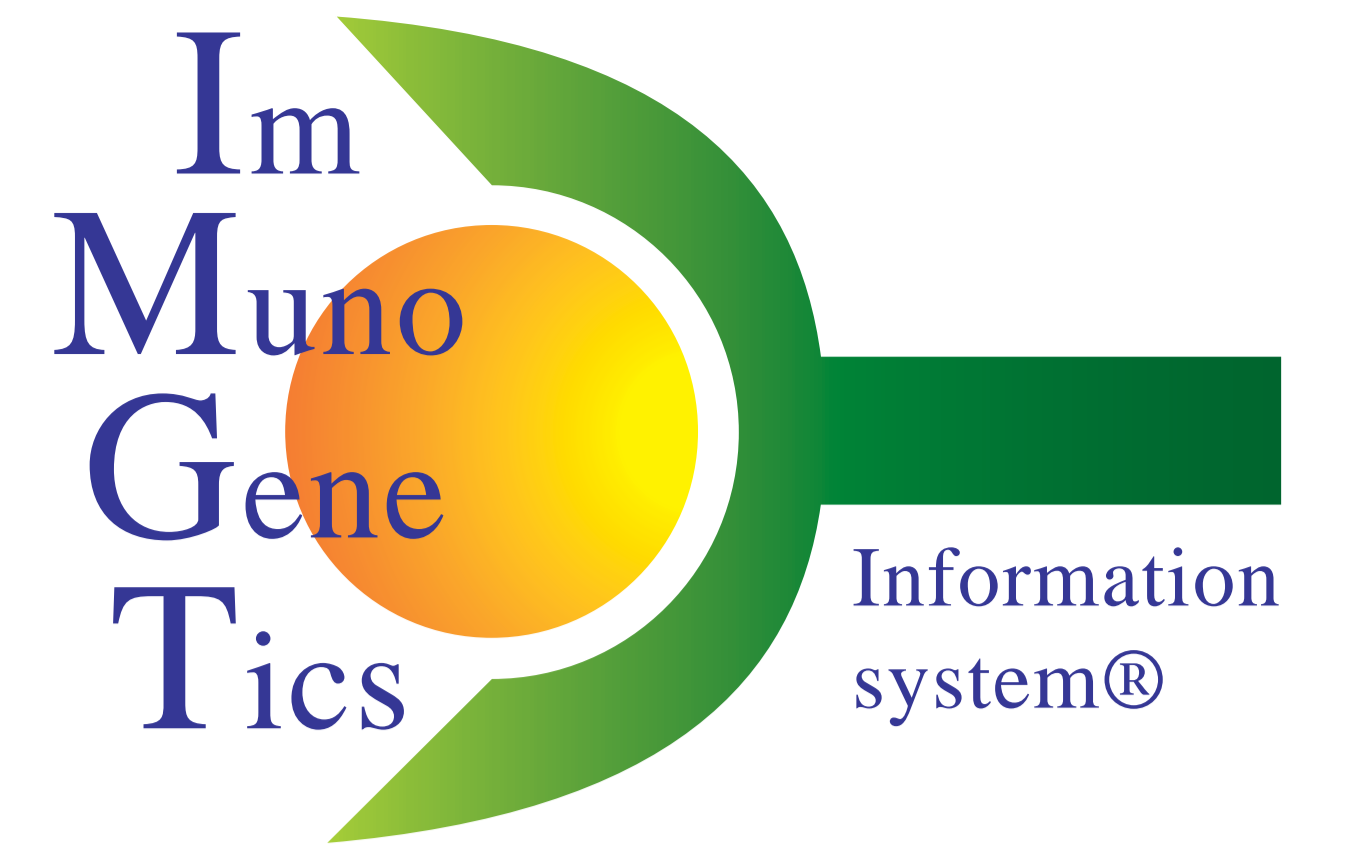


# IMGT-Kaleidoscope, the Formal IMGT-ONTOLOGY paradigm

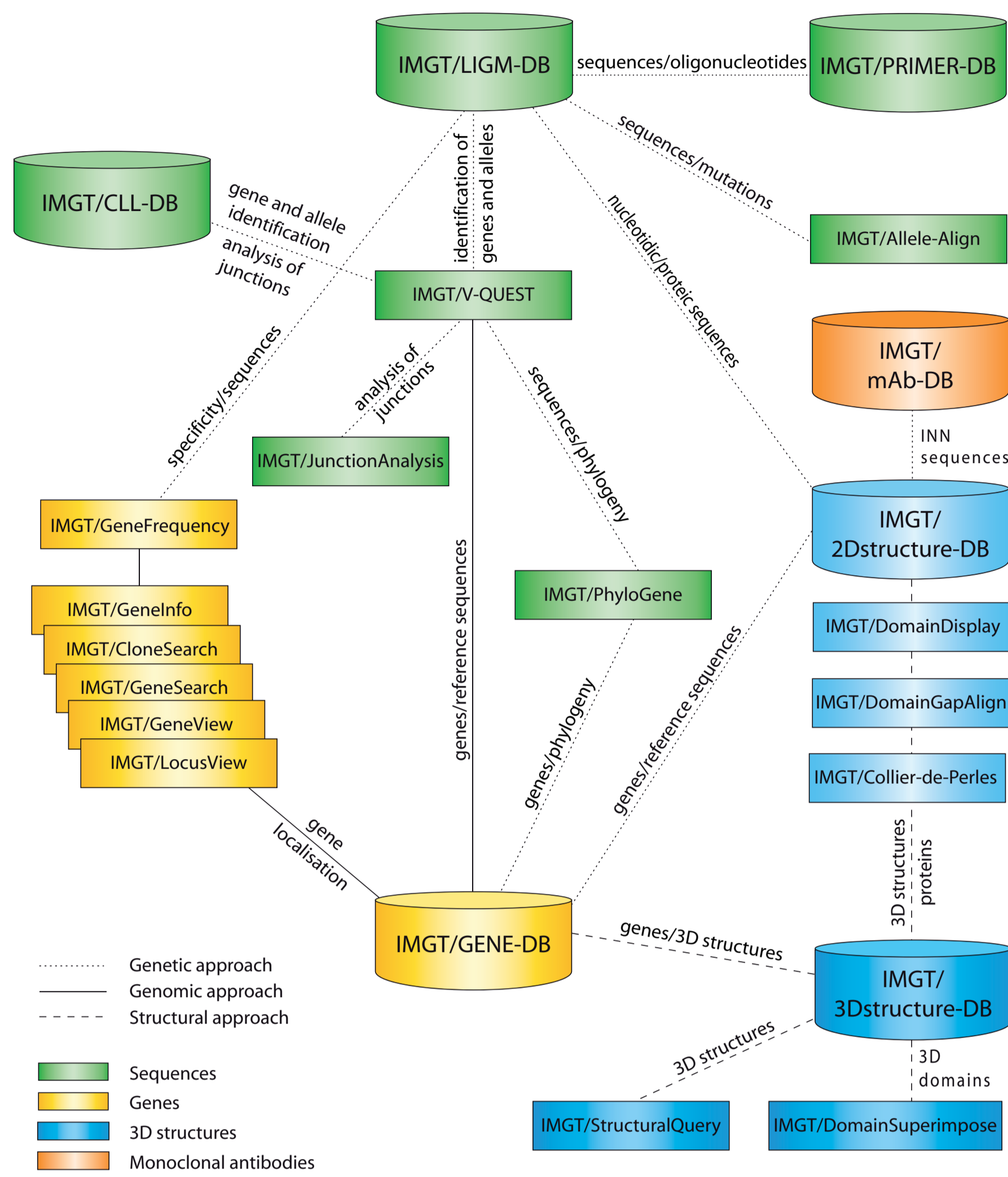
Duroux P, Ehrenmann F, Regnier L, Brochet X, Lane J, Ginestoux C, Lefranc M-P, Giudicelli V

Laboratoire d'ImmunoGénétique Moléculaire (LIGM), Institut de Génétique Humaine (IGH), UPR CNRS 1142, Montpellier (France)



