INSTITUTE OF HUMAN GENETIC

# IMGT® - the international ImMunoGeneTics information systems®


MARIE-PAULE LEFRANC
Marie-Paule.Lefranc@igh.cnrs.fr



**Marie-Paule Lefranc**
**Professor,**
**University Montpellier 2**

Gérard Lefranc,
Emeritus Professor
University Montpellier 2

Patrice Duroux,
Engineer CNRS

Géraldine Folch,
Engineer CNRS

Véronique Giudicelli,
Engineer UM2

Joumana Jabado-Michaloud,
Engineer CNRS

Eltaf Alamyar,
PhD student

Engineers :
Safa Aouinti,
Emilie Carillon,
Hugo Duvergey,
Denis Moreno,
Typhaine Paysan-Lafosse,
Saida Saljoqi,
Souphatta Sasorith,
Caroline Tournier


Our research activities are focused on molecular immunogenetics, immunoinformatics, bioinformatics and rare genetic diseases. We are studying the genetics, structures, functions and repertoires of the immunoglobulins (IG) of B lymphocytes and plasmocytes, and of the T cell receptors (TR) on T lymphocytes, which are essential components of the adaptive immunity in humans and other vertebrates.

In 1989, we created IMGT®, the international ImMunoGeneTics information system® (Montpellier 2 University and CNRS) which is at the birth of immunoinformatics. IMGT® is the global reference in immunogenetics and immunoinformatics. IMGT® is a CNRS registered trademark (EU, Canada and USA) and is certified ISO 9001:2008 by LRQA France since 2010 (renewed in 2013).

IMGT® is specialized in the IG, TR and major histocompatibility (MH) proteins of vertebrates, and in the immunoglobulin superfamily (IgSF), MH superfamily (MhSF) and related proteins of the immune system (RPI). IMGT® is a high-quality integrated knowledge resource which provides a common access to expertly annotated genes, sequences and structures. IMGT® includes seven databases (IMGT/LIGM-DB, a comprehensive database of more than 175,000 IG and TR sequences from 346 species in October 2013; IMGT/GENE-DB, IMGT/CLL-DB, IMGT/PRIMER-DB, IMGT/2Dstructure-DB, IMGT/3Dstructure-DB and IMGT/mAb-DB), seventeen interactive tools and more than 15,000 pages of Web resources. IMGT/DomainGapAlign is widely used for antibody engineering and design of humanized antibodies as it allows the precise definition of FR-IMGT and CDR-IMGT and the easy comparison of amino acid sequences between the nonhuman (mouse, rat…) V domains and the closest human germline genes. IMGT/HighV-QUEST, the only online portal for IG and TR Next Generation Sequencing (NGS) data, has analysed more than 1,200 millions of IG and TR sequences in 2013.

Since July 1995, IMGT® is available on the Web at http://www.imgt.org. IMGT® is used by academic and industrial scientists involved in fundamental research, medical research (autoimmune and infectious diseases, AIDS, leukemia, lymphoma, myeloma), veterinary research, genomics (genome diversity and evolution of the adaptive immune system), biotechnology related to antibody engineering for humanization of therapeutic antibodies, diagnostics (detection of minimal residual diseases) and therapeutic approaches (grafts, immunotherapy, vaccinology). The IMGT® Web server at Montpellier is accessed by more than 80,000 sites per year. IMGT® has an exceptional response with more than 150,000 requests per month.

Antibodies represent a large number of the pharmaceutical substances submitted to the World Health Organization/International Nonproprietary Names (WHO/INN) Programme.

