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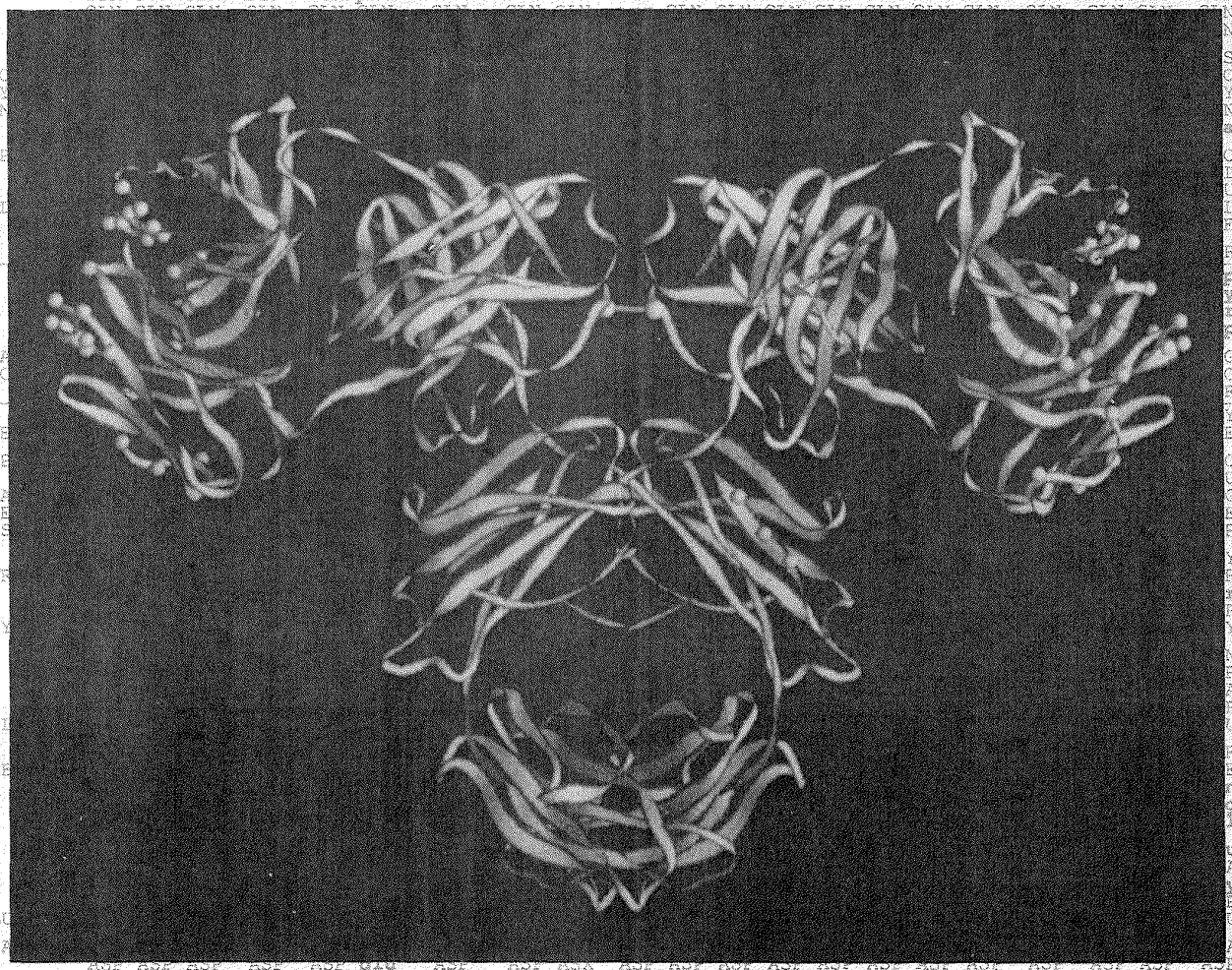

1991

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Frontispiece

Ribbon drawing of a human Mcg IgG1 (lambda) immunoglobulin with a hinge deletion. The complementarity-determining-regions are marked by spheres in appropriate alpha carbon positions at the tips of the Fab arms (only every second residue is highlighted). The interchain disulfide bond between the penultimate residues of the light chains is represented by a ball and stick model in the space between the Fabs. In the CH2 domain on the right, three spheres designate the probable region for docking with complement component C1q in antibodies with intact hinge regions. The hinge by-pass segment connecting CH1 and CH2 domains is the putative site for attachment to the FcRI receptor of human monocytes. Carbohydrate moieties are represented by branched chains between the two CH2 domains. The structure of the IgG1 molecule was determined by Luke Guddat and Allen Edmundson at 2.8 Angstrom resolution (model drawn with algorithm developed by Mike Carson and Charles Bugg, J. Mol. Graphics, 4, 121-122, 1986).

Tabulation and Analysis of Amino Acid and Nucleic Acid Sequences of Precursors, V-Regions, C-Regions, J-Chain, T-Cell Receptors for Antigen, T-Cell Surface Antigens, β_2-Microglobulins, Major Histocompatibility Antigens, Thy-1, Complement, C-Reactive Protein, Thymopoietin, Integrins, Post-gamma Globulin, α_2-Macroglobulins, and Other Related Proteins

1991

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NIH Publication No. 91-3242

Our listing of sequences will be kept up to date. Investigators are invited to send additional sequence data when accepted for publication. Send two copies of the manuscript together with a letter of acceptance from a journal to:

Dr. E.A. Kabat
National Institutes of Health
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9000 Rockville Pike
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