The adaptive immune response is characterized by an extreme diversity of the specific antigens that can be recognized by the immune system. This diversity is achieved through a combination of mechanisms, including somatic hypermutation, gene conversion, and class switching. These mechanisms ensure that each B cell and T cell receptor (TR) has a unique sequence, allowing the immune system to respond to a wide range of antigens. The IMGT® Clonotype (AA) is a selected unique representative sequence that identifies clonal diversity and expression. Amino acid frequency can be determined at each CDR-IMGT and FR-IMGT position.

**IMGT/HighV-QUEST based on IMGT® standard**

The filtered-in sequences comprise the ‘1 copy’ and the ‘More than 1’. The ‘1 copy’ includes the single allele and several alleles (or genes). A high proportion of ‘single allele’ is a good indicator of sequence length and quality.

**Users and Analyses**

Since the availability of IMGT/HighV-QUEST in October 2010, more than 1.4 billions of sequences (from external users) have been submitted. They required more than 720,000 hours of computational resources. About 32 terabytes of results were generated.

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**References**