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Flexibility of human IgG heavy chains constant domains Defined by computational study

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Abstract

Background: Immunoglobulins (Igs) have a vital role in defending the body against infections and eradicating them. Immunoglobulin G (IgG) is an important defensive tool against the microorganisms. The serum IgG rate changes in numerous diseases including immunodeficiencies and autoimmunity. Hence IgG has great diagnostic significance. Careful assessment of IgG needs elusive diagnostic implements such as anti IgG- specific monoclonal antibodies (MAbs). Immunogenic determinants are valuable for producing very accomplished MAbs. More flexible areas in a molecule are more immunogenic. Immunoinformatic is helpful in fine delineation of immunogenic determinants through characterization of their physiochemical traits including flexibility by computational study. In this study the flexibility of human IgG heavy chains constant domains has been evaluated by immunoinformatic.

Methods: Amino acid sequence and third structure of human IgG was achieved in PDB database. Second IgG construction was identified by Phyre 2 software. IgG heavy chains flexible segments were recognized by IEDB software.

Results: Most flexible areas were situated in 111 – 125, 175-241, 275-311, 321-345 and 375-415 amino acid arrangements of IgG heavy chains as was detected by IEDB software.

Conclusion: Conferring to our data, the amino acid sequences sited in 111 – 125, 175-241, 275-311, 321-345 and 375-415 locations which are positioned in constant domains of human IgG heavy chains, establish the most flexible areas and consequently are very valuable tools for definition of more immunogenic determinants of human IgG to making highly sensitive and specific anti - IgG MAbs.

Key words: Human IgG, computational, flexibility