Structure of a Two-domain Chitinase from *Streptomyces Griseus*

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Many glycoside hydrolases consist of multiple domains involved in catalysis and carbohydrate binding, which are connected by interdomain linkers. The widespread occurrence of these linkers suggests their importance in the binding and catalytic functions. However, the number of available structures of full-length glycoside hydrolases has been limited. We first revealed the whole structure of a two-domain chitinase, namely chitinase C from *Streptomyces griseus* HUT6037 (ChiC), classified into glycoside hydrolase family 19. ChiC is composed of an N-terminal chitin-binding domain, a C-terminal catalytic domain, and a linker peptide. Although the cubic crystals of full-length ChiC contain two molecules in an asymmetric unit, the electron densities are assigned to three out of the four domains because of incomplete densities. While the electron densities for the two catalytic domains are clearly defined, that corresponding to the single chitin-binding domain is obscured. This absence and obscurity of electron densities is presumably caused by conformational flexibilities of the linker peptides. The two discrete domains, chitin-binding and catalytic domains, connected by the linker peptide are distantly located without any interactions with each other in the crystal. Great flexibility of the linker must allow the two separated domains to be close to each other in solution, and hence cooperation between the domains is likely to be important for the full activity.

Keywords: chitinase, whole structure, conformational flexibility