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Structure, classification and functions of Antibodies (Part I)

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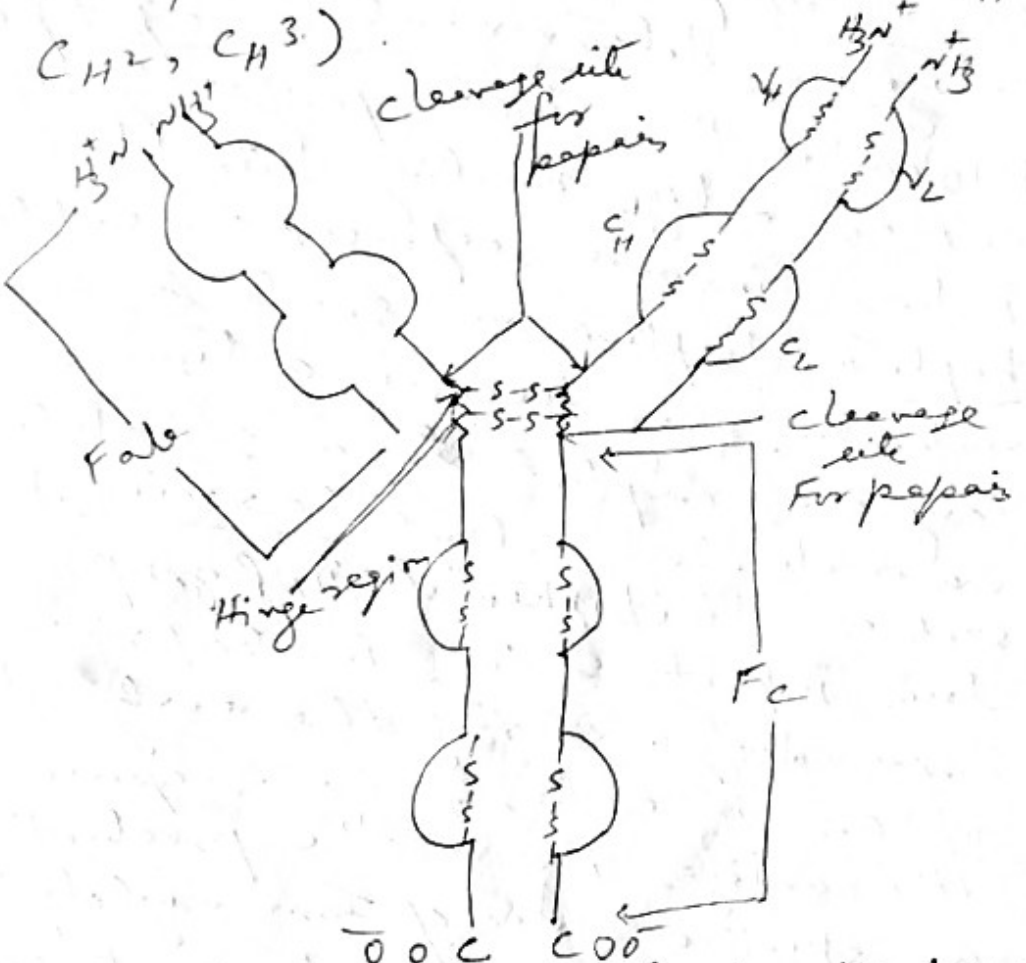
Introduction → The human body is capable of synthesizing more than a million different kinds of Immunoglobulins, each capable of reacting with a different antigen; but all of them appear to share the same fundamental quaternary (globular structure). Typically, an immunoglobulin molecule is a Y-shaped heterimer and composed of two identical heavy (H) polypeptide chains and two smaller identical light (L) chains. Each arm of Y contains a complete L-chain and a part of an H chain and the leg of Y contains the remaining part of the H chains. Near its C-terminus, each L-chain linked to an H chain by disulphide bridge and two additional disulphide bridges link the H-chains together. The H-chains possesses antigenic determinants in the tail segments by

which they can be classified as IgG, IgM, IgA, IgD or IgE, each with its own class of H chains such as γ (Gamma), μ (mu), α (alpha), δ (delta) and ε (Epsilon) respectively. Light chains can likewise be typed as kappa (κ) or lambda (λ). Within a H chain or L chain, C terminal segments exhibit very little variation in primary structure from one individual to another and are called constant regions (C). The amino ends or N-termini of both heavy and light chains, however, are extremely diverse in primary structure, even within a class and are called variable (V) regions. The V_H and V_L regions together form antibody containing site for specific interaction with a homologous antigen molecule. Thus, each Y-shaped antibody has two identical antigen binding sites, one at the tip of each arm of the Y. Because of their two antigen binding sites, antibodies are said to be bivalent. The efficiency of antigen binding and cross-linking of antibodies is greatly increased by the flexible ~~hinge~~ hinge regions in antibody molecules, which allow the distance between the two antigen binding sites to vary.

Further, the proteolytic enzyme papain

Papain digests antibody molecule into different characteristic fragments — two separate and identical Fab (= fragment antigen binding) fragments, each with antigen binding site and one Fc fragment. Each of the four polypeptide chains of an immunoglobulin is also divided into repeating segments called <u>domains</u>, each of which folds independently to form a compact functional unit. Thus, there are two domains in the L chains (i.e. V_L and C_L) and four in the H chains (i.e. V_H, C_{H1}, C_{H2}, C_{H3}).



<u>Structure of Ig Molecule with L and H chains</u>

Recently, it has been found that antigen binding site of the antibody is formed by only about 20 to 30 of amino acids

is the Variable region of both L and H chains. In fact, the variability in the Variable region of both L and H chains is for the most part restricted to 3 small hyper variable regions in each chain. The remaining parts of the variable region known as framework regions are relatively constant. Those parts of the antigen that combine with the antigen binding site on an antibody molecule or on a lymphocyte receptor are called antigenic determinants or Epitopes.

Molecules that bind specifically to such as antigen binding site but cannot induce immune responses are called haptens. Haptens are small organic molecules, they become antigenic if they are coupled to a suitable macromolecule called carrier. Haptens such as dinitrophenyl (DNP group) have been important tools in Experimental Immunology. During the early stages of an infection, the response to the antigen involve the production of a specific class of Immunoglobulins, called IgM, present only in plasma. IgG, is the main Ig. synthesized 10 days after antigen exposure. Opsonic cells bearing make their phagocytosis easier. - - - contd in Part II