Research Communications

βPDGF-IgG chimera demonstrates that human βPDGF Ig-like domains 1 to 3 are sufficient for high affinity PDGF BB binding. M. A. Heidarian, D. Mahadevan, and W. J. LaRoche


Binding of HIV type 1 gp120 to an anti-V3 loop antibody mediates novel antigen induced epitopes. G. Dennisova, Z. Zivickel, and J. M. Gershoni

Structure of anti-idiotypic Fab against feline panleukopenia virus neutralizing antibody and a comparison with the complexed Fab. N. Ban, C. Escobar, K. W. Hasel, J. Day, A. Greenwood, and A. McPherson

Identification of specificity-determining residues in antibodies. E. A. Pedian, C. Abergel, and J. P. Tipper

NMR observation of interactions in the combining site region of an antibody by using a spin-labeled peptide antigen and NOESY difference spectroscopy. T. Scherf, R. Hiltger, and J. Anglist

Intramolecular signalling upon complexation. L. W. Guddet, L. Shan, Zc-fan, K. N. Andersen, R. Rosser, D. S. Linthicum, and A. B. Edmundson

Analysis of antigenic surfaces of proteins. S. Lee and D. Stuart

Oligonucleotide-protein interactions in IgG can modulate recognition by Fcγ receptors. J. Lund, N. Takahashi, J. D. Pound, M. Goodall, H. Nakagawa, and R. Jefferis

Metaantibody design. V. A. Roberts and E. D. Getzoff

Articles in the January issue of The FASEB Journal

Overview

Structural immunology: problems in molecular recognition. L. M. Amzel and B. J. Gaffney

Structural state-of-the-art reviews

Structural features of the reactions between antibodies and protein antigens. B. C. Braden and R. J. Poljak

A structural view of CD4 and CD8. D. J. Leach

Structural studies of classical major histocompatibility complex proteins: insights into antigen presentation. A. C. M. Young, S. G. Nathenson, and J. C. Sacchettini

Antigenic peptides. H. J. Dyson and P. E. Wright

Anti-idiotypic antibodies: biological function and structural studies. Y. Pan, S. C. Yuhas, and L. M. Amzel

Cytoxins and their receptors. D. R. Davies and A. Wdowski

Three-dimensional structures of alpha and beta chemokines. G. M. Clore and A. M. Gronenborn

Three-dimensional structure and actions of immuno-suppressents and their immunoholphins. W. Baur, J. Kallen, V. Míkloš, M. D. Walkinshaw, and K. Wuthrich

Single-chain Fv's. R. Raag and M. Whitlow

COVER: The ribbon diagram describes the conformation of a protein used in the trafficking of hydrophobic compounds within the cytosol of cells. The structure was obtained by X-ray crystallography and is representative of a relatively large family of proteins with the same motif. This motif consists of a 10-stranded beta barrel (not ribbons). One end of the barrel is capped with a helix-turn-helix portion (blue). A fatty acid bound to the crystalline protein is described by the black-and-white ball-and-stick structure visible in the cavity of the barrel. The accompanying article begins a series of reviews summarizing different motifs that are becoming increasingly important in structural biology. See Lalonde et al., pages 1240-1247.

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