<http://www.imgt.org>

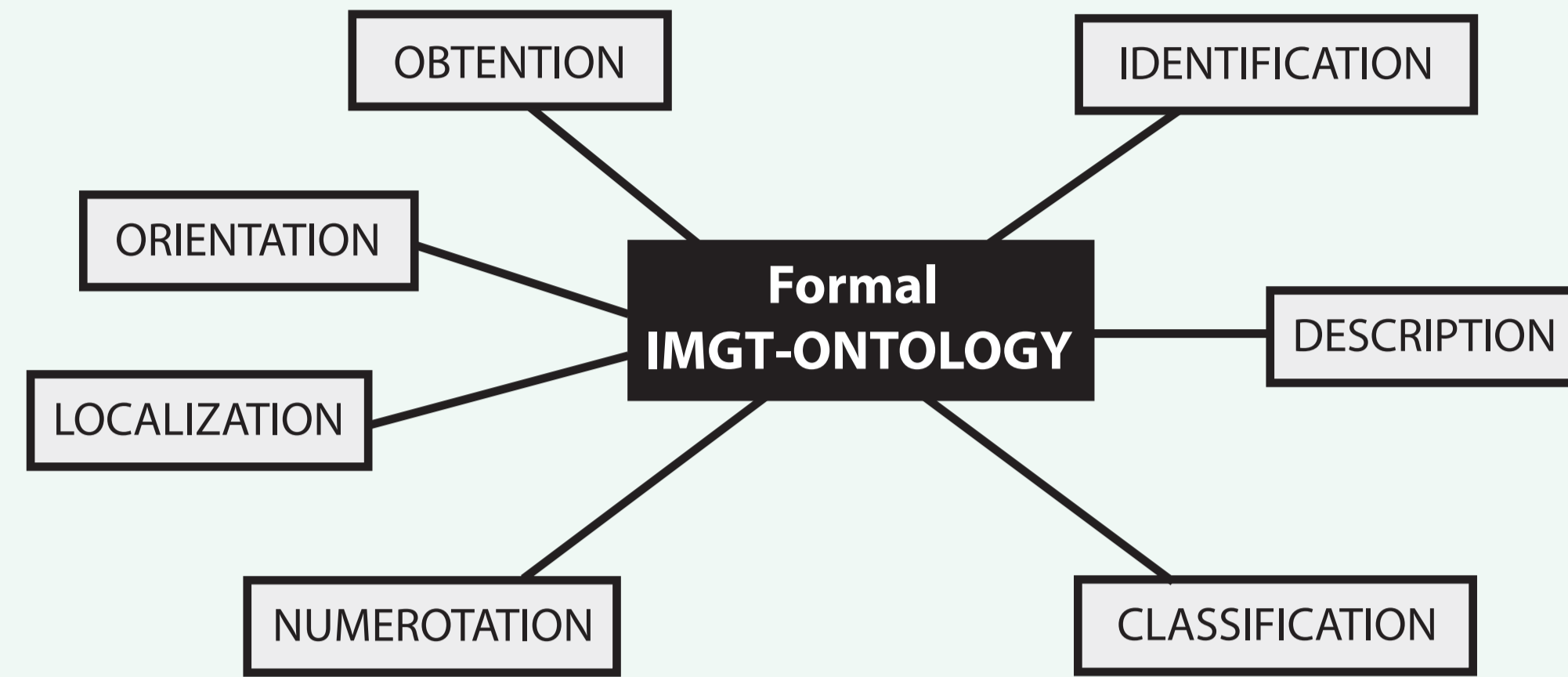
## The IMGT® information system



Lefranc, M.-P. et al., Nucl. Acids Res., 37, D1006-D1012 (2009). PMID: 18978023

## IMGT-Kaleidoscope axioms

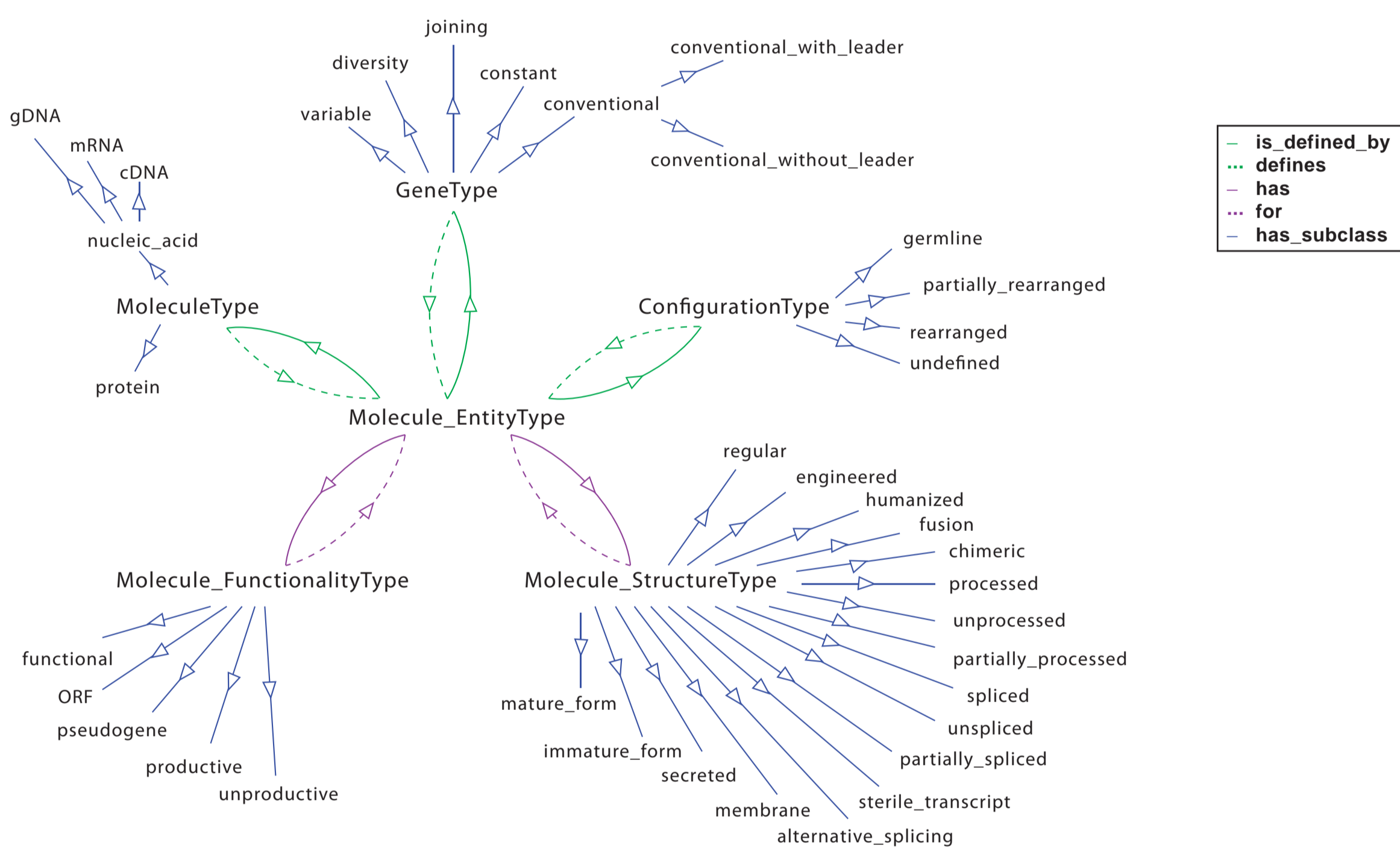
IMGT®, the international ImMunoGeneTics information system (<http://www.imgt.org>) is based on the IMGT-ONTOLOGY concepts. These concepts were generated through the seven axioms of the Formal IMGT-ONTOLOGY or IMGT-Kaleidoscope.



