"Side-Chain Packing and Semidefinite Programming"

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The protein folding problem is an important and difficult problem in
biology today. The side chain positioning problem is a subproblem
which is still very complex, especially for large polypeptides. We
present a semidefinite programming approach to side chain positioning due
to Chazelle, et. al. Specifically, we look at how this approach can be
used to determine the effect of a single amino acid substitution on the
stability of the backbone of Protein G.