

## Crystallization and Preliminary X-Ray Diffraction Study of Recombinant Human Eukaryotic Initiation Factor-4E

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Recombinant human eukaryotic initiation factor-4E (eIF-4E), purified by m<sup>7</sup>GTP-Sepharose 4B affinity chromatography, was used for crystallization. After concentration of the eIF-4E protein (7 mg/ml), the solution was subjected to crystallization by the hanging-drop method. Transparent needle crystals complexed with m<sup>7</sup>GTP were obtained from 50 mM 2-(*N*-morpholino)ethanesulfonic acid-KOH buffer (pH 6.5) containing 25% (w/v) polyethylene glycol 6000 and 0.2 M (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>. The crystals belong to tetragonal space group *P*4<sub>1</sub> or *P*4<sub>3</sub>, of *Z*=4, with unit-cell dimensions of *a*=89.26, *b*=89.26, and *c*=38.51 Å, and diffract beyond 2.1 Å resolution. The *V*<sub>m</sub> value was calculated to be 3.07 Å<sup>3</sup>/Da, which indicates a solvent content of 59.9%.

**Key words:** cap structure, complex, crystallization, eukaryotic initiation factor-4E, m<sup>7</sup>GTP.

Human eukaryotic initiation factor-4E (eIF-4E) is an about 25 kDa polypeptide that is the smallest subunit of eIF-4F, which consists of eIF-4E, eIF-4A, and eIF-4γ, and is required for efficient binding to the mRNA cap structure [m<sup>7</sup>G(5')ppp(5')N..., where N is any nucleotide] during the first stage of protein synthesis (for recent reviews, see Refs. 1-3); eIF-4E also appears to play a key role in the regulation of translation (4, 5). Elucidation of the mechanism underlying recognition of the mRNA cap structure by eIF-4E is necessary for understanding the initiation step of the protein synthetic mechanism. Recently, we succeeded in the construction of a direct expression system for a synthetic gene encoding human eIF-4E under the control of the T7 promoter in *Escherichia coli* (6). We report here the preparation and crystallization of recombinant human eIF-4E, and the results of a preliminary X-ray diffraction study.

Recombinant human eIF-4E was expressed in *E. coli* according to Morino *et al.* (6). Purification of the recombinant human eIF-4E on a m<sup>7</sup>GTP-Sepharose 4B affinity column (Pharmacia LKB Biotechnology) was carried out with according to the method of Rychlik *et al.* (7) with the following modifications. The supernatant of the expressed culture was applied to a 5 ml m<sup>7</sup>GTP-Sepharose 4B column equilibrated with buffer A [20 mM HEPES-KOH (pH 7.5), 1 mM DTT, 0.1 mM EDTA, and 100 mM KCl] at the flow rate of 10 ml/h, the column was thoroughly washed with buffer A until the optical density returned to the base line, and then the bound material was eluted with buffer A containing 100 μM m<sup>7</sup>GTP. The fractions containing eIF-4E were concentrated with a Centricon 10 (Amicon), about 1 ml of 7 mg/ml eIF-4E solution being prepared for crystallization.

Crystallization was carried out by the hanging-drop vapor diffusion method. Each droplet was composed of 3 μl of an aqueous solution containing 7 mg/ml protein and an equal volume of the reservoir solution. Long needle-shaped crystals were obtained within a month at 20°C when 50 mM 2-(*N*-morpholino)ethanesulfonic acid-KOH (pH 6.5) containing 25% (w/v) polyethylene glycol 6000 and 0.2 M (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> was used as the reservoir solution.

Figure 1 shows a micrograph of a complex crystal with the dimensions of 1.0×0.15×0.1 mm. A single crystal together with some mother liquor was mounted in a thin-walled glass capillary, which was then sealed. X-ray diffraction data were collected with an R-AXIS IIC using the imaging plate as the area detector with Ni-filtered Cu-Kα radiation from a Rigaku rotating-anode generator,

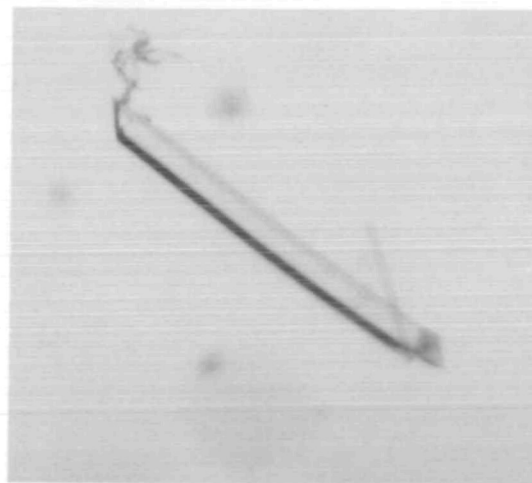


Fig. 1. Photomicrograph of a crystal of the recombinant human eIF-4E-m<sup>7</sup>GTP complex.

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RU-300. The crystals are tetragonal with space group  $P4_1$  or  $P4_3$ , of  $Z=4$ , and cell dimensions of  $a=b=89.26$  Å and  $c=38.51$  Å. The corresponding unit cell volume is  $3.07 \times 10^5$  Å<sup>3</sup>. The  $V_m$  value was calculated to be  $3.07$  Å<sup>3</sup>/Da, assuming one molecule with a molecular weight of 25 kDa per asymmetric unit. This value is within the range observed by Matthews for a variety of protein crystals (8). The solvent content thus could be 59.9%. We collected diffraction data up to 2.1 Å resolution. The data exhibited an  $R$ -merge value of 7.86% and completeness of 81%. Crystal structure determination of the recombinant human eIF-4E-m<sup>7</sup>GTP complex is now in progress.

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