

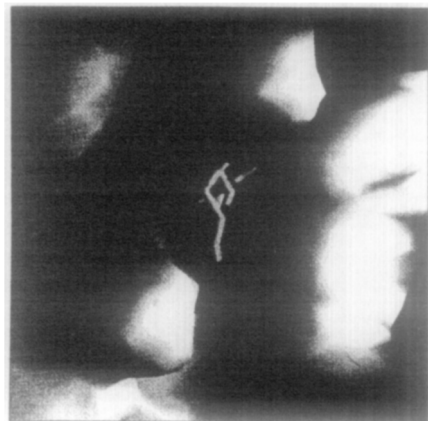
exist. The structure of BPP provides a molecular basis for understanding allergen cross-reactivity, and the detailed chemical and physical description of the major reactive epitopes provides a database for the design of ligands that may reduce the allergic response.

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



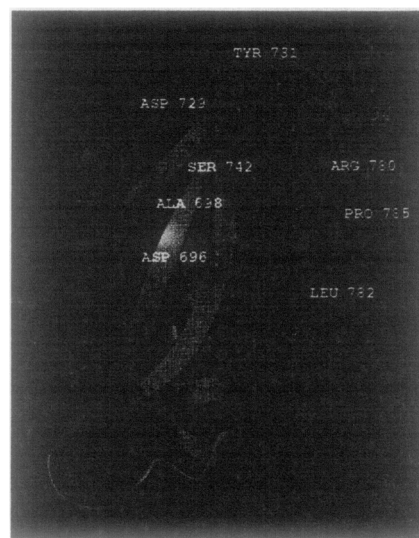
enzymes have evolved their similar chemistry from at least two completely different protein architectures.

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 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