Transplantation direct*, *2*(12).

Dudek, N. L., & Purcell, A. W. (2016). Repertoire of Nonclassical MHC I (HLA-E, HLA-F, HLA-G, and Orthologues). In *Encyclopedia of Immunobiology: Reference Module in Biomedical Sciences* (pp. 215-219). Academic Press.

Duni, A., Kitsos, A., Liapis, G., Tatsis, V., Pappas, C., & Dounousi, E. (2021). Acute kidney transplant rejection after administration of nivolumab in a dialysis patient with a failed graft. *Kidney international reports*, *6*(5), 1459.

Duquesnoy, R. (2001). HLAMMATCHMAKER: a molecularly based donor selection algorithm for highly alloimmunized patients. Transplantation proceedings,

Duquesnoy, R. J. (2002). HLAMatchmaker: a molecularly based algorithm for histocompatibility determination. I. Description of the algorithm. *Human Immunology*, *63*(5), 339-352.

Duquesnoy, R. J. (2006). A structurally based approach to determine HLA compatibility at the humoral immune level. *Human Immunology*, *67*(11), 847-862.

Duquesnoy, R. J. (2008). Clinical usefulness of HLAMatchmaker in HLA epitope matching for organ transplantation. *Current opinion in immunology*, *20*(5), 594-601.

Duquesnoy, R. J. (2011). Humoral alloimmunity in transplantation: relevance of HLA epitope antigenicity and immunogenicity. *Frontiers in immunology*, *2*, 59.

Duquesnoy, R. J. (2017). Are we ready for epitope-based HLA matching in clinical organ transplantation? *Transplantation*, *101*(8), 1755-1765.

Duquesnoy, R. J., & Askar, M. (2007). HLAMatchmaker: a molecularly based algorithm for histocompatibility determination. V. Eplet matching for HLA-DR, HLA-DQ, and HLA-DP. *Human Immunology*, *68*(1), 12-25.

Duquesnoy, R. J., Awadalla, Y., Lomago, J., Jelinek, L., Howe, J., Zern, D., Hunter, B., Martell, J., Girnita, A., & Zeevi, A. (2008). Retransplant candidates have donor-specific antibodies that react with structurally defined HLA-DR, DQ, DP epitopes. *Transplant Immunology*, *18*(4), 352-360.

Duquesnoy, R. J., & Marrari, M. (2009). HLAMatchmaker-based definition of structural human leukocyte antigen epitopes detected by alloantibodies. *Current Opinion in Organ Transplantation*, *14*(4), 403-409.

Duquesnoy, R., Marrari, M., Marroquim, M., Borges, A., da Mata Sousa, L., Socorro, A., & do Monte, S. (2019). Second update of the international registry of HLA epitopes. I. The HLA-ABC epitope database. *Human Immunology*, *80*(2), 103-106.

Duquesnoy, R. J., & Marrari, M. (2017). Usefulness of the ElliPro epitope predictor program in defining the repertoire of HLA-ABC eplets. *Human Immunology*, *78*(7-8), 481-488.

Duquesnoy, R. J., & Marrari, M. (2020). Eplet-based HLA class II matching for transplantation: Design of a repertoire of interlocus eplets shared between HLA-DR,-DQ and-DP alleles. *OBM Transplantation*, *4*(1), 1-1.

Duquesnoy, R. J., Mulder, A., Askar, M., Fernandez-Vina, M., & Claas, F. H. (2005). HLAMatchmaker-based analysis of human monoclonal antibody reactivity

demonstrates the importance of an additional contact site for specific recognition of triplet-defined epitopes. *Human Immunology*, *66*(7), 749-761.

Duquesnoy, R. J., White, L. T., Fierst, J. W., Vanek, M., Banner, B. F., Iwaki, Y., & Starzl, T. E. (1990). Multiscreen serum analysis of highly sensitized renal dialysis patients for antibodies toward public and private class i hla determinants: implications for computer-predicted acceptable and unacceptable donor mismatches in kidney transplantation1. *Transplantation*, *50*(3), 427.

Elez, K., Bonvin, A. M., & Vangone, A. (2018). Distinguishing crystallographic from biological interfaces in protein complexes: role of intermolecular contacts and energetics for classification. *BMC bioinformatics*, *19*(15), 19-28.

Emerson, R. O., Mathew, J. M., Konieczna, I. M., Robins, H. S., & Leventhal, J. R. (2014). Defining the alloreactive T cell repertoire using high-throughput sequencing of mixed lymphocyte reaction culture. *Plos one*, *9*(11), e111943.

Fernando, M. M., Stevens, C. R., Walsh, E. C., De Jager, P. L., Goyette, P., Plenge, R. M., Vyse, T. J., & Rioux, J. D. (2008). Defining the role of the MHC in autoimmunity: a review and pooled analysis. *PLoS genetics*, *4*(4), e1000024.

Friesner, R. A., Murphy, R. B., Repasky, M. P., Frye, L. L., Greenwood, J. R., Halgren, T. A., Sanschagrin, P. C., & Mainz, D. T. (2006). Extra precision glide: Docking and scoring incorporating a model of hydrophobic enclosure for protein− ligand complexes. *Journal of medicinal chemistry*, *49*(21), 6177-6196.

Froimowitz, M. (1993). HyperChem: a software package for computational chemistry and molecular modeling. *Biotechniques*, *14*(6), 1010-1013.

