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Computer-assisted protein engineering analysis and design [abstract only]

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Interactive computer graphics is now established as the most effective means of visualizing and manipulating complex molecular structures. Numerical processors continue to increase in power, and systems designed for symbol manipulation and logic programming are finally emerging from computer science laboratories. Our current research on computer-assisted protein engineering analysis and design, in which we integrate the numeric, symbolic and graphic approaches, is described. The investigator may selectively view, manipulate and modify primary, secondary and tertiary structures, making use of the computational tools that are most effective for each task. Research on protein chain folding, structural modifications related to site-directed mutagenesis, and DNA–protein interactions is described. Progress in molecular graphics techniques is reviewed.

Note. The abstract only is given here because Dr Langridge's paper did not become available after the meeting

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