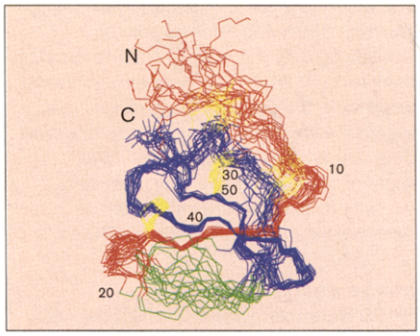
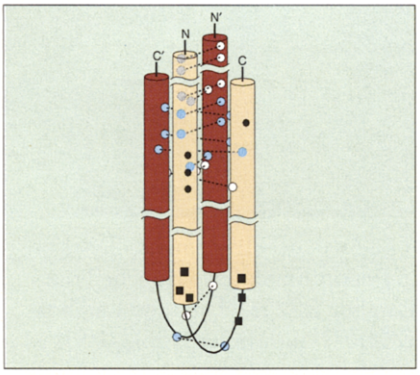
theophylline. The authors joined an FMN- or theophylline-binding domain to a hammerhead ribozyme by different stem II elements and identified a minimal connective bridge comprised of a G·U wobble pair that is responsive to ligand binding. Binding of FMN or theophylline to its allosteric site induces a conformational change in the RNA that stabilizes the wobble pair and favors the active form of the catalytic core. These ligand-sensitive ribozymes exhibit rate enhancements of more than 100-fold in the presence of FMN and of ~40-fold in the presence of theophylline. Conceivably, similar engineering strategies and allosteric mechanisms could be used to create a variety of novel allosteric ribozymes that function with other effector molecules.
23 June 1999, Research Paper, *Structure*.

☐ **Structure of a putative ancestral protein encoded by a single sequence repeat from a multidomain proteinase inhibitor gene from *Nicotiana alata*.**
Martin J Scanlon, Marcus CS Lee, Marilyn A Anderson and David J Craik (1999). *Structure* **7**, 793–802.
The ornamental tobacco *Nicotiana alata* produces a series of proteinase inhibitors (PIs) that are derived from a 43 kDa precursor protein, NaProPI. NaProPI contains six highly



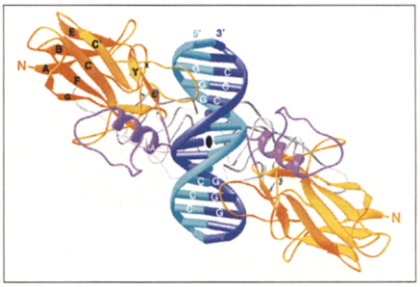
homologous repeats that fold to generate six separate structural domains. Unusually, the structural domains lie across adjacent repeats and the sixth PI domain is generated from fragments of the first and sixth repeats. Although the homology of the repeats suggests that they might have arisen from gene duplication, the observed folding does not appear to support this hypothesis. This structure of a single NaProPI repeat (aPI1) forms a basis for unravelling the mechanism by which this protein might have evolved. The structure of aPI1 closely resembles the triple-stranded antiparallel sheet observed in each of the native PIs. A single repeat from NaProPI is capable of folding into a compact globular domain that displays native-like PI activity. It is therefore possible that a similar single-domain inhibitor represents the ancestral protein from which NaProPI evolved.
24 June 1999, Research Paper, *Structure*.

☐ **The aspartate receptor cytoplasmic domain: *in situ* analysis of structure, mechanism and dynamics.**
Randal B Bass and Joseph J Falke (1999). *Structure* **7**, 829–840.
Site-directed sulfhydryl chemistry and spectroscopy can be used to probe



protein structure, mechanism and dynamics *in situ*. The aspartate receptor of bacterial chemotaxis belongs to a large family of prokaryotic and eukaryotic receptors that regulate histidine kinases in two-component signaling pathways, and has become one of the best characterized transmembrane receptors. The authors use cysteine and disulfide scanning to probe the helix-packing architecture of the cytoplasmic domain of the aspartate receptor. The results have led to a four-helix bundle model for the domain, and have provided constraints on the signalling mechanism and insights into backbone dynamics. The model should be relevant to to other receptors that regulate histidine kinases. The techniques used should continue to be useful for probing a range of systems, particularly complex protein systems.
28 June 1999, Research Paper, *Structure*.

☐ **Structure of the specificity domain of the Dorsal homologue Gambif1 bound to DNA.**
Patrick Cramer, Annabelle Varrot, Carolina Barillas-Mury, Fotis C Kafatos and Christoph W Müller (1999). *Structure* **7**, 841–852.
NF-κB/Rel transcription factors play important roles in immunity and development in mammals and insects. Their activity is regulated by their cellular localization, homo- and heterodimerization and association with other factors on their target gene promoters. Gambif1 from *Anopheles gambiae* is a member of the Rel family



and a close homologue of the morphogen Dorsal, which establishes dorsoventral polarity in the *Drosophila* embryo. The authors present the crystal structure of the amino-terminal specificity domain of Gambif1 bound to DNA. The Gambif1–DNA complex structure illustrates how differences in Dorsal affinity to binding sites in developmental gene promoters are achieved. Comparison with other Rel–DNA complex structures leads to a general model for DNA recognition by Rel proteins.
29 June 1999, Research Paper, *Structure*.