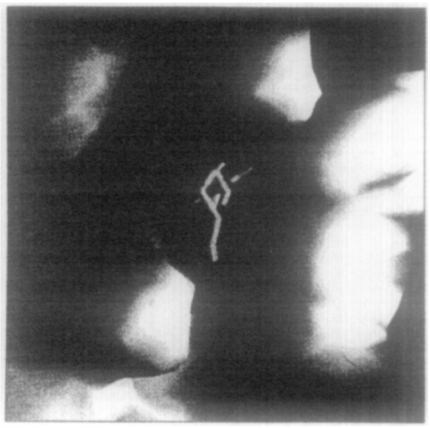
exist. The structure of BPP provides a molecular basis for understanding allergen cross-reactivity, and the detailed chemical and physical description of the major reactive epitopes provides a database for the design of ligands that may reduce the allergic response.
15 January 1997, Research Article, *Structure*

☐ **A new function for a common fold: the crystal structure of quinolinic acid phosphoribosyltransferase.** Janina C Eads, Derya Ozturk, Tom B Wexler, Charles Grubmeyer and James C Sacchettini (1997). *Structure* **5**, 47–58.

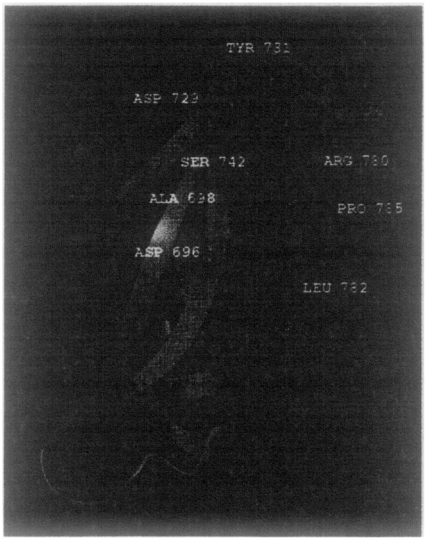
Quinolinic acid (QA) is a neurotoxin that has been shown to be present at high levels in the central nervous system of patients with certain diseases, such as AIDS and meningitis. Quinolinic acid phosphoribosyltransferase (QAPRTase) provides the only route for QA metabolism and is an essential step in *de novo* NAD biosynthesis. QAPRTase catalyzes the synthesis of nicotinic acid mononucleotide (NAMN) from QA and 5-phosphoribosyl-1-pyrophosphate (PRPP). The crystal structure of QAPRTase from *Salmonella typhimurium* was determined with bound QA (2.8 Å resolution) and with bound NAMN (3.0 Å resolution). The enzyme shows a completely novel fold for a PRTase enzyme, comprising a two-domain structure: a mixed α/β amino-terminal domain and an α/β barrel-like domain. The active site is located at the carboxy-terminal ends of the β strands of the α/β barrel, and is bordered by the amino-terminal domain of the second subunit of the dimer. The active site is largely composed of a number of conserved charged residues that appear to be important for substrate binding and catalysis. The structure shows a phosphate-binding site that appears to be conserved among many α/β-barrel enzymes including indole-3-glycerol phosphate synthase and flavocytochrome *b2*. The new fold demonstrates that the PRTase enzymes have evolved their similar chemistry from at least two completely different protein architectures.



15 January 1997, Research Article, *Structure*

☐ **The crystal structure of phenylalanyl-tRNA synthetase from *Thermus thermophilus* complexed with cognate tRNA^{Phe}.** Yehuda Goldgur, Lidia Mosyak, Ludmila Reshetnikova, Valentina Ankilova, Olga Lavrik, Svetlana Khodyreva and Mark Safro (1997). *Structure* **5**, 59–68.

