

## Crystal Structure of RNA 3'-terminal Phosphate Cyclase

G. Palm, and A. Wlodawer (National Cancer Inst.), E. Billy and W. Filipowicz (Friedrich Miescher-Institut)

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We have determined the crystal structure of *Escherichia coli* RNA 3'-terminal phosphate cyclase in several crystal forms by the method of multiple anomalous scattering (MAD). Orthorhombic crystals in the space group  $P2_12_12_1$ ,  $a = 101.8 \text{ \AA}$ ,  $b = 126.6 \text{ \AA}$ ,  $c = 128.8 \text{ \AA}$ , with four molecules in the asymmetric unit, were grown from protein with incorporated selenomethionine and were used for the MAD experiments. Data collected to  $2.1 \text{ \AA}$  resolution from a related crystal in space group  $P2_12_12$ ,  $a = 125.8 \text{ \AA}$ ,  $b = 133.5 \text{ \AA}$ ,  $c = 51.0 \text{ \AA}$ , with two molecules in the asymmetric unit, were used in the final refinement ( $R = 20.4\%$ ,  $R_{\text{free}} = 27.6\%$ ). Completely unexpectedly, the enzyme is found in both crystal forms as a covalent dimer linked by a disulfide bond through Cys308. Topologically, each molecule of RNA cyclase consists of two domains. The larger domain consists of three repeats of a folding unit comprising two parallel helices and a four-stranded sheet, found in the translation initiation factor 3. The three motifs form a domain similar to one of the two domains of EPSP synthase and MurA. The smaller domain uses the same secondary structure elements with different topology, observed in many other proteins, such as thioredoxin. While the active site of RNA cyclase is not unambiguously assigned, the current structure allows us to map it to a region surrounding His309, where a number of amino acids are highly conserved in the enzymes from different sources.