

Determination of amino acids hydrophilicity in constant region of human IgG light chains

Fatemeh Hajighasemi *1, Soheila Rohani 1, Fatemeh Sefid 2

1Department of Immunology, Faculty of Medicine, Shahed University, Tehran, Iran.

2Department of Biology, Faculty of Basic Science, Shahed University, Tehran, Iran.

*e-mail: fatimahajighasemi@gmail.com

Objective: Antibodies (Immunoglobulins) are a group of glycoproteins play essential role in combating against pathogens. Immunoglobulin G (IgG) has very important effect in destruction of microorganisms. Extent of serum IgG is related to severity of a number of diseases including infections. Therefore IgG has special diagnostic importance. Careful quantification of IgG, needs certain assessment tools like IgG- epitope specific monoclonal antibodies (MAbs). Epitopes with high immunogenicity are very valuable for generation of highly effective MAbs. High accumulation of hydrophilic amino acids in a region of a molecule determines the presence of immunogenic epitope(s) in that location. Immunoinformatic is a part of immunology helps in more true definition of immunogenic epitopes through prediction of their immunogenic characteristics such as amino acids hydrophilicity. The aim of present study is determination of hydrophilicity of amino acids in constant region of human immunoglobulin G light chains by immunoinformatic.

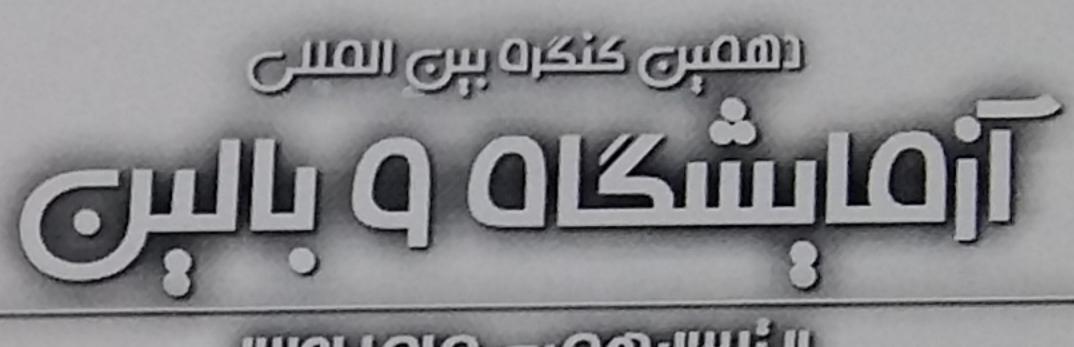
Methods: The sequences of amino acids and third structure of reference human IgG were obtained in PDB database. Second IgG structure was found by Phyre 2 software. IgG light chains constant regionamino acids hydrophilicity was determined by IEDB software.

Results: The amino acids were located in 120 - 130, 150 - 170 and 180-200 positions (in constant region of light chains (CL)) were hydrophilic. The most hydrophilicity was detected in amino acids located to 150 - 170 positions as was determined by IEDB software.

Conclusion: The results of this study show that amino acid sequences located in 150 – 170 positions of IgG light chains have the most hydrophilicity and so could be the most probable site for presence of more immunogenic epitopes. This location is very suitable to predict most proper epitopes to produce anti IgG MAbs with high sensitivity and specificity.

Key words: IgG, immunoinformatic, hydrophilicity





ساعت

دقيقه

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زمان باقیمانده تا شروع همایش:

(REGISTRATION/) ثبت نام کنید



دهمین کنگره بین المللی آزمایشگاه و بالین

و سومین کنگره ملی علوم پایه پزشکی و تولید دانش بنیان

خداوند متعال را شاکریم که بار دیگر جامعه علمی آزمایشگاهیان را توفیق داد تا مقدمات دهمین کنگره بین المللی آزمایشگاه و بالین با رویگر دهای نوین ژنتیکی، مولکولی در تشخیص و درمان و سومین کنگره ملی علوم پایه پزشکی و تولید دانش بنیان را با اهداف عمیق تر و پویاتر در راه پیشرفت و سربلندی کشور برای روزهای 11 لغایت 13 بهمن ماه سال 96 و با شرکت شخصیت های دانشگاهی و علمی کشوری و بین المللی در محل دانشگاه علوم پزشکی ار تش طراحی و برنامه ریزی نماید. از اینرو از همه شما فر هیختگان و اندیشمندان خوزه های مختلف علوم پایه پزشکی و بالینی دعوت می گردد تا همچون همایش های سالیان گذشته و به منظور حضور ارزشمند خود در این رویداد بزر د علمی و برگزاری هر چه با شکوه تر و پربارتر کنگره، شموش ماه خمد با کمهام حستام دماه مدال با با در این رویداد بزر د علمی و برگزاری هر چه با شکوه تر و پربارتر کنگره،