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Evaluation of operational amino acids in human immunoglobulin G light chain by computational Interpro surf software

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Background: Immunoglobulins (Igs) are bifunctional serum glycoproteins protect the body against foreign substances. Igs consist of light and heavy chains. Human immunoglobulin G light chain involves variable (VL) and constant (CL) domains. The variable domain takes part in antigen recognition and the constant domain influence on the antigen binding site conformation. Operational amino acids have a key role in function of proteins. Computational biology softwares are very useful in solving immunologic problems and well understanding of immune cells responses. Recognition of IgG operational amino acids would be useful in determination of vital amino acids in IgG defensive activities. In this study the human IgG light chain functional amino acids were identified by computational Interpro surf software.

Methods: Amino acid sequence and third structure of reference human IgG were attained from PDB database. Second IgG structure was determined via Phyre 2 software. Human IgG light chain operational amino acids were defined using Interpro surf software which is available in <http://curie.utmb.edu/prosurf.html> database.

Results: According to our data **the** operational amino acids of human IgG light chains are generally situated in 1-111 amino acids sequence exist in VL domain.

Conclusion: Our results showed that human IgG light chains functional amino acids are mostly situated in VL domain. This is consistent with well-known amino terminal function of IgG (antigen binding). **These** functional amino acids would be helpful in recognition of IgG idiotypic determinants which are located in its variable regions as well as detection of some IgG dysfunction and related immune disorders.

Key words: IgG, computational software, operational, amino acids