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8423

Assessment of flexible regions in human IgG light chainsby computational analysis

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Background: Immunoglobulins (Igs) are glycoproteins produced by plasma cells, play an essential role in protecting the body against infections and destroying them. Immunoglobulin G (IgG) has an important role in defense against pathogens. The serum IgG level differs in several diseases such as infections and immunodeficiencies. Thus IgG has a very high diagnostic importance. For exact measurement of IgG, we need subtle diagnostic tools such as anti IgG- epitope specific monoclonal antibodies (MAbs). Immunogenic epitopes are beneficial for generating very proficient MAbs. More flexible regions in a molecule have more immunogenicity. Computational immunology helps in well identification of immunogenic epitopes through definition of their physiochemical properties such as flexibility. The aim of this study is evaluation of human IgG light chains flexibilityby computational immunology.
Methods: The amino acid sequence and third construction of reference human IgG was obtained in PDB database. The second IgG structure was specified by Phyre 2 software. IgG light chain flexible regions were distinguished by IEDB software.
Results: The greatest flexible positions were situated in 150 – 160 and in 165-170 amino acid sequences of IgG light chains as was determined by IEDB software.
Conclusion: According to results of this study the amino acid sequences located in 150 – 160 and in 165-170 positions which are placed in constant domain of human IgG light chains, organize the most flexible sites and hence are very useful tools for recognition of more immunogenic epitopes to producing greatly sensitive and specific anti- IgG MAbs.

Keywords: Human IgG, computational analysis, flexibility