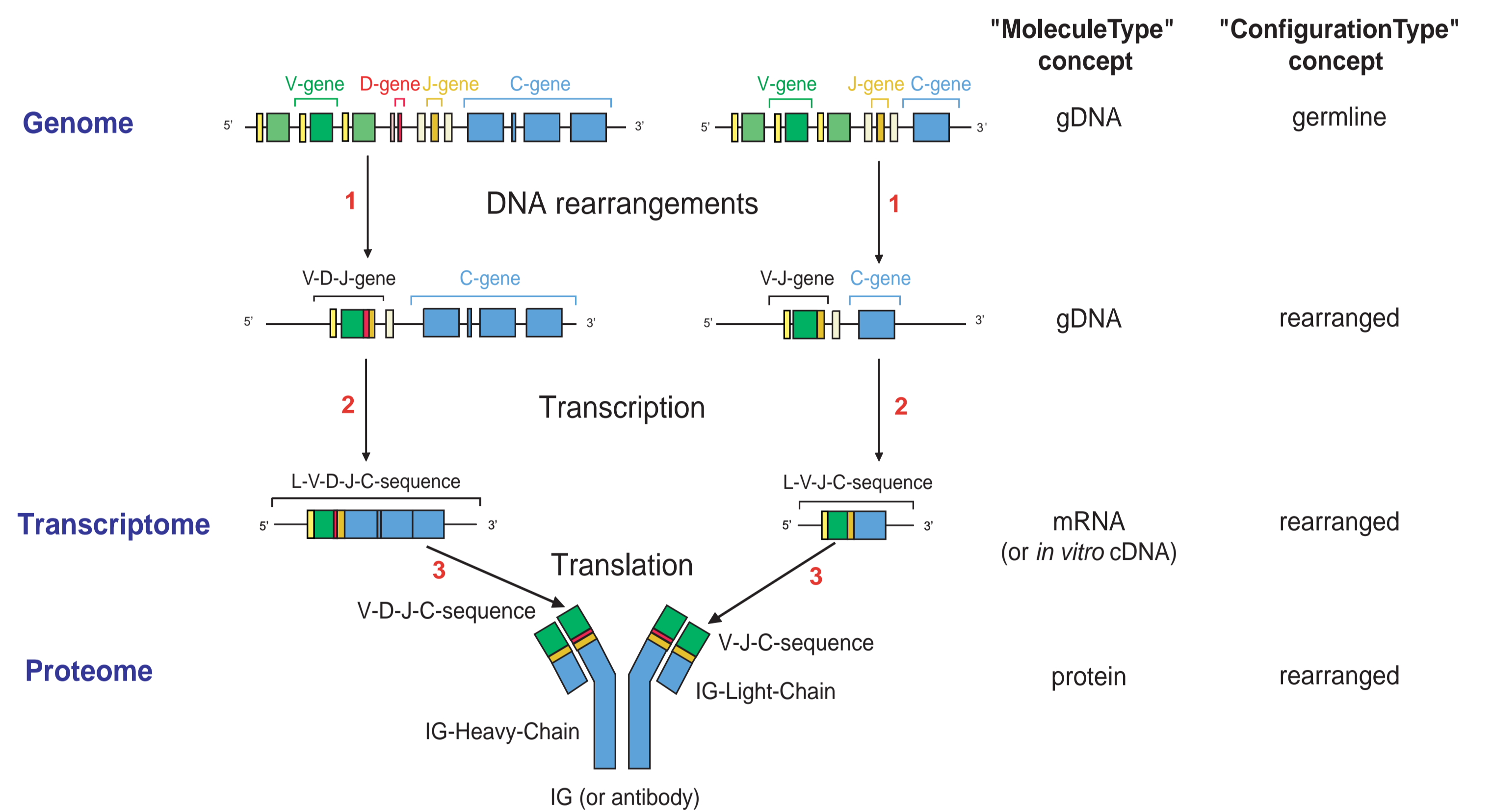
The Formal IMGT-ONTOLOGY or IMGT-Kaleidoscope comprises seven axioms, "IDENTIFICATION", "CLASSIFICATION", "DESCRIPTION", "LOCALIZATION", "NUMEROTATION", "ORIENTATION" and "OBTENTION". These axioms postulate that objects, processes and relations have to be identified, described, classified, numerotated, localized, orientated, and the way they are obtained, determined. The Formal IMGT-ONTOLOGY represents a paradigm for system biology ontologies, which need to identify, to describe, to classify and to numerotate objects, processes and relations at the molecule, cell, tissue, organ, organism or population levels. IMGT-ONTOLOGY is being formalized in OWL. The first version is available on NCBO Biportal site (<http://biportal.bioontology.org/>) and from the 'IMGT downloads' (<http://www.imgt.org>).

Duroux, P. et al., Biochimie, 90, 570-583 (2008).

## IDENTIFICATION



The "Molecule\_EntityType" concept is a major concept of identification. It is defined by the "MoleculeType", "GeneType" and "ConfigurationType" concepts of identification and has relations with the "Functionality" and "StructureType" concepts.