Fujii, S., Senju, S., Chen, Y.-Z., Ando, M., Matsushita, S., & Nishimura, Y. (1998). The CLIP-substituted invariant chain efficiently targets an antigenic peptide to HLA class II pathway in L cells. *Human Immunology*, *59*(10), 607-614.

Gaudreault, F., & Najmanovich, R. J. (2015). FlexAID: revisiting docking on non-native-complex structures. *Journal of chemical information and modeling*, *55*(7), 1323-1336.

Ghosh, P., Amaya, M., Mellins, E., & Wiley, D. C. (1995). The structure of an intermediate in class II MHC maturation: CLIP bound to HLA-DR3. *Nature*, *378*(6556), 457-462.

Gladow, N., Hollmann, C., Ramos, G., Frantz, S., Kerkau, T., Beyersdorf, N., & Hofmann, U. (2020). Treatment of mice with a ligand binding blocking anti-CD28 monoclonal antibody improves healing after myocardial infarction. *Plos one*, *15*(4), e0227734.

Gregers, T. F., Fleckenstein, B., Vartdal, F., Roepstorff, P., Bakke, O., & Sandlie, I. (2003). MHC class II loading of high or low affinity peptides directed by

Ii/peptide fusion constructs: implications for T cell activation. *International immunology*, *15*(11), 1291-1299.

Gromiha, M. M. (2010). *Protein bioinformatics: from sequence to function*. academic press.

Guex, N., Peitsch, M. C., & Schwede, T. (2009). Automated comparative protein structure modeling with SWISS-MODEL and Swiss-PdbViewer: A historical perspective. *Electrophoresis*, *30*(S1), S162-S173.

Gwinner, W. (2007). Renal transplant rejection markers. *World journal of urology*, *25*(5), 445-455.

Haas, M. (2011). Transplant glomerulopathy: it's not always about chronic rejection. *Kidney international*, *80*(8), 801-803.

Han, J., Goldstein, L. A., Gastman, B. R., Froelich, C. J., Yin, X.-M., & Rabinowich, H. (2004). Degradation of Mcl-1 by granzyme B: implications for Bim-mediated mitochondrial apoptotic events. *Journal of Biological Chemistry*, *279*(21), 22020-22029.

Hanf, W., Bonder, C. S., & Coates, P. T. H. (2014). Transplant glomerulopathy: the interaction of HLA antibodies and endothelium. *Journal of immunology research*, *2014*.

Hansen, T. H., & Bouvier, M. (2009). MHC class I antigen presentation: learning from viral evasion strategies. *Nature Reviews Immunology*, *9*(7), 503-513.

Hassan, C., Chabrol, E., Jahn, L., Kester, M. G., De Ru, A. H., Drijfhout, J. W., Rossjohn, J., Falkenburg, J. F., Heemskerk, M. H., & Gras, S. (2015). Naturally processed non-canonical HLA-A* 02: 01 presented peptides. *Journal of Biological Chemistry*, *290*(5), 2593-2603.

Hecker, A., Kaufmann, A., Hecker, M., Padberg, W., & Grau, V. (2009). Expression of interleukin-21, interleukin-21 receptor alpha and related type I cytokines by intravascular graft leukocytes during acute renal allograft rejection. *Immunobiology*, *214*(1), 41-49.

Hood, L., Steinmetz, M., & Malissen, B. (1983). Genes of the major histocompatibility complex of the mouse. *Annual review of immunology*, *1*, 529-568.

Hou, Q., Dutilh, B. E., Huynen, M. A., Heringa, J., & Feenstra, K. A. (2015). Sequence specificity between interacting and non-interacting homologs identifies interface residues–a homodimer and monomer use case. *BMC bioinformatics*, *16*(1), 1-12.

Hurley, C. K. (2021). Naming HLA diversity: a review of HLA nomenclature. *Human Immunology*, *82*(7), 457-465.

Hsia, S., Tong, J. Y., Parris, G. L., Nghiem, D., Cottington, E. M., Rudert, W. A., & Trucco, M. (1993). Molecular compatibility and renal graft survival--the HLA DRB1 genotyping. *Transplantation*, *55*(2), 395-399.

Janeway Jr, C. A., Travers, P., Walport, M., & Shlomchik, M. J. (2001). Responses to alloantigens and transplant rejection. In *Immunobiology: The Immune System in Health and Disease. 5th edition*. Garland Science.

Kamoun, M., Phelan, D., Noreen, H., Marcus, N., Klingman, L., & Gebel, H. (2017). HLA compatibility assessment and management of highly sensitized patients under the new kidney allocation system (KAS): A 2016 status report from twelve HLA laboratories across the US. *Human Immunology*, *78*(1), 19-23.

Karlsson, L. (2005). DM and DO shape the repertoire of peptide–MHC-class-II complexes. *Current opinion in immunology*, *17*(1), 65-70.

Kastritis, P. L., Moal, I. H., Hwang, H., Weng, Z., Bates, P. A., Bonvin, A. M., & Janin, J. (2011). A structure-based benchmark for protein–protein binding affinity. *Protein Science*, *20*(3), 482-491.

Kastritis, P. L., Rodrigues, J. P., Folkers, G. E., Boelens, R., & Bonvin, A. M. (2014). Proteins feel more than they see: fine-tuning of binding affinity by properties of the non-interacting surface. *Journal of molecular biology*, *426*(14), 2632-2652.

Kloc, M., & Ghobrial, R. M. (2014). Chronic allograft rejection: A significant hurdle to transplant success. *Burns & trauma*, *2*(1), 2321-3868.121646.

