**IMGT ALGORITHM AND RULES FOR IMMUNOGLOBULIN AND T-CELL RECEPTOR MOTIF RECOGNITION.**

GIUDICELLI VERONIQUE1, CHAUME DENYS2, MENNESSIER GERARD3, LEFRANC MARIE-PAULE1

1Laboratoire d'ImmunoGenetique Moleculaire, LIGM, Universite Montpellier II, UPR CNRS 1142, 141 rue de la Cardonille, 34396 Montpellier Cedex 5, France;

2CNUSC, Montpellier, France;

3ESA 5032 Montpellier, France

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IMGT, the international ImMunoGeneTics database (http://imgt.cnusc.fr:8104) [1] created by Marie-Paule Lefranc, contains 26000 immunoglobulin (Ig) and T-cell receptor (TcR) DNA sequences from 81 species. Owing to the particularly complex and unique Ig and TcR molecular synthesis and genetics, we developped LIGMotif as an aid for sequence analysis. The algorithm is specific for search of Ig and TcR patterns in DNA sequences. It is based on delimitation rules established by LIGM for exon, splice sites and recombination site recognition, and the unique IMGT numbering [2] defined by Marie-Paule Lefranc for Ig and TcR variable regions of all species. Motifs of interest, such as variable region, can be searched in germline or rearranged DNA or cDNA. Analysis and recognition of genomic regulatory sequences, links to regulatory proteins and integration of data on regulation of gene expression are in development. LIGMotif is integrated in IMGT application in a distributed architecture using a JAVA environment. This approach led to recent major improvments in IMGT: sequence polymorphism description, protein display and structure 3D representation, freely available at the IMGT Marie-Paule page from [http://imgt.cnusc.fr:8104](http://imgt.cnusc.fr:8104/). IMGT rules on gene nomenclature, definition of functionality and IMGT ontology for immunogenetics are described in the IMGT scientific chart, available at the IMGT Marie-Paule page. By providing these data, IMGT has important implications in medical research (repertoire in autoimmune diseases, AIDS, leukemias, lymphomas), therapeutical approaches (antibody engineering), genome diversity and genome evolution studies.

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**References**

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