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Report:

We are elucidating the three-dimensional structure of the photosystem II (PSII) purified from the thermophilic cyanobacterium *Thermosynechococcus elongatus*. The most recent dataset at 3.2 Å resolution suffered from radiation damage and lack of completeness in higher resolution shells.

To overcome this problem, we collected partial datasets from small PSII crystals to fill the segments of data which are missing in the native 3.2 Å dataset. The possibility of merging data from different PSII crystals is limited due to non-isomorphism of the unit cell. Therefore, a total number of 8 partial datasets was collected and three of them could be successfully merged with the 3.2 Å dataset, improving its statistics.

CD26 or dipeptidyl peptidase IV (DPPIV) is engaged in immune functions by co-stimulatory effects on activation and proliferation of T-lymphocytes. We collected native data of the binary complex between human DPPIV and nonapeptide Tat(1-9) up to 2.0 Å resolution (Table 1). The crystal structure was determined by difference Fourier techniques. The ($F_o - F_c$) electron density maps showed the bound peptide Tat(1-9) in the active site of DPPIV (Weihofen *et al.*).

Table 1: Crystallographic Data.

Space group	P2 ₁ 2 ₁ 2 ₁
Unit cell constants (Å)	a = 158.1, b = 168.5, c = 238
Resolution range (Å)	30.0-2.0
Number of observations	548,144
Number of unique	128,898
Completeness (%) ^a	92.2 (87.7)
$\langle I/\sigma(I) \rangle^a$	19.8 (3.1)
R _{sym} (%) ^{a,b}	6.8 (37)

Human acid ceramidase degrades sphingolipids that are major building blocks of eucaryotic plasma membranes. Dysfunctioning of the enzyme leads to metabolic storage diseases which are most prominently observed in the fatal genetic disorder Farber Disease. We collected to heavy atom derivative data sets (platin and iodine) of the human Ceramidase. All attempts to solve the phase problem by the MIR method failed up to now therefore other heavy atom derivatives are needed to improve the phasing.

Reference

Biesiadka, J., Loll, B., Kern, J., Irrgang, K.-D. and Zouni, A. (2004) Crystal structure of cyanobacterial photosystem II at 3.2 Å resolution: a closer look at the Mn-cluster. *Phys Chem Chem Phys*, **6**, 4733-4736.

Weihofen W.A., Liu J., Reutter W., Saenger W., Fan H. (2005) Crystal structures of HIV-1 Tat derived nonapeptides Tat(1-9) and Trp2-Tat(1-9) bound to the active site of dipeptidyl peptidase IV (CD26). *J Biol Chem*. Jan 28; [Epub ahead of print]