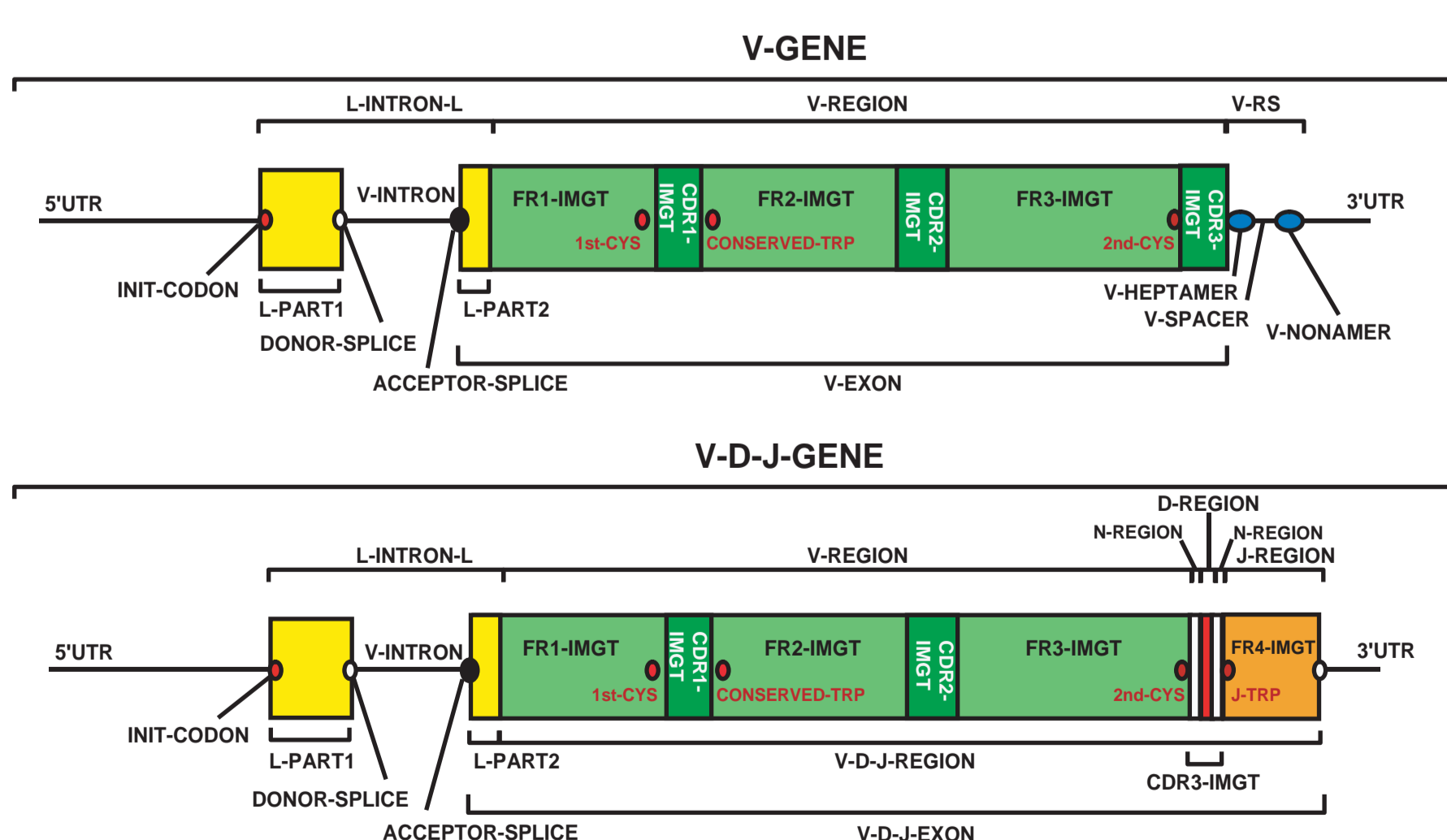


Ten "Molecule\_EntityType" concepts are necessary to identify knowledge, at the molecular level, for the synthesis of an immunoglobulin or antibody in humans: V-gene, D-gene, J-gene, C-gene, V-D-J-gene, V-J-gene, L-V-D-J-C-sequence, L-V-J-C-sequence, V-D-J-C-sequence and V-J-C-sequence.

