

Princeton University
Department of Chemistry
Frick Chemical Laboratory
Princeton, NJ 08544-1009 USA

FAX No. (609) 258-6746

DATE: _____

To: Susan Holtzman

FAX: 415-528-6958

This message includes this cover page plus _____ page(s). If you have any questions, please

contact Schutt at (609) 258-6746.

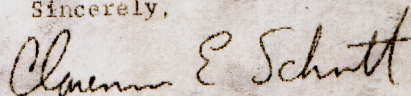
Princeton University

Department of Chemistry
Princeton, New Jersey 08544-1009Clarence E. Schutt
The Henry H. Hoyt Laboratory

September 9, 1989

This is to confirm that Susan Holtzman participated in a general challenge to the scientific community at the AAAS to correctly predict the fold of the Che Y protein. The Che Y structure was determined in my lab and no one outside the scientists working on the structure in the lab had access to the coordinates. This was a double blind and performed in April of 1988. Susan Holtzman received the sequence information and was told that there are no other major molecules bound to Che Y in the crystal. Susan Holtzman correctly predicted a three helix-five strand-two helix motif and also identified another protein which was sequence unrelated, EF-Tu, which contained the 3-5-2 secondary structure motif. The overall topology of the molecule was correctly predicted. Also, the prediction of secondary structural elements which contribute to the topology were mapped onto the crystal structure data and the secondary structure predicted was well-correlated with the data. In addition, a nucleation site was identified and mapped onto the structure and to within experimentally defined accuracy, the atoms in these residues were clustered.

Sincerely,

Clarence E. Schutt
Associate Professor of Chemistry

Princeton University

Department of Chemistry
Princeton, New Jersey 08544-1009

Clarence E. Schutt
The Henry H. Hoyt Laboratory

September 9, 1989

This is to confirm that Susan Holtzman participated in a general challenge to the scientific community at the AAAS to correctly predict the fold of the Che Y protein. The Che Y structure was determined in my lab and no one outside the scientists working on the structure in the lab had access to the coordinates. This was a double blind and performed in April of 1988. Susan Holtzman received the sequence information and was told that there are no other major molecules bound to Che Y in the crystal. Susan Holtzman correctly predicted a three helix-five strand-two helix motif and also identified another protein which was sequence unrelated, EF-Tu, which contained the 3-5-2 secondary structure motif. The overall topology of the molecule was correctly predicted. Also, the prediction of secondary structural elements which contribute to the topology were mapped onto the crystal structure data and the secondary structure predicted was well-correlated with the data. In addition, a nucleation site was identified and mapped onto the structure and to within experimentally defined accuracy, the atoms in these residues were clustered.

Sincerely,



Clarence E. Schutt
Associate Professor of Chemistry