

HLA Informatics Group

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The HLA Informatics group has four main areas of interest:

- Sequence Databases
 - [HLA Nomenclature Information](#) - including details of the forthcoming changes to the HLA nomenclature.
 - [IMGT/HLA Database](#) - Interactive tools for analysing Release 2.25.2
 - [HLA Sequence Data](#) - Static alignments of Release 2.25.2
 - [IPD-KIR Database](#)
 - [IPD-MHC Database](#)
- HSCT Donor/Patient Project
- HLA Diversity Analysis
- The HLA FactsBook

Sequence Databases

The HLA informatics Group has designed and maintains a number of internationally recognised locus specific databases, these include:

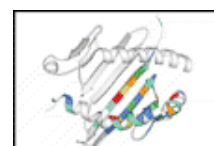
The [IMGT/HLA Database](#) provides a specialist database for sequences of the human major histocompatibility complex (HLA) and includes the official sequences for the WHO Nomenclature Committee For Factors of the HLA System. The IMGT/HLA Database currently contains 3,477 allele sequences. In addition to the physical sequences the database contains detailed information concerning the material from which the sequence was derived and data on the validation of the sequences.



The [IPD-KIR Sequence Database](#) provides a centralised repository for KIR sequences. Killer cell Immunoglobulin-like Receptors or KIRs have been shown to be highly polymorphic at the allelic and haplotypic level. KIRs are members of the immunoglobulin superfamily (IgSF) formerly called Killer cell Inhibitory Receptors. They are composed of two or three Ig-domains, a transmembrane region and cytoplasmic tail which can in turn be short (activatory) or long (inhibitory). The Leukocyte Receptor Complex (LRC) which encodes KIR genes has been shown to be polymorphic, polygenic and complex like the MHC.



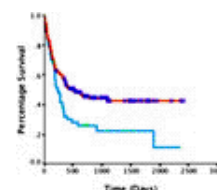
The [IPD-MHC Sequence Database](#) provides a centralised repository for sequences of the major histocompatibility complex from a number of different species. Through a number of international collaborations IPD is able to provide the MHC sequences of different species. The sequences provided by each group are curated by experts in the field and then submitted to the central database.



Currently the database includes sequence data from Domestic Dogs, Wolves, Coyotes, Non Human Primates, Cattle, Rats, Domestic Cats, Sheep, Fish and Pigs.

HSCT Donor/Patient Project

For the past 12 years, the Anthony Nolan Research Institute has co-ordinated a study to investigate the effects of matching or mis-matching a number of different genetic markers on the outcome of haematopoietic stem cell transplants (HSCT) using unrelated donors. This study involves a total of 37 transplant centres throughout the United Kingdom. Over this period we have recruited well over 1500 Anthony Nolan Trust volunteer donors and their respective recipients.

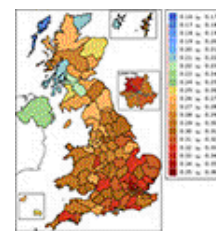


We are utilising the material made available by this project in several studies that have significantly furthered our understanding of the effects of matching HLA at high resolution and in particular the role of the HLA-DPB1 gene. In addition to this, we are now beginning to investigate the role of genes other than HLA on transplant outcome as we believe that there may be a significant contribution when these are taken in to

consideration together with HLA typing. There are two projects being undertaken at this time. The first is trying to establish the effects of NOD2/CARD15 gene polymorphisms on the outcome of unrelated donor haematopoietic stem cell transplants, while the second is investigating the role of KIR genes.

HLA Diversity Analysis of the UK Population

The Anthony Nolan Trust maintains a register of around 390,000 potential bone marrow donors, each of whom have been typed for some of their HLA genes. This data set represents an ideal source of information for studying the HLA genetic diversity in the different UK ethnic groups represented in the register. We are undertaking a project to characterise the geographical HLA genetic diversity of the UK population using donors of North European origin. The results of this project are aimed at aiding the recruitment strategies currently used by the Trust, by the identification of regions with higher diversity. This will contribute to the integration of a more diverse register, and so increase the chances of a patient finding a compatible donor.



Additionally, we are participants of the [15th International Histocompatibility and Immunogenetics Workshop](#), Registry Diversity Group, an international working group whose objective is to establish the standards for the analysis of genetic data from bone marrow registers or similar sources.

The HLA FactsBook

Steven Marsh, Peter Parham, Linda Barber - presents up-to-date and comprehensive information on the HLA genes in a manner that is accessible to both beginner and expert alike. The focus of the book is on the polymorphic HLA genes (HLA-A, B, C, DP, DQ, and DR) that are typed for in clinical HLA laboratories. Each gene has a dedicated section in which individual entries describe the structure, functions, and population distribution of groups of related allotypes. Fourteen introductory chapters provide a beginners' guide to the basic structure, function, and genetics of the HLA genes, as well as to the nomenclature and methods used for HLA typing. Further information on the HLA FactsBook may be found on the [Elsevier](#) site.