## DESCRIPTION

### Sequences

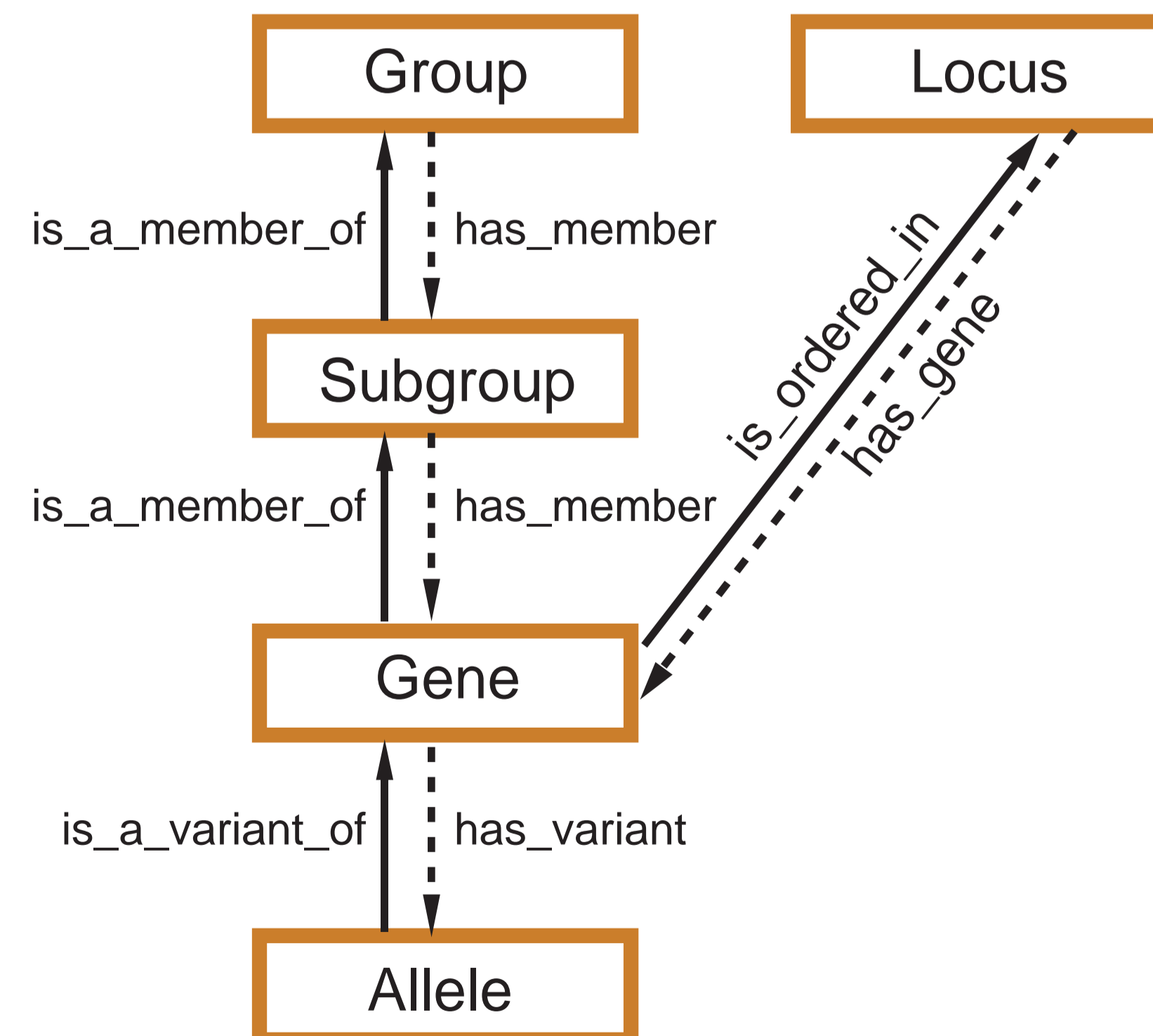
Relation	Reciprocal relation
"adjacent_at_its_5_prime_to"	"adjacent_at_its_3_prime_to"
"included_with_same_5_prime_in"	"includes_with_same_5_prime"
"included_with_same_3_prime_in"	"includes_with_same_3_prime"
"overlaps_at_its_5_prime_with"	"overlaps_at_its_3_prime_with"
"included_in"	"includes"



Graphical representation of two instances of the "Molecule\_EntityPrototype" concept. Twenty-five motifs and ten relations are necessary and sufficient for a complete description of these instances.

