
Identification of functional amino acids in constant region of human Immunoglobulin G heavy chain by computational immunology

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Abstract: Computational immunology is a branch of immunology helps in resolving immunologic complications and good understanding of immune responses and related disorders using computational biology [1, 2]. Immunoglobulins (Igs) are serum proteins have essential role in pathogens eradication. Igs are comprised of light and heavy chains. Every heavy chain consists of variable (VH) and constant (CH) regions. Immunoglobulin G (IgG) is greatest abundant Ig present in sera has an important role in microbial destruction [3]. Identification of IgG functional amino acids would be useful in recognition of key amino acids in IgG defensive activities. In this study the human IgG heavy chain functional amino acids were determined by computational immunology.

Amino acid sequence and third structure of reference human IgG were obtained from PDB database. The second IgG structure was determined by Phyre 2 software. The human IgG heavy chain functional amino acids were determined by Interpro surf software.

The functional amino acids of human IgG heavy chains are mostly situated in 1-100 and 251 - 451 amino acids sequence exist in VH and CH2 – CH3 domains respectively.

According to results of present study human IgG heavy chains functional amino acids are mostly located in VH and CH2 – CH3 domains. This is consistent with well recognized IgG functions such as antigen binding and complement fixation which are associated to VH and CH2 – CH3 domains of IgG heavy chains respectively. These functional amino acids would be helpful in recognition of IgG dysfunction(s) and so the related immune diseases.

Keywords: Human IgG, Immunoinformatic, functional, amino acids

References:

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