-- Li, S., Lefranc, M-P., Miles, JJ., Alamyar, E., Giudicelli, V., Duroux, P. et al. (2013) IMGT/HighV-QUEST paradigm for T cell receptor IMGT clonotype diversity and next generation repertoire immunoprofiling. **Nat. Commun.**, *4*, 2333

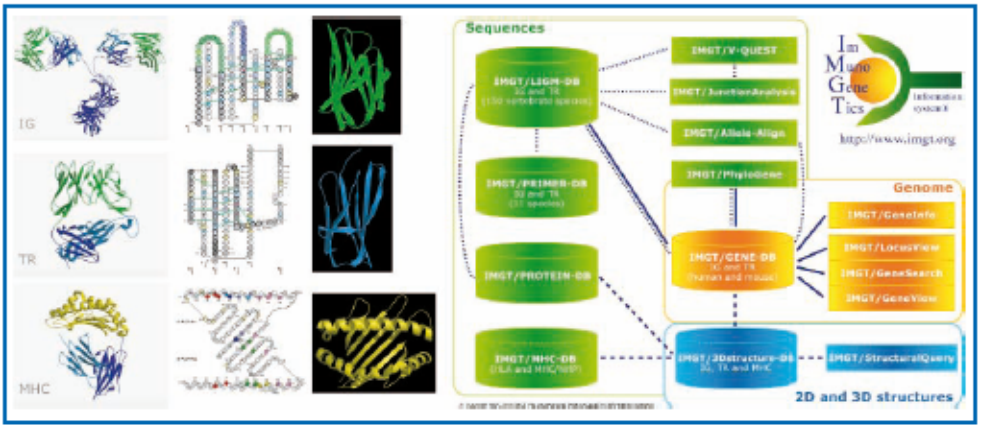
- Giudicelli, V., Lefranc, M-P. (2012) IMGT-ONTOLOGY 2012. **Frontiers in Bioinformatics and Computational Biology. Front Genet.**, *3*, 79.

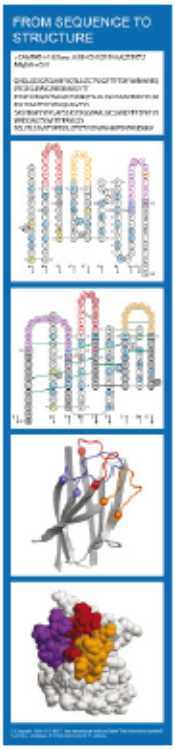
- Lefranc, M-P., Lefranc, G. (2012) Human Gm, Km and Am allotypes and their molecular characterization: a remarkable demonstration of polymorphism. **Methods Mol. Biol.**, *882*, 635-680

.

- Jabara, HH., McDonald, DR., Janssen, E., Massaad, MJ., Ramesh, N. et al. (2012) DOCK8 functions as an adaptor that links TLR-MyD88 signaling to B cell activation. **Nat. Immunol.**, *13*, 6, 612-620.

- Lanternier, F., Pathan, S., Vincent, QB., Liu, L., Cypowyj, S., Prando, C. et al. (2013) Deep Dermatophytosis and Inherited CARD9 Deficiency. **N. Engl. J. Med.** in press.




The INN definition of antibodies is based on the IMGT-ONTOLOGY concepts. Since 2008, amino acid sequences of monoclonal antibodies (mAb, INN suffix -mab), of fusion proteins for immune applications (FPIA, INN suffix -cept) and composite proteins for clinical applications (CPCA) from WHO/INN have been entered into IMGT®. These therapeutic applications emphasize the importance of the IMGT-ONTOLOGY concepts in bridging the gap between antibody sequences and 2D and 3D structures.

Another research interest, in collaboration mainly with the Unit of Medical Genetics, St-Joseph University, Beirut, and also with other teams in Tunisia and Algeria, concerns rare autosomal recessive genetic diseases in consanguineous families (there are as many as 25% of marriages between cousins, often first cousins and even double-first). The patients are autozygous (homozygous by descent) for very rare mutated genes and haplotypes, present in the common ancestor(s) of their parents. These exceptional genotypes are invaluable starting points to allow the identification more quickly of the yet unknown mutated genes. Their functions in the cell organization or in signaling pathways, including the epigenetic and RNA silencing ones, are unmasked and can be investigated. The genetic counselling can be performed in these families.

The better understanding of the molecular basis of the pathophysiology allows better choices in the development of diagnostic tools and innovative therapeutics. This great improvement of knowledge is beneficial not only for the monogenic diseases, but also for the complex ones. Indeed, the consanguinity, responsible also for homozygosity of large chromosomal regions, identical by descent, allows to discover more easily the genetic networks. These statements are also valid for the search of genetic susceptibility or protection against infectious diseases.