Kosmoliaptsis, V., Sharples, L. D., Chaudhry, A. N., Halsall, D. J., Bradley, J. A., & Taylor, C. J. (2011). Predicting HLA class II alloantigen immunogenicity from the number and physiochemical properties of amino acid polymorphisms. *Transplantation*, *91*(2), 183-190.

Kramer, C. S., Koster, J., Haasnoot, G. W., Roelen, D. L., Claas, F. H., & Heidt, S. (2020). HLA-EMMA: a user-friendly tool to analyse HLA class I and class II compatibility on the amino acid level. *Hla*, *96*(1), 43-51.

Kurcinski, M., Jamroz, M., Blaszczyk, M., Kolinski, A., & Kmiecik, S. (2015). CABS-dock web server for the flexible docking of peptides to proteins without prior knowledge of the binding site. *Nucleic acids research*, *43*(W1), W419-W424.

Kurkcuoglu, Z., Koukos, P. I., Citro, N., Trellet, M. E., Rodrigues, J., Moreira, I. S., Roel-Touris, J., Melquiond, A. S., Geng, C., & Schaarschmidt, J. (2018). Performance of HADDOCK and a simple contact-based protein–ligand binding affinity predictor in the D3R Grand Challenge 2. *Journal of computer-aided molecular design*, *32*(1), 175-185.

Kyurkchiev, D. (2017). Cytokines From Mesenchymal Stem Cells Induce Immunosuppressive Cells. In *Cytokine Effector Functions in Tissues* (pp. 257-276). Elsevier.

Lakkis, F. G., Konieczny, B. T., Saleem, S., Baddoura, F. K., Linsley, P. S., Alexander, D. Z., Lowry, R. P., Pearson, T. C., & Larsen, C. P. (1997). Blocking the CD28-B7 T cell costimulation pathway induces long term cardiac allograft acceptance in the absence of IL-4. *The Journal of Immunology*, *158*(5), 2443-2448.

Lamers, M., Berlin, I., & Neefjes, J. (2018). Antigen presentation: Visualizing the MHC Class I peptide-loading bottleneck. *Current Biology*, *28*(2), R83-R86.

Lang, H. L., Jacobsen, H., Ikemizu, S., Andersson, C., Harlos, K., Madsen, L., Hjorth, P., Sondergaard, L., Svejgaard, A., & Wucherpfennig, K. (2002). A functional and structural basis for TCR cross-reactivity in multiple sclerosis. *Nature immunology*, *3*(10), 940-943.

Larkins, N. G., Wong, G., Taverniti, A., & Lim, W. H. (2019). Epitope matching in kidney transplantation: recent advances and current limitations. *Current Opinion in Organ Transplantation*, *24*(4), 370-377.

Larsen, C. P., Elwood, E. T., Alexander, D. Z., Ritchie, S. C., Hendrix, R., Tucker-Burden, C., Cho, H. R., Aruffo, A., Hollenbaugh, D., & Linsley, P. S. (1996). Long-term acceptance of skin and cardiac allografts after blocking CD40 and CD28 pathways. *Nature*, *381*(6581), 434-438.

Launay, G., Ceres, N., & Martin, J. (2017). Non-interacting proteins may resemble interacting proteins: prevalence and implications. *Scientific reports*, *7*(1), 1-12.

Lavant, E. H., Agardh, D. J., Nilsson, A., & Carlson, J. A. (2011). A new PCR-SSP method for HLA DR-DQ risk assessment for celiac disease. *Clinica chimica acta*, *412*(9-10), 782-784.

Lee, H., Heo, L., Lee, M. S., & Seok, C. (2015). GalaxyPepDock: a protein–peptide docking tool based on interaction similarity and energy optimization. *Nucleic acids research*, *43*(W1), W431-W435.

Lee, S., Braun, C. R., Bird, G. H., & Walensky, L. D. (2014). Photoreactive stapled peptides to identify and characterize BCL-2 family interaction sites by mass spectrometry. In *Methods in enzymology* (Vol. 544, pp. 25-48). Elsevier.

Leighton, J., & Wilson, C. (2020). Modern immunosuppression. *Surgery (Oxford)*, *38*(7), 368-374.

Lemaître, F., Viguier, M., Cho, M. S., Fourneau, J. M., Maillère, B., Kourilsky, P., Van Endert, P. M., & Ferradini, L. (2004). Detection of low-frequency human antigen-specific CD4+ T cells using MHC class II multimer bead sorting and immunoscope analysis. *European journal of Immunology*, *34*(10), 2841-2949.

Lemieux, W., Mohammadhassanzadeh, H., Klement, W., Daniel, C., & Sapir-Pichhadze, R. (2021). Matchmaker, matchmaker make me a match: Opportunities and challenges in optimizing compatibility of HLA eplets in transplantation. *International Journal of Immunogenetics*, *48*(2), 135-144.

Leone, P., Shin, E.-C., Perosa, F., Vacca, A., Dammacco, F., & Racanelli, V. (2013). MHC class I antigen processing and presenting machinery: organization, function, and defects in tumor cells. *Journal of the National Cancer Institute*, *105*(16), 1172-1187.

Levin, A., Hemmelgarn, B., Culleton, B., Tobe, S., McFarlane, P., Ruzicka, M., Burns, K., Manns, B., White, C., & Madore, F. (2008). Guidelines for the management of chronic kidney disease. *Cmaj*, *179*(11), 1154-1162.

