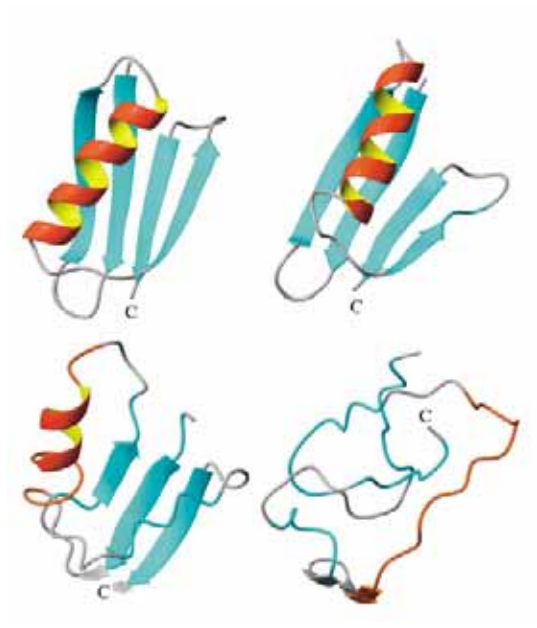**The Role of Sequence and Structure in Protein Folding Kinetics: the Diffusion-Collision Model**

Applied to Proteins L and G

Suhail A. Islam, Martin Karplus,and David L. Weaver,

3   .

,   ,   . 100

.

.

coarse-grain   diffsion-collision

G   L   /   (60   )

. diffsion-collision

(hard sphere)   .

,

,   .

.

61

.   -

1   ,3

.   G   L   15%

.   , N-

C-   4

.   L   G

,   .

-   .

-

.   385K   G

.

, G L -
. G
.

,   ,
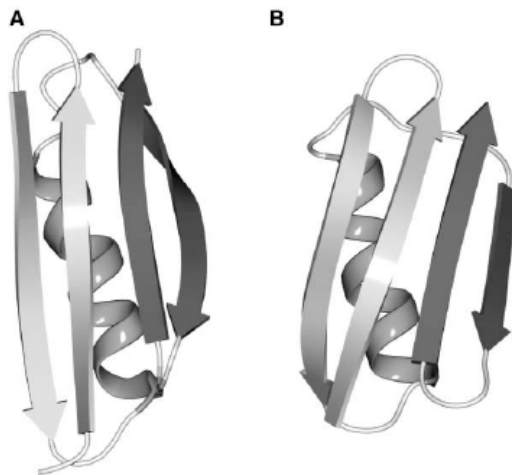.

Figure 1. Schematic Representation of Proteins L and G
(A) B1 segment of the IgG binding domain of peptostreptococcal
protein L (pdb code 2PTL, 62 residues starting with residue 17).
(B) B1 segment of the IgG binding domain of streptococcal protein
G (pdb code 1PGA, 56 residues).