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IMGT unique numbering and tools for antibody humanization and engineering

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The use of IMGT/DomainGapAlign and IMGT/Collier-de-Perles (for amino acid sequences), IMGT/V-QUEST and IMGT/JunctionAnalysis (for nucleotide sequences) provides a standardized way to compare immunoglobulin sequences and to delimit the FR-IMGT and CDR-IMGT in the process of antibody humanization and engineering, whatever the chain type (heavy and light) and whatever the species (e.g. murine and human). Indeed these tools, as the IMGT databases and Web resources are based on the IMGT-ONTOLOGY concepts of classification (IMGT gene and allele nomenclature approved by HGNC and WHO-IUIS [1,2]), of description (IMGT labels), and of numerotation (IMGT unique numbering for V-DOMAIN [3]). The comparison between V domain sequences include determination of the CDR-IMGT lengths (shown between brackets and separated with dots, e.g. [8.8.13]), percentage of identity between FR-IMGT calculated on 91 amino acids for VH (FR1:25, FR2:17, FR3:38, FR4:11) and 89 for V-KAPPA (FR1:26, FR2:17, FR3:36, FR4:10) and evaluation of the number of IMGT physico-chemical classes changes [4,5].

[1] Lefranc and Lefranc. *The Immunoglobulin FactsBook*, Academic Press (2001)

[2] Lefranc. WHO-IUIS report. *Dev Comp Immunol* 32, 461-463 (2008).

[3] Lefranc et al. *Dev Comp Immunol* 27:55-77 (2003).

[4] Pommié et al. *J Mol Recognit* 17:17-32 (2004).

[5] Magdelaine-Beuzelin et al. *Crit Rev Oncol Hemat* 64, 210-225 (2007).

The IMGT unique numbering and tools provide the delimitations of the FR-IMGT and CDR-IMGT for the analysis of antibody paratope or loop grafting in antibody engineering.

The IMGT unique numbering and tools based on the IMGT-ONTOLOGY concepts bridge the gap between sequences and 3D structures facilitating the analysis of antibody/antigen interactions.