Li, X., Lamothe, P. A., Ng, R., Xu, S., Teng, M., Walker, B. D., & Wang, J.-h. (2016). Crystal structure of HLA-B* 5801, a protective HLA allele for HIV-1 infection. *Protein & cell*, *7*(10), 761-765.

Li, X. C., & Raghavan, M. (2010). Structure and function of major histocompatibility complex (MHC) class I antigens. *Current Opinion in Organ Transplantation*, *15*(4), 499.

Lim, W. H., Chapman, J. R., Coates, P. T., Lewis, J. R., Russ, G. R., Watson, N., Holdsworth, R., & Wong, G. (2016). HLA-DQ mismatches and rejection in kidney transplant recipients. *Clinical Journal of the American Society of Nephrology*, *11*(5), 875-883.

Lim, W. H., Wong, G., Heidt, S., & Claas, F. H. (2018). Novel aspects of epitope matching and practical application in kidney transplantation. *Kidney international*, *93*(2), 314-324.

Lindemann, M., Nyadu, B., Heinemann, F. M., Kribben, A., Paul, A., Horn, P. A., & Witzke, O. (2010). High negative predictive value of an amplified flow cytometry crossmatch before living donor kidney transplantation. *Human Immunology*, *71*(8), 771-776.

Litwack, G. (2017). *Human biochemistry*. Academic Press.

Liu, P., Yao, M., Gong, Y., Song, Y., Chen, Y., Ye, Y., Liu, X., Li, F., Dong, H., & Meng, R. (2021). Benchmarking the Human Leukocyte Antigen Typing Performance of Three Assays and Seven Next-Generation Sequencing-Based Algorithms. *Frontiers in immunology*, *12*, 652258.

López-Llano, J., Campos, L., & Sancho, J. (2006). α-helix stabilization by alanine relative to glycine: Roles of polar and apolar solvent exposures and of backbone entropy. *Proteins: Structure, Function, and Bioinformatics*, *64*(3), 769-778.

Macindoe, G., Mavridis, L., Venkatraman, V., Devignes, M.-D., & Ritchie, D. W. (2010). HexServer: an FFT-based protein docking server powered by graphics processors. *Nucleic acids research*, *38*(suppl_2), W445-W449.

Mahdi, B. M. (2013). A glow of HLA typing in organ transplantation. *Clinical and translational medicine*, *2*(1), 1-5.

Malhotra, P., Malu, S., & Kapur, S. (2000). Immunology of transplant rejection. In: Medscape.

McGuire, M. F., Iyengar, M. S., & Mercer, D. W. (2011). Computational approaches for translational clinical research in disease progression. *Journal of Investigative Medicine*, *59*(6), 893-903.

Mehta, A. R. (2009). Renal Transplantation–Mechanisms and Management of Early Rejection. *Apollo Medicine*, *2*(6), 95-99.

Menon, M. C., Cravedi, P., & El Salem, F. (2017). Acute Cellular Rejection. In *Kidney Transplantation, Bioengineering and Regeneration* (pp. 461-474). Elsevier.

Merrill, J. P., Murray, J. E., Harrison, J. H., & Guild, W. R. (1956). Successful homotransplantation of the human kidney between identical twins. *Journal of the American Medical Association*, *160*(4), 277-282.

Metes, D., Logar, A., Rudert, W. A., Zeevi, A., Woodward, J., Demetris, A. J., Abu-Elmagd, K., Eghtesad, B., Shapiro, R., & Fung, J. J. (2003). Four-color flow cytometric analysis of peripheral blood donor cell chimerism. *Human Immunology*, *64*(8), 787-795.

Michalska, K., Korczak-Kowalska, G., NOWACZYK, M., GORSKI, A., PODOBINSKA, I., & DURLIK, M. (2002). Flow cytometry crossmatch in living donor renal transplantation. Transplantation proceedings,

Mintseris, J., Pierce, B., Wiehe, K., Anderson, R., Chen, R., & Weng, Z. (2007). Integrating statistical pair potentials into protein complex prediction. *Proteins: Structure, Function, and Bioinformatics*, *69*(3), 511-520.

Mirdita, M., Von Den Driesch, L., Galiez, C., Martin, M. J., Söding, J., & Steinegger, M. (2017). Uniclust databases of clustered and deeply annotated protein sequences and alignments. *Nucleic acids research*, *45*(D1), D170-D176.

Miyadera, H., Ohashi, J., Lernmark, Å., Kitamura, T., & Tokunaga, K. (2015). Cell-surface MHC density profiling reveals instability of autoimmunity-associated HLA. *The Journal of clinical investigation*, *125*(1), 275-291.

Moal, I. H., Jiménez-García, B., & Fernández-Recio, J. (2015). CCharPPI web server: computational characterization of protein–protein interactions from structure. *Bioinformatics*, *31*(1), 123-125.

Moitessier, N., Pottel, J., Therrien, E., Englebienne, P., Liu, Z., Tomberg, A., & Corbeil, C. R. (2016). Medicinal chemistry projects requiring imaginative structure-based drug design methods. *Accounts of Chemical Research*, *49*(9), 1646-1657.

Morris, P., Fuggle, S., Ting, A., & Wood, K. (1987). HLA and organ transplantation. *British medical bulletin*, *43*(1), 184-202.

Muczynski, K. A., Cotner, T., & Anderson, S. K. (2001). Unusual expression of human lymphocyte antigen class II in normal renal microvascular endothelium. *Kidney international*, *59*(2), 488-497.

