

## **Solution Scattering Studies of Xylanase XYNII from *Trichoderma Longibrachiatum***

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Xylanase (endo-1,4- $\beta$ -xylan xylanohydrolase, EC 3.2.1.8) is an enzyme catalyzing the hydrolysis of  $\beta$ -1,4-D-xylosidic linkages of xylan. *Trichoderma longibrachiatum* has two different xylanases: XYNI and XYNII. Xylanase XYNII is a small protein (21 kDa; 190 a.a).

X-ray solution scattering measurements of XYNII were performed on the EMBL X33 beam line at DESY, Hamburg (Germany). The SAXS/WAXS camera was used to cover the scattering vectors  $0.16 < s < 9.2 \text{ nm}^{-1}$ , with  $s = 4\pi \sin\theta/\lambda$ , where the  $2\theta$  is the scattering angle and  $\lambda = 0.15 \text{ nm}$ . The radius of gyration, forward scattering and distance distribution functions were calculated using the program GNOM [1]. The low resolution structure was restored from experimental data by programs: DAMMIN [2] and GASBOR [3].

The radii of gyration  $R_G$  measured by SAXS were 1.65 nm (pH 3.0) to 1.72 nm (pH 10). The experimental scattering curve was compared to this evaluated from crystal structure. The low resolution structure and also the domain structure (chain compatible spatial distribution model) will be presented.

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[1] Semenyuk A.V., Svergun D.I., *J. Appl. Cryst.*, 1991, **24**, 537. [2] Svergun D.I., *Biophys. J.*, 1999, **76**, 2879. [3] Svergun D.I., Petoukhov M.V., Koch M.H.J., *Biophys. J.*, 2001, **80**, 2946.

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