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Abstract: Cellulosomal cellulases possess an extra noncatalytic module denominated dockerin, which interacts with the scaffolding via cohesion modules to organize the enzymes within the cellulosome. Given the lack of previously solved experimental atomic structures for modular anaerobic fungal cellulases containing dockerin modules, here we employed structural modeling, molecular dynamics simulations, small-angle X-ray scattering, and biochemical analyses to gain new insights into the structure and function of cellulosomal endoglucanase from the anaerobic gut fungus *Piromyces finnis* (*Pf*GH5). Our results revealed that *Pf*GH5 has a nonglobular conformation in solution, exhibiting high molecular flexibility characterized by two principal collective motions: bending and twisting. The removal of the dockerin module decreased the thermostability of the catalytic domain. Interestingly, the removal of the dockerin module resulted in a slight increase in the optimal temperature and pH values of the catalytic domain and favored the random attack on soluble cello-oligosaccharides. The absence of the carbohydrate-binding module led to a slightly reduced activity of the catalytic domain on less soluble substrates. Taken together, our findings indicate that the dockerin module influences both the thermostability and the activity of the catalytic domain. Moreover, the high flexibility in the region encompassing the dockerin module most likely plays an important role in enzyme function. This study provides a valuable basis for further investigation of the role of the dockerin modules in anaerobic fungal cellulases.