Mullen, M. M., Haan, K. M., Longnecker, R., & Jardetzky, T. S. (2002). Structure of the Epstein-Barr virus gp42 protein bound to the MHC class II receptor HLA-DR1. *Molecular cell*, *9*(2), 375-385.

Mulley, W. R., & Kanellis, J. (2011). Understanding crossmatch testing in organ transplantation: A case-based guide for the general nephrologist. *Nephrology*, *16*(2), 125-133.

Münz, C. (2012). Antigen processing for MHC class II presentation via autophagy. *Frontiers in immunology*, *3*, 9.

Murthy, V. L., & Stern, L. J. (1997). The class II MHC protein HLA-DR1 in complex with an endogenous peptide: implications for the structural basis of the specificity of peptide binding. *Structure*, *5*(10), 1385-1396.

Nakamura, T., Shirouzu, T., Nakata, K., Yoshimura, N., & Ushigome, H. (2019). The role of major histocompatibility complex in organ transplantation-donor specific anti-major histocompatibility complex antibodies analysis goes to the next stage. *International Journal of Molecular Sciences*, *20*(18), 4544.

Neal, C. S., Michael, M. Z., Pimlott, L. K., Yong, T. Y., Li, J. Y., & Gleadle, J. M. (2011). Circulating microRNA expression is reduced in chronic kidney disease. *Nephrology Dialysis Transplantation*, *26*(11), 3794-3802.

O'Gorman, M. R., & Donnenberg, A. D. (2008). *Handbook of human immunology*. CRC press.

Olerup, O., & Zetterquist, H. (1992). HLA-DR typing by PCR amplification with sequence-specific primers (PCR-SSP) in 2 hours: an alternative to serological DR typing in clinical practice including donor-recipient matching in cadaveric transplantation. *Tissue antigens*, *39*(5), 225-235.

Ooi, J. D., Petersen, J., Tan, Y. H., Huynh, M., Willett, Z. J., Ramarathinam, S. H., Eggenhuizen, P. J., Loh, K. L., Watson, K. A., & Gan, P. Y. (2017). Dominant protection from HLA-linked autoimmunity by antigen-specific regulatory T cells. *Nature*, *545*(7653), 243-247.

Pang, S. S., Berry, R., Chen, Z., Kjer-Nielsen, L., Perugini, M. A., King, G. F., Wang, C., Chew, S. H., La Gruta, N. L., & Williams, N. K. (2010). The structural basis for autonomous dimerization of the pre-T-cell antigen receptor. *Nature*, *467*(7317), 844-848.

Patel, R., & Terasaki, P. I. (1969). Significance of the positive crossmatch test in kidney transplantation. *New England Journal of Medicine*, *280*(14), 735-739.

Perreault, C., Decary, F., Brochu, S., Gyger, M., Belanger, R., & Roy, D. (1990). Minor histocompatibility antigens. *Blood*, *76*(7), 1269-1280.

Philogene, M. C., Amin, A., Zhou, S., Charnaya, O., Vega, R., Desai, N., Neu, A. M., & Pruette, C. S. (2020). Eplet mismatch analysis and allograft outcome across racially diverse groups in a pediatric transplant cohort: a single-center analysis. *Pediatric nephrology*, *35*(1), 83-94.

Pierce, B. G., Hourai, Y., & Weng, Z. (2011). Accelerating protein docking in ZDOCK using an advanced 3D convolution library. *Plos one*, *6*(9), e24657.

Pierce, B. G., Wiehe, K., Hwang, H., Kim, B.-H., Vreven, T., & Weng, Z. (2014). ZDOCK server: interactive docking prediction of protein–protein complexes and symmetric multimers. *Bioinformatics*, *30*(12), 1771-1773.

Pos, W., Sethi, D. K., Call, M. J., Schulze, M.-S. E., Anders, A.-K., Pyrdol, J., & Wucherpfennig, K. W. (2012). Crystal structure of the HLA-DM–HLA-DR1 complex defines mechanisms for rapid peptide selection. *Cell*, *151*(7), 1557-1568.

Reimann, J., & Schirmbeck, R. (1999). Alternative pathways for processing exogenous and endogenous antigens that can generate peptides for MHC class I-restricted presentation. *Immunological reviews*, *172*(1), 131-152.

Renneberg, R., & Loroch, V. (2016). *Biotechnology for beginners*. Academic Press.

Roche, P. A. (1995). HLA-DM: an in vivo facilitator of MHC class II peptide loading. *Immunity*, *3*(3), 259-262.

Rödström, K. E., Regenthal, P., & Lindkvist-Petersson, K. (2015). Structure of staphylococcal enterotoxin E in complex with TCR defines the role of TCR loop positioning in superantigen recognition. *Plos one*, *10*(7), e0131988.

Rose, M. L., & Hutchinson, I. V. (2006). Transplant immunology II: overcoming acute and chronic rejection. *Surgery (Oxford)*, *24*(3), 79-84.

Sağıroğlu, T., Tozkır, H., Kılıçarslan-Ayna, T., Yağcı, M., Sezer, A., & Carin, M. (2012). Is flow cytometry crossmatch analysis using sera with different dilutions important for pretransplant analysis? A case report. Transplantation proceedings,

Saline, M., Rödström, K. E., Fischer, G., Orekhov, V. Y., Karlsson, B. G., & Lindkvist-Petersson, K. (2010). The structure of superantigen complexed with TCR and MHC reveals novel insights into superantigenic T cell activation. *Nature communications*, *1*(1), 1-9.

