



In Silico Determination of Physicochemical Properties of Human Immunoglobulin-G Heavy Chain Constant Region

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ABSTRACT

Immunoglobulins (Igs), proteins with a key role in body defense against pathogens, consist of light and heavy chains. Heavy (H) chains include of variable (VH) and constant (CH) domains. IgG is the highest Ig exists in human serum combats microorganisms. Serum IgG level is correlated to intensity of numerous diseases including infections and autoimmunity. So IgG has an important diagnostic worth. Identification of physicochemical characteristics of IgG would be valuable in preparation of more specific IgG diagnostic kits. Computational immunology uses bioinformatics methods to fulfill experimental immunology such as exact diagnosis of diseases. In the present study physicochemical features of human IgG- CH domains were recognized by computational immunology. The second and third structures of reference human IgG heavy chain were acquired by Phyre 2 software and PDB database correspondingly. Accessibility, flexibility and hydrophilicity of human IgG- CH region were defined by IEDB software. Most accessible sites in human IgG- CH region are situated in 210-230, 290-300, 350-365, 380-400 and 410-425 amino acids sequence of CH domains. Most flexible positions are sited in 110 -125, 175-200, 210-240, 275-300, 320-345 and 375-405 amino acids sequence of CH domains. Most hydrophilic regions are sited in 130-140, 260-270 and 280-300 amino acids sequence of CH domains. In this study most accessible, flexible and hydrophilic sites of human IgG heavy chains constant domains were determined. These regions might carry best immunogenic epitopes and therefore be valuable for arrangement more specific tools to optimize existing IgG diagnostic assays.

Keywords: In Silico; Human IgG; Physicochemical; Immunoglobulins (Igs)