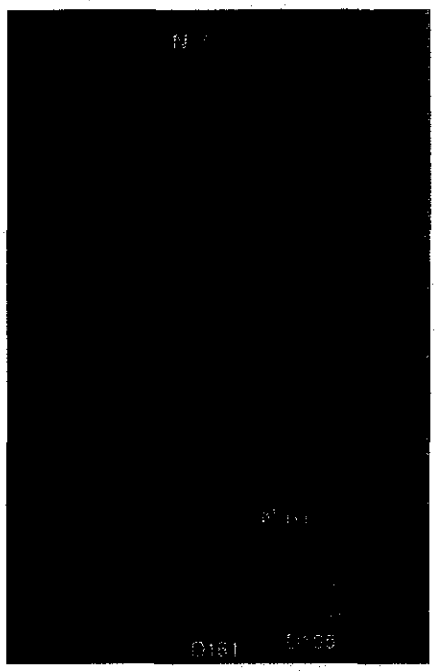
In translating the genetic code each aminoacyl-tRNA synthetase (aaRS) must recognize its cognate tRNA and attach the corresponding amino acid to the acceptor end of tRNA, discriminating all the others. The $(\alpha\beta)_2$ phenylalanyl-tRNA synthetase (PheRS) is one of the most complex enzymes in the aaRS family and is characterized by anomalous charging properties. The crystal structure of *Thermus thermophilus* PheRS complexed with cognate tRNA has been solved (3.28 Å resolution), and shows that one tRNA^{Phe} molecule binds across all four PheRS subunits. The interactions of PheRS with tRNA stabilize the flexible amino-terminal part of the α subunit. Anticodon recognition upon tRNA binding is performed by the B8 domain, which is similar in structure to the RNA-binding domain (RBD) of the small spliceosomal protein U1A. The *Th. thermophilus* PheRS approaches the anticodon loop from the minor groove side. The interactions of tRNA^{Phe} with PheRS, particularly with the coiled-coil domain of the α subunit, result in conformational changes when compared with uncomplexed yeast tRNA^{Phe}. The tRNA^{Phe} is a newly recognized type of RNA molecule specifically interacting with the RBD fold. In addition, a new type of anticodon-binding domain emerges in the aaRS family. The uniqueness of PheRS in charging 2′OH of tRNA is dictated by the size of its adenine-binding pocket and by the local conformation of the tRNA's CCA end. With the availability of this three-dimensional structure of the complex between multisubunit PheRS and tRNA^{Phe}, a fuller picture of the specific tRNA–aaRS interactions is beginning to emerge.



15 January 1997, Research Article, *Structure*

☐ **The novel acidophilic structure of the killer toxin from halotolerant yeast demonstrates remarkable folding similarity with a fungal killer toxin.** Tatsuki Kashiwagi, Naoki Kunishima, Chise Suzuki, Fumihiko Tsuchiya, Sayuki Nikkuni, Yoji Arata and Kosuke Morikawa (1997). *Structure* **5**, 81–94.

Several strains of yeasts and fungi produce proteinaceous substances, termed killer toxins, which kill sensitive strains. The SMK toxin, secreted by the halotolerant yeast *Pichia farinosa* KK1 strain, uniquely exhibits its maximum killer activity under conditions of acidic pH and high salt concentration. The toxin is composed of two distinct subunits, α and β, which tightly interact with each other under acidic conditions, but are easily dissociated under neutral conditions and lose the killer activity. Two crystal structures of the SMK



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.
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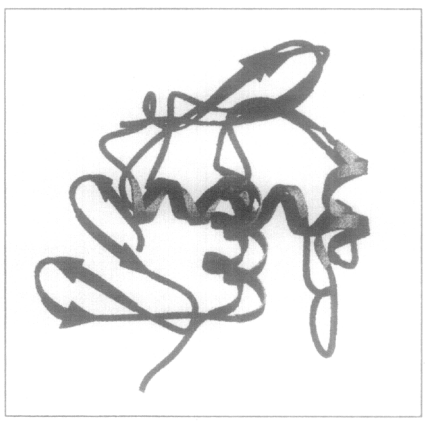
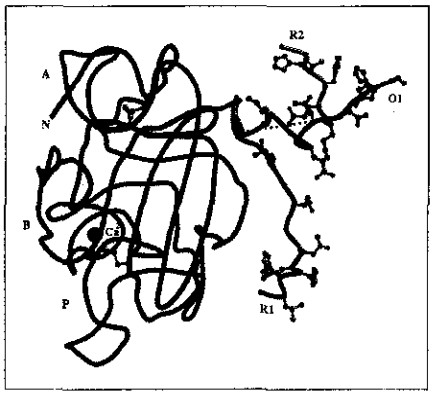


☐ **Crystal structure of a 30 kDa carboxy-terminal fragment from the γ chain of human fibrinogen.** Vivien C Yee, Kathleen P Pratt, Hélène CF Côté, Isolde Le Trong, Dominic W Chung, Earl W Davie, Ronald E Stenkamp and David C Teller (1997). *Structure* **5**, 125–138.

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.



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