Salvalaggio, P. R., Graff, R. J., Pinsky, B., Schnitzler, M. A., Takemoto, S. K., Burroughs, T. E., Santos, L. S., & Lentine, K. L. (2009). Crossmatch testing in kidney transplantation: patterns of practice and associations with rejection and graft

survival. *Saudi journal of kidney diseases and transplantation: an official publication of the Saudi Center for Organ Transplantation, Saudi Arabia*, *20*(4), 577.

Sanchez-Mazas, A. (2020). A review of HLA allele and SNP associations with highly prevalent infectious diseases in human populations. *Swiss medical weekly*(15).

Sapir-Pichhadze, R., Zhang, X., Ferradji, A., Madbouly, A., Tinckam, K. J., Gebel, H. M., Blum, D., Marrari, M., Kim, S. J., & Fingerson, S. (2020). Epitopes as characterized by antibody-verified eplet mismatches determine risk of kidney transplant loss. *Kidney international*, *97*(4), 778-785.

Sapir-Pichhadze, R., Tinckam, K., Quach, K., Logan, A., Laupacis, A., John, R., Beyene, J., & Kim, S. (2015). HLA-DR and-DQ Eplet Mismatches and Transplant Glomerulopathy: A Nested Case–Control Study. *American journal of transplantation*, *15*(1), 137-148.

Schmidt, J., Dojcinovic, D., Guillaume, P., & Luescher, I. (2013). Analysis, isolation, and activation of antigen-specific CD4+ and CD8+ T cells by soluble MHC-peptide complexes. *Frontiers in immunology*, *4*, 218.

Schymkowitz, J., Borg, J., Stricher, F., Nys, R., Rousseau, F., & Serrano, L. (2005). The FoldX web server: an online force field. *Nucleic acids research*, *33*(suppl_2), W382-W388.

Sette, A., Southwood, S., Miller, J., & Appella, E. (1995). Binding of major histocompatibility complex class II to the invariant chain-derived peptide, CLIP, is regulated by allelic polymorphism in class II. *The Journal of experimental medicine*, *181*(2), 677-683.

Smith, A. G., Pereira, S., Jaramillo, A., Stoll, S. T., Khan, F. M., Berka, N., Mostafa, A. A., Pando, M. J., Usenko, C. Y., & Bettinotti, M. P. (2019). Comparison of sequence-specific oligonucleotide probe vs next generation sequencing for HLA-A, B, C, DRB1, DRB3/B4/B5, DQA1, DQB1, DPA1, and DPB1 typing: Toward single-pass high-resolution HLA typing in support of solid organ and hematopoietic cell transplant programs. *Hla*, *94*(3), 296-306.

Shyamala, V., & Ames, G. F.-L. (1989). Genome walking by single-specific-primer polymerase chain reaction: SSP-PCR. *Gene*, *84*(1), 1-8.

Starzl, T. (1988). Achievements in organ transplantation. Why medicine has changed and how. *Arquivos Brasileiros de Cirugia Digestiva/Colegio Brasileiro de Cirugia, Sao Paulo*, *3*(2), 27-28.

Steinegger, M., Meier, M., Mirdita, M., Vöhringer, H., Haunsberger, S. J., & Söding, J. (2019). HH-suite3 for fast remote homology detection and deep protein annotation. *BMC bioinformatics*, *20*(1), 1-15.

Stern, L. J., Brown, J. H., Jardetzky, T. S., Gorga, J. C., Urban, R. G., Strominger, J. L., & Wiley, D. C. (1994). Crystal structure of the human class II MHC protein

HLA-DR1 complexed with an influenza virus peptide. *Nature*, *368*(6468), 215-221.

Sypek, M., Kausman, J., Holt, S., & Hughes, P. (2018). HLA epitope matching in kidney transplantation: an overview for the general nephrologist. *American Journal of Kidney Diseases*, *71*(5), 720-731.

Tambur, A., & Claas, F. (2015). HLA epitopes as viewed by antibodies: what is it all about? *American journal of transplantation*, *15*(5), 1148-1154.

Tambur, A. R. (2018). HLA-epitope matching or eplet risk stratification: the devil is in the details. *Frontiers in immunology*, *9*, 2010.

Tambur, A. R., Kosmoliaptsis, V., Claas, F. H., Mannon, R. B., Nickerson, P., & Naesens, M. (2021). Significance of HLA-DQ in kidney transplantation: time to reevaluate human leukocyte antigen–matching priorities to improve transplant outcomes? An expert review and recommendations. *Kidney international*, *100*(5), 1012-1022.

Tambur, A. R., Rosati, J., Roitberg, S., Glotz, D., Friedewald, J. J., & Leventhal, J. R. (2014). Epitope analysis of HLA-DQ antigens: what does the antibody see? *Transplantation*, *98*(2), 157-166.

Tatusova, T., DiCuccio, M., Badretdin, A., Chetvernin, V., Ciufo, S., & Li, W. (2013). The NCBI handbook. *National Center for Biotechnology Information*.

Terasaki, P. I., & McCLELLAND, J. D. (1964). Microdroplet assay of human serum cytotoxins. *Nature*, *204*(4962), 998-1000.

Thayer, W. P., Ignatowicz, L., Weber, D. A., & Jensen, P. E. (1999). Class II-associated invariant chain peptide-independent binding of invariant chain to class II MHC molecules. *J Immunol*, *162*(3), 1502-1509.