## CLASSIFICATION

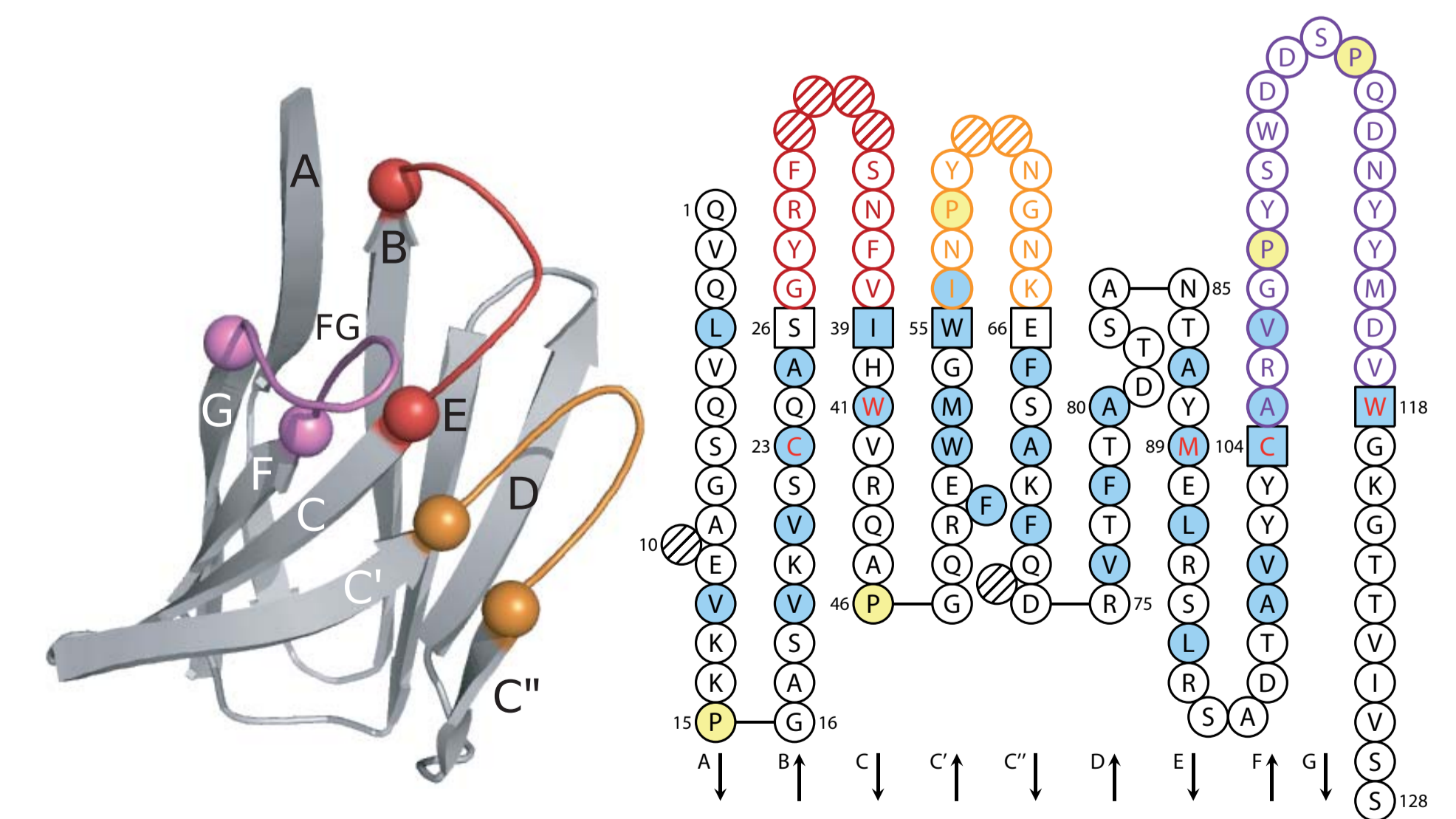
### Genes



Hierarchy of the concepts of classification and their relations. Concepts of classification allowed to define a standardized nomenclature.

## NUMEROTATION

### 2D and 3D structures



V-DOMAIN IMGT Collier de Perles and 3D structure. The "IMGT\_unique\_numbering" concept is illustrated by the "IMGT\_Collier\_de\_Perles" concept which allows two-dimensional (2D) graphical representation of the amino acid sequences of V, C or G type domains and thus bridges the gap between 2D and 3D structures.

Lefranc, M.-P. et al., Dev. Comp. Immunol., 27, 55-77 (2003), 29, 185-203 (2005), 29, 917-938 (2005)