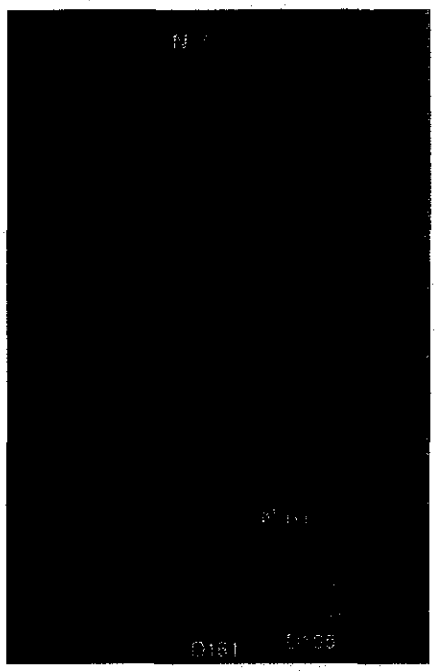
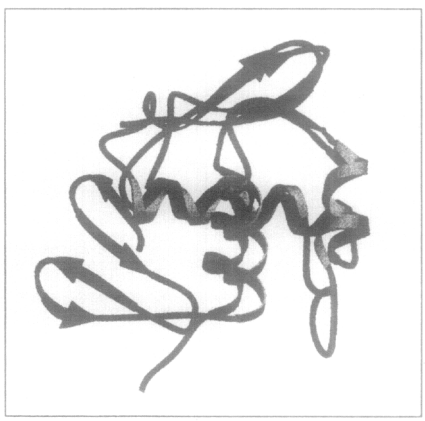


toxin have been determined at 1.8 Å resolution in different ionic strength conditions. The two subunits, α and β, are jointly folded into an ellipsoidal, single domain structure belonging to the α/β-sandwich family. The two killer toxins, SMK and KP4, share a unique folding topology which contains a rare structural motif, suggesting that these toxins are evolutionarily and/or functionally related. The pH-dependent stability of the SMK toxin is a result of intensive hydrogen bond interactions between some carboxyl sidechains; this finding may suggest ways to stabilize the toxin molecule in a broader pH range. The structure of the toxin is hardly affected by the ionic strength, implying that the effect of a high salt concentration on toxicity is mediated by effects on the target cell, not on the toxin.
15 January 1997, Research Article, *Structure*

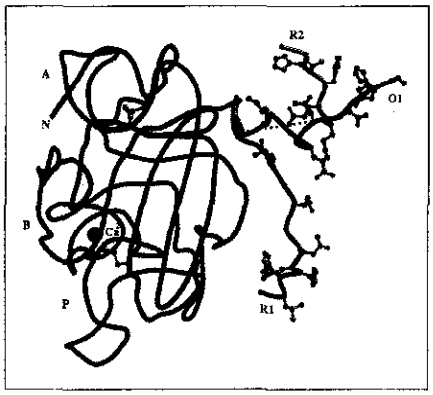
☐ **The DNA-binding domain of OmpR: crystal structures of a winged helix transcription factor.** Erik Martínez-Hackert and Ann M Stock (1997). *Structure* **5**, 109–124.

The differential expression of the *ompF* and *ompC* genes is regulated by two proteins that belong to the two component family of signal transduction proteins: the histidine kinase, EnvZ, and the response regulator, OmpR. OmpR belongs to a subfamily of at least 50 response regulators with homologous carboxy-terminal DNA-binding domains of ~98 amino acids. No sequence homology with DNA-binding proteins of known structure has been detected, and the lack of structural information has, to date, prevented understanding of many of this family's functional properties. The paper describes the crystal structure of the *Escherichia coli* OmpR carboxy-terminal domain at 1.95 Å resolution. The structure consists of three α helices packed against two antiparallel β sheets. Two helices, α2 and α3, and the 10-residue loop connecting them constitute a variation of the helix-turn-helix (HTH) motif. OmpRc thus belongs to the family of 'winged helix-turn-helix' DNA-binding proteins. Helix α3 and the loop connecting the two carboxy-terminal β strands, β6 and β7, are probable DNA-recognition sites. Previous mutagenesis studies indicate that the large loop connecting helices α2 and α3 is the site of interaction with the subunit of RNA polymerase. The structure of OmpRc could be useful in helping to define the positioning of the subunit of RNA polymerase in relation to transcriptional activators that are bound to DNA.
15 January 1997, Research Article, *Structure*



☐ **Crystal structure of a 30 kDa carboxy-terminal fragment from the γ chain of human fibrinogen.** Vivien C Yee, Kathleen P Pratt, Hélène CF Côté, Isolde Le Trong, Dominic W Chung, Earl W Davie, Ronald E Stenkamp and David C Teller (1997). *Structure* **5**, 125–138.

Blood coagulation occurs by a cascade of zymogen activation resulting from minor proteolysis. The final stage of coagulation involves thrombin generation and limited proteolysis of fibrinogen to give spontaneously polymerizing fibrin. The resulting fibrin network is covalently cross linked by factor XIIIa to yield a stable blood clot. Fibrinogen is a 340 kDa glycoprotein composed of six polypeptide chains, $(\alpha\beta\gamma)_2$, held together by 29 disulfide bonds. X-ray crystallographic structure determination of the 30 kDa globular carboxyl terminus of the γ chain of human fibrinogen to 2.5 Å and 2.1 Å resolution has identified three domains, including a carboxyl-terminal fibrin-polymerization domain, which contains a single calcium-binding site and a deep binding pocket that provides the fibrin-polymerization surface. The overall structure has a pronounced dipole moment, and the carboxy-terminal residues appear highly flexible. The polymerization domain in the γ chain is the most variable among a family of fibrinogen-related proteins and contains many acidic residues. These residues contribute to the molecular dipole moment in the structure, which may allow electrostatic steering to guide the alignment of fibrin monomers during the polymerization process. The flexibility of the carboxy-terminal residues, which contain one of the factor XIIIa cross linking sites and the platelet receptor recognition site, may be important in the function of this domain. The structural information obtained for this domain should prove helpful in understanding clot formation.



January 15 1997, Research Article, *Structure*