Tomazin, R., Hill, A. B., Jugovic, P., York, I., Van Endert, P., Ploegh, H. L., Andrews, D. W., & Johnson, D. C. (1996). Stable binding of the herpes simplex virus ICP47 protein to the peptide binding site of TAP. *The EMBO journal*, *15*(13), 3256-3266.

Trott, O., & Olson, A. J. (2010). AutoDock Vina: improving the speed and accuracy of docking with a new scoring function, efficient optimization, and multithreading. *Journal of computational chemistry*, *31*(2), 455-461.

Trowsdale, J. (2011). The MHC, disease and selection. *Immunology letters*, *137*(1-2), 1-8.

Tsai, S., & Santamaria, P. (2013). MHC class II polymorphisms, autoreactive T-cells, and autoimmunity. *Frontiers in immunology*, *4*, 321.

Ullman, E. (1914). Tissue and organ transplantation. *Annals of surgery*, *60*(2), 195.

Van Besouw, N., Zuijderwijk, J., Vaessen, L., Balk, A., Maat, A., Van der Meide, P., & Weimar, W. (2005). The direct and indirect allogeneic presentation pathway during acute rejection after human cardiac transplantation. *Clinical & Experimental Immunology*, *141*(3), 534-540.

van Lith, M., McEwen-Smith, R. M., & Benham, A. M. (2010). HLA-DP, HLA-DQ, and HLA-DR have different requirements for invariant chain and HLA-DM. *Journal of Biological Chemistry*, *285*(52), 40800-40808.

Vangone, A., & Bonvin, A. M. (2015). Contacts-based prediction of binding affinity in protein–protein complexes. *elife*, *4*.

Vangone, A., Schaarschmidt, J., Koukos, P., Geng, C., Citro, N., Trellet, M. E., Xue, L. C., & Bonvin, A. M. (2019). Large-scale prediction of binding affinity in protein–small ligand complexes: The PRODIGY-LIG web server. *Bioinformatics*, *35*(9), 1585-1587.

Vanhove, B., Poirier, N., Soulillou, J.-P., & Blancho, G. (2019). Selective costimulation blockade with antagonist anti-CD28 therapeutics in transplantation. *Transplantation*, *103*(9), 1783-1789.

Visscher, K. M., Kastritis, P. L., & Bonvin, A. M. (2015). Non-interacting surface solvation and dynamics in protein–protein interactions. *Proteins: Structure, Function, and Bioinformatics*, *83*(3), 445-458.

Waithman, J., Moffat, J., Patterson, N., van Beek, A., & Mintern, J. (2014). Antigen Presentation.

Waterhouse, A., Bertoni, M., Bienert, S., Studer, G., Tauriello, G., Gumienny, R., Heer, F. T., de Beer, T. A. P., Rempfer, C., & Bordoli, L. (2018). SWISS-MODEL: homology modelling of protein structures and complexes. *Nucleic acids research*, *46*(W1), W296-W303.

Watson, C., & Dark, J. (2012). Organ transplantation: historical perspective and current practice. *British journal of anaesthesia*, *108*(suppl_1), i29-i42.

Wieczorek M, Sticht J, Stolzenberg S, Günther S, Wehmeyer C, El Habre Z, Álvaro-Benito M, Noé F, Freund C. MHC class II complexes sample intermediate states along the peptide exchange pathway. Nat Commun. 2016 Nov 9;7:13224.

Williams, R. C., Opelz, G., McGarvey, C. J., Weil, E. J., & Chakkera, H. A. (2016). The risk of transplant failure with HLA mismatch in first adult kidney allografts from deceased donors. *Transplantation*, *100*(5), 1094.

Williams, T. M. (2001). Human leukocyte antigen gene polymorphism and the histocompatibility laboratory. *The journal of molecular diagnostics*, *3*(3), 98-104.

Worthington, J. E., Martin, S., Al-Husseini, D. M., Dyer, P. A., & Johnson, R. W. (2003). Posttransplantation production of donor HLA-specific antibodies as a predictor of renal transplant outcome1. *Transplantation*, *75*(7), 1034-1040.

Xiong, P., Zhang, C., Zheng, W., & Zhang, Y. (2017). BindProfX: assessing mutation-induced binding affinity change by protein interface profiles with pseudo-counts. *Journal of molecular biology*, *429*(3), 426-434.

Xue, L. C., Rodrigues, J. P., Kastritis, P. L., Bonvin, A. M., & Vangone, A. (2016). PRODIGY: a web server for predicting the binding affinity of protein–protein complexes. *Bioinformatics*, *32*(23), 3676-3678.

Zavala-Ruiz, Z., Strug, I., Walker, B. D., Norris, P. J., & Stern, L. J. (2004). A hairpin turn in a class II MHC-bound peptide orients residues outside the binding groove for T cell recognition. *Proceedings of the National Academy of Sciences*, *101*(36), 13279-13284.

Zhang, Y., Zhang, X., Ma, L., & Guan, D. (2009). Relationship between platelet activation and acute rejection after renal transplantation. Transplantation proceedings,

APPENDIX

LIST OF PUBLICATIONS

1. Asokan, N. R. T, Aziz, F, Kozhiyil, E. K., Biostatistical Analysis of Relation between HLA-A/B and HLA-DR Eplet Mismatches and Renal Graft Outcome. *International Journal for Research in Applied Science and Engineering Technology* 2023,.50016.

2. Nidheesh Roy T.A., Feroz Aziz., Julia Garvasis, Abraham Joseph and Elyas K.K, Identification of compatible class II HLA DR alleles via tri-molecular docking studies and $\Delta G/K_d$ analysis, American Journal of Transplantation, 2023 - *Communicated.*

OTHER PUBLICATIONS

1. Garvasis, J., Prasad, A. R., Shamsheera, K. O., Roy, T. N., & Joseph, A. (2023). A facile one-pot synthesis of phyto-conjugate superparamagnetic magnetite nanoparticles for the rapid removal of hexavalent chromium from water bodies. *Materials Research Bulletin*, *160*, 112130.

2. Garvasis, J., Prasad, A. R., Shamsheera, K. O., Roy, T. N., & Joseph, A. (2022). Weed to nano seeds: Ultrasonic assisted one-pot fabrication of superparamagnetic magnetite nano adsorbents from Siam weed flower extract for the removal of lead from water. *Journal of Hazardous Materials Advances*, *8*, 100163.

3. Smitha, R. B., Sajith, S., Priji, P., Unni, K. N. N., Roy, T. A. N., & Benjamin, S. (2015). Purification and characterization of amylase from Bacillus thuringiensis subsp. kurstaki. *Bt Research*, *6*(3), 1-8.

4. Unni, K., Faisal, P. A., Priji, P., Sajith, S., Sreedevi, S., Hareesh, E., Roy, T. A. N., & Benjamin, S. (2015). Rubber seed kernel as potent solid substrate for the production of lipase by Pseudomonas aeruginosa strain BUP2. *Advances in Enzyme Research*, *3*(02), 31.

POSTER PRESENTATIONS

1. Nidheesh Roy T. A., Feroz Aziz., and Elyas K. K, Immuno-molecular characterization of HLA alleles and analysis of eplet mismatch using HLA Matchmaker in renal graft outcome - A Case Study, Recent Advances in Molecular Biology & Biotechnology, three-day National Seminar at Kannur University, Thalassery, March 2018

2. Nidheesh Roy T. A., Feroz Aziz., and Elyas K. K, *In silico* analysis of binding affinity between CLIP, peptide antigens, Class II HLA and T cell receptor using ZDOCK & PRODIGY with a view to resolve direct recognition in renal transplantation, International Conference on Advanced Chemical and Structural Biology, PRIST University, Mahabalipuram, Chennai, February 2019

ORAL PRESENTATIONS

1. Nidheesh Roy T. A., Feroz Aziz., and Elyas K. K, In silico analysis of binding affinity between HLA DRβ1 and TCRα1 receptor for the prediction of chronic graft rejection in renal transplantation, Proceedings of XLII All India Botanical Conference & National Symposium on "Innovations & Inventions in Plant Science Research", University of Calicut, Kerala, India, November 2019

2. Nidheesh Roy T. A., Feroz Aziz., and Elyas K. K, Eplet - A unique comrade with the finest expression in transplantation immunology, Proceedings of 9th World Congress on Immunology, Barcelona, Spain, December 2019

LIST OF CONFERENCES & WORKSHOPS

1. NextGen Genomics, Biology, Bioinformatics and Technologies (NGBT) Conference, conducted from Le' Meridien, Kochi, October 2016.
2. In silico Crafts Innovations, National workshop in Cheminformatics, conducted by Department of Biotechnology, University of Calicut, December 2016.
3. Attended a National Workshop on Ethics and Welfare Concerns in Research for Human and Animal Health, conducted from College of Veterinary and Animal Sciences, Pookode, Wayanad, September 2017.
4. Animal handling training from Amala Cancer Center Studies based on the topic, Anti-tumor & Anti-hypersensitivity in Relevant Animal Models, November 2017.
5. Attended a three-day Hands-on Training on Statistical Data Analysis for Researchers and Students, TIES, Velloor, Kottayam, May 2018.
6. CME on Updates in Immunology & Microbiology, conducted from Malabar Cancer Center, Thalassery, November 2018.
7. Webinar on Next Generation Sequencing, conducted by Department of Biotechnology, University of Calicut, May 2021.
8. Frontiers in Chemical Science, three-day international seminar conducted by Department of Chemistry, University of Calicut, March 2022.

OTHER CONTRIBUTIONS

1. Resource person, Recent Advances in Bioinformatics, one day workshop conducted by Department of Biotechnology, University of Calicut, March 2019.
2. Resource person, Biotechnology & Bioinformatics, three-day workshop conducted by Department of Biotechnology, University of Calicut, February 2022.

CERTIFICATE
OF RECOGNITION

PULSUS

WWW.PULSUSCONFERENCE.COM

Pulsus
40 Bloomsbury Way, Lower Ground Floor, London, UK, WC1A 2SE
Ph: +44-203-769-1778

PULSUS and the Editors of Journal of Immune Disorders & Therapy and Journal of Immunopathology wish to thank

~~Prof/Dr/~~Mr. ***Nidheesh Roy T A***

University of Calicut, India

for his phenomenal and worthy oral presentation on

"Eplet: A unique comrade with the finest expression in transplantation immunology"

at the "9th World Congress on Immunology"
held during December 09-10, 2019 in Barcelona, Spain

Ricardo Moutinho Guilherme Alves Soares
Hospital Quirónsalud Madrid, Spain

Hussein Fayyad-Kazan
Lebanese University, Lebanon

World Immunology 2019 Organizing Committee Members

Kaihong Su
University of Nebraska, USA

Veronica Ann Varney
The Royal Brompton Hospital, UK

Ian James Martins
Edith Cowan University, Australia

"The more you know, the more you know that you don't know"

- **Socrates**